



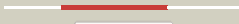
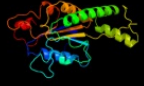
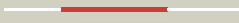




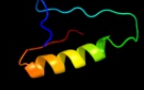










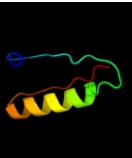
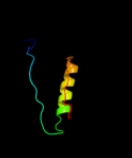


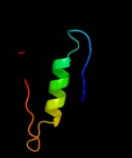
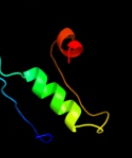
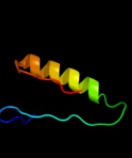

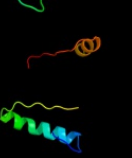


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1e9ra_</a>	 Alignment		100.0	29	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
2	<a href="#">c2iutA_</a>	 Alignment		99.3	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna translocase ftsk; <b>PDBTitle:</b> p. aeruginosa ftsk motor domain, dimeric
3	<a href="#">c2iusB_</a>	 Alignment		99.3	17	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna translocase ftsk; <b>PDBTitle:</b> e. coli ftsk motor domain
4	<a href="#">c2iuuE_</a>	 Alignment		99.3	15	<b>PDB header:</b> membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> dna translocase ftsk; <b>PDBTitle:</b> p. aeruginosa ftsk motor domain, hexamer
5	<a href="#">d2i3ba1</a>	 Alignment		97.4	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
6	<a href="#">d1okkd2</a>	 Alignment		97.3	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
7	<a href="#">d1vmaa2</a>	 Alignment		97.3	24	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
8	<a href="#">c3jvvA_</a>	 Alignment		97.2	20	<b>PDB header:</b> atp binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> twitching mobility protein; <b>PDBTitle:</b> crystal structure of p. aeruginosa pilt with bound amp-pcp
9	<a href="#">c2cnwF_</a>	 Alignment		97.2	22	<b>PDB header:</b> signal recognition <b>Chain:</b> F: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> gdpalf4 complex of the srp gtpases ffh and ftsy
10	<a href="#">d2qy9a2</a>	 Alignment		97.2	24	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
11	<a href="#">c3lfuA_</a>	 Alignment		97.2	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna helicase ii; <b>PDBTitle:</b> crystal structure of e. coli uvrd

12	<a href="#">dl1s1a2</a>	Alignment		97.1	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
13	<a href="#">c2ja1A</a>	Alignment		97.1	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thymidine kinase; <b>PDBTitle:</b> thymidine kinase from b. cereus with ttp bound as phosphate2 donor.
14	<a href="#">c2j7pA</a>	Alignment		97.1	21	<b>PDB header:</b> signal recognition <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle protein; <b>PDBTitle:</b> gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
15	<a href="#">dlqzxa3</a>	Alignment		97.1	24	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
16	<a href="#">dlp9ra</a>	Alignment		97.1	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
17	<a href="#">c1pjrA</a>	Alignment		97.1	11	<b>PDB header:</b> helicase <b>Chain:</b> A: <b>PDB Molecule:</b> pcra; <b>PDBTitle:</b> structure of dna helicase
18	<a href="#">c2og2A</a>	Alignment		97.0	19	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative signal recognition particle receptor; <b>PDBTitle:</b> crystal structure of chloroplast ftsy from arabidopsis2 thaliana
19	<a href="#">c2qy9A</a>	Alignment		97.0	24	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> structure of the ng+1 construct of the e. coli srp receptor2 ftsy
20	<a href="#">c2f1rA</a>	Alignment		97.0	21	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin-guanine dinucleotide biosynthesis <b>PDBTitle:</b> crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
21	<a href="#">dlnp6a</a>	Alignment	not modelled	97.0	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
22	<a href="#">dlg6oa</a>	Alignment	not modelled	97.0	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
23	<a href="#">dlbyia</a>	Alignment	not modelled	97.0	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
24	<a href="#">d2bmfa2</a>	Alignment	not modelled	97.0	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
25	<a href="#">c3b9qA</a>	Alignment	not modelled	96.9	20	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> chloroplast srp receptor homolog, alpha subunit <b>PDBTitle:</b> the crystal structure of cpfts from arabidopsis thaliana
26	<a href="#">c1zu4A</a>	Alignment	not modelled	96.9	29	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> fts;f; <b>PDBTitle:</b> crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
27	<a href="#">c1vmaA</a>	Alignment	not modelled	96.9	22	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
28	<a href="#">c3dm5A</a>	Alignment	not modelled	96.9	28	<b>PDB header:</b> rna binding protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition

						particle3 from the archaeon pyrococcus furiosus. <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
29	<a href="#">d1uaaa1</a>	Alignment	not modelled	96.9	12	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> protein (atp-dependent dna helicase rep.); <b>PDBTitle:</b> e. coli rep helicase/dna complex
30	<a href="#">c1uaaB_</a>	Alignment	not modelled	96.9	11	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of n-terminal domain of zonular occludens toxin from2 neisseria meningitidis
31	<a href="#">c2r2aB_</a>	Alignment	not modelled	96.9	20	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> structure of the e. coli srp receptor ftsy
32	<a href="#">c2yhsA_</a>	Alignment	not modelled	96.9	24	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> helicase/nucleoside triphosphatase; <b>PDBTitle:</b> crystal structure of catalytic domain of japanese2 encephalitis virus ns3 helicase/nucleoside triphosphatase3 at a resolution 1.8
33	<a href="#">c2z83A_</a>	Alignment	not modelled	96.9	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
34	<a href="#">d1pjra1</a>	Alignment	not modelled	96.9	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle receptor; <b>PDBTitle:</b> structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
35	<a href="#">c3dmdA_</a>	Alignment	not modelled	96.9	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease subunit ns3; <b>PDBTitle:</b> dengue virus 4 ns3 helicase in complex with amppnp
36	<a href="#">c2jlrA_</a>	Alignment	not modelled	96.9	14	<b>PDB header:</b> rna-binding <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle protein ffh; <b>PDBTitle:</b> structure of the e. coli signal recognition particle2 bound to a translating ribosome
37	<a href="#">c2iy3A_</a>	Alignment	not modelled	96.8	21	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dnaa-related protein; <b>PDBTitle:</b> solution structure of protein nmb1076 from neisseria meningitidis.2 northeast structural genomics consortium target mr101b.
38	<a href="#">c2kjqA_</a>	Alignment	not modelled	96.8	17	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase dob1; <b>PDBTitle:</b> structure of ntr4, a dexh helicase involved in nuclear rna2 processing and surveillance
39	<a href="#">c2xgiA_</a>	Alignment	not modelled	96.8	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> reverse gyrase helicase domain; <b>PDBTitle:</b> helicase domain of reverse gyrase from thermotoga maritima
40	<a href="#">c3oiyB_</a>	Alignment	not modelled	96.8	16	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> crystal structure of thermotoga maritima reca
41	<a href="#">c3hr8A_</a>	Alignment	not modelled	96.8	18	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> dna helicase ii; <b>PDBTitle:</b> crystal structure of uvrd-dna-adpmgf3 ternary complex
42	<a href="#">c2is6B_</a>	Alignment	not modelled	96.8	10	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
43	<a href="#">d1r6bx2</a>	Alignment	not modelled	96.8	24	<b>PDB header:</b> protein transport <b>Chain:</b> E: <b>PDB Molecule:</b> twitching motility protein pilt; <b>PDBTitle:</b> structure of a. aeolicus pilt with 6 monomers per2 asymmetric unit
44	<a href="#">c2gszE_</a>	Alignment	not modelled	96.8	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> type iv secretion system protein virb11; <b>PDBTitle:</b> crystal structure of the virb11 atpase from the brucella suis type iv2 secretion system in complex with sulphate
45	<a href="#">c2gzaB_</a>	Alignment	not modelled	96.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> genome polyprotein [contains: flavivirin <b>PDBTitle:</b> crystal structure of yellow fever virus ns3 helicase2 complexed with adp
46	<a href="#">c1ymfA_</a>	Alignment	not modelled	96.8	13	<b>PDB header:</b> helicase <b>Chain:</b> A: <b>PDB Molecule:</b> recg; <b>PDBTitle:</b> structure of recg bound to three-way dna junction
47	<a href="#">c1gm5A_</a>	Alignment	not modelled	96.8	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> l-seryl-trna(sec) kinase; <b>PDBTitle:</b> crystal structure of archaeal o-phosphoseryl-trna(sec)2 kinase
48	<a href="#">c3a4mB_</a>	Alignment	not modelled	96.8	26	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dethiobiotin synthetase; <b>PDBTitle:</b> crystal structure of a dethiobiotin synthetase from francisella2 tularensis subsp. tularensis schu s4
49	<a href="#">c3of5A_</a>	Alignment	not modelled	96.7	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> reca protein; <b>PDBTitle:</b> "deinococcus radiodurans reca in complex with atp-gamma-s"
50	<a href="#">c1xp8A_</a>	Alignment	not modelled	96.7	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Helicase-like "domain" of reverse gyrase
51	<a href="#">d1gkub1</a>	Alignment	not modelled	96.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> 1: <b>PDB Molecule:</b> type ii secretion system protein; <b>PDBTitle:</b> crystal structure of the archaeal secretion atpase gspe in complex2 with phosphate
52	<a href="#">c2oaq1_</a>	Alignment	not modelled	96.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna replication factor; <b>PDBTitle:</b> crystal structure of a putative dna replication regulator hda2 (sama_1916) from shewanella amazonensis sb2b at 1.75 a
53	<a href="#">c3bosA_</a>	Alignment	not modelled	96.7	18	

						resolution
54	<a href="#">c1xx6B_</a>	Alignment	not modelled	96.7	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thymidine kinase; <b>PDBTitle:</b> x-ray structure of clostridium acetobutylicum thymidine kinase with2 adp. northeast structural genomics target car26.
55	<a href="#">c4a4zA_</a>	Alignment	not modelled	96.7	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> antiviral helicase ski2; <b>PDBTitle:</b> crystal structure of the s. cerevisiae dexh helicase ski2 bound to2 amppnp
56	<a href="#">c3b85A_</a>	Alignment	not modelled	96.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphate starvation-inducible protein; <b>PDBTitle:</b> crystal structure of predicted phosphate starvation-induced atpase2 phoh2 from corynebacterium glutamicum
57	<a href="#">d2qm8a1</a>	Alignment	not modelled	96.6	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
58	<a href="#">c2wv9A_</a>	Alignment	not modelled	96.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> flavivirin protease ns2b regulatory subunit, flavivirin <b>PDBTitle:</b> crystal structure of the ns3 protease-helicase from murray2 valley encephalitis virus
59	<a href="#">d1gl9b1</a>	Alignment	not modelled	96.6	13	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Helicase-like "domain" of reverse gyrase
60	<a href="#">c2eyuA_</a>	Alignment	not modelled	96.6	28	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> twitching motility protein pilt; <b>PDBTitle:</b> the crystal structure of the c-terminal domain of aquifex2 aeolicus pilt
61	<a href="#">c2px0D_</a>	Alignment	not modelled	96.6	23	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> D: <b>PDB Molecule:</b> flagellar biosynthesis protein flhf; <b>PDBTitle:</b> crystal structure of flhf complexed with gmpnp/mg(2+)
62	<a href="#">c2p6uA_</a>	Alignment	not modelled	96.6	10	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> afuhel308 helicase; <b>PDBTitle:</b> apo structure of the hel308 superfamily 2 helicase
63	<a href="#">c2xzlA_</a>	Alignment	not modelled	96.6	12	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent helicase nam7; <b>PDBTitle:</b> upf1-rna complex
64	<a href="#">c2j37W_</a>	Alignment	not modelled	96.5	22	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> signal recognition particle 54 kda protein <b>PDBTitle:</b> model of mammalian srp bound to 80s rncs
65	<a href="#">c2qeqA_</a>	Alignment	not modelled	96.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> flavivirin protease ns3 catalytic subunit; <b>PDBTitle:</b> crystal structure of kunjin virus ns3 helicase
66	<a href="#">d1fnna2</a>	Alignment	not modelled	96.5	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
67	<a href="#">c2wjyA_</a>	Alignment	not modelled	96.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> regulator of nonsense transcripts 1; <b>PDBTitle:</b> crystal structure of the complex between human nonsense2 mediated decay factors upf1 and upf2 orthorhombic form
68	<a href="#">d1yrba1</a>	Alignment	not modelled	96.5	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
69	<a href="#">c2vbcA_</a>	Alignment	not modelled	96.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dengue 4 ns3 full-length protein; <b>PDBTitle:</b> crystal structure of the ns3 protease-helicase from dengue2 virus
70	<a href="#">c2v6jA_</a>	Alignment	not modelled	96.5	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> rna helicase; <b>PDBTitle:</b> kokobera virus helicase: mutant met47thr
71	<a href="#">c3i5yA_</a>	Alignment	not modelled	96.5	16	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase mss116; <b>PDBTitle:</b> structure of mss116p bound to ssrna containing a single 5-bru and amp-2 pnp
72	<a href="#">c2v3cC_</a>	Alignment	not modelled	96.5	24	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> crystal structure of the srp54-srp19-7s.s srp rna complex2 of m. jannaschii
73	<a href="#">c3l9oA_</a>	Alignment	not modelled	96.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase dob1; <b>PDBTitle:</b> crystal structure of mtr4, a co-factor of the nuclear exosome
74	<a href="#">c2recB_</a>	Alignment	not modelled	96.5	17	<b>PDB header:</b> helicase <b>PDB COMPND:</b>
75	<a href="#">d1xjca_</a>	Alignment	not modelled	96.5	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
76	<a href="#">d1g41a_</a>	Alignment	not modelled	96.5	30	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
77	<a href="#">d1l8qa2</a>	Alignment	not modelled	96.4	28	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
78	<a href="#">c2w0mA_</a>	Alignment	not modelled	96.4	20	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sso2452; <b>PDBTitle:</b> crystal structure of sso2452 from sulfolobus solfataricus2 p2
79	<a href="#">c1zu1A_</a>	Alignment	not modelled	96.4	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> shikimate kinase;

79	<a href="#">c1z9tA</a>	Alignment	not modelled	96.4	31	<b>PDBTitle:</b> structural basis for shikimate-binding specificity of helicobacter2 pylori shikimate kinase <b>PDB header:</b> recombination <b>Chain:</b> G: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
80	<a href="#">c3cmvG</a>	Alignment	not modelled	96.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pre-mrna-splicing factor atp-dependent rna <b>PDBTitle:</b> crystal structure of prp43p in complex with adp
81	<a href="#">c3kx2A</a>	Alignment	not modelled	96.4	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
82	<a href="#">d1c4oa1</a>	Alignment	not modelled	96.4	13	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
83	<a href="#">d2eyqa3</a>	Alignment	not modelled	96.4	26	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
84	<a href="#">c1w36G</a>	Alignment	not modelled	96.4	15	<b>PDB header:</b> recombination <b>Chain:</b> G: <b>PDB Molecule:</b> exodeoxyribonuclease v alpha chain; <b>PDBTitle:</b> recbcd:dna complex
85	<a href="#">d1u94a1</a>	Alignment	not modelled	96.4	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
86	<a href="#">d1ubea1</a>	Alignment	not modelled	96.3	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
87	<a href="#">c1gl9B</a>	Alignment	not modelled	96.3	10	<b>PDB header:</b> topoisomerase <b>Chain:</b> B: <b>PDB Molecule:</b> reverse gyrase; <b>PDBTitle:</b> archaeoglobus fulgidus reverse gyrase complexed with adpnp
88	<a href="#">d1a1va1</a>	Alignment	not modelled	96.3	24	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
89	<a href="#">c2w58B</a>	Alignment	not modelled	96.3	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> primosome component (helicase loader); <b>PDBTitle:</b> crystal structure of the dnaI
90	<a href="#">c2qmoA</a>	Alignment	not modelled	96.3	25	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dethiobiotin synthetase; <b>PDBTitle:</b> crystal structure of dethiobiotin synthetase (biotd) from helicobacter2 pylori
91	<a href="#">c2va8A</a>	Alignment	not modelled	96.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ski2-type helicase; <b>PDBTitle:</b> dna repair helicase hel308
92	<a href="#">c1u9iA</a>	Alignment	not modelled	96.3	22	<b>PDB header:</b> circadian clock protein <b>Chain:</b> A: <b>PDB Molecule:</b> kaic; <b>PDBTitle:</b> crystal structure of circadian clock protein kaic with phosphorylation2 sites
93	<a href="#">c2qq0B</a>	Alignment	not modelled	96.3	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thymidine kinase; <b>PDBTitle:</b> thymidine kinase from thermotoga maritima in complex with2 thymidine + appnnp
94	<a href="#">c3e1sA</a>	Alignment	not modelled	96.3	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exodeoxyribonuclease v, subunit recd; <b>PDBTitle:</b> structure of an n-terminal truncation of deinococcus radiodurans recd2
95	<a href="#">d1w36d1</a>	Alignment	not modelled	96.3	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
96	<a href="#">d1ye8a1</a>	Alignment	not modelled	96.3	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
97	<a href="#">c2dr3A</a>	Alignment	not modelled	96.3	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0273 protein ph0284; <b>PDBTitle:</b> crystal structure of reca superfamily atpase ph0284 from pyrococcus2 horikoshii ot3
98	<a href="#">d1xp8a1</a>	Alignment	not modelled	96.3	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
99	<a href="#">d1zaka1</a>	Alignment	not modelled	96.3	11	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
100	<a href="#">c3c8uA</a>	Alignment	not modelled	96.3	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fructokinase; <b>PDBTitle:</b> crystal structure of putative fructose transport system kinase2 (yp_612366.1) from silicibacter sp. tm1040 at 1.95 a resolution
101	<a href="#">c2zroA</a>	Alignment	not modelled	96.2	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> msreca adp form iv
102	<a href="#">c1wp9D</a>	Alignment	not modelled	96.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> atp-dependent rna helicase, putative; <b>PDBTitle:</b> crystal structure of pyrococcus furiosus hef helicase domain
103	<a href="#">c3nxsA</a>	Alignment	not modelled	96.2	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> lao/ao transport system atpase; <b>PDBTitle:</b> crystal structure of lao/ao transport system from mycobacterium2 smegmatis bound to gdp
104	<a href="#">d1kaga</a>	Alignment	not modelled	96.2	38	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Shikimate kinase (AroK)
						<b>PDB header:</b> hydrolase/dna



105	<a href="#">c2pirF_</a>	Alignment	not modelled	96.2	11	<b>Chain:</b> F: <b>PDB Molecule:</b> protein (helicase pcra); <b>PDBTitle:</b> helicase product complex
106	<a href="#">c1fnnB_</a>	Alignment	not modelled	96.2	21	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> cell division control protein 6; <b>PDBTitle:</b> crystal structure of cdc6p from pyrobaculum aerophilum
107	<a href="#">dlnksa_</a>	Alignment	not modelled	96.2	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
108	<a href="#">c2ce7B_</a>	Alignment	not modelled	96.2	24	<b>PDB header:</b> cell division protein <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsh; <b>PDBTitle:</b> edta treated
109	<a href="#">dlofha_</a>	Alignment	not modelled	96.2	31	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
110	<a href="#">d1tf7a2</a>	Alignment	not modelled	96.2	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
111	<a href="#">c3eihB_</a>	Alignment	not modelled	96.2	18	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 4; <b>PDBTitle:</b> crystal structure of s.cerevisiae vps4 in the presence of atpgammas
112	<a href="#">c2hcbC_</a>	Alignment	not modelled	96.2	28	<b>PDB header:</b> replication <b>Chain:</b> C: <b>PDB Molecule:</b> chromosomal replication initiator protein dnaa; <b>PDBTitle:</b> structure of amppcp-bound dnaa from aquifex aeolicus
113	<a href="#">dlyksa1</a>	Alignment	not modelled	96.2	12	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
114	<a href="#">d1jbka_</a>	Alignment	not modelled	96.2	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
115	<a href="#">d1mo6a1</a>	Alignment	not modelled	96.1	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
116	<a href="#">d1qvra2</a>	Alignment	not modelled	96.1	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
117	<a href="#">d1ny5a2</a>	Alignment	not modelled	96.1	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
118	<a href="#">c2z0hA_</a>	Alignment	not modelled	96.1	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thymidylate kinase; <b>PDBTitle:</b> crystal structure of thymidylate kinase in complex with dtdp2 and adp from thermotoga maritima
119	<a href="#">d1nn5a_</a>	Alignment	not modelled	96.1	27	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
120	<a href="#">c1qhha_</a>	Alignment	not modelled	96.1	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (pcra (subunit)); <b>PDBTitle:</b> structure of dna helicase with adpnp