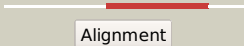



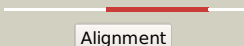







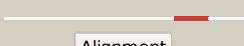











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2748c_(ftsK)_3059865_3062516
Date	Wed Aug 7 12:50:40 BST 2019
Unique Job ID	f4f597a388e3bdff

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2iuuE_	 Alignment		100.0	50	PDB header: membrane protein Chain: E; PDB Molecule: dna translocase ftsk; PDBTitle: p. aeruginosa ftsk motor domain, hexamer
2	c2iutA_	 Alignment		100.0	50	PDB header: membrane protein Chain: A; PDB Molecule: dna translocase ftsk; PDBTitle: p. aeruginosa ftsk motor domain, dimeric
3	c2iusB_	 Alignment		100.0	51	PDB header: membrane protein Chain: B; PDB Molecule: dna translocase ftsk; PDBTitle: e. coli ftsk motor domain
4	c4nh0A_	 Alignment		100.0	28	PDB header: cell cycle Chain: A; PDB Molecule: cell divisionftsK/spoiiiE; PDBTitle: cytoplasmic domain of the thermomonospora curvata type vii secretion2 atpase eccc
5	c4lyaA_	 Alignment		100.0	16	PDB header: cell cycle Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: escC (atpases 2 and 3) from geobacillus thermodenitrificans (semet)
6	c4n1aE_	 Alignment		100.0	22	PDB header: protein binding/protein binding Chain: E; PDB Molecule: cell divisionftsK/spoiiiE; PDBTitle: thermomonospora curvata eccc (atpases 2 and 3) in complex with a2 signal sequence peptide
7	d2j5pa1	 Alignment		99.9	34	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: FtsK C-terminal domain-like
8	d2ve8a1	 Alignment		99.9	35	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: FtsK C-terminal domain-like
9	c4kfuC_	 Alignment		99.9	19	PDB header: hydrolase Chain: C; PDB Molecule: genome packaging ntpase b204; PDBTitle: structure of the genome packaging ntpase b204 from sulfobolus turreted2 icosahedral virus 2 in complex with amppcp
10	c4d2iB_	 Alignment		99.8	17	PDB header: hydrolase Chain: B; PDB Molecule: hera; PDBTitle: crystal structure of the hera hexameric dna translocase2 from sulfobolus solfataricus bound to amp-ppp
11	c4ag5A_	 Alignment		99.8	20	PDB header: hydrolase Chain: A; PDB Molecule: type iv secretory pathway virb4 components-like protein; PDBTitle: structure of virb4 of thermoanaerobacter pseudethanolicus

12	c5dcfA_	Alignment		99.7	32	PDB header: recombination Chain: A: PDB Molecule: tyrosine recombinase xerd,dna translocase ftsk; PDBTitle: c-terminal domain of xerd recombinase in complex with gamma domain of2 ftsk
13	d1e9ra_	Alignment		99.3	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
14	c4ag5D_	Alignment		99.1	15	PDB header: hydrolase Chain: D: PDB Molecule: type iv secretory pathway virb4 components-like protein; PDBTitle: structure of virb4 of thermoanaerobacter pseudethanolicus
15	c2ztsB_	Alignment		97.5	13	PDB header: atp-binding protein Chain: B: PDB Molecule: putative uncharacterized protein ph0186; PDBTitle: crystal structure of kaic-like protein ph0186 from hyperthermophilic2 archaea pyrococcus horikoshii ot3
16	c6gefB_	Alignment		97.4	26	PDB header: hydrolase Chain: B: PDB Molecule: type iv secretion system protein dotb; PDBTitle: x-ray structure of the yersinia pseudotuberculosis atpase dotb
17	c4xgcD_	Alignment		97.2	24	PDB header: dna binding protein Chain: D: PDB Molecule: origin recognition complex subunit 4; PDBTitle: crystal structure of the eukaryotic origin recognition complex
18	d1p9ra_	Alignment		97.2	37	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
19	c5f4hF_	Alignment		97.2	23	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
20	c1q57G_	Alignment		97.2	14	PDB header: transferase Chain: G: PDB Molecule: dna primase/helicase; PDBTitle: the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
21	c4ydsA_	Alignment	not modelled	97.1	16	PDB header: hydrolase Chain: A: PDB Molecule: flagella-related protein h; PDBTitle: flah from sulfolobus acidocaldarius with atp and mg-ion
22	c4phtC_	Alignment	not modelled	97.1	38	PDB header: protein transport Chain: C: PDB Molecule: general secretory pathway protein e; PDBTitle: atpase gspe in complex with the cytoplasmic domain of gspl from the2 vibrio vulnificus type ii secretion system
23	c2vyeA_	Alignment	not modelled	97.1	13	PDB header: hydrolase/dna Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of the dnac-ssdna complex
24	c4nmnA_	Alignment	not modelled	97.1	18	PDB header: replication Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: aquifex aeolicus replicative helicase (dnab) complexed with adp, at2 3.3 resolution
25	c3jvvA_	Alignment	not modelled	97.1	27	PDB header: atp binding protein Chain: A: PDB Molecule: twitching mobility protein; PDBTitle: crystal structure of p. aeruginosa pilt with bound amp-ppc
26	c5l3rC_	Alignment	not modelled	97.0	20	PDB header: protein transport Chain: C: PDB Molecule: signal recognition particle 54 kda protein, chloroplastic; PDBTitle: structure of the gtpase heterodimer of chloroplast srp54 and ftsy from2 arabidopsis thaliana
27	c6gebK_	Alignment	not modelled	97.0	27	PDB header: hydrolase Chain: K: PDB Molecule: dotb; PDBTitle: x-ray structure of the legionella pneumophila atpase dotb
28	c2j7pA_	Alignment	not modelled	97.0	13	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
29	c5udhD_	Alignment	not modelled	96.9	14	PDB header: replication Chain: D: PDB Molecule: origin recognition complex subunit 4;

