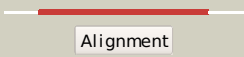
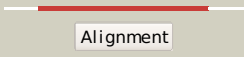
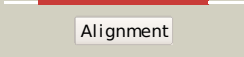
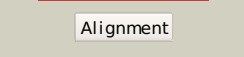
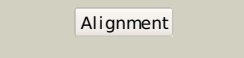
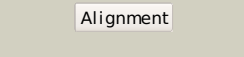
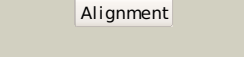
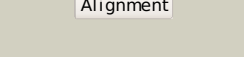
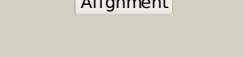
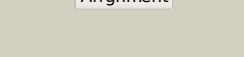
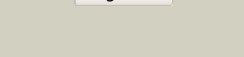
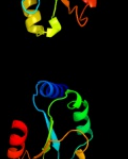
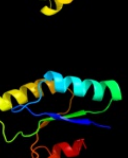
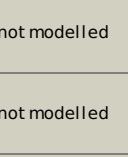


| #  | Template                | Alignment Coverage                                                                            | 3D Model                                                                            | Confidence | % i.d. | Template Information                                                                                                                                                                                                                                                 |
|----|-------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1  | <a href="#">c2qthA_</a> |  Alignment   |    | 99.3       | 16     | <b>PDB header:</b> nucleotide binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein;<br><b>PDBTitle:</b> crystal structure of a gtp-binding protein from the2 hyperthermophilic archaeon sulfolobus solfataricus in3 complex with gdp         |
| 2  | <a href="#">c2e87A_</a> |  Alignment   |    | 99.2       | 14     | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph1320;<br><b>PDBTitle:</b> crystal structure of hypothetical gtp-binding protein ph1320 from2 pyrococcus horikoshii ot3, in complex with gdp |
| 3  | <a href="#">c2hjaA_</a> |  Alignment   |    | 99.2       | 17     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein enga;<br><b>PDBTitle:</b> the crystal structure of the b. subtilis yphc gtpase in2 complex with gdp                                                                        |
| 4  | <a href="#">c1lnzA_</a> |  Alignment   |   | 99.2       | 22     | <b>PDB header:</b> cell cycle<br><b>Chain:</b> A: <b>PDB Molecule:</b> spo0b-associated gtp-binding protein;<br><b>PDBTitle:</b> structure of the obg gtp-binding protein                                                                                            |
| 5  | <a href="#">c1udxA_</a> |  Alignment |  | 99.2       | 22     | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> the gtp-binding protein obg;<br><b>PDBTitle:</b> crystal structure of the conserved protein tt1381 from thermus2 thermophilus hb8                                                        |
| 6  | <a href="#">c4a2iV_</a> |  Alignment |  | 99.0       | 17     | <b>PDB header:</b> ribosome/hydrolase<br><b>Chain:</b> V: <b>PDB Molecule:</b> putative ribosome biogenesis gtpase rsga;<br><b>PDBTitle:</b> cryo-electron microscopy structure of the 30s subunit in complex with2 the yjeq biogenesis factor                       |
| 7  | <a href="#">c2rcnA_</a> |  Alignment |  | 99.0       | 17     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable gtpase engc;<br><b>PDBTitle:</b> crystal structure of the ribosomal interacting gtpase yjeq from the2 enterobacterial species salmonella typhimurium.                                 |
| 8  | <a href="#">c1mkvA_</a> |  Alignment |  | 98.9       | 15     | <b>PDB header:</b> ligand binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable gtp-binding protein enga;<br><b>PDBTitle:</b> structural analysis of the domain interactions in der, a2 switch protein containing two gtpase domains                     |
| 9  | <a href="#">c2yv5A_</a> |  Alignment |  | 98.9       | 20     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> yjeq protein;<br><b>PDBTitle:</b> crystal structure of yjeq from aquifex aeolicus                                                                                                              |
| 10 | <a href="#">d1puja_</a> |  Alignment |  | 98.9       | 21     | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                                           |
| 11 | <a href="#">c1g7tA_</a> |  Alignment |  | 98.8       | 24     | <b>PDB header:</b> translation<br><b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor if2/eif5b;<br><b>PDBTitle:</b> x-ray structure of translation initiation factor if2/eif5b2 complexed with gdpnp                                                |

|                                      |                         |           |                                                                                     |      |    |                                                                                                                                                                                                                                                       |
|--------------------------------------|-------------------------|-----------|-------------------------------------------------------------------------------------|------|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12                                   | <a href="#">c2ywfA_</a> | Alignment |     | 98.8 | 20 | <b>PDB header:</b> translation<br><b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein lepa;<br><b>PDBTitle:</b> crystal structure of gmppnp-bound lepa from aquifex aeolicus                                                                    |
