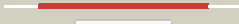



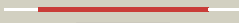








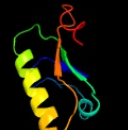







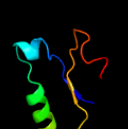
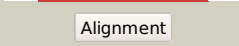


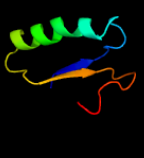



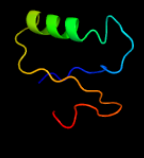
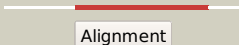

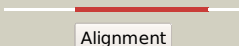

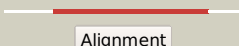



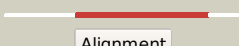
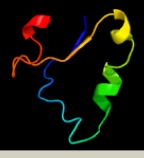
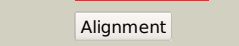
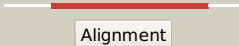
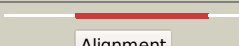

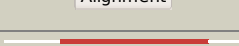
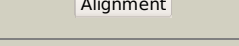
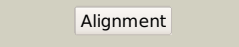


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2856B_(RVBD2856B)_3168222_3168437
 Date Wed Aug 7 12:50:52 BST 2019
 Unique Job ID a94a0fe256f70036

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1 | c5xktA_ |  Alignment |  | 99.3 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: urease accessory protein ureg; PDBTitle: klebsiella pneumoniae ureg in complex with gmppnp and nickel |
| 2 | c2wsmB_ |  Alignment |  | 99.3 | 33 | PDB header: metal binding protein Chain: B: PDB Molecule: hydrogenase expression/formation protein (hybp); PDBTitle: crystal structure of hydrogenase maturation factor hybp from2 archaeoglobus fulgidus |
| 3 | c4hi0F_ |  Alignment |  | 99.3 | 23 | PDB header: metal binding protein Chain: F: PDB Molecule: urease accessory protein ureg; PDBTitle: crystal structure of helicobacter pylori urease accessory protein2 uref/h/g complex |
| 4 | c4lpsA_ |  Alignment |  | 99.3 | 28 | PDB header: metal binding protein Chain: A: PDB Molecule: hydrogenase/urease nickel incorporation protein hybp; PDBTitle: crystal structure of hybp from helicobacter pylori in complex with2 nickel |
| 5 | c2hf9A_ |  Alignment |  | 99.0 | 27 | PDB header: hydrolase, metal binding protein Chain: A: PDB Molecule: probable hydrogenase nickel incorporation PDBTitle: crystal structure of hybp from methanocaldococcus2 jannaschii in the triphosphate form |
| 6 | c3nxsA_ |  Alignment |  | 98.6 | 16 | PDB header: transport protein Chain: A: PDB Molecule: lao/ao transport system atpase; PDBTitle: crystal structure of lao/ao transport system from mycobacterium2 smegmatis bound to gdp |
| 7 | c3md0A_ |  Alignment |  | 98.5 | 17 | PDB header: transport protein Chain: A: PDB Molecule: arginine/ornithine transport system atpase; PDBTitle: crystal structure of arginine/ornithine transport system atpase from2 mycobacterium tuberculosis bound to gdp (a ras-like gtpase3 superfamily protein) |
| 8 | d1nija1 |  Alignment |  | 98.3 | 15 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like |
| 9 | c1mkYA_ |  Alignment |  | 98.2 | 20 | PDB header: ligand binding protein Chain: A: PDB Molecule: probable gtp-binding protein engA; PDBTitle: structural analysis of the domain interactions in der, a switch2 protein containing two gtpase domains |
| 10 | c2hjgA_ |  Alignment |  | 98.2 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: gtp-binding protein engA; PDBTitle: the crystal structure of the b. subtilis yphc gtpase in complex with2 gdp |
| 11 | c3j4jA_ |  Alignment |  | 97.9 | 30 | PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-2; PDBTitle: model of full-length t. thermophilus translation initiation factor 22 refined against its cryo-em density from a 30s initiation complex map |

| | | | | | | |
|----|-------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | c1nijA |  Alignment |  | 97.9 | 15 | PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein yjia; PDBTitle: yjia protein |
| 13 | c3ievA |  Alignment |  | 97.9 | 19 | PDB header: nucleotide binding protein/rna Chain: A; PDB Molecule: gtp-binding protein era; PDBTitle: crystal structure of era in complex with mggnp and the 3' end of 16s2 rrna |
| 14 | c1lnzA |  Alignment |  | 97.8 | 14 | PDB header: cell cycle Chain: A; PDB Molecule: spo0b-associated gtp-binding protein; PDBTitle: structure of the obg gtp-binding protein |
| 15 | c4kzD |  Alignment |  | 97.8 | 30 | PDB header: translation Chain: D; PDB Molecule: translation initiation factor if-2; PDBTitle: crystal structure of thermus thermophilus if2, apo and gdp-bound forms2 (2-474) |
| 16 | c4b3xA |  Alignment |  | 97.7 | 32 | PDB header: translation Chain: A; PDB Molecule: translation initiation factor if-2; PDBTitle: bacterial translation initiation factor if2 (1-363), apo form |
| 17 | c2qthA |  Alignment |  | 97.7 | 15 | PDB header: nucleotide binding protein Chain: A; PDB Molecule: gtp-binding protein; PDBTitle: crystal structure of a gtp-binding protein from the hyperthermophilic2 archaeon sulfobolus solfataricus in complex with gdp |
| 18 | c4csu9 |  Alignment |  | 97.7 | 15 | PDB header: ribosome Chain: 9; PDB Molecule: gtpase obge/cgta; PDBTitle: cryo-em structures of the 50s ribosome subunit bound with obge |
| 19 | c1u0IB |  Alignment |  | 97.7 | 27 | PDB header: hydrolase Chain: B; PDB Molecule: probable gtpase engc; PDBTitle: crystal structure of yjeq from thermotoga maritima |
| 20 | c6h4dA |  Alignment |  | 97.7 | 22 | PDB header: rna binding protein Chain: A; PDB Molecule: small ribosomal subunit biogenesis gtpase rsga; PDBTitle: crystal structure of rsga from pseudomonas aeruginosa |
| 21 | c1legaB |  Alignment | not modelled | 97.6 | 22 | PDB header: hydrolase Chain: B; PDB Molecule: protein (gtp-binding protein era); PDBTitle: crystal structure of a widely conserved gtpase era |
| 22 | d2qm8a1 |  Alignment | not modelled | 97.6 | 18 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like |
| 23 | c3j8gX |  Alignment | not modelled | 97.6 | 18 | PDB header: ribosome Chain: X; PDB Molecule: gtpase der; PDBTitle: electron cryo-microscopy structure of enga bound with the 50s2 ribosomal subunit |
| 24 | d2p67a1 |  Alignment | not modelled | 97.6 | 13 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like |
| 25 | c2yv5A |  Alignment | not modelled | 97.6 | 24 | PDB header: hydrolase Chain: A; PDB Molecule: yjeq protein; PDBTitle: crystal structure of yjeq from aquifex aeolicus |
| 26 | d1yrba1 |  Alignment | not modelled | 97.5 | 25 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like |
| 27 | d1u0la2 |  Alignment | not modelled | 97.5 | 27 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins |
| 28 | c2rcnA |  Alignment | not modelled | 97.5 | 24 | PDB header: hydrolase Chain: A; PDB Molecule: probable gtpase engc; PDBTitle: crystal structure of the ribosomal interacting gtpase yjeq from the2 enterobacterial species salmonella typhimurium. |
| 29 | c5dn8A |  Alignment | not modelled | 97.5 | 18 | PDB header: gtp-binding protein Chain: A; PDB Molecule: gtpase der; |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 29 | c6un6A | Alignment | not modelled | 97.3 | 10 | PDBTitle: 1.76 angstrom crystal structure of gtp-binding protein der from2 coxiella burnetii in complex with gdp. PDB header: hydrolase |
