Phyre^2

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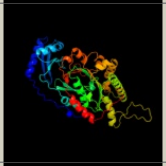
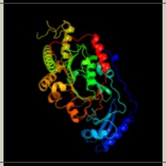
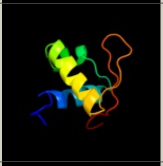
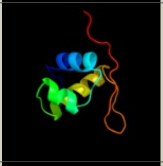
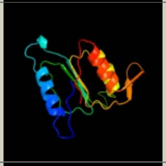
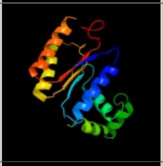
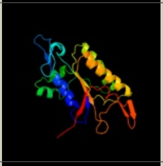
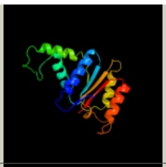
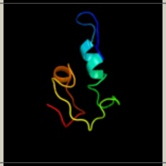
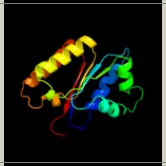
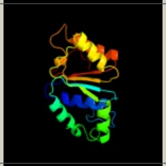
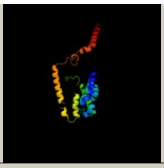
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2iuuE_	Alignment		100.0	64	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**dna translocase ftsk; **PDBTitle:** p. aeruginosa ftsk motor domain, hexamer
2	c2iutA_	Alignment		100.0	64	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**dna translocase ftsk; **PDBTitle:** p. aeruginosa ftsk motor domain, dimeric
3	c2iusB_	Alignment		100.0	99	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**dna translocase ftsk; **PDBTitle:** e. coli ftsk motor domain
4	d2j5pa1	Alignment		99.9	100	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**FtsK C-terminal domain-like
5	d2ve8a1	Alignment		99.9	62	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**FtsK C-terminal domain-like
6	d1e9ra_	Alignment		98.8	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
7	c3jvvA_	Alignment		97.2	33	**PDB header:**atp binding protein **Chain:** A: **PDB Molecule:**twitching mobility protein; **PDBTitle:** crystal structure of p. aeruginosa pilt with bound amp-pcp
8	c1q57G_	Alignment		97.0	16	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna primase/helicase; **PDBTitle:** the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
9	d2i1qa2	Alignment		97.0	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
10	c2vyeA_	Alignment		96.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**replicative dna helicase; **PDBTitle:** crystal structure of the dnac-ssdna complex
11	c2ztsB_	Alignment		96.6	18	**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

12	c3bh0A_	Alignment		96.5	16	**PDB header:**replication **Chain:** A: **PDB Molecule:**dnab-like replicative helicase; **PDBTitle:** atpase domain of g40p
13	c2gzaB_	Alignment		96.4	39	**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
14	c1u9iA_	Alignment		96.3	23	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**kaic; **PDBTitle:** crystal structure of circadian clock protein kaic with phosphorylation2 sites
15	d1cr2a_	Alignment		96.3	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
16	d1tf7a2	Alignment		96.2	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
17	c3bgwD_	Alignment		96.1	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
18	c1szpC_	Alignment		96.1	14	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** a crystal structure of the rad51 filament
19	d1nlfa_	Alignment		96.0	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
20	c3ldaA_	Alignment		96.0	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** yeast rad51 h352y filament interface mutant
21	c3te6A_	Alignment	not modelled	95.9	11	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**regulatory protein sir3; **PDBTitle:** crystal structure of the s. cerevisiae sir3 aaa+ domain
22	d1p9ra_	Alignment	not modelled	95.9	38	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
23	d1n0wa_	Alignment	not modelled	95.9	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
24	d1v5wa_	Alignment	not modelled	95.8	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
25	c2v1uA_	Alignment	not modelled	95.8	15	**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
26	c2w0mA_	Alignment	not modelled	95.7	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**sso2452; **PDBTitle:** crystal structure of sso2452 from sulfolobus solfataricus2 p2
27	c2r2aB_	Alignment	not modelled	95.6	24	**PDB header:**toxin **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of n-terminal domain of zonular occludens toxin from2 neisseria meningitidis

28	c3b9yA_	Alignment		95.5	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter family rh-like protein; **PDBTitle:** crystal structure of the nitrosomonas europaea rh protein
29	c2cvhB_	Alignment	not modelled	95.3	14	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna repair and recombination protein radb; **PDBTitle:** crystal structure of the radb recombinase
30	c2q6tB_	Alignment	not modelled	95.3	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dnab replication fork helicase; **PDBTitle:** crystal structure of the thermus aquaticus dnab monomer
31	c2p6uA_	Alignment	not modelled	95.3	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**afuhel308 helicase; **PDBTitle:** apo structure of the hel308 superfamily 2 helicase
32	d1g6oa_	Alignment	not modelled	95.3	35	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
33	d1tf7a1	Alignment	not modelled	95.2	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
34	c1iqpF_	Alignment	not modelled	95.1	24	**PDB header:**replication **Chain:** F: **PDB Molecule:**rfcs; **PDBTitle:** crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
35	c2v6jA_	Alignment	not modelled	94.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna helicase; **PDBTitle:** kokobera virus helicase: mutant met47thr
36	c2zmeB_	Alignment	not modelled	94.9	17	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**vacuolar protein-sorting-associated protein 36; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
37	c1xx6B_	Alignment	not modelled	94.8	24	**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.
