Phyre^2

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Description	P09980
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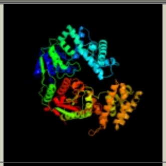
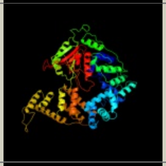
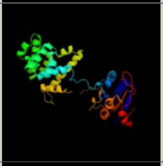
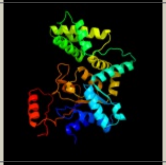
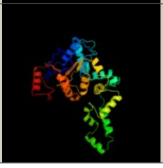
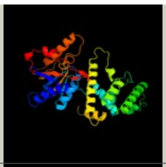
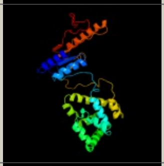
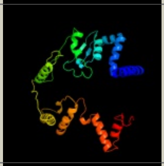
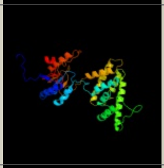
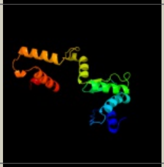
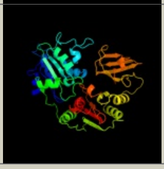
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1uaaB_	Alignment		100.0	100	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**protein (atp-dependent dna helicase rep.); **PDBTitle:** e. coli rep helicase/dna complex
2	c2is6B_	Alignment		100.0	37	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**dna helicase ii; **PDBTitle:** crystal structure of uvrd-dna-adpmgf3 ternary complex
3	c1w36E_	Alignment		100.0	20	**PDB header:**recombination **Chain:** E: **PDB Molecule:**exodeoxyribonuclease v beta chain; **PDBTitle:** recbcd:dna complex
4	c1pjrA_	Alignment		100.0	42	**PDB header:**helicase **Chain:** A: **PDB Molecule:**pcra; **PDBTitle:** structure of dna helicase
5	c3lfuA_	Alignment		100.0	37	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna helicase ii; **PDBTitle:** crystal structure of e. coli uvrd
6	c2pjrF_	Alignment		100.0	40	**PDB header:**hydrolase/dna **Chain:** F: **PDB Molecule:**protein (helicase pcra); **PDBTitle:** helicase product complex
7	c1w36F_	Alignment		100.0	15	**PDB header:**recombination **Chain:** F: **PDB Molecule:**exodeoxyribonuclease v gamma chain; **PDBTitle:** recbcd:dna complex
8	d1uaaa2	Alignment		100.0	98	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
9	d1uaaa1	Alignment		100.0	100	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
10	d1pjra1	Alignment		100.0	45	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
11	d1w36b1	Alignment		100.0	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain

12	d1pjra2	Alignment		100.0	39	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
13	d1w36b2	Alignment		100.0	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
14	c2wjyA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of nonsense transcripts 1; **PDBTitle:** crystal structure of the complex between human nonsense2 mediated decay factors upf1 and upf2 orthorhombic form
15	c2xzlA_	Alignment		100.0	20	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**atp-dependent helicase nam7; **PDBTitle:** upf1-rna complex
16	c1qhhB_	Alignment		100.0	46	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein (pcra (subunit)); **PDBTitle:** structure of dna helicase with adpnp
17	d1w36c2	Alignment		100.0	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
18	c2gk7A_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of nonsense transcripts 1; **PDBTitle:** structural and functional insights into the human upf1 helicase core
19	c1qhhA_	Alignment		100.0	45	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (pcra (subunit)); **PDBTitle:** structure of dna helicase with adpnp
20	c3e1sA_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exodeoxyribonuclease v, subunit recd; **PDBTitle:** structure of an n-terminal truncation of deinococcus radiodurans recd2
21	c1w36G_	Alignment	not modelled	100.0	24	**PDB header:**recombination **Chain:** G: **PDB Molecule:**exodeoxyribonuclease v alpha chain; **PDBTitle:** recbcd:dna complex
22	c2pjrB_	Alignment	not modelled	99.9	56	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**protein (helicase pcra); **PDBTitle:** helicase product complex
23	c1qhhD_	Alignment	not modelled	99.9	54	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**protein (pcra (subunit)); **PDBTitle:** structure of dna helicase with adpnp
24	c3dmnA_	Alignment	not modelled	99.9	35	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative dna helicase; **PDBTitle:** the crystal structure of the c-terminal domain of a possilbe dna2 helicase from lactobacillus plantarun wcfs1
25	d1w36d1	Alignment	not modelled	99.7	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
26	d1w36d2	Alignment	not modelled	99.6	32	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
27	c3b85A_	Alignment	not modelled	99.6	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphate starvation-inducible protein; **PDBTitle:** crystal structure of predicted phosphate starvation-induced atpase2 phoh2 from corynebacterium glutamicum
28	c3i5yA_	Alignment	not modelled	98.7	20	**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
						PDB header:hydrolase

29	c2va8A_	Alignment	not modelled	98.6	25	**Chain:** A: **PDB Molecule:**ski2-type helicase; **PDBTitle:** dna repair helicase hel308
30	d1gkub1	Alignment	not modelled	98.6	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Helicase-like "domain" of reverse gyrase
31	c3tbkA_	Alignment	not modelled	98.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rig-i helicase domain; **PDBTitle:** mouse rig-i atpase domain
32	c2xgjA_	Alignment	not modelled	98.5	20	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dob1; **PDBTitle:** structure of mtr4, a dexh helicase involved in nuclear rna2 processing and surveillance
33	c2zj2A_	Alignment	not modelled	98.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ski2-type helicase; **PDBTitle:** archaeal dna helicase hjm apo state in form 1
34	c1gm5A_	Alignment	not modelled	98.5	21	**PDB header:**helicase **Chain:** A: **PDB Molecule:**recg; **PDBTitle:** structure of recg bound to three-way dna junction
35	c3oiyB_	Alignment	not modelled	98.5	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**reverse gyrase helicase domain; **PDBTitle:** helicase domain of reverse gyrase from thermotoga maritima
36	c3l9oA_	Alignment	not modelled	98.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dob1; **PDBTitle:** crystal structure of mtr4, a co-factor of the nuclear exosome
37	c4a4zA_	Alignment	not modelled	98.5	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**antiviral helicase ski2; **PDBTitle:** crystal structure of the s. cerevisiae dexh helicase ski2 bound to2 amppnp
38	c2z0mA_	Alignment	not modelled	98.4	16	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**337aa long hypothetical atp-dependent rna **PDBTitle:** crystal structure of hypothetical atp-dependent rna2 helicase from sulfolobus tokodaii
39	c3tmiA_	Alignment	not modelled	98.4	18	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**atp-dependent rna helicase ddx58; **PDBTitle:** structural basis for rna recognition and activation of rig-i
40	c2p6uA_	Alignment	not modelled	98.4	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**afuhel308 helicase; **PDBTitle:** apo structure of the hel308 superfamily 2 helicase
41	c1xtkA_	Alignment	not modelled	98.4	14	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**probable atp-dependent rna helicase p47; **PDBTitle:** structure of decd to dead mutation of human uap56
42	d1gl9b1	Alignment	not modelled	98.4	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Helicase-like "domain" of reverse gyrase
43	c3dkpA_	Alignment	not modelled	98.4	20	**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
44	c2db3D_	Alignment	not modelled	98.3	17	**PDB header:**hydrolase/rna **Chain:** D: **PDB Molecule:**atp-dependent rna helicase vasa; **PDBTitle:** structural basis for rna unwinding by the dead-box protein2 drosophila vasa
45	d1rifa_	Alignment	not modelled	98.3	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**DNA helicase UvsW
46	c2hxyC_	Alignment	not modelled	98.3	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**probable atp-dependent rna helicase ddx48; **PDBTitle:** crystal structure of human apo-eif4aiii
47	c1wp9D_	Alignment	not modelled	98.3	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**atp-dependent rna helicase, putative; **PDBTitle:** crystal structure of pyrococcus furiosus hef helicase domain
48	c1s2mA_	Alignment	not modelled	98.3	17	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**putative atp-dependent rna helicase dhh1; **PDBTitle:** crystal structure of the dead box protein dhh1p
49	c2ocaA_	Alignment	not modelled	98.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent dna helicase uvsw; **PDBTitle:** the crystal structure of t4 uvsw
50	c1gl9B_	Alignment	not modelled	98.2	13	**PDB header:**topoisomerase **Chain:** B: **PDB Molecule:**reverse gyrase; **PDBTitle:** archaeoglobus fulgidus reverse gyrase complexed with adpnp
51	c3fhtA_	Alignment	not modelled	98.2	14	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**atp-dependent rna helicase ddx19b; **PDBTitle:** crystal structure of human dbp5 in complex with amppnp and rna
52	c2wv9A_	Alignment	not modelled	98.2	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flavivirin protease ns2b regulatory subunit, flavivirin **PDBTitle:** crystal structure of the ns3 protease-helicase from murray2 valley encephalitis virus
53	c3bxzA_	Alignment	not modelled	98.2	22	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**preprotein translocase subunit seca; **PDBTitle:** crystal structure of the isolated dead motor domains from2 escherichia coli seca
54	c2eyqA_	Alignment	not modelled	98.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**transcription-repair coupling factor; **PDBTitle:** crystal structure of escherichia coli transcription-repair2

						coupling factor
55	c2fwrA_	Alignment	not modelled	98.2	30	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad25; **PDBTitle:** structure of archaeoglobus fulgidis xpb
56	c3ewsA_	Alignment	not modelled	98.2	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase ddx19b; **PDBTitle:** human dead-box rna-helicase ddx19 in complex with adp
57	c3pexA_	Alignment	not modelled	98.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dbp5; **PDBTitle:** s. cerevisiae dbp5 l327v bound to gle1 h337r and ip6
58	d2eyqa3	Alignment	not modelled	98.2	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
59	c3kx2A_	Alignment	not modelled	98.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pre-mrna-splicing factor atp-dependent rna **PDBTitle:** crystal structure of prp43p in complex with adp
60	c2vbcA_	Alignment	not modelled	98.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dengue 4 ns3 full-length protein; **PDBTitle:** crystal structure of the ns3 protease-helicase from dengue2 virus
61	c2jlrA_	Alignment	not modelled	98.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine protease subunit ns3; **PDBTitle:** dengue virus 4 ns3 helicase in complex with amppnp
62	c1ymfA_	Alignment	not modelled	98.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**genome polyprotein [contains: flavivirin **PDBTitle:** crystal structure of yellow fever virus ns3 helicase2 complexed with adp
63	c1hv8B_	Alignment	not modelled	98.1	19	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**putative atp-dependent rna helicase mj0669; **PDBTitle:** crystal structure of a dead box protein from the2 hyperthermophile methanococcus jannaschii
64	c2kbeA_	Alignment	not modelled	98.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dbp5; **PDBTitle:** solution structure of amino-terminal domain of dbp5p
65	c3ly5A_	Alignment	not modelled	98.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase ddx18; **PDBTitle:** ddx18 dead-domain
66	d1c4oa1	Alignment	not modelled	98.1	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
67	c2qeqA_	Alignment	not modelled	98.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flavivirin protease ns3 catalytic subunit; **PDBTitle:** crystal structure of kunjin virus ns3 helicase
68	c2vsxA_	Alignment	not modelled	98.0	17	**PDB header:**translation/hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase eif4a; **PDBTitle:** crystal structure of a translation initiation complex
69	c2pl3A_	Alignment	not modelled	98.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable atp-dependent rna helicase ddx10; **PDBTitle:** human dead-box rna helicase ddx10, dead domain in complex with adp
70	d1wp9a1	Alignment	not modelled	98.0	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
71	d2p6ra3	Alignment	not modelled	98.0	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
72	c3b6eA_	Alignment	not modelled	98.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**interferon-induced helicase c domain-containing protein 1; **PDBTitle:** crystal structure of human dech-box rna helicase mda5 (melanoma2 differentiation-associated protein 5), dech-domain
73	c1a1vA_	Alignment	not modelled	98.0	17	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**protein (ns3 protein); **PDBTitle:** hepatitis c virus ns3 helicase domain complexed with single2 stranded sdna
74	c3fe2B_	Alignment	not modelled	97.9	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable atp-dependent rna helicase ddx5; **PDBTitle:** human dead-box rna helicase ddx5 (p68), conserved domain i in complex2 with adp
75	c1c4oA_	Alignment	not modelled	97.9	17	**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
76	c2z83A_	Alignment	not modelled	97.9	22	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**helicase/nucleoside triphosphatase; **PDBTitle:** crystal structure of catalytic domain of japanese2 encephalitis virus ns3 helicase/nucleoside triphosphatase3 at a resolution 1.8
77	c3llmB_	Alignment	not modelled	97.9	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp-dependent rna helicase a; **PDBTitle:** crystal structure analysis of a rna helicase
78	c2v1xB_	Alignment	not modelled	97.8	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp-dependent dna helicase q1; **PDBTitle:** crystal structure of human recq-like dna helicase
79	c2vl7A_	Alignment	not modelled	97.8	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**xpd; **PDBTitle:** structure of s. tokodaii xpd4

80	c2f55C_	Alignment	not modelled	97.8	18	**PDB header:**hydrolase/dna **Chain:** C: **PDB Molecule:**polyprotein; **PDBTitle:** two hepatitis c virus ns3 helicase domains complexed with2 the same strand of dna
81	c2d7dA_	Alignment	not modelled	97.8	16	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**uvrabc system protein b; **PDBTitle:** structural insights into the cryptic dna dependent atp-ase2 activity of uvrb
82	c2v6jA_	Alignment	not modelled	97.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna helicase; **PDBTitle:** kokobera virus helicase: mutant met47thr
83	d1q0ua_	Alignment	not modelled	97.8	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
84	c1oywA_	Alignment	not modelled	97.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent dna helicase; **PDBTitle:** structure of the recq catalytic core
85	c3iuyB_	Alignment	not modelled	97.8	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable atp-dependent rna helicase ddx53; **PDBTitle:** crystal structure of ddx53 dead-box domain
86	c3crw1_	Alignment	not modelled	97.8	15	**PDB header:**hydrolase **Chain:** 1: **PDB Molecule:**xpd/rad3 related dna helicase; **PDBTitle:** "xpd_apo"
87	d1gm5a3	Alignment	not modelled	97.8	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
88	d2fwra2	Alignment	not modelled	97.8	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
89	d1s2ma1	Alignment	not modelled	97.7	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
90	d2fz4a1	Alignment	not modelled	97.7	31	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
91	c2w74B_	Alignment	not modelled	97.7	16	**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
92	d1oywa2	Alignment	not modelled	97.7	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
93	c1xx6B_	Alignment	not modelled	97.6	20	**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.
94	d1nkta3	Alignment	not modelled	97.6	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
95	c2gxqA_	Alignment	not modelled	97.6	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**heat resistant rna dependent atpase; **PDBTitle:** hera n-terminal domain in complex with amp, crystal form 1
96	d1t6na_	Alignment	not modelled	97.6	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
97	d1qdea_	Alignment	not modelled	97.6	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
98	c2oxcA_	Alignment	not modelled	97.6	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable atp-dependent rna helicase ddx20; **PDBTitle:** human dead-box rna helicase ddx20, dead domain in complex2 with adp
99	c3fmoB_	Alignment	not modelled	97.6	13	**PDB header:**oncoprotein/hydrolase **Chain:** B: **PDB Molecule:**atp-dependent rna helicase ddx19b; **PDBTitle:** crystal structure of the nucleoporin nup214 in complex with the dead-2 box helicase ddx19
100	d1wrba1	Alignment	not modelled	97.6	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
101	c2cnwF_	Alignment	not modelled	97.6	18	**PDB header:**signal recognition **Chain:** F: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** gdpalf4 complex of the srp gtpases ffh and ftsy
102	c3dmdA_	Alignment	not modelled	97.6	24	**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
103	c1cu1B_	Alignment	not modelled	97.5	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein (protease/helicase ns3); **PDBTitle:** crystal structure of an enzyme complex from hepatitis c2 virus
104	c2yhsA_	Alignment	not modelled	97.5	20	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the e. coli srp receptor ftsy
						Fold:P-loop containing nucleoside triphosphate hydrolases

105	d2bmfa2	Alignment	not modelled	97.5	19	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
106	c2j7pA_	Alignment	not modelled	97.5	17	**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
107	d1a5ta2	Alignment	not modelled	97.5	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
108	d1a1va1	Alignment	not modelled	97.5	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
109	c3h1tA_	Alignment	not modelled	97.5	17	**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
110	c3jvvA_	Alignment	not modelled	97.5	20	**PDB header:**atp binding protein **Chain:** A: **PDB Molecule:**twitching mobility protein; **PDBTitle:** crystal structure of p. aeruginosa pilt with bound amp-pcp
111	d1tf5a3	Alignment	not modelled	97.5	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
112	c3berA_	Alignment	not modelled	97.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable atp-dependent rna helicase ddx47; **PDBTitle:** human dead-box rna-helicase ddx47, conserved domain i in complex with2 amp
113	c2og2A_	Alignment	not modelled	97.4	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**putative signal recognition particle receptor; **PDBTitle:** crystal structure of chloroplast ftsy from arabidopsis2 thaliana
114	c3b9qA_	Alignment	not modelled	97.4	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**chloroplast srp receptor homolog, alpha subunit **PDBTitle:** the crystal structure of cpftsy from arabidopsis thaliana
115	c1z63A_	Alignment	not modelled	97.4	11	**PDB header:**hydrolase/dna complex **Chain:** A: **PDB Molecule:**helicase of the snf2/rad54 hamily; **PDBTitle:** sulfolobus solfataricus swi2/snf2 atpase core in complex2 with dsdna
116	c1zu4A_	Alignment	not modelled	97.4	20	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**ftsy; **PDBTitle:** crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
117	c1vmaA_	Alignment	not modelled	97.4	17	**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
118	d2j0sa1	Alignment	not modelled	97.4	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
119	c3ezkB_	Alignment	not modelled	97.4	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dna packaging protein gp17; **PDBTitle:** bacteriophage t4 gp17 motor assembly based on crystal2 structures and cryo-em reconstructions
120	c2iy3A_	Alignment	not modelled	97.4	17	**PDB header:**rna-binding **Chain:** A: **PDB Molecule:**signal recognition particle protein ffh; **PDBTitle:** structure of the e. coli signal recognition particle2 bound to a translating ribosome