

CsKTN1-CCMC	MGS. .NTLVFQDHLKARVYALEGLYDTSIIFFGCAICIKHLSTVDDPLMFAKVVWVKKALSEEIEMKCLDAERKARKEITMNG.FFAASPPIFAKSS.EVFCPLDEYPTSS.APPM	115
CsKTN1-mp	MGS. .NTLVFQDHLKARVYALEGLYDTSIIFFGCAICIKHLSTVDDPLMFAKVVWVKKALSEEIEMKCLDAERKARKEITMNG.FFAASPPIFAKSS.EVFCPLDEYPTSS.APPM	115
CmKTN1	MGS. .NTLVFQDHLKARVYALEGLYDTSIIFFGCAICIKHLSTVDDPLMFAKVVWVKKALSEEIEMKCLDAERKARKEITMNG.FFAASPPIFAKSS.EVFCPLDEYPTSS.APPM	115
GhKTN1	MVG. .NSLASFQDHLKARVYALEGLYDTSIIFFGCAICIKHLANLDDPLIEMKVVWVKKALSEEIEMKCLDAERRSRKEITMNG.FRPPSSPPIFAKSS.EVFCPLDEYPTSS.GAPV	115
AIKTN1	MVGSNSLAFQDHLKARVYALEGLYDTSIIFFGCAICIKHLNTLDDPLATKVVWVKKALMEEIEMKCLDAERFARKEITMNG.FFAASPPINTKSS.EVFCPLDEYPTSSGGGFM	118
SIKTN1	MVG. .ASLAFQDHLKARVYALEGLYDTSIIFFGCAICIKHVVNTLDDPLIEMKVVWVKKALSEEIEMKCLDAERGRFKEITMNG.FRPNSPPISTKSS.EVFCPLDEYPTSS.GAPM	115
NKTN1	MVG. .SALAFQDHLKARVYALEGLYDTSIIFFGCAICIKHLNTLDDPLIEMKVVWVKKALSEEIEMKCLDAERKARKEITMNG.FRPPSSPPISTKSS.EVFCPLDEYPTSS.GAPM	117
BdKTN1	NAT. .PLAFQDHLKARVYALEGLYDTSIIFFGCAICIKYLLSTLDDALIEMKVVWVKKALCEEVEIEMKCLDAQLKSRKEITMNG.FRPPSSPPIRSN.KSLEVFCPLDEYPTSS.PPTF	114
HvKTN1	NAN. .PLAFQDHLKARVYALEGLYDTSIIFFGCAICIKHLASLDDNFMKVVWVKKALCEEVEIEMKCLDAQLKSRKEITMNG.FRPPSSPPIRSN.KSLEVFCPLDEYPTSS.PTTF	115
OskTN1	MVS. .ALAFQDHLKARVYALEGLYDTSIIFFGCAICIKHLNTLDDALIEMKVVWVKKALCEEVEIEMKCLDAQLKSRKEITMNG.FRPPSSPPIRSN.KSLEVFCPLDEYPTSS.PPTF	115
SbKTN1	NAN. .PLAFQDHLKARVYALEGLYDTSIIFFGCAICIKHLNTLDDALIEMKVVWVKKALCEEVEIEMKCLDAQLKSRKEITMNG.FRPPSSPPIRSN.KSLEVFCPLDEYPTSS.PAPP	115
CsKTN1-CCMC	DDPDVVFPPSRCS. SSRFAFAAGCVGRKSPDCGAVAFGSSITTRPNTTARCAKACGSSFANSQVRASTAGKSSCAT.GKSSSDSANGD.DDEKSKKGOYEGFPDLDLAAMLERDVLDTSP	232
CsKTN1-mp	DDPDVVFPPSRCS. SSRFAFAAGCVGRKSPDCGAVAFGSSITTRPNTTARCAKACGSSFANSQVRASTAGKSSCAT.GKSSSDSANGD.DDEKSKKGOYEGFPDLDLAAMLERDVLDTSP	232
CmKTN1	DDPDVVFPPSRCS. SSRFAFAAGCVGRKSPDCGAVAFGSSITTRPNTTARCAKACGSSFANSQVRASTAGKSSCAT.GKSSSDSANGD.DDEKSKKGOYEGFPDLDLAAMLERDVLDTSP	232
GhKTN1	DDPDVVFPPSRCT. SSRFAFAAGCVGRKSPDCGAVAFGSSITTRPNTTARCAKACGSSSRTNTCARASTGKKGTGS. GKSTKCSANGDCEKSKKGOYEGFPDLDLAAMLERDVLDTSP	231
AIKTN1	DDPDVVFPPTRFD. SSRFAFAAGCVGRKSPDCGAVAFGPTTRTGFASGGRGATSKSTAGARSTAGKGAAS. .KSNNAESMNGDCEKSKKGOYEGFPDLDLAAMLERDVLDTSP	234
SIKTN1	DDPDVVFPPSR. .TTRFPGAAGCGGRKSPDCGAVAFASTTRTGTITIGRGGTSGSTKACTGVRSSITGKKAPGK. . . . .SAKSDSTDCGEEPEEKSKKGOYEGFPDLDLAAMLERDVLDTSP	229
NKTN1	DDPDVVFPPSR. .TTRFSAFAAGCVGRKSPDCGAVAFGSSITTRPNTTARCAKACGSSSRTNTCARASTGKKGTGS. . . . .STKADSTDCGEEPEEKSKKGOYEGFPDLDLAAMLERDVLDTSP	230
BdKTN1	DDPDVVFPPRCS. .SNRSTRT. CGSSARKSPDCGAVAFGSSITTRPNTTARCAKACGSSSRTNTCARASTGKKGTGS. . . . .KASFAVRSATASSTGCRKCKSSSKPDSASSDAEECKSKKGOYEGFPDLDLAAMLERDVLDTSP	229
HvKTN1	DDPDVVFPPR. .SNRSTRT. CGSSARKSPDCGAVAFGSSITTRPNTTARCAKACGSSSRTNTCARASTGKKGTGS. . . . .KASFAVRSATASSTGCRKCKSSSKPDSASSDAEECKSKKGOYEGFPDLDLAAMLERDVLDTSP	232
OskTN1	DDPDVVFPPR. .SNRSTRT. CGSSARKSPDCGAVAFGSSITTRPNTTARCAKACGSSSRTNTCARASTGKKGTGS. . . . .KASFAVRSATASSTGCRKCKSSSKPDSASSDAEECKSKKGOYEGFPDLDLAAMLERDVLDTSP	230
SbKTN1	DDPDVVFPPR. .SNRSTRT. CGSSARKSPDCGAVAFGSSITTRPNTTARCAKACGSSSRTNTCARASTGKKGTGS. . . . .KASFAVRSATASSTGCRKCKSSSKPDSASSDAEECKSKKGOYEGFPDLDLAAMLERDVLDTSP	230
CsKTN1-CCMC	QVRVDDVAGLSEAKRLLLEAVVPLVWPEYFCGRRPVKCVLWFCPPGCTGKTLAKAVATECGTTFNVSATLASKVRCESERWRCFLDLARAYAPSTIFIDEIDSLQVARGASGEHE	352
CsKTN1-mp	QVRVDDVAGLSEAKRLLLEAVVPLVWPEYFCGRRPVKCVLWFCPPGCTGKTLAKAVATECGTTFNVSATLASKVRCESERWRCFLDLARAYAPSTIFIDEIDSLQVARGASGEHE	352
CmKTN1	QVRVDDVAGLSEAKRLLLEAVVPLVWPEYFCGRRPVKCVLWFCPPGCTGKTLAKAVATECGTTFNVSATLASKVRCESERWRCFLDLARAYAPSTIFIDEIDSLQVARGASGEHE	352
GhKTN1	QVRVDDVAGLSEAKRLLLEAVVPLVWPEYFCGRRPVKCVLWFCPPGCTGKTLAKAVATECGTTFNVSATLASKVRCESERWRCFLDLARAYAPSTIFIDEIDSLQVARGASGEHE	351
AIKTN1	QVRVDDVAGLSEAKRLLLEAVVPLVWPEYFCGRRPVKCVLWFCPPGCTGKTLAKAVATECGTTFNVSATLASKVRCESERWRCFLDLARAYAPSTIFIDEIDSLQVARGASGEHE	354
SIKTN1	QVRVDDVAGLSEAKRLLLEAVVPLVWPEYFCGRRPVKCVLWFCPPGCTGKTLAKAVATECGTTFNVSATLASKVRCESERWRCFLDLARAYAPSTIFIDEIDSLQVARGASGEHE	349
NKTN1	QVRVDDVAGLSEAKRLLLEAVVPLVWPEYFCGRRPVKCVLWFCPPGCTGKTLAKAVATECGTTFNVSATLASKVRCESERWRCFLDLARAYAPSTIFIDEIDSLQVARGASGEHE	350
BdKTN1	QVRVDDVAGLSEAKRLLLEAVVPLVWPEYFCGRRPVKCVLWFCPPGCTGKTLAKAVATECGTTFNVSATLASKVRCESERWRCFLDLARAYAPSTIFIDEIDSLQVARGASGEHE	349
HvKTN1	QVRVDDVAGLSEAKRLLLEAVVPLVWPEYFCGRRPVKCVLWFCPPGCTGKTLAKAVATECGTTFNVSATLASKVRCESERWRCFLDLARAYAPSTIFIDEIDSLQVARGASGEHE	352
OskTN1	QVRVDDVAGLSEAKRLLLEAVVPLVWPEYFCGRRPVKCVLWFCPPGCTGKTLAKAVATECGTTFNVSATLASKVRCESERWRCFLDLARAYAPSTIFIDEIDSLQVARGASGEHE	350
SbKTN1	QVRVDDVAGLSEAKRLLLEAVVPLVWPEYFCGRRPVKCVLWFCPPGCTGKTLAKAVATECGTTFNVSATLASKVRCESERWRCFLDLARAYAPSTIFIDEIDSLQVARGASGEHE	350
CsKTN1-CCMC	SRRVKSSELLVQDGVNNSSTNEDGCRKIVVWLAATNFPVDI DEALRRRLLEKRIYIPLPFESRKLRIENLRTVEVAEVDI DEVARFTEGYSDDLTVNCRDASINCVRRKIAKGTDR	472
CsKTN1-mp	SRRVKSSELLVQDGVNNSSTNEDGCRKIVVWLAATNFPVDI DEALRRRLLEKRIYIPLPFESRKLRIENLRTVEVAEVDI DEVARFTEGYSDDLTVNCRDASINCVRRKIAKGTDR	472
CmKTN1	SRRVKSSELLVQDGVNNSSTNEDGCRKIVVWLAATNFPVDI DEALRRRLLEKRIYIPLPFESRKLRIENLRTVEVAEVDI DEVARFTEGYSDDLTVNCRDASINCVRRKIAKGTDR	472
GhKTN1	SRRVKSSELLVQDGVNNSSTNEDGCRKIVVWLAATNFPVDI DEALRRRLLEKRIYIPLPFESRKLRIENLRTVEVAEVDI DEVARFTEGYSDDLTVNCRDASINCVRRKIAKGTDR	471
AIKTN1	SRRVKSSELLVQDGVNNSSTNEDGCRKIVVWLAATNFPVDI DEALRRRLLEKRIYIPLPFESRKLRIENLRTVEVAEVDI DEVARFTEGYSDDLTVNCRDASINCVRRKIAKGTDR	474
SIKTN1	SRRVKSSELLVQDGVNNSSTNEDGCRKIVVWLAATNFPVDI DEALRRRLLEKRIYIPLPFESRKLRIENLRTVEVAEVDI DEVARFTEGYSDDLTVNCRDASINCVRRKIAKGTDR	469
NKTN1	SRRVKSSELLVQDGVNNSSTNEDGCRKIVVWLAATNFPVDI DEALRRRLLEKRIYIPLPFESRKLRIENLRTVEVAEVDI DEVARFTEGYSDDLTVNCRDASINCVRRKIAKGTDR	470
BdKTN1	SRRVKSSELLVQDGVNNSSTNEDGCRKIVVWLAATNFPVDI DEALRRRLLEKRIYIPLPFESRKLRIENLRTVEVAEVDI DEVARFTEGYSDDLTVNCRDASINCVRRKIAKGTDR	469
HvKTN1	SRRVKSSELLVQDGVNNSSTNEDGCRKIVVWLAATNFPVDI DEALRRRLLEKRIYIPLPFESRKLRIENLRTVEVAEVDI DEVARFTEGYSDDLTVNCRDASINCVRRKIAKGTDR	472
OskTN1	SRRVKSSELLVQDGVNNSSTNEDGCRKIVVWLAATNFPVDI DEALRRRLLEKRIYIPLPFESRKLRIENLRTVEVAEVDI DEVARFTEGYSDDLTVNCRDASINCVRRKIAKGTDR	470
SbKTN1	SRRVKSSELLVQDGVNNSSTNEDGCRKIVVWLAATNFPVDI DEALRRRLLEKRIYIPLPFESRKLRIENLRTVEVAEVDI DEVARFTEGYSDDLTVNCRDASINCVRRKIAKGTDR	470
CsKTN1-CCMC	ENNAKDI SKDPVAMCDREALLKVGQSVSAADI ERHEKVFSEFGS	520
CsKTN1-mp	ENNAKDI SKDPVAMCDREALLKVGQSVSAADI ERHEKVFSEFGS	520
CmKTN1	ENNAKDI SKDPVAMCDREALLKVGQSVSAADI ERHEKVFSEFGS	520
GhKTN1	ENNAKDI SKDPVAMCDREALLKVGQSVSAADI ERHEKVFSEFGS	519
AIKTN1	ENNAKDI SKDPVAMCDREALLKVGQSVSAADI ERHEKVFSEFGS	522
SIKTN1	ENNAKDI SKDPVAMCDREALLKVGQSVSAADI ERHEKVFSEFGS	517
NKTN1	ENNAKDI SKDPVAMCDREALLKVGQSVSAADI ERHEKVFSEFGS	518
BdKTN1	ENNAKDI SKDPVAMCDREALLKVGQSVSPDI ERHEKVAEFGS	517
HvKTN1	ENNAKDI SKDPVAMCDREALLKVGQSVSPDI ERHEKVAEFGS	520
OskTN1	ENNAKDI SKDPVAMCDREALLKVGQSVSPDI ERHEKVAEFGS	518
SbKTN1	ENNAKDI SKDPVAMCDREALLKVGQSVSPDI ERHEKVAEFGS	518

**Fig. S4** Sequence alignment of Katanin p60 homologs. Green line, the AAA+ type ATPase domain; red rectangle, amino acid substitution in CsKTN1 protein of *mp* mutant.