| 30 | c1wf3A | Alignment | not modelled | 97.5 | 12 | Chain: A; PDB Molecule: gtp-binding protein; PDBTitle: crystal structure of gtp-binding protein tt1341 from thermus2 thermophilus hb8 |
| 31 | c2e87A | Alignment | not modelled | 97.5 | 21 | PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein ph1320; PDBTitle: crystal structure of hypothetical gtp-binding protein ph1320 from2 pyrococcus horikoshii ot3, in complex with gdp |
| 32 | c4a2iV | Alignment | not modelled | 97.5 | 24 | PDB header: ribosome/hydrolase Chain: V; PDB Molecule: putative ribosome biogenesis gtpase rsga; PDBTitle: cryo-electron microscopy structure of the 30s subunit in complex with2 the yjeq biogenesis factor |
| 33 | c1t9hA | Alignment | not modelled | 97.4 | 15 | PDB header: hydrolase Chain: A; PDB Molecule: probable gtpase engc; PDBTitle: the crystal structure of yloq, a circularly permuted gtpase. |
| 34 | c5k0yS | Alignment | not modelled | 97.4 | 24 | PDB header: translation Chain: S; PDB Molecule: eukaryotic initiation factor 2 gamma subunit (eif2-gamma); PDBTitle: m48s late-stage initiation complex, purified from rabbit reticulocytes2 lysates, displaying eif2 ternary complex and eif3 i and g subunits3 relocated to the intersubunit face |
| 35 | c4upyB | Alignment | not modelled | 97.4 | 45 | PDB header: ribosome Chain: B; PDB Molecule: eif5b; PDBTitle: mammalian 80s hcv-ires initiation complex with eif5b pre-like state |
| 36 | c4zu9A | Alignment | not modelled | 97.4 | 23 | PDB header: translation Chain: A; PDB Molecule: elongation factor selb; PDBTitle: crystal structure of bacterial selenocysteine-specific elongation2 factor ef-sec |
| 37 | c3wyaA | Alignment | not modelled | 97.3 | 22 | PDB header: translation Chain: A; PDB Molecule: elongation factor 1-alpha; PDBTitle: crystal structure of gdp-bound ef1alpha from pyrococcus horikoshii |
| 38 | c3j81k | Alignment | not modelled | 97.3 | 18 | PDB header: ribosome Chain: K; PDB Molecule: es10; PDBTitle: cryoem structure of a partial yeast 48s preinitiation complex |
| 39 | d1ky3a | Alignment | not modelled | 97.3 | 15 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins |
| 40 | d1jny3 | Alignment | not modelled | 97.3 | 23 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins |
| 41 | c2plfA | Alignment | not modelled | 97.3 | 16 | PDB header: translation Chain: A; PDB Molecule: translation initiation factor 2 gamma subunit; PDBTitle: the structure of aif2gamma subunit from the archaeon2 sulfobolus solfataricus in the nucleotide-free form. |
| 42 | c3j65o | Alignment | not modelled | 97.2 | 12 | PDB header: ribosome Chain: O; PDB Molecule: 60s ribosomal protein I15; PDBTitle: arx1 pre-60s particle. this entry contains the r-proteins and2 biogenesis factors. |
| 43 | d1t9ha2 | Alignment | not modelled | 97.2 | 20 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins |
| 44 | c2wwwB | Alignment | not modelled | 97.2 | 18 | PDB header: transport protein Chain: B; PDB Molecule: methylmalonic aciduria type a protein, PDBTitle: crystal structure of methylmalonic acidemia type a protein |
| 45 | c5fg3A | Alignment | not modelled | 97.2 | 32 | PDB header: translation Chain: A; PDB Molecule: probable translation initiation factor if-2; PDBTitle: crystal structure of gdp-bound aif5b from aeropyrum pernix |
| 46 | c3wbkB | Alignment | not modelled | 97.1 | 30 | PDB header: biosynthetic protein Chain: B; PDB Molecule: eukaryotic translation initiation factor 5b; PDBTitle: crystal structure analysis of eukaryotic translation initiation factor2 5b and 1a complex |