| 13                                   | <a href="#">c3izyP_</a> | Alignment |    | 98.8 | 19 | <b>PDB header:</b> rna, ribosomal protein<br><b>Chain:</b> P: <b>PDB Molecule:</b> translation initiation factor if-2, mitochondrial;<br><b>PDBTitle:</b> mammalian mitochondrial translation initiation factor 2                                     |
| 14                                   | <a href="#">c3cb4D_</a> | Alignment |    | 98.8 | 21 | <b>PDB header:</b> translation<br><b>Chain:</b> D: <b>PDB Molecule:</b> gtp-binding protein lepa;<br><b>PDBTitle:</b> the crystal structure of lepa                                                                                                   |
| 15                                   | <a href="#">c1kk3A_</a> | Alignment |    | 98.8 | 15 | <b>PDB header:</b> translation<br><b>Chain:</b> A: <b>PDB Molecule:</b> eif2gamma;<br><b>PDBTitle:</b> structure of the wild-type large gamma subunit of2 initiation factor eif2 from pyrococcus abyssi complexed3 with gdp-mg2+                      |
| 16                                   | <a href="#">c2wsmB_</a> | Alignment |    | 98.8 | 14 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> hydrogenase expression/formation protein (hypb);<br><b>PDBTitle:</b> crystal structure of hydrogenase maturation factor hypb from2 archaeoglobus fulgidus           |
| 17                                   | <a href="#">c2plfA_</a> | Alignment |   | 98.8 | 18 | <b>PDB header:</b> translation<br><b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor 2 gamma subunit;<br><b>PDBTitle:</b> the structure of aif2gamma subunit from the archaeon2 sulfobolus solfataricus in the nucleotide-free form. |
| 18                                   | <a href="#">c3ievA_</a> | Alignment |  | 98.8 | 13 | <b>PDB header:</b> nucleotide binding protein/rna<br><b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein era;<br><b>PDBTitle:</b> crystal structure of era in complex with mggnp and the 3' end of 16s2 rrna                                    |
| 19                                   | <a href="#">c1u0lB_</a> | Alignment |  | 98.8 | 19 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> probable gtpase engc;<br><b>PDBTitle:</b> crystal structure of yjeq from thermotoga maritima                                                                                    |
| 20                                   | <a href="#">d1u0la2</a> | Alignment |  | 98.7 | 19 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                            |
| 21                                   | <a href="#">c1t9hA_</a> | Alignment | not modelled                                                                        | 98.7 | 20 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable gtpase engc;<br><b>PDBTitle:</b> the crystal structure of yloq, a circularly permuted gtpase.                                                                          |
| 22                                   | <a href="#">c1wf3A_</a> | Alignment | not modelled                                                                        | 98.7 | 14 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein;<br><b>PDBTitle:</b> crystal structure of gtp-binding protein tt1341 from thermus2 thermophilus hb8                                                         |
| 23                                   | <a href="#">c3degC_</a> | Alignment | not modelled                                                                        | 98.7 | 20 | <b>PDB header:</b> ribosome<br><b>Chain:</b> C: <b>PDB Molecule:</b> gtp-binding protein lepa;<br><b>PDBTitle:</b> complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp                                                         |
| 24                                   | <a href="#">c3qq5A_</a> | Alignment | not modelled                                                                        | 98.7 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> small gtp-binding protein;<br><b>PDBTitle:</b> crystal structure of the [fe]-hydrogenase maturation protein hydF                                                           |
| 25                                   | <a href="#">c1wb1C_</a> | Alignment | not modelled                                                                        | 98.7 | 23 | <b>PDB header:</b> protein synthesis<br><b>Chain:</b> C: <b>PDB Molecule:</b> translation elongation factor selb;<br><b>PDBTitle:</b> crystal structure of translation elongation factor selb2 from methanococcus maripaludis in complex with gdp     |
| 26                                   | <a href="#">c1xzqA_</a> | Alignment | not modelled                                                                        | 98.7 | 16 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable trna modification gtpase trme;<br><b>PDBTitle:</b> structure of the gtp-binding protein trme from thermotoga2 maritima complexed with 5-formyl-thf                     |
