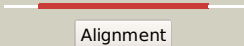

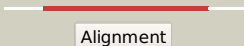

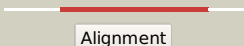


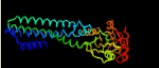




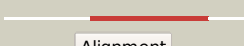




















Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2725c_(hflX)_3037437_3038924
 Date Wed Aug 7 12:50:38 BST 2019
 Unique Job ID 19b840ff79a3410a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5ady6_	 Alignment		100.0	40	PDB header: ribosome Chain: 6: PDB Molecule: gtpase hflx; PDBTitle: cryo-em structures of the 50s ribosome subunit bound with hflx
2	c2qthA_	 Alignment		100.0	31	PDB header: nucleotide binding protein Chain: A: PDB Molecule: gtp-binding protein; PDBTitle: crystal structure of a gtp-binding protein from the hyperthermophilic2 archaeon sulfolobus solfataricus in complex with gdp
3	c2e87A_	 Alignment		100.0	19	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
4	c3j65o_	 Alignment		100.0	17	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.
5	c4a9aB_	 Alignment		100.0	29	PDB header: translation Chain: B: PDB Molecule: ribosome-interacting gtpase 1; PDBTitle: structure of rbg1 in complex with tma46 dfrp domain
6	c1xzqA_	 Alignment		100.0	22	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	c6em5b_	 Alignment		100.0	18	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
8	c3gehA_	 Alignment		100.0	26	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
9	c1udxA_	 Alignment		100.0	28	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
10	c4csu9_	 Alignment		100.0	22	PDB header: ribosome Chain: 9: PDB Molecule: gtpase obge/cgta; PDBTitle: cryo-em structures of the 50s ribosome subunit bound with obge
11	c1lnzA_	 Alignment		100.0	24	PDB header: cell cycle Chain: A: PDB Molecule: spo0b-associated gtp-binding protein; PDBTitle: structure of the obg gtp-binding protein

12	c5dn8A	Alignment		100.0	26	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.
13	c3j8gX	Alignment		100.0	24	PDB header: ribosome Chain: X; PDB Molecule: gtpase der; PDBTitle: electron cryo-microscopy structure of enga bound with the 50s2 ribosomal subunit
14	c4b3xA	Alignment		100.0	19	PDB header: translation Chain: A; PDB Molecule: translation initiation factor if-2; PDBTitle: bacterial translation initiation factor if2 (1-363), apo form
15	c3ievA	Alignment		100.0	24	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
16	c4kjdD	Alignment		100.0	22	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)
17	c1wf3A	Alignment		100.0	24	PDB header: hydrolase Chain: A; PDB Molecule: gtp-binding protein; PDBTitle: crystal structure of gtp-binding protein tt1341 from thermus2 thermophilus hb8
18	c3j4jA	Alignment		99.9	20	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
19	c1mkya	Alignment		99.9	26	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
20	c3k53B	Alignment		99.9	23	PDB header: metal transport Chain: B; PDB Molecule: ferrous iron transport protein b; PDBTitle: crystal structure of nfeob from p. furiosus
21	c1legaB	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: B; PDB Molecule: protein (gtp-binding protein era); PDBTitle: crystal structure of a widely conserved gtpase era
22	c3a1vB	Alignment	not modelled	99.9	22	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	c2higA	Alignment	not modelled	99.9	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
24	c5ee1A	Alignment	not modelled	99.9	27	PDB header: hydrolase Chain: A; PDB Molecule: obg-like atpase 1; PDBTitle: crystal structure of osychf1 at ph 7.85
25	c3nxsA	Alignment	not modelled	99.9	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
26	c3md0A	Alignment	not modelled	99.9	18	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)
27	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
28	d2bv3a2	Alignment	not modelled	99.9	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins

29	c3lx8A_	Alignment	not modelled	99.9	22	PDB header: metal transport Chain: A: PDB Molecule: ferrous iron uptake transporter protein b; PDBTitle: crystal structure of gdp-bound nfeob from s. thermophilus
30	c1kk3A_	Alignment	not modelled	99.9	21	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+
31	c3i8sC_	Alignment	not modelled	99.9	24	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
32	c3ibyA_	Alignment	not modelled	99.9	20	PDB header: transport protein Chain: A: PDB Molecule: ferrous iron transport protein b; PDBTitle: structure of cytosolic domain of l. pneumophila feob
33	c3izyP_	Alignment	not modelled	99.9	26	PDB header: rna, ribosomal protein Chain: P: PDB Molecule: translation initiation factor if-2, mitochondrial; PDBTitle: mammalian mitochondrial translation initiation factor 2
34	d2p67a1	Alignment	not modelled	99.9	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
35	d2dy1a2	Alignment	not modelled	99.9	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
36	c4zu9A_	Alignment	not modelled	99.9	24	PDB header: translation Chain: A: PDB Molecule: elongation factor selb; PDBTitle: crystal structure of bacterial selenocysteine-specific elongation2 factor ef-sec
37	c1jalA_	Alignment	not modelled	99.9	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ychf protein; PDBTitle: ychf protein (hi0393)
38	c5k0yS_	Alignment	not modelled	99.9	20	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
39	c4upyB_	Alignment	not modelled	99.9	23	PDB header: ribosome Chain: B: PDB Molecule: eif5b; PDBTitle: mammalian 80s hcv-ires initiation complex with eif5b pre-like state
40	c5fg3A_	Alignment	not modelled	99.9	27	PDB header: translation Chain: A: PDB Molecule: probable translation initiation factor if-2; PDBTitle: crystal structure of gdp-bound aif5b from aeropyrum pernix
41	c2wwwB_	Alignment	not modelled	99.9	21	PDB header: transport protein Chain: B: PDB Molecule: methylmalonic aciduria type a protein, PDBTitle: crystal structure of methylmalonic acidemia type a protein
42	c1ni3A_	Alignment	not modelled	99.9	27	PDB header: hydrolase Chain: A: PDB Molecule: ychf gtp-binding protein; PDBTitle: structure of the schizosaccharomyces pombe ychf gtpase
43	c4dheA_	Alignment	not modelled	99.9	16	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
44	c4nclB_	Alignment	not modelled	99.9	24	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
45	c1wb1C_	Alignment	not modelled	99.9	23	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
46	c1zo1l_	Alignment	not modelled	99.9	27	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
47	c3wbkB_	Alignment	not modelled	99.9	25	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
48	d2qm8a1	Alignment	not modelled	99.9	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
49	c2ywfA_	Alignment	not modelled	99.9	23	PDB header: translation Chain: A: PDB Molecule: gtp-binding protein lepa; PDBTitle: crystal structure of gmppnp-bound lepa from aquifex aeolicus
50	c3j81k_	Alignment	not modelled	99.9	21	PDB header: ribosome Chain: K: PDB Molecule: es10; PDBTitle: cryoem structure of a partial yeast 48s preinitiation complex
51	c3degC_	Alignment	not modelled	99.9	22	PDB header: ribosome Chain: C: PDB Molecule: gtp-binding protein lepa; PDBTitle: complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp
52	c2dwqB_	Alignment	not modelled	99.9	27	PDB header: hydrolase Chain: B: PDB Molecule: gtp-binding protein; PDBTitle: thermus thermophilus ychf gtp-binding protein
53	c2ohfA_	Alignment	not modelled	99.9	26	PDB header: hydrolase Chain: A: PDB Molecule: gtp-binding protein 9; PDBTitle: crystal structure of human ola1 in complex with amppcp

54	c4lpsA	Alignment	not modelled	99.9	10	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
55	c1g7tA	Alignment	not modelled	99.9	27	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
56	c2plfA	Alignment	not modelled	99.9	24	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.
57	d1lnza2	Alignment	not modelled	99.9	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
58	c3w5lB	Alignment	not modelled	99.9	16	PDB header: metal transport Chain: B: PDB Molecule: ferrous iron transport protein b; PDBTitle: crystal structure of nfeob from gallionella capsiferriformans
59	d1ni3a1	Alignment	not modelled	99.9	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
60	d1h65a	Alignment	not modelled	99.9	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
61	d1svia	Alignment	not modelled	99.9	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
62	d1tq4a	Alignment	not modelled	99.9	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
63	c6bbqA	Alignment	not modelled	99.8	22	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
64	c4qjty	Alignment	not modelled	99.8	24	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
65	c5izmA	Alignment	not modelled	99.8	19	PDB header: translation Chain: A: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: the crystal structure of human eefsec in complex with gdpnp
66	c4n3nA	Alignment	not modelled	99.8	26	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
67	c5oxfB	Alignment	not modelled	99.8	21	PDB header: lipid binding protein Chain: B: PDB Molecule: gtp-binding protein; PDBTitle: an oligomerised bacterial dynamin pair provides a mechanism for the2 long range sensing and tethering of membranes
68	c2qptA	Alignment	not modelled	99.8	17	PDB header: endocytosis Chain: A: PDB Molecule: eh domain-containing protein-2; PDBTitle: crystal structure of an ehd atpase involved in membrane remodelling
69	c5izkB	Alignment	not modelled	99.8	23	PDB header: translation Chain: B: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: the crystal structure of human eefsec in complex with gdp
70	c2bvnB	Alignment	not modelled	99.8	21	PDB header: elongation factor Chain: B: PDB Molecule: elongation factor tu; PDBTitle: e. coli ef-tu:gdpnp in complex with the antibiotic enacyloxin iia
71	c3geiB	Alignment	not modelled	99.8	27	PDB header: hydrolase Chain: B: PDB Molecule: trna modification gtpase mnme; PDBTitle: crystal structure of mnme from chlorobium tepidum in complex2 with gcp
72	c4wnrA	Alignment	not modelled	99.8	21	PDB header: signaling protein Chain: A: PDB Molecule: leucine-rich-repeat protein; PDBTitle: structure of methanosarcina barkeri roco2 roccordc bound to gdp
73	c2wsmB	Alignment	not modelled	99.8	18	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
74	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
75	c2xtpA	Alignment	not modelled	99.8	17	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
76	d1udxa2	Alignment	not modelled	99.8	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
77	d1wxqa1	Alignment	not modelled	99.8	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
78	c5ymxB	Alignment	not modelled	99.8	20	PDB header: signaling protein, hydrolase Chain: B: PDB Molecule: mutual gliding-motility protein mgla; PDBTitle: myxococcus xanthus mgla in gdp bound conformation

79	c3agiC	Alignment	not modelled	99.8	21	PDB header: translation/hydrolase Chain: C: PDB Molecule: elongation factor 1-alpha; PDBTitle: crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
80	c4aurA	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: leoa; PDBTitle: leoa bacterial dynamin gtpase from etec
81	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
82	c3pqcA	Alignment	not modelled	99.8	22	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
83	c1d2eA	Alignment	not modelled	99.8	18	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
84	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
85	c2wjJB	Alignment	not modelled	99.8	25	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
86	c3lxwA	Alignment	not modelled	99.8	21	PDB header: immune system Chain: A: PDB Molecule: gtpase imap family member 1; PDBTitle: crystal structure of human gtpase imap family member 1
87	c3lxA	Alignment	not modelled	99.8	19	PDB header: immune system Chain: A: PDB Molecule: gtpase imap family member 4; PDBTitle: crystal structure of human gtpase imap family member 4
88	c4byxV	Alignment	not modelled	99.8	27	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
89	d1f60a3	Alignment	not modelled	99.8	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
90	d1wf3a1	Alignment	not modelled	99.8	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
91	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
92	d1kk1a3	Alignment	not modelled	99.8	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
93	c4zciA	Alignment	not modelled	99.8	22	PDB header: gtp-binding protein Chain: A: PDB Molecule: gtp-binding protein typa/bipa; PDBTitle: crystal structure of escherichia coli gtpase bipa/typa
94	d1jala1	Alignment	not modelled	99.8	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
95	c3r7wC	Alignment	not modelled	99.8	15	PDB header: protein transport Chain: C: PDB Molecule: gtp-binding protein gtr1; PDBTitle: crystal structure of gtr1p-gtr2p complex
96	c5kszA	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: A: PDB Molecule: mitochondrial rho gtpase 1; PDBTitle: hmiro ef hand and cgtpase domains in the gmppcp-bound state
97	c3wyaA	Alignment	not modelled	99.8	20	PDB header: translation Chain: A: PDB Molecule: elongation factor 1-alpha; PDBTitle: crystal structure of gdp-bound ef1alpha from pyrococcus horikoshii
98	d1zunb3	Alignment	not modelled	99.8	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
99	c6cesA	Alignment	not modelled	99.8	13	PDB header: signaling protein Chain: A: PDB Molecule: ras-related gtp-binding protein a; PDBTitle: cryo-em structure of gator1-rag
100	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
101	d1egaa1	Alignment	not modelled	99.8	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
102	c2j69D	Alignment	not modelled	99.8	25	PDB header: hydrolase Chain: D: PDB Molecule: bacterial dynamin-like protein; PDBTitle: bacterial dynamin-like protein bdlp
103	d1yrba1	Alignment	not modelled	99.8	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
104	c2elfA	Alignment	not modelled	99.8	22	PDB header: translation Chain: A: PDB Molecule: protein translation elongation factor 1a; PDBTitle: crystal structure of the selb-like elongation factor ef-pyl from2 methanosarcina mazei PDB header: hydrolase, metal binding protein

105	c2hf9A_	Alignment	not modelled	99.8	18	Chain: A: PDB Molecule: probable hydrogenase nickel incorporation PDBTitle: crystal structure of hybp from methanocaldococcus2 jannaschii in the triphosphate form
106	c2gedB_	Alignment	not modelled	99.8	24	PDB header: protein transport, signaling protein Chain: B: PDB Molecule: signal recognition particle receptor beta subunit; PDBTitle: signal recognition particle receptor beta-subunit in nucleotide-free2 dimerized form
107	c3a1wA_	Alignment	not modelled	99.8	24	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
108	c3lvrE_	Alignment	not modelled	99.8	22	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
109	c4byrP_	Alignment	not modelled	99.8	24	PDB header: ribosome Chain: P: PDB Molecule: eukaryotic translation initiation factor 5b; PDBTitle: cryo-em reconstruction of the 80s-eif5b-met-itnmet2 eukaryotic translation initiation complex
110	d2gj8a1	Alignment	not modelled	99.8	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
111	c2dy1A_	Alignment	not modelled	99.8	28	PDB header: signaling protein, translation Chain: A: PDB Molecule: elongation factor g; PDBTitle: crystal structure of ef-g-2 from thermus thermophilus
112	d2cxa1	Alignment	not modelled	99.8	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
113	d1d2ea3	Alignment	not modelled	99.8	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
114	c5mvfA_	Alignment	not modelled	99.8	16	PDB header: endocytosis Chain: A: PDB Molecule: eh domain-containing protein 4; PDBTitle: active structure of ehd4 complexed with adp
115	c3o47A_	Alignment	not modelled	99.8	21	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
116	c1mj1A_	Alignment	not modelled	99.8	21	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
117	d1puia_	Alignment	not modelled	99.8	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
118	d2c78a3	Alignment	not modelled	99.8	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
119	c3zjcC_	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: C: PDB Molecule: gtpase imap family member 7; PDBTitle: crystal structure of gmppnp-bound human gimap7 I100q variant
120	c2h5eB_	Alignment	not modelled	99.8	27	PDB header: translation Chain: B: PDB Molecule: peptide chain release factor rf-3; PDBTitle: crystal structure of e.coli polypeptide release factor rf3