38	c2dr3A_	Alignment	not modelled	94.7	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0273 protein ph0284; **PDBTitle:** crystal structure of reca superfamily atpase ph0284 from pyrococcus2 horikoshii ot3
39	c3h1tA_	Alignment	not modelled	94.6	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**type i site-specific restriction-modification **PDBTitle:** the fragment structure of a putative hsdr subunit of a type2 i restriction enzyme from vibrio vulnificus yj016
40	c2oaq1_	Alignment	not modelled	94.5	34	**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
41	d1gkub1	Alignment	not modelled	94.3	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Helicase-like "domain" of reverse gyrase
42	c1t4gA_	Alignment	not modelled	94.2	12	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna repair and recombination protein rada; **PDBTitle:** atpase in complex with amp-pnp
43	d1szpa2	Alignment	not modelled	94.2	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
44	c2dflA_	Alignment	not modelled	94.1	15	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna repair and recombination protein rada; **PDBTitle:** crystal structure of left-handed rada filament
45	c1cu1B_	Alignment	not modelled	94.1	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein (protease/helicase ns3); **PDBTitle:** crystal structure of an enzyme complex from hepatitis c2 virus
46	c2d3wB_	Alignment	not modelled	94.0	21	**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
47	c3pvsA_	Alignment	not modelled	94.0	22	**PDB header:**recombination **Chain:** A: **PDB Molecule:**replication-associated recombination protein a; **PDBTitle:** structure and biochemical activities of escherichia coli mgsa
48	d1a1va1	Alignment	not modelled	93.9	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
49	c2gszE_	Alignment	not modelled	93.8	37	**PDB header:**protein transport **Chain:** E: **PDB Molecule:**twitching motility protein pilt; **PDBTitle:** structure of a. aeolicus pilt with 6 monomers per2 asymmetric unit
50	d1z3ix2	Alignment	not modelled	93.5	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
51	c2j7pA_	Alignment	not modelled	93.5	22	**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
						Fold:P-loop containing nucleoside triphosphate hydrolases

52	d1u94a1	Alignment	not modelled	93.3	25	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
53	c2eyuA_	Alignment	not modelled	93.2	33	**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
54	c1pznG_	Alignment	not modelled	93.2	16	**PDB header:**recombination **Chain:** G: **PDB Molecule:**dna repair and recombination protein rad51; **PDBTitle:** rad51 (rada)
55	d1w5sa2	Alignment	not modelled	93.2	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
56	c2zmeA_	Alignment	not modelled	93.1	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar-sorting protein snf8; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
57	c3llmB_	Alignment	not modelled	93.1	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp-dependent rna helicase a; **PDBTitle:** crystal structure analysis of a rna helicase
58	d3b60a1	Alignment	not modelled	93.0	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
59	d1jj7a_	Alignment	not modelled	92.9	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
60	d1l7vc_	Alignment	not modelled	92.8	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
61	d1pzna2	Alignment	not modelled	92.5	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
62	d1rifa_	Alignment	not modelled	92.4	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**DNA helicase UvsW
63	c3u5zM_	Alignment	not modelled	92.4	17	**PDB header:**dna binding protein/dna **Chain:** M: **PDB Molecule:**dna polymerase accessory protein 44; **PDBTitle:** structure of t4 bacteriophage clamp loader bound to the t4 clamp,2 primer-template dna, and atp analog