| 27                                   | <a href="#">d1yrba1</a> | Alignment | not modelled                                                                        | 98.7 | 16 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nitrogenase iron protein-like                                                         |
| 28                                   | <a href="#">c1egaB_</a> | Alignment | not modelled                                                                        | 98.6 | 14 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> protein (gtp-binding protein era);<br><b>PDBTitle:</b> crystal structure of a widely conserved gtpase era                                                                       |
| <b>PDB header:</b> signaling protein |                         |           |                                                                                     |      |    |                                                                                                                                                                                                                                                       |

|    |                         |           |              |      |    |                                                                                                                                                                                                                                                                                                       |
|----|-------------------------|-----------|--------------|------|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 29 | <a href="#">c3c5hA_</a> | Alignment | not modelled | 98.6 | 21 | <b>Chain:</b> A: <b>PDB Molecule:</b> glucocorticoid receptor dna-binding factor 1;<br><b>PDBTitle:</b> crystal structure of the ras homolog domain of human grlf12 (p190rhogap)                                                                                                                      |
| 30 | <a href="#">c1zo1l_</a> | Alignment | not modelled | 98.5 | 25 | <b>PDB header:</b> translation/rna<br><b>Chain:</b> I: <b>PDB Molecule:</b> translation initiation factor 2;<br><b>PDBTitle:</b> if2, if1, and trna fitted to cryo-em data of e. coli 70s2 initiation complex                                                                                         |
| 31 | <a href="#">c3lvrE_</a> | Alignment | not modelled | 98.5 | 13 | <b>PDB header:</b> protein transport<br><b>Chain:</b> E: <b>PDB Molecule:</b> arf-gap with sh3 domain, ank repeat and ph domain-<br><b>PDBTitle:</b> the crystal structure of asap3 in complex with arf6 in transition2 state soaked with calcium                                                     |
| 32 | <a href="#">c3gehA_</a> | Alignment | not modelled | 98.5 | 22 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> trna modification gtpase mnme;<br><b>PDBTitle:</b> crystal structure of mnme from nostoc in complex with gdp, folinic2 acid and zn                                                                                              |
| 33 | <a href="#">d1t9ha2</a> | Alignment | not modelled | 98.5 | 18 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                                                                            |
| 34 | <a href="#">c3md0A_</a> | Alignment | not modelled | 98.4 | 28 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> arginine/ornithine transport system atpase;<br><b>PDBTitle:</b> crystal structure of arginine/ornithine transport system2 atpase from mycobacterium tuberculosis bound to gdp (a ras-3 like gtpase superfamily protein) |
| 35 | <a href="#">d1svia_</a> | Alignment | not modelled | 98.4 | 12 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                                                                            |
| 36 | <a href="#">c3nxsA_</a> | Alignment | not modelled | 98.3 | 21 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> lao/ao transport system atpase;<br><b>PDBTitle:</b> crystal structure of lao/ao transport system from mycobacterium2 smegmatis bound to gdp                                                                             |
| 37 | <a href="#">d1puia_</a> | Alignment | not modelled | 98.2 | 20 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                                                                            |
| 38 | <a href="#">c3h2yA_</a> | Alignment | not modelled | 98.2 | 24 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> gtpase family protein;<br><b>PDBTitle:</b> crystal structure of yqeh gtpase from bacillus anthracis with dgdp2 bound                                                                                                            |
| 39 | <a href="#">c3ec1A_</a> | Alignment | not modelled | 98.2 | 18 | <b>PDB header:</b> hydrolase, signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> yqeh gtpase;<br><b>PDBTitle:</b> structure of yqeh gtpase from geobacillus stearothermophilus2 (an atnos1 / atnoa1 ortholog)                                                                                 |
