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Description	P33030
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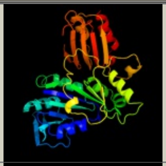
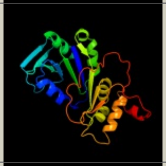
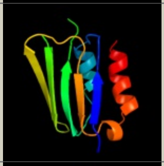
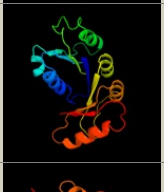
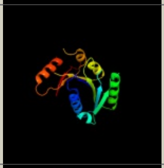
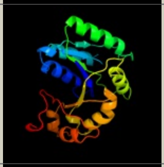
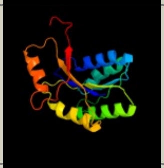
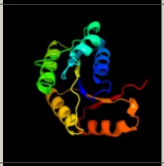
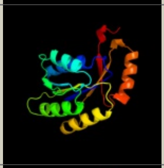
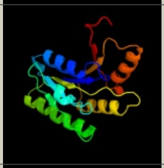
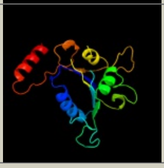
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1nijA_	Alignment		100.0	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yjia; **PDBTitle:** yjia protein
2	d1nija1	Alignment		100.0	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
3	c2hf9A_	Alignment		99.7	18	**PDB header:**hydrolase, metal binding protein **Chain:** A: **PDB Molecule:**probable hydrogenase nickel incorporation **PDBTitle:** crystal structure of hypb from methanocaldococcus2 jannaschii in the triphosphate form
4	d1nija2	Alignment		99.7	16	**Fold:**Hypothetical protein YjiA, C-terminal domain **Superfamily:**Hypothetical protein YjiA, C-terminal domain **Family:**Hypothetical protein YjiA, C-terminal domain
5	c2wsmB_	Alignment		99.5	19	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**hydrogenase expression/formation protein (hypb); **PDBTitle:** crystal structure of hydrogenase maturation factor hypb from2 archaeoglobus fulgidus
6	c3nxsA_	Alignment		99.5	21	**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	d1yrba1	Alignment		99.5	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
8	d2qm8a1	Alignment		99.3	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
9	c2f1rA_	Alignment		99.3	15	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin-guanine dinucleotide biosynthesis **PDBTitle:** crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
10	d1qzxa3	Alignment		99.2	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
11	c3md0A_	Alignment		99.1	22	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**arginine/ornithine transport system atpase; **PDBTitle:** crystal structure of arginine/ornithine transport system2 atpase from mycobacterium tuberculosis bound to gdp (a ras-3 like gtpase superfamily protein)
						

12	c3dmdA_	Alignment		99.1	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**signal recognition particle receptor; **PDBTitle:** structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
13	d2p67a1	Alignment		99.1	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
14	d1ls1a2	Alignment		99.0	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
15	c2cnwF_	Alignment		99.0	16	**PDB header:**signal recognition **Chain:** F: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** gdpalf4 complex of the srp gtpases ffh and ftsy
16	c3dm5A_	Alignment		99.0	16	**PDB header:**rna binding protein, transport protein **Chain:** A: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
17	c1zu4A_	Alignment		98.9	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**ftsy; **PDBTitle:** crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
18	c2j7pA_	Alignment		98.9	18	**PDB header:**signal recognition **Chain:** A: **PDB Molecule:**signal recognition particle protein; **PDBTitle:** gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
19	c2iy3A_	Alignment		98.8	19	**PDB header:**rna-binding **Chain:** A: **PDB Molecule:**signal recognition particle protein ffh; **PDBTitle:** structure of the e. coli signal recognition particle2 bound to a translating ribosome
20	c2wwwB_	Alignment		98.8	20	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**methylmalonic aciduria type a protein, **PDBTitle:** crystal structure of methylmalonic acidemia type a protein
21	d1vmaa2	Alignment	not modelled	98.8	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
22	c2yhsA_	Alignment	not modelled	98.8	15	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the e. coli srp receptor ftsy
23	c2v3cC_	Alignment	not modelled	98.8	17	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** crystal structure of the srp54-srp19-7s.s srp rna complex2 of m. jannaschii
24	c2qy9A_	Alignment	not modelled	98.8	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the ng+1 construct of the e. coli srp receptor2 ftsy
