Phyre^2

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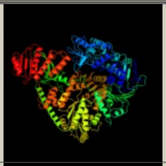
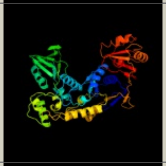
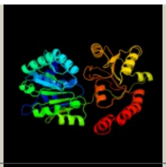
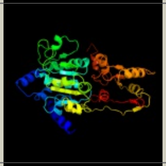
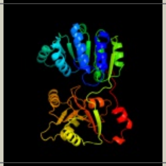
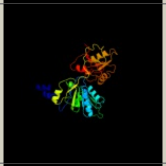
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2eyqA_	 Alignment		100.0	100	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**transcription-repair coupling factor; **PDBTitle:** crystal structure of escherichia coli transcription-repair2 coupling factor
2	c3hjhA_	 Alignment		100.0	100	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**transcription-repair-coupling factor; **PDBTitle:** a rigid n-terminal clamp restrains the motor domains of the bacterial2 transcription-repair coupling factor
3	c1gm5A_	 Alignment		100.0	37	**PDB header:**helicase **Chain:** A: **PDB Molecule:**recg; **PDBTitle:** structure of recg bound to three-way dna junction
4	d2eyqa4	 Alignment		100.0	100	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
5	d2b2na1	 Alignment		100.0	100	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
6	d1t5la1	 Alignment		100.0	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
7	d2eyqa5	 Alignment		100.0	100	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
8	d2eyqa3	 Alignment		100.0	100	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
9	c2v1xB_	 Alignment		100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp-dependent dna helicase q1; **PDBTitle:** crystal structure of human recq-like dna helicase
10	c2xgjA_	 Alignment		100.0	22	**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
11	c4a4zA_	 Alignment		100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**antiviral helicase ski2; **PDBTitle:** crystal structure of the s. cerevisiae dexh helicase ski2 bound to2 amppnp

12	c1oywA_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent dna helicase; **PDBTitle:** structure of the recq catalytic core
13	c3bxzA_	Alignment		100.0	19	**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
14	c3l9oA_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dob1; **PDBTitle:** crystal structure of mtr4, a co-factor of the nuclear exosome
15	d1gm5a3	Alignment		100.0	35	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
16	c1gl9B_	Alignment		100.0	17	**PDB header:**topoisomerase **Chain:** B: **PDB Molecule:**reverse gyrase; **PDBTitle:** archaeoglobus fulgidus reverse gyrase complexed with adpnp
17	c2vbcA_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dengue 4 ns3 full-length protein; **PDBTitle:** crystal structure of the ns3 protease-helicase from dengue2 virus
18	c2va8A_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ski2-type helicase; **PDBTitle:** dna repair helicase hel308
19	c3rc8A_	Alignment		100.0	15	**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
20	c2fsgA_	Alignment		100.0	20	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**preprotein translocase seca subunit; **PDBTitle:** complex seca:atp from escherichia coli
21	c2zj2A_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ski2-type helicase; **PDBTitle:** archaeal dna helicase hjm apo state in form 1
22	c2p6uA_	Alignment	not modelled	100.0	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**afuhel308 helicase; **PDBTitle:** apo structure of the hel308 superfamily 2 helicase
23	c1ymfA_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**genome polyprotein [contains: flavivirin **PDBTitle:** crystal structure of yellow fever virus ns3 helicase2 complexed with adp
24	c2jlrA_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine protease subunit ns3; **PDBTitle:** dengue virus 4 ns3 helicase in complex with amppnp
25	d1gm5a4	Alignment	not modelled	100.0	39	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
26	c2ocaA_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent dna helicase uvsw; **PDBTitle:** the crystal structure of t4 uvsw
27	c2d7dA_	Alignment	not modelled	100.0	24	**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
28	c1hv8B_	Alignment	not modelled	100.0	20	**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

29	c3kx2A_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pre-mrna-splicing factor atp-dependent rna **PDBTitle:** crystal structure of prp43p in complex with adp
30	c2db3D_	Alignment	not modelled	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
31	c1c4oA_	Alignment	not modelled	100.0	24	**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
32	c2wv9A_	Alignment	not modelled	100.0	21	**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
33	c2v6jA_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna helicase; **PDBTitle:** kokobera virus helicase: mutant met47thr
34	c3i5yA_	Alignment	not modelled	100.0	19	**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
35	c3ewsA_	Alignment	not modelled	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
36	c3oiyB_	Alignment	not modelled	100.0	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**reverse gyrase helicase domain; **PDBTitle:** helicase domain of reverse gyrase from thermotoga maritima
37	c3tmiA_	Alignment	not modelled	100.0	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
38	c1s2mA_	Alignment	not modelled	100.0	23	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**putative atp-dependent rna helicase dhh1; **PDBTitle:** crystal structure of the dead box protein dhh1p
39	c2z83A_	Alignment	not modelled	100.0	18	**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
40	c3fhtA_	Alignment	not modelled	100.0	19	**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
41	c3pexA_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dbp5; **PDBTitle:** s. cerevisiae dbp5 l327v bound to gle1 h337r and ip6
42	c2z0mA_	Alignment	not modelled	100.0	18	**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
43	c1xtkA_	Alignment	not modelled	100.0	19	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**probable atp-dependent rna helicase p47; **PDBTitle:** structure of decd to dead mutation of human uap56
44	d2eyqa6	Alignment	not modelled	100.0	100	**Fold:**TRCF domain-like **Superfamily:**TRCF domain-like **Family:**TRCF domain
45	c1wp9D_	Alignment	not modelled	100.0	26	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**atp-dependent rna helicase, putative; **PDBTitle:** crystal structure of pyrococcus furiosus hef helicase domain
46	c2hxyC_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**probable atp-dependent rna helicase ddx48; **PDBTitle:** crystal structure of human apo-eif4aiii
47	c2qeqA_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flavivirin protease ns3 catalytic subunit; **PDBTitle:** crystal structure of kunjin virus ns3 helicase
48	c2fwrA_	Alignment	not modelled	100.0	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad25; **PDBTitle:** structure of archaeoglobus fulgidis xpb
49	c2vsxA_	Alignment	not modelled	100.0	18	**PDB header:**translation/hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase eif4a; **PDBTitle:** crystal structure of a translation initiation complex
50	c3fpnB_	Alignment	not modelled	100.0	29	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**geobacillus stearothermophilus uvrb interaction **PDBTitle:** crystal structure of uvra-uvrb interaction domains
51	c1a1vA_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**protein (ns3 protein); **PDBTitle:** hepatitis c virus ns3 helicase domain complexed with single2 stranded sdna
52	c2i4iA_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase ddx3x; **PDBTitle:** crystal structure of human dead-box rna helicase ddx3x
53	c1tf2A_	Alignment	not modelled	100.0	20	**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
54	c2gsrA	Alignment	not modelled	100.0	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription-repair coupling factor;

54	c2qsrA_	Alignment	not modelled	100.0	25	**PDBTitle:** crystal structure of c-terminal domain of transcription-repair2 coupling factor
55	c3dl8B_	Alignment	not modelled	100.0	21	**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
56	d2bmfa2	Alignment	not modelled	100.0	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
57	c2f55C_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase/dna **Chain:** C: **PDB Molecule:**polyprotein; **PDBTitle:** two hepatitis c virus ns3 helicase domains complexed with2 the same strand of dna
58	c2w74B_	Alignment	not modelled	100.0	17	**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
59	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
60	c3tbkA_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rig-i helicase domain; **PDBTitle:** mouse rig-i atpase domain
61	c3dmqA_	Alignment	not modelled	100.0	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
62	c1z3iX_	Alignment	not modelled	99.9	16	**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
63	d1c4oa1	Alignment	not modelled	99.9	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
64	c3mwyW_	Alignment	not modelled	99.9	17	**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
65	c1cu1B_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein (protease/helicase ns3); **PDBTitle:** crystal structure of an enzyme complex from hepatitis c2 virus
66	d1nkta3	Alignment	not modelled	99.9	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
67	c1z63A_	Alignment	not modelled	99.9	16	**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
68	d2eyqa1	Alignment	not modelled	99.9	100	**Fold:**SH3-like barrel **Superfamily:**CarD-like **Family:**CarD-like
69	c2w00B_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hsdr; **PDBTitle:** crystal structure of the hsdr subunit of the ecor124i2 restriction enzyme in complex with atp
70	c3ly5A_	Alignment	not modelled	99.9	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase ddx18; **PDBTitle:** ddx18 dead-domain
71	d1oywa2	Alignment	not modelled	99.9	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
72	c3fe2B_	Alignment	not modelled	99.9	23	**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
73	d1t5la2	Alignment	not modelled	99.9	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
74	d1gl9b1	Alignment	not modelled	99.9	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Helicase-like "domain" of reverse gyrase
75	c3crw1_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** 1: **PDB Molecule:**xpd/rad3 related dna helicase; **PDBTitle:** "xpd_apo"
76	d1c4oa2	Alignment	not modelled	99.9	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
77	d1oywa3	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
78	d1hv8a1	Alignment	not modelled	99.8	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
79	d1gkub1	Alignment	not modelled	99.8	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases

						Family: Helicase-like "domain" of reverse gyrase
80	c3i32A_	Alignment	not modelled	99.8	17	**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
81	d1rifa_	Alignment	not modelled	99.8	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**DNA helicase UvsW
82	d1tf5a3	Alignment	not modelled	99.8	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
83	d1hv8a2	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
84	d1wp9a1	Alignment	not modelled	99.8	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
85	c3dkpA_	Alignment	not modelled	99.8	22	**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
86	d2j0sa2	Alignment	not modelled	99.8	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
87	d1s2ma1	Alignment	not modelled	99.8	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
88	c2kbeA_	Alignment	not modelled	99.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dbp5; **PDBTitle:** solution structure of amino-terminal domain of dbp5p
89	c2oxcA_	Alignment	not modelled	99.8	20	**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
90	c2pl3A_	Alignment	not modelled	99.8	23	**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
91	d1s2ma2	Alignment	not modelled	99.8	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
92	c3berA_	Alignment	not modelled	99.8	23	**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
93	d2p6ra4	Alignment	not modelled	99.8	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
94	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
95	c2vl7A_	Alignment	not modelled	99.8	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**xpd; **PDBTitle:** structure of s. tokodaii xpd4
96	c2hjvB_	Alignment	not modelled	99.8	18	**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
97	c3iuyB_	Alignment	not modelled	99.8	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable atp-dependent rna helicase ddx53; **PDBTitle:** crystal structure of ddx53 dead-box domain
98	d2p6ra3	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
99	d2fz4a1	Alignment	not modelled	99.8	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
100	c2p6nA_	Alignment	not modelled	99.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase ddx41; **PDBTitle:** human dead-box rna helicase ddx41, helicase domain
101	d2fwra2	Alignment	not modelled	99.8	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
102	d2g2ja1	Alignment	not modelled	99.8	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
103	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
104	d2j0sa1	Alignment	not modelled	99.7	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate

104	d2j0sa1	Alignment	not modelled	99.7	18	hydrolases **Family:**Tandem AAA-ATPase domain
105	c3b6eA_	Alignment	not modelled	99.7	26	**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
106	d1qdea_	Alignment	not modelled	99.7	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
107	d1t6na_	Alignment	not modelled	99.7	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
108	d2eyqa2	Alignment	not modelled	99.7	100	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
109	d1a1va2	Alignment	not modelled	99.7	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
110	c2vdaA_	Alignment	not modelled	99.7	23	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**translocase subunit seca; **PDBTitle:** solution structure of the seca-signal peptide complex
111	c3earA_	Alignment	not modelled	99.7	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hera; **PDBTitle:** novel dimerization motif in the dead box rna helicase hera: form 1,2 partial dimer
112	c1nl3B_	Alignment	not modelled	99.7	21	**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
113	d1veca_	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
114	d1t5ia_	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
115	d1tf5a4	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
116	c2jgnB_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp-dependent rna helicase ddx3x; **PDBTitle:** ddx3 helicase domain
117	c3juxA_	Alignment	not modelled	99.7	22	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein translocase subunit seca; **PDBTitle:** structure of the translocation atpase seca from thermotoga2 maritima
118	d1a1va1	Alignment	not modelled	99.7	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
119	c3dinB_	Alignment	not modelled	99.7	19	**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
120	d1wrba1	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