| 40 | <a href="#">c3o47A_</a> | Alignment | not modelled | 98.2 | 14 | <b>PDB header:</b> hydrolase, hydrolase activator<br><b>Chain:</b> A: <b>PDB Molecule:</b> adp-ribosylation factor gtpase-activating protein 1, adp-<br><b>PDBTitle:</b> crystal structure of arfgap1-arf1 fusion protein                                                                             |
| 41 | <a href="#">c2elfA_</a> | Alignment | not modelled | 98.2 | 18 | <b>PDB header:</b> translation<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein translation elongation factor 1a;<br><b>PDBTitle:</b> crystal structure of the selb-like elongation factor ef-pyl2 from methanosarcina mazei                                                                          |
| 42 | <a href="#">c1skqB_</a> | Alignment | not modelled | 98.2 | 19 | <b>PDB header:</b> translation<br><b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor 1-alpha;<br><b>PDBTitle:</b> the crystal structure of sulfobolus solfataricus elongation2 factor 1-alpha in complex with magnesium and gdp                                                                  |
| 43 | <a href="#">c3c5cC_</a> | Alignment | not modelled | 98.2 | 16 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> ras-like protein 12;<br><b>PDBTitle:</b> crystal structure of human ras-like, family 12 protein in2 complex with gdp                                                                                                    |
| 44 | <a href="#">d1m7ba_</a> | Alignment | not modelled | 98.2 | 19 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                                                                            |
| 45 | <a href="#">c1gwnA_</a> | Alignment | not modelled | 98.2 | 19 | <b>PDB header:</b> gtpase<br><b>Chain:</b> A: <b>PDB Molecule:</b> rho-related gtp-binding protein rhoe;<br><b>PDBTitle:</b> the crystal structure of the core domain of rhoe/rnd3 - a2 constitutively activated small g protein                                                                      |
| 46 | <a href="#">d2atxa1</a> | Alignment | not modelled | 98.2 | 20 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                                                                            |
| 47 | <a href="#">c2wkqA_</a> | Alignment | not modelled | 98.2 | 23 | <b>PDB header:</b> transferase, cell adhesion<br><b>Chain:</b> A: <b>PDB Molecule:</b> nph1-1, ras-related c3 botulinum toxin substrate<br><b>PDBTitle:</b> structure of a photoactivatable rac1 containing the lov22 c450a mutant                                                                    |
| 48 | <a href="#">c2bvnB_</a> | Alignment | not modelled | 98.2 | 18 | <b>PDB header:</b> elongation factor<br><b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor tu;<br><b>PDBTitle:</b> e. coli ef-tu:gdpnp in complex with the antibiotic2 enacyloxin iia                                                                                                            |
| 49 | <a href="#">d1yzga1</a> | Alignment | not modelled | 98.1 | 9  | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                                                                            |
| 50 | <a href="#">c2x77B_</a> | Alignment | not modelled | 98.1 | 12 | <b>PDB header:</b> gtp-binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> adp-ribosylation factor;<br><b>PDBTitle:</b> crystal structure of leishmania major adp ribosylation2 factor-like 1.                                                                                                   |
| 51 | <a href="#">c1d2eA_</a> | Alignment | not modelled | 98.1 | 20 | <b>PDB header:</b> rna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor tu (ef-tu);<br><b>PDBTitle:</b> crystal structure of mitochondrial ef-tu in complex with gdp                                                                                                        |
| 52 | <a href="#">d2p67a1</a> | Alignment | not modelled | 98.1 | 20 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nitrogenase iron protein-like                                                                                                         |
| 53 | <a href="#">d1ky3a_</a> | Alignment | not modelled | 98.1 | 19 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases                                                                                                                                                         |

|    |                         |           |              |      |                                                                                                                                                                                                                                                            |
|----|-------------------------|-----------|--------------|------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|    |                         |           |              |      | <b>Family:</b> G proteins                                                                                                                                                                                                                                  |