25	c3b9qA_	Alignment	not modelled	98.7	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**chloroplast srp receptor homolog, alpha subunit **PDBTitle:** the crystal structure of cpftsy from arabidopsis thaliana
26	c2og2A_	Alignment	not modelled	98.7	17	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**putative signal recognition particle receptor; **PDBTitle:** crystal structure of chloroplast ftsy from arabidopsis2 thaliana
27	c2j37W_	Alignment	not modelled	98.7	11	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**signal recognition particle 54 kda protein **PDBTitle:** model of mammalian srp bound to 80s rncs
28	d2qy9a2	Alignment	not modelled	98.7	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
						PDB header:protein transport

29	c1vmaA_	Alignment	not modelled	98.7	16	**Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
30	d1okkd2	Alignment	not modelled	98.5	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
31	c2e87A_	Alignment	not modelled	98.5	18	**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	c2qptA_	Alignment	not modelled	98.5	19	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**eh domain-containing protein-2; **PDBTitle:** crystal structure of an ehd atpase involved in membrane remodelling
33	d1xjca_	Alignment	not modelled	98.4	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
34	c2px0D_	Alignment	not modelled	98.4	15	**PDB header:**biosynthetic protein **Chain:** D: **PDB Molecule:**flagellar biosynthesis protein flhf; **PDBTitle:** crystal structure of flhf complexed with gmppnp/mg(2+)
35	c2gzaB_	Alignment	not modelled	98.3	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**type iv secretion system protein virb11; **PDBTitle:** crystal structure of the virb11 atpase from the brucella suis type iv2 secretion system in complex with sulphate
36	c1qzwC_	Alignment	not modelled	98.3	16	**PDB header:**signaling protein/rna **Chain:** C: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication
37	c1egaB_	Alignment	not modelled	98.3	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein (gtp-binding protein era); **PDBTitle:** crystal structure of a widely conserved gtpase era
38	c2qthA_	Alignment	not modelled	98.3	16	**PDB header:**nucleotide binding protein **Chain:** A: **PDB Molecule:**gtp-binding protein; **PDBTitle:** crystal structure of a gtp-binding protein from the2 hyperthermophilic archaeon sulfolobus solfataricus in3 complex with gdp
39	d1g6oa_	Alignment	not modelled	98.3	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
40	c1wb1C_	Alignment	not modelled	98.2	19	**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
41	c2j289_	Alignment	not modelled	98.2	19	**PDB header:**ribosome **Chain:** 9: **PDB Molecule:**signal recognition particle 54; **PDBTitle:** model of e. coli srp bound to 70s rncs
42	c2qa5A_	Alignment	not modelled	98.2	17	**PDB header:**cell cycle, structural protein **Chain:** A: **PDB Molecule:**septin-2; **PDBTitle:** crystal structure of sept2 g-domain
43	c2gedB_	Alignment	not modelled	98.1	18	**PDB header:**protein transport, signaling protein **Chain:** B: **PDB Molecule:**signal recognition particle receptor beta **PDBTitle:** signal recognition particle receptor beta-subunit in2 nucleotide-free dimerized form
44	c2oaq1_	Alignment	not modelled	98.1	22	**PDB header:**hydrolase **Chain:** 1: **PDB Molecule:**type ii secretion system protein; **PDBTitle:** crystal structure of the archaeal secretion atpase gspe in complex2 with phosphate
45	c1kk3A_	Alignment	not modelled	98.1	16	**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+
46	d1np6a_	Alignment	not modelled	98.0	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
47	c1d2eA_	Alignment	not modelled	98.0	11	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**elongation factor tu (ef-tu); **PDBTitle:** crystal structure of mitochondrial ef-tu in complex with gdp
48	c3t5dC_	Alignment	not modelled	98.0	19	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**septin-7; **PDBTitle:** crystal structure of septin 7 in complex with gdp
49	c2plfA_	Alignment	not modelled	97.9	16	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor 2 gamma subunit; **PDBTitle:** the structure of aif2gamma subunit from the archaeon2 sulfolobus solfataricus in the nucleotide-free form.