29	c3u0bD	Alignment	not modelled	96.9	14	PDBTitle: structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1 PDB header: circadian clock protein
30	c1u9iA	Alignment	not modelled	96.9	20	Chain: A: PDB Molecule: kaic; PDBTitle: crystal structure of circadian clock protein kaic with phosphorylation2 sites
31	c3bh0A	Alignment	not modelled	96.9	14	PDB header: replication Chain: A: PDB Molecule: dnab-like replicative helicase; PDBTitle: atpase domain of g40p
32	d1cr2a	Alignment	not modelled	96.9	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
33	c4a1fB	Alignment	not modelled	96.9	18	PDB header: hydrolase Chain: B: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of c-terminal domain of helicobacter2 pylori dnab helicase
34	c3bgwD	Alignment	not modelled	96.8	14	PDB header: replication Chain: D: PDB Molecule: dnab-like replicative helicase; PDBTitle: the structure of a dnab-like replicative helicase and its interactions2 with primase
35	c5tshF	Alignment	not modelled	96.8	31	PDB header: atp-binding protein Chain: F: PDB Molecule: type iv pilus biogenesis atpase pilb; PDBTitle: pilb from geobacter metallireducens bound to amp-pnp
36	c2w0mA	Alignment	not modelled	96.7	14	PDB header: unknown function Chain: A: PDB Molecule: sso2452; PDBTitle: crystal structure of sso2452 from sulfolobus solfataricus p2
37	c2q6tB	Alignment	not modelled	96.7	13	PDB header: hydrolase Chain: B: PDB Molecule: dnab replication fork helicase; PDBTitle: crystal structure of the thermus aquaticus dnab monomer
38	c2eyuA	Alignment	not modelled	96.7	31	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
39	c3ldaA	Alignment	not modelled	96.7	17	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: yeast rad51 h352y filament interface mutant
40	d2i1qa2	Alignment	not modelled	96.7	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
41	c4xgcE	Alignment	not modelled	96.6	18	PDB header: dna binding protein Chain: E: PDB Molecule: origin recognition complex subunit 5; PDBTitle: crystal structure of the eukaryotic origin recognition complex
42	d1tf7a1	Alignment	not modelled	96.6	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
43	c5zfQA	Alignment	not modelled	96.6	30	PDB header: transport protein Chain: A: PDB Molecule: twitching motility pilus retraction protein; PDBTitle: crystal structure of pilt-4, a retraction atpase motor of type iv2 pilus , from geobacter sulfurreducens
44	c5jwqA	Alignment	not modelled	96.6	17	PDB header: transcription regulator Chain: A: PDB Molecule: circadian clock protein kinase kaic; PDBTitle: crystal structure of kaic s431e in complex with foldswitch-stabilized2 kaib from thermosynechococcus elongatus
45	c1szpC	Alignment	not modelled	96.5	19	PDB header: dna binding protein Chain: C: PDB Molecule: dna repair protein rad51; PDBTitle: a crystal structure of the rad51 filament
46	c4zc0A	Alignment	not modelled	96.4	16	PDB header: hydrolase Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: structure of a dodecameric bacterial helicase
47	c5l3qB	Alignment	not modelled	96.4	22	PDB header: protein transport Chain: B: PDB Molecule: signal recognition particle receptor subunit alpha; PDBTitle: structure of the gtpase heterodimer of human srp54 and sralpha
48	c2qbyA	Alignment	not modelled	96.4	14	PDB header: replication/dna Chain: A: PDB Molecule: cell division control protein 6 homolog 1; PDBTitle: crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus)
49	c2r2aB	Alignment	not modelled	96.4	21	PDB header: toxin Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of n-terminal domain of zonular occludens toxin from2 neisseria meningitidis
50	d1w5sa2	Alignment	not modelled	96.3	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
51	c3dkpA	Alignment	not modelled	96.2	18	PDB header: hydrolase Chain: A: PDB Molecule: probable atp-dependent rna helicase ddx52; PDBTitle: human dead-box rna-helicase ddx52, conserved domain i in complex with2 adp
52	d1szpa2	Alignment	not modelled	96.2	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
53	c3dmdA	Alignment	not modelled	96.2	20	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
54	c2qy9A	Alignment	not modelled	96.2	19	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
						Fold: P-loop containing nucleoside triphosphate hydrolases

55	d1n0wa_	Alignment	not modelled	96.1	15	Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
56	c2df1A_	Alignment	not modelled	96.1	17	PDB header: recombination Chain: A: PDB Molecule: dna repair and recombination protein rada; PDBTitle: crystal structure of left-handed rada filament
57	d1ubea1	Alignment	not modelled	96.1	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
58	c2v1uA_	Alignment	not modelled	96.1	22	PDB header: replication Chain: A: PDB Molecule: cell division control protein 6 homolog; PDBTitle: structure of the aeropyrum pernix orc1 protein in complex2 with dna
59	c5f13A_	Alignment	not modelled	96.1	33	PDB header: transport protein Chain: A: PDB Molecule: pili retraction protein pilt; PDBTitle: pilt2 from thermus thermophilus
60	d1ewqa2	Alignment	not modelled	96.0	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
61	c2gzaB_	Alignment	not modelled	96.0	38	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
62	c6bbmA_	Alignment	not modelled	96.0	15	PDB header: replication Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: mechanisms of opening and closing of the bacterial replicative2 helicase: the dnab helicase and lambda p helicase loader complex
63	c4kssC_	Alignment	not modelled	95.9	44	PDB header: protein transport Chain: C: PDB Molecule: type ii secretion system protein e, hemolysin-coregulated PDBTitle: crystal structure of vibrio cholerae atpase gspse hexamer
64	c5l3sF_	Alignment	not modelled	95.9	18	PDB header: protein transport Chain: F: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: structure of the gtpase heterodimer of crenarchaeal srp54 and ftsy
65	c1in8A_	Alignment	not modelled	95.9	14	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: thermotoga maritima ruvb t158v
66	d1tf7a2	Alignment	not modelled	95.9	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
67	c3b85A_	Alignment	not modelled	95.8	19	PDB header: hydrolase Chain: A: PDB Molecule: phosphate starvation-inducible protein; PDBTitle: crystal structure of predicted phosphate starvation-induced atpase2 pho2 from corynebacterium glutamicum
68	c5udbE_	Alignment	not modelled	95.8	8	PDB header: replication Chain: E: PDB Molecule: origin recognition complex subunit 5; PDBTitle: structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
69	d1g6oa_	Alignment	not modelled	95.8	42	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
70	d1fnna2	Alignment	not modelled	95.7	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
71	c5irrB_	Alignment	not modelled	95.7	37	PDB header: hydrolase Chain: B: PDB Molecule: septin-like protein; PDBTitle: crystal structure of septin gtpase domain from chlamydomonas2 reinhardtii
72	c2recB_	Alignment	not modelled	95.6	21	PDB header: helicase PDB COMPND:
73	c3te6A_	Alignment	not modelled	95.6	6	PDB header: gene regulation Chain: A: PDB Molecule: regulatory protein sir3; PDBTitle: crystal structure of the s. cerevisiae sir3 aaa+ domain
74	c4ii7D_	Alignment	not modelled	95.6	35	PDB header: hydrolase Chain: D: PDB Molecule: flai atpase; PDBTitle: archaellum assembly atpase flai
75	d1qzxa3	Alignment	not modelled	95.4	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
76	c5it5B_	Alignment	not modelled	95.4	43	PDB header: transport protein Chain: B: PDB Molecule: atp binding motif-containing protein pilf; PDBTitle: thermus thermophilus pilb core atpase region
77	c2cvhB_	Alignment	not modelled	95.4	15	PDB header: dna binding protein Chain: B: PDB Molecule: dna repair and recombination protein radb; PDBTitle: crystal structure of the radb recombinase
78	c6qelB_	Alignment	not modelled	95.3	17	PDB header: replication Chain: B: PDB Molecule: replicative dna helicase; PDBTitle: e. coli dnabc apo complex
79	d1v5wa_	Alignment	not modelled	95.3	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
80	c5owvC_	Alignment	not modelled	95.3	40	PDB header: lipid binding protein Chain: C: PDB Molecule: gtp-binding protein; PDBTitle: an oligomerised bacterial dynamin pair provides a mechanism for the2 long-range sensing and tethering of membranes
81	c3ec2A_	Alignment	not modelled	95.3	18	PDB header: replication Chain: A: PDB Molecule: dna replication protein dnac; PDBTitle: crystal structure of the dnac helicase loader

82	c2dr3A_	Alignment	not modelled	95.3	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: supf0273 protein ph0284; PDBTitle: crystal structure of reca superfamily atpase ph0284 from pyrococcus2 horikoshii ot3
83	c5zr1A_	Alignment	not modelled	95.3	20	PDB header: dna binding protein/dna Chain: A: PDB Molecule: origin recognition complex subunit 1; PDBTitle: saccharomyces cerevisiae origin recognition complex bound to a 72-bp2 origin dna containing acs and b1 element
84	d1nlfA_	Alignment	not modelled	95.3	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
85	c3dm5A_	Alignment	not modelled	95.2	22	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 assembling the2 ribonucleic core of the signal recognition particle from the archaeon3 pyrococcus furiosus.
86	c2oaq1_	Alignment	not modelled	95.2	27	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
87	c5x06G_	Alignment	not modelled	95.1	12	PDB header: replication Chain: G: PDB Molecule: dnaa regulatory inactivator hda; PDBTitle: dna replication regulation protein
88	c2d3wB_	Alignment	not modelled	95.1	17	PDB header: biosynthetic protein Chain: B: PDB Molecule: probable atp-dependent transporter sufC; PDBTitle: crystal structure of escherichia coli sufC, an atpase2 compenent of the suf iron-sulfur cluster assembly machinery
89	c2yhsA_	Alignment	not modelled	95.1	19	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the e. coli srp receptor ftsy
90	d1xp8a1	Alignment	not modelled	95.0	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
91	c2gszE_	Alignment	not modelled	95.0	45	PDB header: protein transport Chain: E: PDB Molecule: twitching motility protein pilt; PDBTitle: structure of a. aeolicus pilt with 6 monomers per asymmetric unit
92	c1xx6B_	Alignment	not modelled	95.0	26	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.
93	c1fnnB_	Alignment	not modelled	95.0	16	PDB header: cell cycle Chain: B: PDB Molecule: cell division control protein 6; PDBTitle: crystal structure of cdc6p from pyrobaculum aerophilum
94	c1pznA_	Alignment	not modelled	95.0	16	PDB header: recombination Chain: A: PDB Molecule: dna repair and recombination protein rad51; PDBTitle: rad51 (rada)
95	c2qagB_	Alignment	not modelled	94.9	37	PDB header: cell cycle, structural protein Chain: B: PDB Molecule: septin-6; PDBTitle: crystal structure of human septin trimer 2/6/7
96	d1vmaa2	Alignment	not modelled	94.9	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
97	c1ymfA_	Alignment	not modelled	94.8	24	PDB header: hydrolase Chain: A: PDB Molecule: genome polyprotein [contains: flavivirin protease ns3 PDBTitle: crystal structure of yellow fever virus ns3 helicase complexed with2 adp
98	c2cnwF_	Alignment	not modelled	94.8	23	PDB header: signal recognition Chain: F: PDB Molecule: cell division protein ftsy; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsy
99	d1u94a1	Alignment	not modelled	94.8	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
100	c5wsge_	Alignment	not modelled	94.8	13	PDB header: rna binding protein/rna Chain: E: PDB Molecule: saccharomyces cerevisiae s288c snr6 snrna; PDBTitle: cryo-em structure of the catalytic step ii spliceosome (c* complex) at2 4.0 angstrom resolution
101	c5ujmE_	Alignment	not modelled	94.7	21	PDB header: replication Chain: E: PDB Molecule: origin recognition complex subunit 5; PDBTitle: structure of the active form of human origin recognition complex and2 its atpase motor module
102	c1vmaA_	Alignment	not modelled	94.7	21	PDB header: protein transport 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
103	d1wb9a2	Alignment	not modelled	94.7	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
104	c2qbyB_	Alignment	not modelled	94.7	15	PDB header: replication/dna Chain: B: PDB Molecule: cell division control protein 6 homolog 3; PDBTitle: crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus)
105	c5mvfA_	Alignment	not modelled	94.7	27	PDB header: endocytosis Chain: A: PDB Molecule: eh domain-containing protein 4; PDBTitle: active structure of ehd4 complexed with adp
106	c6epcj_	Alignment	not modelled	94.7	18	PDB header: hydrolase Chain: J: PDB Molecule: 26s proteasome regulatory subunit 8; PDBTitle: ground state 26s proteasome (gs2)
107	c3t5dC_	Alignment	not modelled	94.7	47	PDB header: signaling protein Chain: C: PDB Molecule: septin-7; PDBTitle: crystal structure of septin 7 in complex with gdp