| 54 | <a href="#">c2h57A_</a> | Alignment | not modelled | 98.1 | 14<br><b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> adp-ribosylation factor-like protein 6;<br><b>PDBTitle:</b> crystal structure of human adp-ribosylation factor-like 6                                                  |
| 55 | <a href="#">c2rexD_</a> | Alignment | not modelled | 98.1 | 18<br><b>PDB header:</b> signaling protein/lipoprotein<br><b>Chain:</b> D: <b>PDB Molecule:</b> rho-related gtp-binding protein rho6;<br><b>PDBTitle:</b> crystal structure of the effector domain of plxnbl bound with rnd12 gtpase                       |
| 56 | <a href="#">d1moza_</a> | Alignment | not modelled | 98.0 | 16<br><b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 57 | <a href="#">d1zj6a1</a> | Alignment | not modelled | 98.0 | 10<br><b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 58 | <a href="#">c2wwwB_</a> | Alignment | not modelled | 98.0 | 20<br><b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> methylmalonic aciduria type a protein,<br><b>PDBTitle:</b> crystal structure of methylmalonic acidemia type a protein                                                  |
| 59 | <a href="#">d2ngra_</a> | Alignment | not modelled | 98.0 | 18<br><b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 60 | <a href="#">c3t1tC_</a> | Alignment | not modelled | 98.0 | 17<br><b>PDB header:</b> hydrolase<br><b>Chain:</b> C: <b>PDB Molecule:</b> gliding protein mgla;<br><b>PDBTitle:</b> mgla bound to gdp in p1 tetrameric arrangement                                                                                       |
| 61 | <a href="#">c1g7cA_</a> | Alignment | not modelled | 98.0 | 16<br><b>PDB header:</b> translation<br><b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor 1-alpha;<br><b>PDBTitle:</b> yeast eef1a:eef1ba in complex with gdpnp                                                                                      |
| 62 | <a href="#">c3bwdD_</a> | Alignment | not modelled | 98.0 | 18<br><b>PDB header:</b> plant protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> rac-like gtp-binding protein arac6;<br><b>PDBTitle:</b> crystal structure of the plant rho protein rop5                                                                    |
| 63 | <a href="#">d1ds6a_</a> | Alignment | not modelled | 98.0 | 18<br><b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 64 | <a href="#">d1s0ua3</a> | Alignment | not modelled | 98.0 | 13<br><b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 65 | <a href="#">d1z6xa1</a> | Alignment | not modelled | 98.0 | 16<br><b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 66 | <a href="#">d2gjsa1</a> | Alignment | not modelled | 97.9 | 17<br><b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 67 | <a href="#">d1vg8a_</a> | Alignment | not modelled | 97.9 | 21<br><b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 68 | <a href="#">c3l82B_</a> | Alignment | not modelled | 97.9 | 8<br><b>PDB header:</b> cell cycle<br><b>Chain:</b> B: <b>PDB Molecule:</b> f-box only protein 4;<br><b>PDBTitle:</b> x-ray crystal structure of trf1 and fbx4 complex                                                                                     |
| 69 | <a href="#">c3cnlA_</a> | Alignment | not modelled | 97.9 | 11<br><b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of gnp-bound ylfq from t. maritima                                                             |
| 70 | <a href="#">d1z2ca1</a> | Alignment | not modelled | 97.9 | 20<br><b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 71 | <a href="#">d1udxa2</a> | Alignment | not modelled | 97.9 | 25<br><b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 72 | <a href="#">d1byua_</a> | Alignment | not modelled | 97.9 | 14<br><b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 73 | <a href="#">c3oesA_</a> | Alignment | not modelled | 97.9 | 18<br><b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> gtpase rhebl1;<br><b>PDBTitle:</b> crystal structure of the small gtpase rhebl1                                                                                                |
| 74 | <a href="#">d1r8sa_</a> | Alignment | not modelled | 97.9 | 12<br><b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 75 | <a href="#">c2hdnl_</a> | Alignment | not modelled | 97.9 | 19<br><b>PDB header:</b> translation<br><b>Chain:</b> J: <b>PDB Molecule:</b> elongation factor ef-tu;<br><b>PDBTitle:</b> trypsin-modified elongation factor tu in complex with2 tetracycline at 2.8 angstrom resolution                                  |
| 76 | <a href="#">d1f60a3</a> | Alignment | not modelled | 97.9 | 18<br><b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 77 | <a href="#">c3pqcA_</a> | Alignment | not modelled | 97.9 | 18<br><b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable gtp-binding protein engb;<br><b>PDBTitle:</b> crystal structure of thermotoga maritima ribosome biogenesis gtp-2 binding protein engb (ysxc/yiha) in complex with gdp |
| 78 | <a href="#">c2g3yA_</a> | Alignment | not modelled | 97.9 | 22<br><b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein gem;<br><b>PDBTitle:</b> crystal structure of the human small gtpase gem                                                                           |
| 79 | <a href="#">d2g3ya1</a> | Alignment | not modelled | 97.9 | 22<br><b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases                                                                                                        |

|     |                         |           |              |      |    |                                                                                                                                                                                                                                                      |
|-----|-------------------------|-----------|--------------|------|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|     |                         |           |              |      |    | <b>Family:</b> G proteins<br><b>PDB header:</b> translation,transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor ts, elongation factor tu 1, linker, q<br><b>PDBTitle:</b> structure of viral polymerase form ii                   |
| 80  | <a href="#">c3agqA_</a> | Alignment | not modelled | 97.8 | 24 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 81  | <a href="#">d2c78a3</a> | Alignment | not modelled | 97.8 | 17 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> adp-ribosylation factor-like protein 8a;<br><b>PDBTitle:</b> structure of human adp-ribosylation factor-like 10b (arl10b)                                              |
| 82  | <a href="#">c2h18A_</a> | Alignment | not modelled | 97.8 | 13 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 83  | <a href="#">d2bcgy1</a> | Alignment | not modelled | 97.8 | 18 | <b>PDB header:</b> hydrolase, metal binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable hydrogenase nickel incorporation<br><b>PDBTitle:</b> crystal structure of hypb from methanocaldococcus2 jannaschii in the triphosphate form    |
| 84  | <a href="#">c2hf9A_</a> | Alignment | not modelled | 97.8 | 11 | <b>PDB header:</b> translation<br><b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor 2 gamma subunit;<br><b>PDBTitle:</b> eif2gamma apo                                                                                             |
| 85  | <a href="#">c1s0uA_</a> | Alignment | not modelled | 97.8 | 16 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 86  | <a href="#">d1i2ma_</a> | Alignment | not modelled | 97.8 | 12 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 87  | <a href="#">d1kk1a3</a> | Alignment | not modelled | 97.8 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> elongation factor tu 2, elongation factor ts;<br><b>PDBTitle:</b> structure of the qb replicase, an rna-dependent rna polymerase2 consisting of viral and host proteins      |
| 88  | <a href="#">c3mmpC_</a> | Alignment | not modelled | 97.8 | 21 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 89  | <a href="#">d1kmqa_</a> | Alignment | not modelled | 97.8 | 19 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 90  | <a href="#">d2qm8a1</a> | Alignment | not modelled | 97.8 | 21 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nitrogenase iron protein-like                                                        |
| 91  | <a href="#">d1jnya3</a> | Alignment | not modelled | 97.8 | 14 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 92  | <a href="#">c1m2oD_</a> | Alignment | not modelled | 97.8 | 17 | <b>PDB header:</b> protein transport/signaling protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> gtp-binding protein sar1;<br><b>PDBTitle:</b> crystal structure of the sec23-sar1 complex                                                            |
| 93  | <a href="#">c2wjJB_</a> | Alignment | not modelled | 97.8 | 13 | <b>PDB header:</b> metal transport<br><b>Chain:</b> B: <b>PDB Molecule:</b> ferrous iron transport protein b homolog;<br><b>PDBTitle:</b> structure and function of the feob g-domain from2 methanococcus jannaschii                                 |
| 94  | <a href="#">d1z0aa1</a> | Alignment | not modelled | 97.8 | 22 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 95  | <a href="#">d2b6ha1</a> | Alignment | not modelled | 97.8 | 13 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 96  | <a href="#">d2qn6a3</a> | Alignment | not modelled | 97.8 | 16 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 97  | <a href="#">c2zejA_</a> | Alignment | not modelled | 97.8 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> leucine-rich repeat kinase 2;<br><b>PDBTitle:</b> structure of the roc domain from the parkinson's disease-associated2 leucine-rich repeat kinase 2 reveals a dimeric gtpase |
| 98  | <a href="#">d1zd9a1</a> | Alignment | not modelled | 97.8 | 9  | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 99  | <a href="#">d2al7a1</a> | Alignment | not modelled | 97.8 | 14 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 100 | <a href="#">d1x1ra1</a> | Alignment | not modelled | 97.8 | 20 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 101 | <a href="#">d2f9la1</a> | Alignment | not modelled | 97.8 | 16 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 102 | <a href="#">d2g6ba1</a> | Alignment | not modelled | 97.8 | 17 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 103 | <a href="#">d2a5da1</a> | Alignment | not modelled | 97.7 | 14 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                           |
| 104 | <a href="#">c3cbqA_</a> | Alignment | not modelled | 97.7 | 20 | <b>PDB header:</b> nucleotide binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein rem 2;<br><b>PDBTitle:</b> crystal structure of the human rem2 gtpase with bound                                                          |

|     |                         |           |              |      |    |                                                                                                                                                                                                                                                                  |
|-----|-------------------------|-----------|--------------|------|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|     |                         |           |              |      |    | gdp                                                                                                                                                                                                                                                              |
| 105 | <a href="#">d1wmsa_</a> | Alignment | not modelled | 97.7 | 17 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                                       |
| 106 | <a href="#">d1zunb3</a> | Alignment | not modelled | 97.7 | 11 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                                       |
| 107 | <a href="#">c2j0vD_</a> | Alignment | not modelled | 97.7 | 16 | <b>PDB header:</b> nucleotide-binding protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> rac-like gtp-binding protein arac7;<br><b>PDBTitle:</b> the crystal structure of arabidopsis thaliana rac7-rop9:2 the first ras superfamily gtpase from the plant kingdom |
| 108 | <a href="#">c3conA_</a> | Alignment | not modelled | 97.7 | 20 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> gtpase nras;<br><b>PDBTitle:</b> crystal structure of the human nras gtpase bound with gdp                                                                                                 |
| 109 | <a href="#">c2dykB_</a> | Alignment | not modelled | 97.7 | 20 | <b>PDB header:</b> ribosome<br><b>Chain:</b> B: <b>PDB Molecule:</b> gtp-binding protein;<br><b>PDBTitle:</b> crystal structure of n-terminal gtp-binding domain of enga from2 thermus thermophilus hb8                                                          |
| 110 | <a href="#">c3lx8A_</a> | Alignment | not modelled | 97.7 | 13 | <b>PDB header:</b> metal transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> ferrous iron uptake transporter protein b;<br><b>PDBTitle:</b> crystal structure of gdp-bound nfeob from s. thermophilus                                                             |
| 111 | <a href="#">d1z0ja1</a> | Alignment | not modelled | 97.7 | 19 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                                       |
| 112 | <a href="#">d1fzqa_</a> | Alignment | not modelled | 97.6 | 13 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                                       |
| 113 | <a href="#">c2fg5A_</a> | Alignment | not modelled | 97.6 | 23 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> ras-related protein rab-31;<br><b>PDBTitle:</b> crystal structure of human rab31 in complex with a gtp2 analogue                                                                   |
| 114 | <a href="#">d2fg5a1</a> | Alignment | not modelled | 97.6 | 23 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                                       |
| 115 | <a href="#">d2qtvb1</a> | Alignment | not modelled | 97.6 | 17 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                                       |
| 116 | <a href="#">d1xzpa2</a> | Alignment | not modelled | 97.6 | 20 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                                       |
| 117 | <a href="#">c2nzjB_</a> | Alignment | not modelled | 97.6 | 18 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> gtp-binding protein rem 1;<br><b>PDBTitle:</b> the crystal structure of rem1 in complex with gdp                                                                                   |
| 118 | <a href="#">c3clvA_</a> | Alignment | not modelled | 97.6 | 17 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> rab5 protein, putative;<br><b>PDBTitle:</b> crystal structure of rab5a from plasmodium falciparum,2 pfb0500c                                                                       |
| 119 | <a href="#">d1yzna1</a> | Alignment | not modelled | 97.6 | 18 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins                                                                                       |
| 120 | <a href="#">c3a1wA_</a> | Alignment | not modelled | 97.6 | 27 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> iron(ii) transport protein b;<br><b>PDBTitle:</b> crystal structue of the g domain of t. maritima feob iron2 iransporter                                                           |