50	c3jvvA_	Alignment	not modelled	97.9	23	**PDB header:**atp binding protein **Chain:** A: **PDB Molecule:**twitching mobility protein; **PDBTitle:** crystal structure of p. aeruginosa pilt with bound amp-pcp
51	c2qagB_	Alignment	not modelled	97.9	23	**PDB header:**cell cycle, structural protein **Chain:** B: **PDB Molecule:**septin-6; **PDBTitle:** crystal structure of human septin trimer 2/6/7
52	c1wf3A_	Alignment	not modelled	97.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gtp-binding protein; **PDBTitle:** crystal structure of gtp-binding protein tt1341 from thermus2 thermophilus hb8
53	d1p9ra_	Alignment	not modelled	97.9	28	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
54	c3gehA_	Alignment	not modelled	97.8	17	**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
55	c2bvnB_	Alignment	not modelled	97.8	11	**PDB header:**elongation factor **Chain:** B: **PDB Molecule:**elongation factor tu; **PDBTitle:** e. coli ef-tu:gdpnp in complex with the antibiotic2 enacyloxin iia
56	c3k53B_	Alignment	not modelled	97.8	19	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**ferrous iron transport protein b; **PDBTitle:** crystal structure of nfeob from p. furiosus
57	c3ftqA_	Alignment	not modelled	97.8	19	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**septin-2; **PDBTitle:** crystal structure of septin 2 in complex with gppnhp and2 mg2+
58	d2c78a3	Alignment	not modelled	97.8	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
59	c1mkyA_	Alignment	not modelled	97.8	20	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**probable gtp-binding protein enga; **PDBTitle:** structural analysis of the domain interactions in der, a2 switch protein containing two gtpase domains
60	d2dy1a2	Alignment	not modelled	97.8	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
61	c2qagC_	Alignment	not modelled	97.8	23	**PDB header:**cell cycle, structural protein **Chain:** C: **PDB Molecule:**septin-7; **PDBTitle:** crystal structure of human septin trimer 2/6/7
62	c2xtpA_	Alignment	not modelled	97.8	13	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gtpase imap family member 2; **PDBTitle:** crystal structure of nucleotide-free human gimap2, amino2 acid residues 1-260
63	c1xzqA_	Alignment	not modelled	97.8	23	**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
64	c3lx8A_	Alignment	not modelled	97.7	18	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**ferrous iron uptake transporter protein b; **PDBTitle:** crystal structure of gdp-bound nfeob from s. thermophilus
65	c1s0uA_	Alignment	not modelled	97.7	13	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor 2 gamma subunit; **PDBTitle:** eif2gamma apo
66	d1u94a1	Alignment	not modelled	97.7	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
67	c2gszE_	Alignment	not modelled	97.7	21	**PDB header:**protein transport **Chain:** E: **PDB Molecule:**twitching motility protein pilt; **PDBTitle:** structure of a. aeolicus pilt with 6 monomers per2 asymmetric unit
68	c1mj1A_	Alignment	not modelled	97.7	15	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**elongation factor tu; **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
69	c2qagA_	Alignment	not modelled	97.7	18	**PDB header:**cell cycle, structural protein **Chain:** A: **PDB Molecule:**septin-2; **PDBTitle:** crystal structure of human septin trimer 2/6/7
70	d1ubea1	Alignment	not modelled	97.7	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
71	c1udxA_	Alignment	not modelled	97.7	16	**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
72	c1lnzA_	Alignment	not modelled	97.7	25	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**spo0b-associated gtp-binding protein; **PDBTitle:** structure of the obg gtp-binding protein
73	c1g7tA_	Alignment	not modelled	97.7	17	**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
74	d1mo6a1	Alignment	not modelled	97.7	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
75	c3la6P_	Alignment	not modelled	97.7	19	**PDB header:**transferase **Chain:** P: **PDB Molecule:**tyrosine-protein kinase wzc; **PDBTitle:** octameric kinase domain of the e. coli tyrosine kinase wzc with bound2 adp
76	c2recB_	Alignment	not modelled	97.6	23	**PDB header:**helicase **PDB COMPND:**
77	c2eyuA_	Alignment	not modelled	97.6	21	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**twitching motility protein pilt; **PDBTitle:** the crystal structure of the c-terminal domain of aquifex2 aeolicus pilt
78	c2h5eB_	Alignment	not modelled	97.6	17	**PDB header:**translation **Chain:** B: **PDB Molecule:**peptide chain release factor rf-3; **PDBTitle:** crystal structure of e.coli polypeptide release factor rf3
79	c3ievA_	Alignment	not modelled	97.6	16	**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
80	c2ywfA_	Alignment	not modelled	97.6	19	**PDB header:**translation **Chain:** A: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** crystal structure of gmppnp-bound lepa from aquifex aeolicus

81	c2zroA_	Alignment	not modelled	97.6	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein reca; **PDBTitle:** msreca adp form iv
82	c2elfA_	Alignment	not modelled	97.6	23	**PDB header:**translation **Chain:** A: **PDB Molecule:**protein translation elongation factor 1a; **PDBTitle:** crystal structure of the selb-like elongation factor ef-pyl2 from methanosarcina mazei
83	c3hr8A_	Alignment	not modelled	97.6	22	**PDB header:**recombination **Chain:** A: **PDB Molecule:**protein reca; **PDBTitle:** crystal structure of thermotoga maritima reca
84	c2vyeA_	Alignment	not modelled	97.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**replicative dna helicase; **PDBTitle:** crystal structure of the dnac-ssdna complex
85	c3cioA_	Alignment	not modelled	97.6	13	**PDB header:**signaling protein, transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase etk; **PDBTitle:** the kinase domain of escherichia coli tyrosine kinase etk
86	c1zo1I_	Alignment	not modelled	97.5	12	**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
87	c3mcaA_	Alignment	not modelled	97.5	17	**PDB header:**translation regulation/hydrolase **Chain:** A: **PDB Molecule:**elongation factor 1 alpha-like protein; **PDBTitle:** structure of the dom34-hbs1 complex and implications for its role in2 no-go decay
88	d2fh5b1	Alignment	not modelled	97.5	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
89	c2hjgA_	Alignment	not modelled	97.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gtp-binding protein enga; **PDBTitle:** the crystal structure of the b. subtilis yphc gtpase in2 complex with gdp
90	d1f60a3	Alignment	not modelled	97.5	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
91	d2bv3a2	Alignment	not modelled	97.5	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
92	d1xp8a1	Alignment	not modelled	97.5	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
93	c2vedA_	Alignment	not modelled	97.5	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**membrane protein capa1, protein tyrosine kinase; **PDBTitle:** crystal structure of the chimerical mutant capabk55m2 protein
94	c3p1jC_	Alignment	not modelled	97.4	10	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**gtpase imap family member 2; **PDBTitle:** crystal structure of human gtpase imap family member 2 in the2 nucleotide-free state
95	c1xp8A_	Alignment	not modelled	97.4	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**reca protein; **PDBTitle:** "deinococcus radiodurans reca in complex with atp-gamma-s"
96	c3lxxA_	Alignment	not modelled	97.4	12	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gtpase imap family member 4; **PDBTitle:** crystal structure of human gtpase imap family member 4
97	c2q3fB_	Alignment	not modelled	97.4	16	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**ras-related gtp-binding protein d; **PDBTitle:** x-ray crystal structure of putative human ras-related gtp2 binding d in complex with gmppnp
98	c3tr5C_	Alignment	not modelled	97.4	17	**PDB header:**translation **Chain:** C: **PDB Molecule:**peptide chain release factor 3; **PDBTitle:** structure of a peptide chain release factor 3 (prfc) from coxiella2 burnetii
99	d1puia_	Alignment	not modelled	97.4	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
100	c2ja1A_	Alignment	not modelled	97.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidine kinase; **PDBTitle:** thymidine kinase from b. cereus with ttp bound as phosphate2 donor.
101	c3lxwA_	Alignment	not modelled	97.4	12	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gtpase imap family member 1; **PDBTitle:** crystal structure of human gtpase imap family member 1
102	d1zunb3	Alignment	not modelled	97.4	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
103	c2q6tB_	Alignment	not modelled	97.3	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dnab replication fork helicase; **PDBTitle:** crystal structure of the thermus aquaticus dnab monomer
104	c3r7wC_	Alignment	not modelled	97.3	15	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**gtp-binding protein gtr1; **PDBTitle:** crystal structure of gtr1p-gtr2p complex
105	c1jalA_	Alignment	not modelled	97.3	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ychf protein; **PDBTitle:** ychf protein (hi0393)
106	c2xexA_	Alignment	not modelled	97.3	18	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor g; **PDBTitle:** crystal structure of staphylococcus aureus elongation factor2 g
						PDB header:elongation factor

107	c2bm0A_	Alignment	not modelled	97.3	21	**Chain:** A: **PDB Molecule:**elongation factor g; **PDBTitle:** ribosomal elongation factor g (ef-g) fusidic acid resistant2 mutant t84a
108	d1g3qa_	Alignment	not modelled	97.3	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
109	c2dy1A_	Alignment	not modelled	97.3	19	**PDB header:**signaling protein, translation **Chain:** A: **PDB Molecule:**elongation factor g; **PDBTitle:** crystal structure of ef-g-2 from thermus thermophilus
110	c2xtnA_	Alignment	not modelled	97.3	9	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gtpase imap family member 2; **PDBTitle:** crystal structure of gtp-bound human gimap2, amino acid2 residues 1-234
111	c1xx6B_	Alignment	not modelled	97.3	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thymidine kinase; **PDBTitle:** x-ray structure of clostridium acetobutylicum thymidine kinase with2 adp. northeast structural genomics target car26.
112	d1svia_	Alignment	not modelled	97.3	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
113	c3mmpC_	Alignment	not modelled	97.2	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**elongation factor tu 2, elongation factor ts; **PDBTitle:** structure of the qb replicase, an rna-dependent rna polymerase2 consisting of viral and host proteins
114	c1skqB_	Alignment	not modelled	97.2	17	**PDB header:**translation **Chain:** B: **PDB Molecule:**elongation factor 1-alpha; **PDBTitle:** the crystal structure of sulfolobus solfataricus elongation2 factor 1-alpha in complex with magnesium and gdp
115	d1qhxa_	Alignment	not modelled	97.2	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Chloramphenicol phosphotransferase
116	c3degC_	Alignment	not modelled	97.2	14	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp
117	c3cmvG_	Alignment	not modelled	97.2	23	**PDB header:**recombination **Chain:** G: **PDB Molecule:**protein reca; **PDBTitle:** mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
118	d1tf7a2	Alignment	not modelled	97.2	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
119	d1ihua2	Alignment	not modelled	97.2	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
120	c2ztsB_	Alignment	not modelled	97.2	20	**PDB header:**atp-binding protein **Chain:** B: **PDB Molecule:**putative uncharacterized protein ph0186; **PDBTitle:** crystal structure of kaic-like protein ph0186 from2 hyperthermophilic archaea pyrococcus horikoshii ot3