108	c3sopB	Alignment	not modelled	94.5	40	PDB header: hydrolase Chain: B: PDB Molecule: neuronal-specific septin-3; PDBTitle: crystal structure of human septin 3 gtpase domain
109	c3zjcC	Alignment	not modelled	94.5	47	PDB header: hydrolase Chain: C: PDB Molecule: gtpase imap family member 7; PDBTitle: crystal structure of gmpnp-bound human gimap7 I100q variant
110	d1h65a	Alignment	not modelled	94.5	55	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
111	d1jwyb	Alignment	not modelled	94.4	39	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
112	c6djqa	Alignment	not modelled	94.4	41	PDB header: hydrolase Chain: A: PDB Molecule: vps1 gtpase-bse; PDBTitle: vps1 gtpase-bse fusion complexed with gdp.alf4-
113	c5xdrA	Alignment	not modelled	94.4	21	PDB header: hydrolase Chain: A: PDB Molecule: pre-mrna-splicing factor atp-dependent rna helicase dhx15; PDBTitle: crystal structure of human deah-box rna helicase dhx15 in complex with2 adp
114	c4bejB	Alignment	not modelled	94.3	25	PDB header: hydrolase Chain: B: PDB Molecule: dynamin 1-like protein; PDBTitle: nucleotide-free dynamin 1-like protein (dnm1l, drp1, dlp1)
115	c3nxsA	Alignment	not modelled	94.3	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
116	c1sxB	Alignment	not modelled	94.3	20	PDB header: replication Chain: B: PDB Molecule: activator 1 37 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
117	c4yqfA	Alignment	not modelled	94.3	37	PDB header: hydrolase Chain: A: PDB Molecule: septin-9; PDBTitle: gtpase domain of human septin 9
118	c3ftqA	Alignment	not modelled	94.2	50	PDB header: cell cycle Chain: A: PDB Molecule: septin-2; PDBTitle: crystal structure of septin 2 in complex with gppnhp and2 mg2+
119	c2j3eA	Alignment	not modelled	94.2	55	PDB header: protein transport Chain: A: PDB Molecule: t7i23.11 protein; PDBTitle: dimerization is important for the gtpase activity of2 chloroplast translocon components attoc33 and pstoc159
120	c2qa5A	Alignment	not modelled	94.2	45	PDB header: cell cycle, structural protein Chain: A: PDB Molecule: septin-2; PDBTitle: crystal structure of sept2 g-domain