| 47 | c4n3nA | Alignment | not modelled | 97.1 | 28 | PDB header: translation Chain: A; PDB Molecule: eukaryotic translation initiation factor 5b-like protein, PDBTitle: crystal structure of eukaryotic translation initiation factor eif5b2 (517-1116) from chaetomium thermophilum, apo form |
| 48 | c5hcnA | Alignment | not modelled | 97.1 | 19 | PDB header: hydrolase Chain: A; PDB Molecule: gpn-loop gtpase 1; PDBTitle: gpn-loop gtpase npa3 in complex with gmppcp |
| 49 | c1kk3A | Alignment | not modelled | 97.1 | 29 | PDB header: translation Chain: A; PDB Molecule: eif2gamma; PDBTitle: structure of the wild-type large gamma subunit of2 initiation factor eif2 from pyrococcus abyssi complexed3 with gdp-mg2+ |
| 50 | c3izyP | Alignment | not modelled | 97.1 | 25 | PDB header: rna, ribosomal protein Chain: P; PDB Molecule: translation initiation factor if-2, mitochondrial; PDBTitle: mammalian mitochondrial translation initiation factor 2 |
| 51 | c5uz4Z | Alignment | not modelled | 97.1 | 22 | PDB header: ribosome/hydrolase Chain: Z; PDB Molecule: small ribosomal subunit biogenesis gtpase rsga; PDBTitle: the cryo-em structure of yjeq bound to the 30s subunit suggests a2 fidelity checkpoint function for this protein in ribosome assembly |
| 52 | c4ku4B | Alignment | not modelled | 97.0 | 16 | PDB header: signaling protein Chain: B; PDB Molecule: ras-3 from cryphonectria parasitica; PDBTitle: crystal structure of a ras-like protein from cryphonectria parasitica2 in complex with gdp |
| 53 | c3degC | Alignment | not modelled | 97.0 | 34 | PDB header: ribosome Chain: C; PDB Molecule: gtp-binding protein lepa; PDBTitle: complex of elongating escherichia coli 70s ribosome and |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| | | | | | | ef4(lepa)-2 gmppnp |
| 54 | c3c5cC_ | Alignment | not modelled | 96.9 | 11 | PDB header: signaling protein Chain: C: PDB Molecule: ras-like protein 12; PDBTitle: crystal structure of human ras-like, family 12 protein in complex with2 gdp |
| 55 | c3agiC_ | Alignment | not modelled | 96.9 | 20 | PDB header: translation/hydrolase Chain: C: PDB Molecule: elongation factor 1-alpha; PDBTitle: crystal structure of archaeal pelota and gtp-bound ef1 alpha complex |
| 56 | c5ady6_ | Alignment | not modelled | 96.9 | 24 | PDB header: ribosome Chain: 6: PDB Molecule: gtpase hflx; PDBTitle: cryo-em structures of the 50s ribosome subunit bound with hflx |
| 57 | c1wb1C_ | Alignment | not modelled | 96.9 | 20 | PDB header: protein synthesis Chain: C: PDB Molecule: translation elongation factor selb; PDBTitle: crystal structure of translation elongation factor selb2 from methanococcus maripaludis in complex with gdp |
| 58 | c1xzqA_ | Alignment | not modelled | 96.9 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: probable trna modification gtpase trme; PDBTitle: structure of the gtp-binding protein trme from thermotoga2 maritima complexed with 5-formyl-thf |
| 59 | d1z0aa1 | Alignment | not modelled | 96.9 | 20 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins |
| 60 | c5ck3F_ | Alignment | not modelled | 96.9 | 16 | PDB header: signaling protein Chain: F: PDB Molecule: putative signal recognition particle protein; PDBTitle: signal recognition particle receptor srb-gtp/srx complex from2 chaetomium thermophilum |
| 61 | c2ywfA_ | Alignment | not modelled | 96.9 | 32 | PDB header: translation Chain: A: PDB Molecule: gtp-binding protein lepa; PDBTitle: crystal structure of gmppnp-bound lepa from aquifex aeolicus |
| 62 | c3qq5A_ | Alignment | not modelled | 96.8 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: small gtp-binding protein; PDBTitle: crystal structure of the [fefe]-hydrogenase maturation protein hydF |
| 63 | d2g3ya1 | Alignment | not modelled | 96.8 | 18 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins |
| 64 | c2g3yA_ | Alignment | not modelled | 96.8 | 18 | PDB header: signaling protein Chain: A: PDB Molecule: gtp-binding protein gem; PDBTitle: crystal structure of the human small gtpase gem |
| 65 | c3oesA_ | Alignment | not modelled | 96.8 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: gtpase rheb11; PDBTitle: crystal structure of the small gtpase rheb11 |
| 66 | c3cb4D_ | Alignment | not modelled | 96.8 | 34 | PDB header: translation Chain: D: PDB Molecule: gtp-binding protein lepa; PDBTitle: the crystal structure of lepa |
| 67 | d2gjsa1 | Alignment | not modelled | 96.7 | 20 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins |
| 68 | c5yoza_ | Alignment | not modelled | 96.7 | 16 | PDB header: endocytosis Chain: A: PDB Molecule: rab5a; PDBTitle: solution structure of truncated rab5a from leishmania donovani |
| 69 | c1zo1l | Alignment | not modelled | 96.7 | 25 | PDB header: translation/rna Chain: I: PDB Molecule: translation initiation factor 2; PDBTitle: if2, if1, and trna fitted to cryo-em data of e. coli 70s2 initiation complex |
| 70 | c3cbqA_ | Alignment | not modelled | 96.7 | 11 | PDB header: nucleotide binding protein Chain: A: PDB Molecule: gtp-binding protein rem 2; PDBTitle: crystal structure of the human rem2 gtpase with bound gdp |
| 71 | c4klza_ | Alignment | not modelled | 96.7 | 20 | PDB header: protein binding Chain: A: PDB Molecule: gtp-binding protein rit1; PDBTitle: inhibition of small gtpases by stabilization of the gdp complex, a2 novel approach applied to rit1, a target for rheumatoid arthritis |
| 72 | d1f60a3 | Alignment | not modelled | 96.7 | 20 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins |
| 73 | c5kutB_ | Alignment | not modelled | 96.6 | 11 | PDB header: hydrolase Chain: B: PDB Molecule: mitochondrial rho gtpase 2; PDBTitle: hmiro2 c-terminal gtpase domain, gdp-bound |
| 74 | d1u8za_ | Alignment | not modelled | 96.6 | 20 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins |
| 75 | c1skqB_ | Alignment | not modelled | 96.6 | 23 | PDB header: translation Chain: B: PDB Molecule: elongation factor 1-alpha; PDBTitle: the crystal structure of sulfolobus solfataricus elongation factor 1-2 alpha in complex with magnesium and gdp |
| 76 | c5jcpB_ | Alignment | not modelled | 96.6 | 16 | PDB header: signaling protein,hydrolase Chain: B: PDB Molecule: arf-gap with rho-gap domain, ank repeat and ph domain- PDBTitle: rhogap domain of arap3 in complex with rhoa in the transition state |
| 77 | c5izmA_ | Alignment | not modelled | 96.6 | 28 | PDB header: translation Chain: A: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: the crystal structure of human eefsec in complex with gdpnp |
| 78 | c1g7tA_ | Alignment | not modelled | 96.5 | 36 | PDB header: translation Chain: A: PDB Molecule: translation initiation factor if2/eif5b; PDBTitle: x-ray structure of translation initiation factor if2/eif5b2 complexed with gdpnp |
| 79 | d2f9la1 | Alignment | not modelled | 96.5 | 18 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases |

| | | | | | | |
|-----|-------------------------|-----------|--------------|------|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| | | | | | | Family: G proteins |
| 80 | d1moza_ | Alignment | not modelled | 96.5 | 21 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins |
| 81 | d1puia_ | Alignment | not modelled | 96.5 | 19 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins |
| 82 | d1svia_ | Alignment | not modelled | 96.5 | 20 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins |
| 83 | d2g6ba1 | Alignment | not modelled | 96.5 | 18 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins |
| 84 | d1puja_ | Alignment | not modelled | 96.5 | 19 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins |
| 85 | c4wnrA_ | Alignment | not modelled | 96.5 | 18 | PDB header: signaling protein Chain: A: PDB Molecule: leucine-rich-repeat protein; PDBTitle: structure of methanosarcina barkeri roco2 roccordc bound to gdp |
| 86 | c3c5hA_ | Alignment | not modelled | 96.4 | 20 | PDB header: signaling protein Chain: A: PDB Molecule: glucocorticoid receptor dna-binding factor 1; PDBTitle: crystal structure of the ras homolog domain of human grif12 (p190rhogap) |
| 87 | d1zj6a1 | Alignment | not modelled | 96.4 | 15 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins |
| 88 | c1r5nA_ | Alignment | not modelled | 96.4 | 24 | PDB header: translation Chain: A: PDB Molecule: eukaryotic peptide chain release factor gtp- PDBTitle: crystal structure analysis of sup35 complexed with gdp |
| 89 | d1x1ra1 | Alignment | not modelled | 96.4 | 16 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins |
| 90 | d1yzna1 | Alignment | not modelled | 96.4 | 16 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins |
| 91 | c5izkB_ | Alignment | not modelled | 96.4 | 30 | PDB header: translation Chain: B: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: the crystal structure of human eefsec in complex with gdp |
| 92 | c2fg5A_ | Alignment | not modelled | 96.4 | 14 | PDB header: signaling protein Chain: A: PDB Molecule: ras-related protein rab-31; PDBTitle: crystal structure of human rab31 in complex with a gtp analogue |
| 93 | d2fg5a1 | Alignment | not modelled | 96.4 | 14 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins |
| 94 | d1vg8a_ | Alignment | not modelled | 96.3 | 20 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins |
| 95 | c4qjty_ | Alignment | not modelled | 96.3 | 30 | PDB header: ribosome Chain: Y: PDB Molecule: PDBTitle: crystal structure of elongation factor 4 (ef4/lepa) bound to the2 thermus thermophilus 70s ribosome, 30s subunit of the 70s ribosome |
| 96 | d2d7ca1 | Alignment | not modelled | 96.3 | 16 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins |
| 97 | d2ew1a1 | Alignment | not modelled | 96.3 | 18 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins |
| 98 | c2ew1A_ | Alignment | not modelled | 96.3 | 18 | PDB header: signaling protein Chain: A: PDB Molecule: ras-related protein rab-30; PDBTitle: crystal structure of rab30 in complex with a gtp analogue |
| 99 | c1udxA_ | Alignment | not modelled | 96.3 | 29 | PDB header: protein binding Chain: A: PDB Molecule: the gtp-binding protein obg; PDBTitle: crystal structure of the conserved protein tt1381 from thermus2 thermophilus hb8 |
| 100 | c6bbqA_ | Alignment | not modelled | 96.3 | 14 | PDB header: lipid binding protein Chain: A: PDB Molecule: cytohesin-3,adp-ribosylation factor 6; PDBTitle: model for extended volume of truncated monomeric cytohesin-3 (grp1;2 amino acids 63-399) e161a arf6 q67l fusion protein |
| 101 | d2a5ja1 | Alignment | not modelled | 96.3 | 23 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins |
| 102 | c2nzjB_ | Alignment | not modelled | 96.2 | 16 | PDB header: signaling protein Chain: B: PDB Molecule: gtp-binding protein rem 1; PDBTitle: the crystal structure of rem1 in complex with gdp |
| 103 | c3a1wA_ | Alignment | not modelled | 96.2 | 25 | PDB header: transport protein Chain: A: PDB Molecule: iron(ii) transport protein b; PDBTitle: crystal structure of the g domain of t. maritima feob iron2 iransporter |
| 104 | c3gehA_ | Alignment | not modelled | 96.2 | 22 | PDB header: hydrolase Chain: A: PDB Molecule: trna modification gtpase mnme; PDBTitle: crystal structure of mnme from nostoc in complex with gdp, folinic2 acid and zn |
| 105 | c4ncrB_ | Alignment | not modelled | 96.2 | 30 | PDB header: translation Chain: B: PDB Molecule: eukaryotic translation initiation factor 5b-like protein; |

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|-----|-------------------------|-----------|--------------|------|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 105 | c4ncb_ | Alignment | not modelled | 96.2 | 30 | PDBTitle: crystal structure of eukaryotic translation initiation factor eif5b2 (517-970) from chaetomium thermophilum in complex with gdp |
| 106 | d2bcgy1 | Alignment | not modelled | 96.2 | 18 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins |
| 107 | d1d5ca_ | Alignment | not modelled | 96.2 | 18 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins |
| 108 | c3o47A_ | Alignment | not modelled | 96.2 | 18 | PDB header: hydrolase, hydrolase activator Chain: A: PDB Molecule: adp-ribosylation factor gtpase-activating protein 1, adp- PDBTitle: crystal structure of arfgap1-arf1 fusion protein |
| 109 | d1z2aa1 | Alignment | not modelled | 96.2 | 14 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins |
| 110 | c4drzA_ | Alignment | not modelled | 96.1 | 20 | PDB header: protein transport Chain: A: PDB Molecule: ras-related protein rab-14; PDBTitle: crystal structure of human rab14 |
| 111 | c2f9lA_ | Alignment | not modelled | 96.1 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: rab11b, member ras oncogene family; PDBTitle: 3d structure of inactive human rab11b gtpase |
| 112 | c2atvA_ | Alignment | not modelled | 96.1 | 23 | PDB header: signaling protein Chain: A: PDB Molecule: ras-like estrogen-regulated growth inhibitor; PDBTitle: the crystal structure of human reg in the gdp bound state |
| 113 | d2atva1 | Alignment | not modelled | 96.1 | 23 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins |
| 114 | c2hupB_ | Alignment | not modelled | 96.0 | 11 | PDB header: signaling protein Chain: B: PDB Molecule: ras-related protein rab-43; PDBTitle: crystal structure of human rab43 in complex with gdp |
| 115 | c3bbpA_ | Alignment | not modelled | 96.0 | 18 | PDB header: protein transport/splicing Chain: A: PDB Molecule: ras-related protein rab-6a; PDBTitle: rab6-gtp:ccc185 rab binding domain complex |
| 116 | c3t1tC_ | Alignment | not modelled | 96.0 | 20 | PDB header: hydrolase Chain: C: PDB Molecule: gliding protein mgla; PDBTitle: mgla bound to gdp in p1 tetrameric arrangement |
| 117 | c4byxV_ | Alignment | not modelled | 96.0 | 36 | PDB header: ribosome Chain: V: PDB Molecule: eukaryotic translation initiation factor 5b, probable PDBTitle: cryo-em reconstruction of the 80s-eif5b-met-itnamet eukaryotic2 translation initiation complex |
| 118 | c3pqcA_ | Alignment | not modelled | 96.0 | 24 | PDB header: hydrolase Chain: A: PDB Molecule: probable gtp-binding protein engb; PDBTitle: crystal structure of thermotoga maritima ribosome biogenesis gtp-2 binding protein engb (ysxc/yiha) in complex with gdp |
| 119 | c2wkqA_ | Alignment | not modelled | 96.0 | 24 | PDB header: transferase, cell adhesion Chain: A: PDB Molecule: nph1-1, ras-related c3 botulinum toxin substrate 1; PDBTitle: structure of a photoactivatable rac1 containing the lov2 c450a mutant |
| 120 | c3lvrE_ | Alignment | not modelled | 96.0 | 14 | PDB header: protein transport Chain: E: PDB Molecule: arf-gap with sh3 domain, ank repeat and ph domain- PDBTitle: the crystal structure of asap3 in complex with arf6 in transition2 state soaked with calcium |