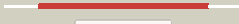



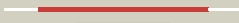







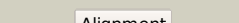









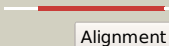

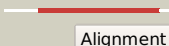







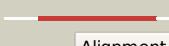









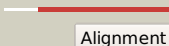
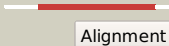
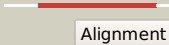
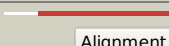




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2364c_era_2645781_2646683
Date	Mon Aug 5 13:25:51 BST 2019
Unique Job ID	752384f7e3ad556d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ievA_	 Alignment		100.0	34	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
2	c1wf3A_	 Alignment		100.0	39	PDB header: hydrolase Chain: A: PDB Molecule: gtp-binding protein; PDBTitle: crystal structure of gtp-binding protein tt1341 from thermus2 thermophilus hb8
3	c1egaB_	 Alignment		100.0	33	PDB header: hydrolase Chain: B: PDB Molecule: protein (gtp-binding protein era); PDBTitle: crystal structure of a widely conserved gtpase era
4	d1wf3a2	 Alignment		100.0	46	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
5	d1egaa2	 Alignment		100.0	33	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
6	c1xzqA_	 Alignment		100.0	24	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
7	c2e87A_	 Alignment		100.0	25	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
8	c4csu9_	 Alignment		100.0	20	PDB header: ribosome Chain: 9: PDB Molecule: gtpase obge/cgta; PDBTitle: cryo-em structures of the 50s ribosome subunit bound with obge
9	d1ni3a1	 Alignment		100.0	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
10	c6em5b_	 Alignment		100.0	14	PDB header: ribosome Chain: B: PDB Molecule: 60s ribosomal protein l3; PDBTitle: state d architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes
11	d1egaa1	 Alignment		100.0	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins

12	c1udxA	 Alignment		100.0	25	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
13	c5ady6	 Alignment		100.0	21	PDB header: ribosome Chain: 6: PDB Molecule: gtpase hflx; PDBTitle: cryo-em structures of the 50s ribosome subunit bound with hflx
14	c3gehA	 Alignment		100.0	25	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
15	d1wf3a1	 Alignment		99.9	35	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
16	c3j65o	 Alignment		99.9	20	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l15; PDBTitle: arx1 pre-60s particle. this entry contains the r-proteins and2 biogenesis factors.
17	c5dn8A	 Alignment		99.9	31	PDB header: gtp-binding protein Chain: A: PDB Molecule: gtpase der; PDBTitle: 1.76 angstrom crystal structure of gtp-binding protein der from2 coxiella burnetii in complex with gdp.
18	c1lnzA	 Alignment		99.9	24	PDB header: cell cycle Chain: A: PDB Molecule: spo0b-associated gtp-binding protein; PDBTitle: structure of the obg gtp-binding protein
19	c3j8gX	 Alignment		99.9	24	PDB header: ribosome Chain: X: PDB Molecule: gtpase der; PDBTitle: electron cryo-microscopy structure of enga bound with the 50s2 ribosomal subunit
20	c4b3xA	 Alignment		99.9	21	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-2; PDBTitle: bacterial translation initiation factor if2 (1-363), apo form
21	c3j4jA	 Alignment	not modelled	99.9	22	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
22	c3a1vB	 Alignment	not modelled	99.9	19	PDB header: transport protein Chain: B: PDB Molecule: iron(ii) transport protein b; PDBTitle: crystal structure of the cytosolic domain of t. maritima feob2 iron transporter in apo form
23	c3k53B	 Alignment	not modelled	99.9	23	PDB header: metal transport Chain: B: PDB Molecule: ferrous iron transport protein b; PDBTitle: crystal structure of nfeob from p. furiousus
24	c2qthA	 Alignment	not modelled	99.9	23	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
25	d2bv3a2	 Alignment	not modelled	99.9	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
26	c3lx8A	 Alignment	not modelled	99.9	17	PDB header: metal transport Chain: A: PDB Molecule: ferrous iron uptake transporter protein b; PDBTitle: crystal structure of gdp-bound nfeob from s. thermophilus
27	c2higA	 Alignment	not modelled	99.9	26	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
28	c4kzD	 Alignment	not modelled	99.9	23	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)
29	c3ibyA_	Alignment	not modelled	99.9	17	PDB header: transport protein Chain: A: PDB Molecule: ferrous iron transport protein b; PDBTitle: structure of cytosolic domain of l. pneumophila feob
30	c3wbkB_	Alignment	not modelled	99.9	24	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
31	c2wwwB_	Alignment	not modelled	99.9	20	PDB header: transport protein Chain: B: PDB Molecule: methylmalonic aciduria type a protein, PDBTitle: crystal structure of methylmalonic acidemia type a protein
32	c1mkYA_	Alignment	not modelled	99.9	29	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
33	c1zo1I_	Alignment	not modelled	99.9	23	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
34	c3md0A_	Alignment	not modelled	99.9	19	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)
35	c3izyP_	Alignment	not modelled	99.9	24	PDB header: rna, ribosomal protein Chain: P: PDB Molecule: translation initiation factor if-2, mitochondrial; PDBTitle: mammalian mitochondrial translation initiation factor 2
36	c5fg3A_	Alignment	not modelled	99.9	30	PDB header: translation Chain: A: PDB Molecule: probable translation initiation factor if-2; PDBTitle: crystal structure of gdp-bound aif5b from aeropyrum pernix
37	c3i8sC_	Alignment	not modelled	99.9	18	PDB header: transport protein Chain: C: PDB Molecule: ferrous iron transport protein b; PDBTitle: structure of the cytosolic domain of e. coli feob, nucleotide-free2 form
38	c4nclB_	Alignment	not modelled	99.9	23	PDB header: translation Chain: B: PDB Molecule: eukaryotic translation initiation factor 5b-like protein; PDBTitle: crystal structure of eukaryotic translation initiation factor eif5b2 (517-970) from chaetomium thermophilum in complex with gdp
39	c4dheA_	Alignment	not modelled	99.9	21	PDB header: cell cycle Chain: A: PDB Molecule: probable gtp-binding protein engb; PDBTitle: crystal structure of a probable gtp-binding protein engb from2 burkholderia thailandensis
40	c1kk3A_	Alignment	not modelled	99.9	22	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+
41	c2xtpA_	Alignment	not modelled	99.9	15	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
42	c4upyB_	Alignment	not modelled	99.9	29	PDB header: ribosome Chain: B: PDB Molecule: eif5b; PDBTitle: mammalian 80s hcv-ires initiation complex with eif5b pre-like state
43	c4a9aB_	Alignment	not modelled	99.9	27	PDB header: translation Chain: B: PDB Molecule: ribosome-interacting gtpase 1; PDBTitle: structure of rbg1 in complex with tma46 dfrp domain
44	c1wb1C_	Alignment	not modelled	99.9	22	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
45	c3w5iB_	Alignment	not modelled	99.9	19	PDB header: metal transport Chain: B: PDB Molecule: ferrous iron transport protein b; PDBTitle: crystal structure of nfeob from gallionella capsiferiformans
46	d2dy1a2	Alignment	not modelled	99.9	35	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
47	d2qm8a1	Alignment	not modelled	99.9	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
48	c1g7tA_	Alignment	not modelled	99.9	26	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
49	d2p67a1	Alignment	not modelled	99.9	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
50	c3nxsA_	Alignment	not modelled	99.9	18	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
51	c4n3nA_	Alignment	not modelled	99.9	24	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
52	c2wjJB_	Alignment	not modelled	99.9	20	PDB header: metal transport Chain: B: PDB Molecule: ferrous iron transport protein b homolog; PDBTitle: structure and function of the feob g-domain from2 methanococcus jannaschii
						PDB header: hydrolase

53	c3pqcA	Alignment	not modelled	99.9	24	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
54	d2gj8a1	Alignment	not modelled	99.9	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
55	c6cesC	Alignment	not modelled	99.9	12	PDB header: signaling protein Chain: C: PDB Molecule: ras-related gtp-binding protein c; PDBTitle: cryo-em structure of gator1-rag
56	d1lnza2	Alignment	not modelled	99.9	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
57	c4lpsA	Alignment	not modelled	99.9	17	PDB header: metal binding protein Chain: A: PDB Molecule: hydrogenase/urease nickel incorporation protein hypb; PDBTitle: crystal structure of hypb from helicobacter pylori in complex with2 nickel
58	c4zu9A	Alignment	not modelled	99.9	23	PDB header: translation Chain: A: PDB Molecule: elongation factor selb; PDBTitle: crystal structure of bacterial selenocysteine-specific elongation2 factor ef-sec
59	c2ywfA	Alignment	not modelled	99.9	19	PDB header: translation Chain: A: PDB Molecule: gtp-binding protein lepa; PDBTitle: crystal structure of gmppnp-bound lepa from aquifex aeolicus
60	c5k0yS	Alignment	not modelled	99.9	19	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
61	c3degC	Alignment	not modelled	99.9	20	PDB header: ribosome Chain: C: PDB Molecule: gtp-binding protein lepa; PDBTitle: complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp
62	c3qq5A	Alignment	not modelled	99.9	23	PDB header: oxidoreductase Chain: A: PDB Molecule: small gtp-binding protein; PDBTitle: crystal structure of the [fefe]-hydrogenase maturation protein hydF
63	d1kk1a3	Alignment	not modelled	99.9	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
64	c2xtnA	Alignment	not modelled	99.9	15	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
65	d1jala1	Alignment	not modelled	99.9	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
66	c3j81k	Alignment	not modelled	99.9	20	PDB header: ribosome Chain: K: PDB Molecule: es10; PDBTitle: cryoem structure of a partial yeast 48s preinitiation complex
67	c4byxV	Alignment	not modelled	99.8	24	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
68	c6bbqA	Alignment	not modelled	99.8	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
69	d1svia	Alignment	not modelled	99.8	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
70	d1tq4a	Alignment	not modelled	99.8	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
71	c3zjcC	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: C: PDB Molecule: gtpase imap family member 7; PDBTitle: crystal structure of gmppnp-bound human gimap7 l100q variant
72	c5hcnA	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: A: PDB Molecule: gpn-loop gtpase 1; PDBTitle: gpn-loop gtpase npa3 in complex with gmppcp
73	c2qu8A	Alignment	not modelled	99.8	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative nucleolar gtp-binding protein 1; PDBTitle: crystal structure of putative nucleolar gtp-binding protein 1 pff0625w2 from plasmodium falciparum
74	c5ee1A	Alignment	not modelled	99.8	23	PDB header: hydrolase Chain: A: PDB Molecule: obg-like atpase 1; PDBTitle: crystal structure of osychf1 at ph 7.85
75	c2plfA	Alignment	not modelled	99.8	23	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.
76	d1udxa2	Alignment	not modelled	99.8	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
77	d1wb1a4	Alignment	not modelled	99.8	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins

78	c4byrP	Alignment	not modelled	99.8	25	PDB header: ribosome Chain: P: PDB Molecule: eukaryotic translation initiation factor 5b; PDBTitle: cryo-em reconstruction of the 80s-eif5b-met-itramet2 eukaryotic translation initiation complex
79	d1d2ea3	Alignment	not modelled	99.8	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
80	c4wnrA	Alignment	not modelled	99.8	14	PDB header: signaling protein Chain: A: PDB Molecule: leucine-rich-repeat protein; PDBTitle: structure of methanosarcina barkeri roco2 roccordc bound to gdp
81	c5izmA	Alignment	not modelled	99.8	25	PDB header: translation Chain: A: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: the crystal structure of human eefsec in complex with gdpnp
82	c3a1wA	Alignment	not modelled	99.8	22	PDB header: transport protein Chain: A: PDB Molecule: iron(ii) transport protein b; PDBTitle: crystal structue of the g domain of t. maritima feob iron2 iransporter
83	c5ucvA	Alignment	not modelled	99.8	16	PDB header: cell cycle Chain: A: PDB Molecule: probable gtp-binding protein engb; PDBTitle: crystal structure of a ribosome biogenesis gtp-binding protein (ysxc)2 from neisseria gonorrhoeae with bound gdp
84	c4qjty	Alignment	not modelled	99.8	19	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
85	c5izkB	Alignment	not modelled	99.8	28	PDB header: translation Chain: B: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: the crystal structure of human eefsec in complex with gdp
86	d1zunb3	Alignment	not modelled	99.8	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
87	c2lkcA	Alignment	not modelled	99.8	23	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-2; PDBTitle: free b.st if2-g2
88	c1ni3A	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: yhcH gtp-binding protein; PDBTitle: structure of the schizosaccharomyces pombe yhcH gtpase
89	c2j3eA	Alignment	not modelled	99.8	20	PDB header: protein transport Chain: A: PDB Molecule: t7i23.11 protein; PDBTitle: dimerization is important for the gtpase activity of2 chloroplast translocon components atoc33 and pstoc159
90	c2hf9A	Alignment	not modelled	99.8	14	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
91	c2dykB	Alignment	not modelled	99.8	24	PDB header: ribosome Chain: B: PDB Molecule: gtp-binding protein; PDBTitle: crystal structure of n-terminal gtp-binding domain of enga from2 thermus thermophilus hb8
92	c5c2kA	Alignment	not modelled	99.8	20	PDB header: hydrolase activator Chain: A: PDB Molecule: transforming protein rhoa,rac gtpase-activating protein 1; PDBTitle: crystal structure of the fusion protein linked by rhoa and the gap2 domain of mgracgap
93	d2cxa1	Alignment	not modelled	99.8	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
94	d1g7sa4	Alignment	not modelled	99.8	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
95	c4yqfA	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: A: PDB Molecule: septin-9; PDBTitle: gtpase domain of human septin 9
96	d1h65a	Alignment	not modelled	99.8	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
97	c3o47A	Alignment	not modelled	99.8	20	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
98	d1f60a3	Alignment	not modelled	99.8	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
99	c5ymxB	Alignment	not modelled	99.8	17	PDB header: signaling protein, hydrolase Chain: B: PDB Molecule: mutual gliding-motility protein mgla; PDBTitle: myxococcus xanthus mgla in gdp bound conformation
100	c2ohfA	Alignment	not modelled	99.8	29	PDB header: hydrolase Chain: A: PDB Molecule: gtp-binding protein 9; PDBTitle: crystal structure of human ola1 in complex with amppcp
101	d1xzpa2	Alignment	not modelled	99.8	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
102	c5kutB	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: B: PDB Molecule: mitochondrial rho gtpase 2; PDBTitle: hmiro2 c-terminal gtpase domain, gdp-bound
103	c3lxA	Alignment	not modelled	99.8	16	PDB header: immune system Chain: A: PDB Molecule: gtpase imap family member 1; PDBTitle: crystal structure of human gtpase imap family member 1 PDB header: elongation factor

104	c2bvnB_	Alignment	not modelled	99.8	22	Chain: B: PDB Molecule: elongation factor tu; PDBTitle: e. coli ef-tu:gdnpn in complex with the antibiotic enacyloxin iia
105	d1puia_	Alignment	not modelled	99.8	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
106	d2qn6a3	Alignment	not modelled	99.8	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
107	c2wsmB_	Alignment	not modelled	99.8	14	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
108	c3p1jC_	Alignment	not modelled	99.8	17	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
109	d1r5ba3	Alignment	not modelled	99.8	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
110	c1d2eA_	Alignment	not modelled	99.8	22	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
111	c3vr1B_	Alignment	not modelled	99.8	28	PDB header: translation Chain: B: PDB Molecule: peptide chain release factor 3; PDBTitle: crystal structure analysis of the translation factor rf3
112	c6cesA_	Alignment	not modelled	99.8	14	PDB header: signaling protein Chain: A: PDB Molecule: ras-related gtp-binding protein a; PDBTitle: cryo-em structure of gator1-rag
113	c2wkqA_	Alignment	not modelled	99.8	18	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
114	c5xktA_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: urease accessory protein ureg; PDBTitle: klebsiella pneumoniae ureg in complex with gmppnp and nickel
115	d2c78a3	Alignment	not modelled	99.8	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
116	d1z0ja1	Alignment	not modelled	99.8	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
117	c1jalA_	Alignment	not modelled	99.8	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ychf protein; PDBTitle: ychf protein (hi0393)
118	c3lvrE_	Alignment	not modelled	99.8	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
119	d2qtvb1	Alignment	not modelled	99.8	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
120	c2h57A_	Alignment	not modelled	99.7	16	PDB header: transport protein Chain: A: PDB Molecule: adp-ribosylation factor-like protein 6; PDBTitle: crystal structure of human adp-ribosylation factor-like 6