64	c3dkpA_	Alignment	not modelled	92.3	32	**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
65	c2ce7B_	Alignment	not modelled	92.3	25	**PDB header:**cell division protein **Chain:** B: **PDB Molecule:**cell division protein ftsh; **PDBTitle:** edta treated
66	d1qvra2	Alignment	not modelled	92.3	28	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
67	c1a1vA_	Alignment	not modelled	92.2	17	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**protein (ns3 protein); **PDBTitle:** hepatitis c virus ns3 helicase domain complexed with single2 stranded sdna
68	c3cuqA_	Alignment	not modelled	92.2	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar-sorting protein snf8; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
69	c2qagB_	Alignment	not modelled	92.0	37	**PDB header:**cell cycle, structural protein **Chain:** B: **PDB Molecule:**septin-6; **PDBTitle:** crystal structure of human septin trimer 2/6/7
70	c1w7pD_	Alignment	not modelled	91.9	8	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**vps36p, ylr417w; **PDBTitle:** the crystal structure of endosomal complex escrt-ii2 (vps22/vps25/vps36)
71	d1l8qa2	Alignment	not modelled	91.9	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
72	c2dhrC_	Alignment	not modelled	91.7	22	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ftsh; **PDBTitle:** whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
73	d1gm5a3	Alignment	not modelled	91.6	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
74	c3t5dC_	Alignment	not modelled	91.6	42	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**septin-7; **PDBTitle:** crystal structure of septin 7 in complex with gdp
75	d1ubea1	Alignment	not modelled	91.5	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
76	c2qa5A_	Alignment	not modelled	91.4	40	**PDB header:**cell cycle, structural protein **Chain:** A: **PDB Molecule:**septin-2; **PDBTitle:** crystal structure of sept2 g-domain
77	c1yqtA_	Alignment	not modelled	91.2	17	**PDB header:**hydrolyase/translation **Chain:** A: **PDB Molecule:**rnase l inhibitor; **PDBTitle:** rnase-l inhibitor
						Fold:P-loop containing nucleoside triphosphate hydrolases

78	d1uaaa1	Alignment	not modelled	91.2	23	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
79	d2onka1	Alignment	not modelled	91.2	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
80	c3ftqA_	Alignment	not modelled	91.0	44	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**septin-2; **PDBTitle:** crystal structure of septin 2 in complex with gppnhp and2 mg2+
81	d1h65a_	Alignment	not modelled	91.0	50	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
82	c2recB_	Alignment	not modelled	91.0	22	**PDB header:**helicase **PDB COMPND:**
83	c3d3qB_	Alignment	not modelled	90.9	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate **PDBTitle:** crystal structure of trna delta(2)-isopentenylpyrophosphate2 transferase (se0981) from staphylococcus epidermidis.3 northeast structural genomics consortium target ser100
84	d1jwyb_	Alignment	not modelled	90.7	33	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
85	c2yyzA_	Alignment	not modelled	90.7	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sugar abc transporter, atp-binding protein; **PDBTitle:** crystal structure of sugar abc transporter, atp-binding protein
86	c2j3eA_	Alignment	not modelled	90.6	50	**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
87	c1xp8A_	Alignment	not modelled	90.6	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**reca protein; **PDBTitle:** "deinococcus radiodurans reca in complex with atp-gamma-s"
88	c3gfoA_	Alignment	not modelled	90.5	17	**PDB header:**atp binding protein **Chain:** A: **PDB Molecule:**cobalt import atp-binding protein cbio 1; **PDBTitle:** structure of cbio1 from clostridium perfringens: part of2 the abc transporter complex cbionq.
89	c3tbkA_	Alignment	not modelled	90.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rig-i helicase domain; **PDBTitle:** mouse rig-i atpase domain
90	c2cbzA_	Alignment	not modelled	90.5	18	**PDB header:**transport **Chain:** A: **PDB Molecule:**multidrug resistance-associated protein 1; **PDBTitle:** structure of the human multidrug resistance protein 12 nucleotide binding domain 1
91	c3kx2A_	Alignment	not modelled	90.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pre-mrna-splicing factor atp-dependent rna **PDBTitle:** crystal structure of prp43p in complex with adp
92	d1tq4a_	Alignment	not modelled	90.3	45	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
93	d1xp8a1	Alignment	not modelled	90.2	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
94	c2qagA_	Alignment	not modelled	90.1	42	**PDB header:**cell cycle, structural protein **Chain:** A: **PDB Molecule:**septin-2; **PDBTitle:** crystal structure of human septin trimer 2/6/7
95	c3g5uB_	Alignment	not modelled	89.9	20	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**multidrug resistance protein 1a; **PDBTitle:** structure of p-glycoprotein reveals a molecular basis for2 poly-specific drug binding
96	c3p1jC_	Alignment	not modelled	89.7	35	**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
97	c2ocaA_	Alignment	not modelled	89.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent dna helicase uvsw; **PDBTitle:** the crystal structure of t4 uvsw
98	c3b9pA_	Alignment	not modelled	89.5	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cg5977-pa, isoform a; **PDBTitle:** spastin
99	d1okkd2	Alignment	not modelled	89.4	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
100	c1c4oA_	Alignment	not modelled	89.4	25	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna nucleotide excision repair enzyme uvrb; **PDBTitle:** crystal structure of the dna nucleotide excision repair enzyme uvrb2 from thermus thermophilus
101	d1sxjb2	Alignment	not modelled	89.4	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
102	c1sxjD_	Alignment	not modelled	89.3	31	**PDB header:**replication **Chain:** D: **PDB Molecule:**activator 1 41 kda subunit; **PDBTitle:** crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3

						(proliferating cell nuclear antigen, pcna)
103	c2x2fD_	Alignment	not modelled	89.3	29	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**dynamin-1; **PDBTitle:** dynamin 1 gtpase dimer, short axis form
104	c2j69D_	Alignment	not modelled	89.3	48	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**bacterial dynamin-like protein; **PDBTitle:** bacterial dynamin-like protein bdlp
105	c3lxwA_	Alignment	not modelled	89.1	42	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gtpase imap family member 1; **PDBTitle:** crystal structure of human gtpase imap family member 1
106	c1fnnB_	Alignment	not modelled	89.1	14	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cell division control protein 6; **PDBTitle:** crystal structure of cdc6p from pyrobaculum aerophilum
107	c1wp9D_	Alignment	not modelled	89.0	24	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**atp-dependent rna helicase, putative; **PDBTitle:** crystal structure of pyrococcus furiosus hef helicase domain
108	d1b0ua_	Alignment	not modelled	89.0	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
109	c2d2fA_	Alignment	not modelled	89.0	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**sufc protein; **PDBTitle:** crystal structure of atypical cytoplasmic abc-atpase sufc from thermus2 thermophilus hb8
110	c3dmdA_	Alignment	not modelled	88.9	15	**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
111	d1mo6a1	Alignment	not modelled	88.9	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
112	c2w74B_	Alignment	not modelled	88.8	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**type i restriction enzyme ecor124ii r protein; **PDBTitle:** mutant (k220r) of the hsdr subunit of the ecor124i2 restriction enzyme in complex with atp
113	c2xtpA_	Alignment	not modelled	88.7	37	**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
114	c1sxjB_	Alignment	not modelled	88.7	29	**PDB header:**replication **Chain:** B: **PDB Molecule:**activator 1 37 kda subunit; **PDBTitle:** crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
115	c2qagC_	Alignment	not modelled	88.6	42	**PDB header:**cell cycle, structural protein **Chain:** C: **PDB Molecule:**septin-7; **PDBTitle:** crystal structure of human septin trimer 2/6/7
116	d1w36b1	Alignment	not modelled	88.5	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
117	d1sq5a_	Alignment	not modelled	88.5	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
118	c3i5yA_	Alignment	not modelled	88.4	21	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**atp-dependent rna helicase mss116; **PDBTitle:** structure of mss116p bound to ssrna containing a single 5-bru and amp-2 pnp
119	c3qmzA_	Alignment	not modelled	88.4	26	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**cytoplasmic dynein heavy chain; **PDBTitle:** crystal structure of the cytoplasmic dynein heavy chain motor domain
120	d1sxjd2	Alignment	not modelled	88.2	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain