Phyre^2

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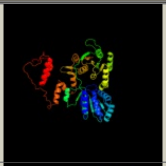
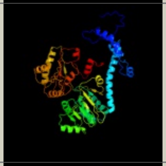
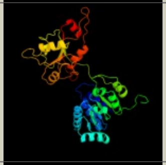
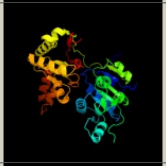
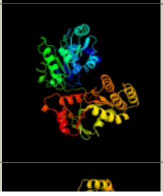
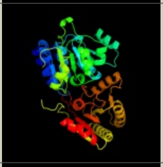
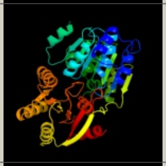
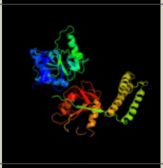
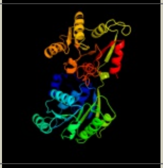
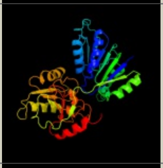
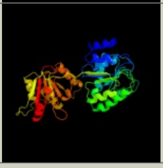
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2eyqA_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**transcription-repair coupling factor; **PDBTitle:** crystal structure of escherichia coli transcription-repair2 coupling factor
2	c1gm5A_	Alignment		100.0	19	**PDB header:**helicase **Chain:** A: **PDB Molecule:**recg; **PDBTitle:** structure of recg bound to three-way dna junction
3	c2xgjA_	Alignment		100.0	17	**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
4	c4a4zA_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**antiviral helicase ski2; **PDBTitle:** crystal structure of the s. cerevisiae dexh helicase ski2 bound to2 amppnp
5	c2v1xB_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp-dependent dna helicase q1; **PDBTitle:** crystal structure of human recq-like dna helicase
6	c1oywA_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent dna helicase; **PDBTitle:** structure of the recq catalytic core
7	c3l9oA_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dob1; **PDBTitle:** crystal structure of mtr4, a co-factor of the nuclear exosome
8	c2va8A_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ski2-type helicase; **PDBTitle:** dna repair helicase hel308
9	c1gl9B_	Alignment		100.0	18	**PDB header:**topoisomerase **Chain:** B: **PDB Molecule:**reverse gyrase; **PDBTitle:** archaeoglobus fulgidus reverse gyrase complexed with adpnp
10	c3bxzA_	Alignment		100.0	15	**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
11	c2zj2A_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ski2-type helicase; **PDBTitle:** archaeal dna helicase hjm apo state in form 1
						

12	c1c4oA_	Alignment		100.0	20	**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
13	c2p6uA_	Alignment		100.0	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**afuhel308 helicase; **PDBTitle:** apo structure of the hel308 superfamily 2 helicase
14	c3i5yA_	Alignment		100.0	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
15	c2db3D_	Alignment		100.0	19	**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
16	c3tmiA_	Alignment		100.0	15	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**atp-dependent rna helicase ddx58; **PDBTitle:** structural basis for rna recognition and activation of rig-i
17	c1hv8B_	Alignment		100.0	21	**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
18	c3rc8A_	Alignment		100.0	18	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**atp-dependent rna helicase supv3l1, mitochondrial; **PDBTitle:** human mitochondrial helicase suv3 in complex with short rna fragment
19	c2d7dA_	Alignment		100.0	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
20	c3ewsA_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase ddx19b; **PDBTitle:** human dead-box rna-helicase ddx19 in complex with adp
21	c1wp9D_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**atp-dependent rna helicase, putative; **PDBTitle:** crystal structure of pyrococcus furiosus hef helicase domain
22	c3kx2A_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pre-mrna-splicing factor atp-dependent rna **PDBTitle:** crystal structure of prp43p in complex with adp
23	c2ocaA_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent dna helicase uvsw; **PDBTitle:** the crystal structure of t4 uvsw
24	c2jlrA_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine protease subunit ns3; **PDBTitle:** dengue virus 4 ns3 helicase in complex with amppnp
25	c1s2mA_	Alignment	not modelled	100.0	16	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**putative atp-dependent rna helicase dhh1; **PDBTitle:** crystal structure of the dead box protein dhh1p
26	c3fhtA_	Alignment	not modelled	100.0	17	**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
27	c1xtkA_	Alignment	not modelled	100.0	17	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**probable atp-dependent rna helicase p47; **PDBTitle:** structure of decd to dead mutation of human uap56
28	c2vbcA_	Alignment	not modelled	100.0	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
						PDB header:rna binding protein **Chain:** A: **PDB Molecule:**337aa long hypothetical atp-dependent

29	c2z0mA_	Alignment	not modelled	100.0	23	rna **PDBTitle:** crystal structure of hypothetical atp-dependent rna2 helicase from sulfolobus tokodaii
30	c3pexA_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dbp5; **PDBTitle:** s. cerevisiae dbp5 l327v bound to gle1 h337r and ip6
31	c3oiyB_	Alignment	not modelled	100.0	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**reverse gyrase helicase domain; **PDBTitle:** helicase domain of reverse gyrase from thermotoga maritima
32	c2v6jA_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna helicase; **PDBTitle:** kokobera virus helicase: mutant met47thr
33	c2fwrA_	Alignment	not modelled	100.0	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad25; **PDBTitle:** structure of archaeoglobus fulgidis xpb
34	c2w74B_	Alignment	not modelled	100.0	13	**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
35	c2hxyC_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**probable atp-dependent rna helicase ddx48; **PDBTitle:** crystal structure of human apo-eif4aiii
36	c2wv9A_	Alignment	not modelled	100.0	18	**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
37	c2z83A_	Alignment	not modelled	100.0	20	**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
38	c2fsgA_	Alignment	not modelled	100.0	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**preprotein translocase seca subunit; **PDBTitle:** complex seca:atp from escherichia coli
39	c1ymfA_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**genome polyprotein [contains: flavivirin **PDBTitle:** crystal structure of yellow fever virus ns3 helicase2 complexed with adp
40	c2vsxA_	Alignment	not modelled	100.0	17	**PDB header:**translation/hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase eif4a; **PDBTitle:** crystal structure of a translation initiation complex
41	c2i4iA_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase ddx3x; **PDBTitle:** crystal structure of human dead-box rna helicase ddx3x
42	c3tbkA_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rig-i helicase domain; **PDBTitle:** mouse rig-i atpase domain
43	d2eyqa3	Alignment	not modelled	100.0	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
44	c1a1vA_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**protein (ns3 protein); **PDBTitle:** hepatitis c virus ns3 helicase domain complexed with single2 stranded sdna
45	c2qeqA_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flavivirin protease ns3 catalytic subunit; **PDBTitle:** crystal structure of kunjin virus ns3 helicase
46	d1gm5a3	Alignment	not modelled	100.0	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
47	c3h1tA_	Alignment	not modelled	100.0	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
48	c1tf2A_	Alignment	not modelled	100.0	18	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**preprotein translocase seca subunit; **PDBTitle:** crystal structure of seca:adp in an open conformation from2 bacillus subtilis
49	c2f55C_	Alignment	not modelled	100.0	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
50	c3dl8B_	Alignment	not modelled	100.0	20	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein translocase subunit seca; **PDBTitle:** structure of the complex of aquifex aeolicus secyeg and2 bacillus subtilis seca
51	c2d7gD_	Alignment		100.0	100	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**primosomal protein n; **PDBTitle:** crystal structure of the aa complex of the n-terminal2 domain of pria
52	d2bmfa2	Alignment	not modelled	100.0	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
53	c3mwyW_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** W: **PDB Molecule:**chromo domain-containing protein 1; **PDBTitle:** crystal structure of the chromodomain-atpase portion of

						the yeast chd12 chromatin remodeler
54	c1z3iX_	Alignment	not modelled	99.9	15	**PDB header:**recombination/dna binding **Chain:** X: **PDB Molecule:**similar to rad54-like; **PDBTitle:** structure of the swi2/snf2 chromatin remodeling domain of eukaryotic2 rad54
55	c1cu1B_	Alignment	not modelled	99.9	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein (protease/helicase ns3); **PDBTitle:** crystal structure of an enzyme complex from hepatitis c2 virus
56	c2w00B_	Alignment	not modelled	99.9	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hsdr; **PDBTitle:** crystal structure of the hsdr subunit of the ecor124i2 restriction enzyme in complex with atp
57	c3dmqA_	Alignment	not modelled	99.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna polymerase-associated protein rapa; **PDBTitle:** crystal structure of rapa, a swi2/snf2 protein that2 recycles rna polymerase during transcription
58	c3crw1_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase **Chain:** 1: **PDB Molecule:**xpd/rad3 related dna helicase; **PDBTitle:** "xpd_apo"
59	c1z63A_	Alignment	not modelled	99.9	13	**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
60	d1oywa2	Alignment	not modelled	99.9	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
61	c3dkpA_	Alignment	not modelled	99.9	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
62	c3fe2B_	Alignment	not modelled	99.9	18	**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
63	c3ly5A_	Alignment	not modelled	99.9	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase ddx18; **PDBTitle:** ddx18 dead-domain
64	d2eyqa5	Alignment	not modelled	99.9	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
65	d1gl9b1	Alignment	not modelled	99.9	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Helicase-like "domain" of reverse gyrase
66	c2vl7A_	Alignment	not modelled	99.9	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**xpd; **PDBTitle:** structure of s. tokodaii xpd4
67	d1gkub1	Alignment	not modelled	99.9	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Helicase-like "domain" of reverse gyrase
68	c2pl3A_	Alignment	not modelled	99.9	21	**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
69	c2kbeA_	Alignment	not modelled	99.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dbp5; **PDBTitle:** solution structure of amino-terminal domain of dbp5p
70	d1s2ma1	Alignment	not modelled	99.8	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
71	d1hv8a1	Alignment	not modelled	99.8	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
72	d2j0sa1	Alignment	not modelled	99.8	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
73	d1q0ua_	Alignment	not modelled	99.8	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
74	d1rifa_	Alignment	not modelled	99.8	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**DNA helicase UvsW
75	c2gxqA_	Alignment	not modelled	99.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**heat resistant rna dependent atpase; **PDBTitle:** hera n-terminal domain in complex with amp, crystal form 1
76	c3berA_	Alignment	not modelled	99.8	21	**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
77	c3iuyB_	Alignment	not modelled	99.8	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable atp-dependent rna helicase ddx53; **PDBTitle:** crystal structure of ddx53 dead-box domain
78	d2p6ra3	Alignment	not modelled	99.8	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases

						Family: Tandem AAA-ATPase domain
79	d2fwra2	Alignment	not modelled	99.8	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
80	c3b6eA_	Alignment	not modelled	99.8	17	**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
81	d1wp9a1	Alignment	not modelled	99.8	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
82	c2oxcA_	Alignment	not modelled	99.8	15	**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
83	d1gm5a4	Alignment	not modelled	99.8	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
84	d1wrba1	Alignment	not modelled	99.8	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
85	d1qdea_	Alignment	not modelled	99.8	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
86	d1a1va1	Alignment	not modelled	99.8	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
87	d2fz4a1	Alignment	not modelled	99.8	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
88	d1veca_	Alignment	not modelled	99.8	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
89	c3llmB_	Alignment	not modelled	99.8	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp-dependent rna helicase a; **PDBTitle:** crystal structure analysis of a rna helicase
90	d1t5la2	Alignment	not modelled	99.8	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
91	d1t6na_	Alignment	not modelled	99.8	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
92	d1oywa3	Alignment	not modelled	99.8	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
93	c3fmoB_	Alignment	not modelled	99.8	22	**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
94	d1c4oa2	Alignment	not modelled	99.7	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
95	c3fhcB_	Alignment	not modelled	99.7	21	**PDB header:**transport protein/hydrolase **Chain:** B: **PDB Molecule:**atp-dependent rna helicase ddx19b; **PDBTitle:** crystal structure of human dbp5 in complex with nup214
96	d1nkta3	Alignment	not modelled	99.7	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
97	d1tf5a3	Alignment	not modelled	99.7	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
98	d2g9na1	Alignment	not modelled	99.7	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
99	c3fmpD_	Alignment	not modelled	99.7	22	**PDB header:**oncoprotein/hydrolase **Chain:** D: **PDB Molecule:**atp-dependent rna helicase ddx19b; **PDBTitle:** crystal structure of the nucleoporin nup214 in complex with the dead-2 box helicase ddx19
100	d1yksa1	Alignment	not modelled	99.7	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
101	d2j0sa2	Alignment	not modelled	99.7	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
102	c2vsfA_	Alignment	not modelled	99.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna repair helicase rad3 related protein; **PDBTitle:** structure of xpd from thermoplasma acidophilum
103	c2vdaA_	Alignment	not modelled	99.7	20	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**translocase subunit seca; **PDBTitle:** solution structure of the seca-signal peptide complex
						Fold:P-loop containing nucleoside triphosphate hydrolases

104	d1hv8a2	Alignment	not modelled	99.7	22	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
105	d1c4oa1	Alignment	not modelled	99.7	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
106	c1nl3B_	Alignment	not modelled	99.6	20	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**preprotein translocase seca 1 subunit; **PDBTitle:** crystal structure of the seca protein translocation atpase2 from mycobacterium tuberculosis in apo form
107	d1s2ma2	Alignment	not modelled	99.6	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
108	c3i32A_	Alignment	not modelled	99.6	26	**PDB header:**rna binding protein,hydrolase **Chain:** A: **PDB Molecule:**heat resistant rna dependent atpase; **PDBTitle:** dimeric structure of a hera helicase fragment including the c-terminal2 reca domain, the dimerization domain, and the rna binding domain
109	c3juxA_	Alignment	not modelled	99.6	22	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein translocase subunit seca; **PDBTitle:** structure of the translocation atpase seca from thermotoga2 maritima
110	d2p6ra4	Alignment	not modelled	99.6	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
111	c2hjvB_	Alignment	not modelled	99.6	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp-dependent rna helicase dbpa; **PDBTitle:** structure of the second domain (residues 207-368) of the2 bacillus subtilis yxin protein
112	c2p6nA_	Alignment	not modelled	99.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase ddx41; **PDBTitle:** human dead-box rna helicase ddx41, helicase domain
113	c2ipcB_	Alignment	not modelled	99.6	19	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**preprotein translocase seca subunit; **PDBTitle:** crystal structure of the translocation atpase seca from thermus2 thermophilus reveals a parallel, head-to-head dimer
114	c3dinB_	Alignment	not modelled	99.6	22	**PDB header:**membrane protein, protein transport **Chain:** B: **PDB Molecule:**protein translocase subunit seca; **PDBTitle:** crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
115	c3earA_	Alignment	not modelled	99.5	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hera; **PDBTitle:** novel dimerization motif in the dead box rna helicase hera: form 1,2 partial dimer
116	d2g2ja1	Alignment	not modelled	99.5	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
117	d1t5ia_	Alignment	not modelled	99.5	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
118	d1wp9a2	Alignment	not modelled	99.5	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
119	d1z3ix2	Alignment	not modelled	99.4	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
120	d1nkta4	Alignment	not modelled	99.4	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain