

Additional File 8. Alignment and domain analysis of Triticeae MKKs. The amino acid sequences from multiple genomic copies, along with the accessions reported in Additional File 3, of all Triticeae MKKs identified were aligned in Clustal Omega (www.ebi.ac.uk/Tools/msa/clustalo/) under default settings. A lower case 'p' next to the gene name indicates that only a partial sequence was identified for the given gene. The protein kinase domain is in black font, and the N- and C-terminal extensions in teal font. Missing sequence information, namely 'X' residues, are shown in pink font. Highlighted sequences are the ATP binding signature (blue) which carries the P-loop consensus sequence (GxGxxG), the catalytic C-loop (red) with the DΨK consensus (where Ψ refers to the aliphatic amino acids L/I/V, but not M), the activation T-loop (black), NTF2 domain (pink). Sequence deviations from the S/TxxxxS/T activation loop of plant MKKs are marked in yellow font. Other deviations from consensus are highlighted in yellow. An asterix indicates a stop codon.

MKK3

GxGxxxG

TaMKK3 (3B)p	-----	
TuMKK3p	-----	
HvMKK3-3 (6H)	MAGLEELKRRLQPIFFDADGNVPPPAADGTHDDSSDDCEVTLDGGTVNLLSRSSDEYNI SKLGFHKRTRPDGDYATDKAYRCSCHDMHIFDS	VGNGASSVVHRAIYVPVHRVLALKK
TaMKK3-3 (5AL)	MAGLEDLKRRLQPIFFDADGNVPPPAADGTSDDSSDDCEV-LDSGTVNLLSRSSDEYNI SKLGFHKRTRPDGDYATDKAYRCSCHDMHIFDS	VGIGASSVVHRAIYVPVHRVLALKK
TuMKK3-3	MAGLEDLKRRLQPIFFDADGNVPPPAADGTSDDSSDDCEV-LDSGTVNLLSRSSDEYNI SKLGFHKRTRPDGDYATDKAYRCSCHDMHIFDS	VGIGASSVVHRAIYVPVHRVLALKK
TaMKK3-3 (5BL)	MAGLEDLKRRLQPIFFDADGNVPPPAADGTSDDSSDDCEV-LDSGTVNLLSRSSDEYNI SKLGFHKRTRPDGDYATDKAYRCSCHDMHIFDS	VGNGASSVVYRAIYVPVHRVLALKK
TsMKK3-3 (U)	MAGLEDLKRRLQPIFFDADGNVPPPAADGTSDDSSDDCEV-LDSGTVNLLSRSSDEYNI SKLGFHKRTRPDGDYATDKAYRCSCHDMHIFDS	VGNGASSVVHRAIYVPVHRVLALKK
ScMKK3-3	MAGLEELKRRLQPIFFDADGNVPPPAADGTSDDSSDDCEV-LDGGTVNLLSRSSDEYNI SKLGFHKRTRPDGDYATDKAYRCSCHDMHIFDS	VGNGASSVVHRAIYVPVHRVLALKK
TaMKK3-3 (5DL)	MAGLEELKRRLQPIFFDADGNVPPPAADGTSDDSSDDCEV-LDGGTVNLLSRSSDEYNI SKLGFHKRTRPDGDYATDKAYRCCCHDMHIFDS	VGNGASSVVHRAIYVPVHRVLALKK
TsMKK3-2 (U2)p	MSGLEELKKKLQPLLFDDTDKGGVSTRV---FPEDTCDSYVSDGGTINLLSRSFGEYNINEHGFHKRSTGPEEPDSGEKAYRCASEDMHIFGP	IGNGASSVVQRAIFIPVHRILALKK
BAJ96085.1	-----MKVSDGGTINLLSRSFGEYNINEHGFHKRSTGPEEPDTGEKAYRCASEDMHIFGP	IGNGASSVVQRAIFIPVHRILALKK
AKS50325.1	MAGLEELKKKLQPLLFDDSDKGGVSTRV---FPEDTCDSYVSDGGTINLLSRSFGEYNINEHGFHKRSTGPEEPDTGEKAYRCASEDMHIFGP	IGNGASSVVQRAIFIPVHRILALKK
TuMKK3-2	MSGLEELKKKLQPLLFDDTDKGGVSTRV---FPEDTCDSYVSDGGTINLLSRSFGEYNINEHGFHKRSTGPEEPDTGEKAYRCASEDMHIFGP	IGNGASSVVQRAIFIPVHRILALKK
ScMKK3-1	MSGLEELKKKLQPLLFDDSDKGGVSTRV---FPEDTCDSYVSDGGTINLLSRSFGEYNINEHGFHKRSTGPEEPDTGEKAYRCASEDMHIFGP	IGNGASSVVQRAIFIPVHRILALKK
TsMKK3-2 (U1)	MAGLEELKKKLQPLLFDDSDKGGVSTRV---FPEDTCDSYVSDGGTINLLSRSFGEYNINEHGFHKRSTGPEEPDTGEKAYRCASEDMHIFGP	IGSGASSVVQRAIFIPVHRILALKK
HvMKK3-2 (5H)	MAGLEELKKKLQPLLFDDSDKGGVSTRV---FPEDTCDSYVSDGGTINLLSRSFGEYNINEHGFHKRSTGPEEPDTGEKAYRCASEDMHIFGP	IGNGASSVVQRAIFIPVHRILALKK
BAU62004.1	MAGLEELKKKLQPLLFDDSDKGGVSTRV---FPEDTCDSYVSDGGTINLLSRSFGEYNINEHGFHKRSTGPEEPDTGEKAYRCASEDMHIFGP	IGNGASSVVQRAIFIPVHRILALKK
TaMKK3-2 (5BL)	MAGLEELKKKLQPLLFDDSDKGGVSTRV---FPEDTCDSYVSDGGTINLLSRSFGEYNINEHGFHKRSTGPEEPDTGEKAYRCASEDMHIFGP	IGSGASSVVQRAIFIPVHRILALKK
TsMKK3-2 (B)	MAGLEELKKKLQPLLFDDSDKGGVSTRV---FPEDTCDSYVSDGGTINLLSRSFGEYNINEHGFHKRSTGPEEPDTGEKAYRCASEDMHIFGP	IGSGASSVVQRAIFIPVHRILALKK
AetMKK3-2	MAGLEELKKKLQPLLFDDSDKGGVSTRV---FPEDTCDSYVSDGGTINLLSRSFGEYNINEHGFHKRSTGPEEPDTGEKAYRCASEDMHIFGP	IGSGASSVVQRAIFIPVHRILALKK
TaMKK3-2 (5DL)	MSGLEELKKKLQPLLFDDSDKGGVSTRV---FPEDTCDSYVSDGGTINLLSRSFGEYNINEHGFHKRSTGPEEPDTGEKAYRCASEDMHIFGP	IGNGASSVVQRAIFIPVHRILALKK

MKK3 continued

DΨK

TaMKK3(3B)p -----KIADFGV SAGLD
 TuMKK3p -----KIADFGV SAGLD
 HvMKK3-3(5H) INIFEKEKRQQILNEIRTLAASCYPGLVEFQGVFYTPDSGEIYFALEYMDGGSLADIRVKKFITEPVLSHMLQKVLLALRYLHEVRRLVHRDIKPANLLLNLKGDTKITDFGVTSGLH
 TaMKK3-3(5AL) ISIFDKEKRQQILNEITTLAASCYPGLVEFQGFYTPDSGEIYFALEYMDGGSLADIRVKKFITEPVLSHMLQKVLLALRYLHEVRRLVHRDIKPANLLLNLKRDTKITDFGVTSGLH
 TuMKK3-3 ISIFDKEKRQQILNEITTLAASCYPGLVEFQGFYTPDSGEIYFALEYMDGGSLADIRVKKFITEPVLSHMLQKVLLALRYLHEVRRLVHRDIKPANLLLNLKGDTKITDFGVTSGLH
 TaMKK3-3(5BL) INIFDKERRQQILNEIRTLAASCYPGLVEFQGVFYTPDSGEIYFALEYMDGGSLADIRVKKFITEPVLSHMLQKVLLALRYLHEVRRLVHRDIKPANLLLNLKGDTKITDFGVTSGLH
 TsMKK3-3(U) INIFDKERRQQILNEIRTLAASCYPGLVEFQGVFYTPDSGEIYFALEYMDGGSLADIRVKKFITEPVLSHMLQKVLLALRYLHEVRRLVHRDIKPANLLLNLKGDTKITDFGVTSGLH
 ScMKK3-3 IN-FEKEKRQQILNEIRTLAASCYPGLVEFQGVFYTPDSGEIYFALEYMDGGSLADIRVKKFITEPVLSHMLQKVLLALRYLHEVRRLVHRDIKPANLLLNLKGDTKITDFGVTSGLH
 TaMKK3-3(5DL) INIFDKEKRQQILNEIRTLAASCYPGLVEFQGVFYTPDSGEIYFALEYMDGGSLADIRVKKFITEPVLSHMLQKVLLALRYLHEVRRLVHRDIKPANLLLNLKGDTKITDFGVSSGLH
 TsMKK3-2(U2)p INIFEKEKRQQILNEMRTLCEASCYPGLVEFQGFYMPDSGQISIALEYMDGGSLADVIRVKKSIPEPVLAHMLLKVLLGLKYLHEVRHLVHRDLKPANILVNLKGEAKITDFGV SAGLD
 BAJ96085.1 INIFEKEKRQQILNEMRTLCEASCYPGLVEFQGFYMPDSGQISIALEYMDGGSLADVIRVKKSIPEPVLAHMLLKVLLGLKYLHEARHLVHRDLKPANILVNLKGEAKITDFGV SAGLD
 AKS50325.1 INIFEKEKRQQILNEMRTLCEASCYPGLVEFQGFYMPDSGQISIALEYMDGGSLADVIRVKKSIPEPVLAHMLQKVLLGLKYLHEVRHLVHRDLKPANLLVNLKGEAKITDFGV SAGLD
 TuMKK3-2 INIFEKEKRQQILNEMRTLCEASCYPGLVEFQGFYMPDSGQISIALEYMDGGSLADVIRVKKSIPEPVLAHMLQKVLLGLKYLHEVRHLVHRDLKPANLLVNLKGEAKITDFGV SAGLD
 ScMKK3-1 INIFEKEKRQQILNEMRTLCEASCYPGLVEFQGFYMPDSGQISIALEYMDGGSLADVIRVKKSIPEPVLAHMLLKVLLGLKYLHEVRHLVHRDLKPANILVNLKGEAKITDFGV SAGLD
 TsMKK3-2(U1) INIFEKEKRQQILNEMRTLCEASCYPGLVEFQGFYMPDSGQISIALEYMDGGSLADVIRVKKSIPEPVLAHMLLKVLLGLKYLHEVRHLVHRDLKPANILVNLKGEAKITDFGV SAGLD
 HvMKK3-2(5H) INIFEKEKRQQILNEMRTLCEASCYPGLVEFQGFYMPDSGQISIALEYMDGGSLADVIRVKKSIPEPVLAHMLLKVLLGLKYLHEARHLVHRDLKPANILVNLKGEAKITDFGV SAGLD
 BAU62004.1 INIFEKEKRQQILNEMRTLCEASCYPGLVEFQGFYMPDSGQISIALEYMDGGSLADVIRVKKSIPEPVLAHMLLKVLLGLKYLHEARHLVHRDLKPANILVNLKGEAKITDFGL SAGLD
 TaMKK3-2(5BL) INIFEKEKRQQILNEMRTLCEASCYPGLVEFQGFYMPDSGQISIALEYMDGGSLADVIRVKKSIPEPVLAHMLLKVLLGLKYLHEVRHLVHRDLKPANILVNLKGEAKITDFGV SAGLD
 TsMKK3-2(B) INIFEKEKRQQILNEMRTLCEASCYPGLVEFQGFYMPDSGQISIALEYMDGGSLADVIRVKKSIPEPVLAHMLLKVLLGLKYLHEVRHLVHRDLKPANILVNLKGEAKITDFGV SAGLD
 AetMKK3-2 INIFEKEKRQQILNEMRTLCEASCYPGLVEFQGFYMPDSGQISIALEYMDGGSLADVIRVKKSIPEPVLAHMLLKVLLGLKYLHEVRHLVHRDLKPANILVNLKGEAKITDFGV SAGLD
 TaMKK3-2(5DL) INIFEKEKRQQILNEMRTLCEASCYPGLVEFQGFYMPDSGQISIALEYMDGGSLADVIRVKKSIPEPVLAHMLLKVLLGLKYLHEVRHLVHRDLKPANILVNLKGEAKITDFGV SAGLD

MKK3 continued

TaMKK3 (3B)p -----PDARPTCEQLLSHPFIKRYEEAGVDLAAYV
TuMKK3p GTMAMRATFVGTVTYMLPERIRGDNLYAADIWSLGLTVLECATGKFPYDFSEGPTNLMLQILDDPSPTPPEDAYSPEFRSFIDDCLQKEPDARSTCEQLLSHPFIKRYEEAGVDLAAYV
HvMKK3-3 (5H) DSITMCATFLGSVTYMSPERIRNENYSYAADIWSLGLTALECATGRYPYDVSGGEADLMLQILEDPSPTPPQHMHSEEFCSFIDACLQKDADARPTCDQLLSHAFIKKYEKPGVDLAEYN
TaMKK3-3 (5AL) DSVTMCATFLGSVTYMSPERIRNENYSYAADIWSLGLTALECATGRYPYDVNGGEADLMLQILEDPSPTPPQHMHSEEFCSFIDACLQKDADARPTCNELLSHSFIKRYEGPGVDLAEYN
TuMKK3-3 DSVTMCATFLGSVTYMSPERIRNENYSYAADIWSLGLTALECATGRYPYDVNGGEADLMLQILEDPSPTPPQHMHSEEFCSFIDACLQKDADARPTCNELLSHSFIKRYEGPGVDLAEYN
TaMKK3-3 (5BL) DSVTMCATFLGSVTYMSPERIRNENYSYAADIWSLGLTALECATGRYPYDVNGGEADLMLQILEDPSPTPPQHMHSEEFCLFIDACLQKDADARPTCDELLSHSFIKRYEGPGVDLAEYN
TsMKK3-3 (U) DSVTMCATFLGSVTYMSPERIRNENYSYAADIWSLGLTALECATGRYPYDVSGGEADLMLQILEDPSPTPPQHMHSEEFCSFIDACLQKDADARPTCDELLSHSFIKRYEGPGVDLAEYN
ScMKK3-3 DSVTMCTTFLGSVTYMSPERIRNENYSYAADIWSLGLTALECATGRYPYDVSGGEADLMLQILEDPSPTPPQHMHSEEFCSFIDACLQKDADARPTCDQLLSHAFIKKYEKPGVDLAEYN
TaMKK3-3 (5DL) DSVTMCATFLGSVTYMSPERIRNENYSYAADIWSLGLTALECATGRYPYDVNGGEADLMLQILEDPSPTPPQHMHSEEFCSFIDACLQKDADARPTCDQLLSHAFIKKYEKPGVDLAEYN
TsMKK3-2 (U2)p NTMAMCATFVGTVTYMSPERIRNENYSYAADIWSLGLTILECATGKFPYVNEGPANLMLQILDDPSAPPADGYTPEFCSFINDCLRKDADARPTCEQLLSHAFIKRYEQTGVDLAAYV
BAJ96085.1 NTMAMCATFVGTVTYMSPERIRNENYSYAADIWSLGLTILECATGKFPYVNEGPANLMLQILDDPSAPPEDAYTPEFCSFINDCLRKDADARPTCEQLLSHPFIKRYEETRVDLAAYV
AKS50325.1 NTMAMCATFVGTVTYMSPERIRNENYSYAADIWSLGLTILECATGKFPYVNEGPANLMLQILDDPSPTPPEDAYTPEFCSFINDCLRKDADARPTCEQLLSHPFIKRYEQTGVDLAAYV
TuMKK3-2 NTMAMCATFVGTVTYMSPERIRNENYSYAADIWSLGLTILECATGKFPYVNEGPANLMLQILDDPSPTPPEDAYTPEFCSFINDCLRKDADARPTCEQLLSHAFIKRYEQTGVDLAAYV
ScMKK3-1 NTMAMCATFVGTVTYMSPERIRNENYSYAADIWSLGLTILECATGKFPYVNEGPANLMLQILDDPSAPPADGYTPEFCSFINDCLRKDADTRPTCEQLLSHPFIKRYEPTGVDLAAYV
TsMKK3-2 (U1) NTMAMCATFVGTVTYMSPERIRNENYSYAADIWSLGLTILECATGKFPYVNEGPANLMLQILDDPSAPPEDAYTPEFCSFINDCLRKDADARPTCEQLLSHPFIKRYEPTGVDLAAYV
HvMKK3-2 (5H) NTMAMCATFVGTVTYMSPERIRNENYSYAADIWSLGLTILECATGKFPYVNEGPANLMLQILDDPSAPPEDAYTPEFCSFINDCLRKDADARPTCEQLLSHPFIKRYEETGVDLAAYV
BAU62004.1 NTMAMCATFVGTVTYMSPERIRNENYSYAADIWSLGLTILECATGKFPYVNEGPANLMLQILDDPSAPPEDAYTPEFCSFINDCLRKDADARPTCEQLLSHPFIKRYEETRVDLAAYV
TaMKK3-2 (5BL) NTMAMCATFVGTVTYMSPERIRNENYSYAADIWSLGLTILECATGKFPYVNEGPANLMLQILDDPSAPPEDAYTPEFCSFINDCLRKDADARPTCEQLLSHPFIKRYEQTGVDLAAYV
TsMKK3-2 (B) NTMAMCATFVGTVTYMSPERIRNENYSYAADIWSLGLTILECATGKFPYVNEGPANLMLQILDDPSAPPEDAYTPEFCSFINDCLRKDADARPTCEQLLSHPFIKRYEQTGVDLAAYV
AetMKK3-2 NTMAMCATFVGTVTYMSPERIRNENYSYAADIWSLGLTILECATGKFPYVNEGPANLMLQILDDPSAPPEDAYTPEFCSFIKDCLWKDADARPTCEQLLSHPFIKRYEQTGVDLAAYV
TaMKK3-2 (5DL) NTMAMCATFVGTVTYMSPERIRNENYSYAADIWSLGLTILECATGKFPYVNEGPANLMLQILDDPSAPPEDAYTPEFCSFINDCLRKYADARPTCEQLLSHPFIKRYEQTGVDLAAYV
: **:***** **:* ** * * *

MKK3 continued

TaMKK3(3B)p GGVVDPTESLKQ IAEMLAVHYLLFNGSDGSWNHMKTLMEESSFSFLGNVCVEQSVIFDTLSTIRNKCLKGDQPGGGIVHVVEKIHYGANGEREITVRVFGPFIVGNQFLVLGEGLOAEG
 TuMKK3p GGVVNPTERLKQ IAEMLVVHYLLFNGSDGSWHHMETPYMEESSFRFSRNVYVGQSAIFDTLSTIRNFKGDQPSGGIFHVVEKIHCGADGEREITVRVSGSFIVGNQFLILGEGLOAEG
 HvMKK3-3(5H) KSVHDPSEERLSQ IAHMLAVHYLLIFDGGDDQWCHMKSFYEQDSTFSFSEETHFGKSDIFDTLSRIREMLKDNSRCKKIGRVMKVKYCRAGHEEGMSVRVSGSFIMGNEFLVCADGFCAEG
 TaMKK3-3(5AL) KSVHDPSEERLSQ IAHMLAVHYLLIF-----HMKSFYEQDSTFSFSGETHVGKSDIFDTLSRIREMLKGNRCEKIGRVMKVKYCRAGHEEGMSVRVSGSFIMGNEFLVCADGFCAEG
 TuMKK3-3 KSVHDPSEERLSQ IAHMLAVHYLLIF-----HMKSFYEQDSTFSFSGETHVGKSDIFDTLSRIREMLKGNRCEKIGRVMKVKYCRAGHEEGMSVRVSGSFIMGNEFLVCADGFCAEG
 TaMKK3-3(5BL) RSVHDPSEERLSQ IAHMLAVHYLLIFDGGDDQWHHMKSFYEQDSTFSFSGETHVGKSDIFDTLSRIREMLKGNRCEKIGRVMKVKY-RAHGEEGTSVRVSGSFIMGNEFLVCADGFCAEG
 TsMKK3-3(U) RSVHDPSEERLSQ IAHMLAVHYLLIFDGGDDQWHHMKSFYEQDSTFSFSGETHVGKSDIFDTLSRIREMLKGNRCEKIGRVMKVKY-RAHGEEGMSVRVSGSFIMGNEFLVCADGFCAEG
 ScMKK3-3 KSVHDPSEERLSQ IAHMLAVHYLLIFDGGDDQWRHMKSFYEQDSTFSFSGETHVGKSDIFDTLSRIREMLKGNRCEKIGRVMKVKYCRAGHEEGMSVRVSGSFIMGNEFLVCADGFCAEG
 TaMKK3-3(5DL) KSVHDPSEERLSQ IAHMLAVHYLLIFDGGDDQWRHMKSFYEQDSTFSFSGETHVGKSDIFDTLSRIREMLKGNRCEKIGRVMKVKYCRAGHEEGMSVRVSGSFIMGNEFLVCADGFCAEG
 TsMKK3-2(U2)p RDVVNPTERLKQ IAEMLAVHYLLFNGSEGPWNMKTFFYKEESSFSFSGNVYVGQSAIFDTLSNIRKCLKGDRPREKIVHVVEKLHCRAKWNRCYPCVWIIHHGQP-----
 BAJ96085.1 RGVVNPTERLKQ IAEMLAVHYLLFNGSEGPWNHMKTFYREESSFRYLRCYIL*-----
 AKS50325.1 RGVVNPTERLKQ IAEMLAVHYLLFNGSEGPWNMKTFFYKEESSFSFSGNVYVGQSAIFDTLSNIRKCLKGDRPREKIVHVVEKLHCRRANGETEIAIRVSGSFITGNQFLIFGEGLOAEG
 TuMKK3-2 RGVVNPTERLKQ IAEMLAVHYLLFNGSEGPWNMKTFFYKEESSFSFSGNVYVGQSAIFDTLSNIRKCLKGDRPREKIVHVVEKLHCRRANGETEIAIRVSGSFITGNQFLIFGEGLOAEG
 ScMKK3-1 RGVVNPTERLKQ IAEMLAVHYLLFDGSEGPWNHMKTFYKEESSFSFSGNVYVGQSAIFDTLSNIRKCLKGDRPREKIVHVVEKLHCRRANGESEIAIRVSGSFITGNQFLIFGEGLOAEG
 TsMKK3-2(U1) RGVVNPTERLKQ IAEMLAVHYLLFDGSEGPWNHMKTFYKEESSFSFSGNVYVGQSAIFDTLSNIRKCLKGDRPREKIVHVVEKLHCRRANGESEIAIRVSGSFITGNQFLIFGEGLOAEG
 HvMKK3-2(5H) RGVVNPTERLKQ IAEMLAVHYLLFDGSEGPWNHMKTFYREESSFSFSGNVYVGQSAIFDTLSNIRKCLKGDRPREKIVHVVEKLHCRRANGETEIAIRVSGSFITGNQFLIFGEGLOAEG
 BAU62004.1 RGVVNPTERLKQ IAEMLAVHYLLFNGSEGPWNHMKTFYREESSFSFSGNVYVGQSAIFDTLSNIRKCLKGDRPREKIVHVVEKLHCRRANGETEIAIRVSGSFITGNQFLIFGEGLOAEG
 TaMKK3-2(5BL) RGVVNPTERLKQ IAEMLAVHYLLFNGSEGPWNHMKTFYREESSFSFSGNVYVGQSAIFDTLSNIRKCLKGDRPREKIVHVVEKLHCRRANGETEIAIRVSGSFITGNQFLIFGEGLOAEG
 TsMKK3-2(B) RGVVNPTERLKQ IAEMLAVHYLLFNGSEGPWNHMKTFYREESSFSFSGNVYVGQSAIFDTLSNIRKCLKGDRPREKIVHVVEKLHCRRANGETEIAIRVSGSFITGNQFLIFGEGLOAEG
 AetMKK3-2 RGVVNPTERLKQ IAEMLAVHYLLFNGSEGPWNHMKTFYREESSFSFSGNVYVGQSAIFDTLSNIRKCLKGDRPREKIVHVVEKLHCRRANGETEIAIRVSGSFITGNQFLIFGEGLOAEG
 TaMKK3-2(5DL) RGVVNPTERLKQ IAEMLAVHYLLFNGSEGPWDHMKTFYREESSFSFSGNVYVGQSAIFDTLSNIRKCLKGDRPREKIVHVVEKLHCRRANGETEIAIRVSGSFITGNQFLISGEGLOAEG
 * :*: * .***.***.*****:* :*: * :*: * : . .

MKK3 continued

TaMKK3 (3B)p MP SLDELTVDI PRIRVGQFREQFIMQPGISM ECYYSRQDLYI IQS*
 TuMKK3p MP GPDELAIDIPSNRAGQFREQFIMQPGISM ECYYP RQDLYI S*--
 HvMKK3-3 (5H) ML SIVEISPDILSKQACHFQEDFFMEPGTAMGCYVISRQELHI PVS*
 TaMKK3-3 (5AL) ML SMVELSPDILSKQAGHFQEDFFMEPGTAMGCYVISKQELHI GVS*
 TuMKK3-3 ML SMVELSPDILSKQAGHFQEDFFMEPGTAMGCYVISKQELHI GVS*
 TaMKK3-3 (5BL) ML SIVELSPDILSKQAGHFQEDFFMEPGTAMGCYVISRQELHI GVS*
 TsMKK3-3 (U) ML SM-ELSPDILSKQAGHFQEDFFMEPGTAMGCYVISRQELHI GVS*
 ScMKK3-3 ML SIVELSPDILSKQAGHFQEDFFMEPGTAMGCYVISRQELHI AVS*
 TaMKK3-3 (5DL) ML SIVELSPDILSKQAGHFQEDFFMEPGTAMGCYVISRQELHI GVS*
 TsMKK3-2 (U2)p I PDIW-----
 BAJ96085.1 -----
 AKS50325.1 MP SLEEIDIDIPSKRVGQFREQFTVHPGTSMGCYYIARQDLYI IQA*
 TuMKK3-2 MP SLEEIDIDIPSKRVGQFREQFTVHPGTSMGCYYIAKQDLYI IVQS*
 ScMKK3-1 MP SLDEIGVDIPSKRVGQFREQFTVLPGTSMGCYYIAKQDLYI IVQS*
 TsMKK3-2 (U1) MP SLDEIGVDIPSKRVGQFREQFTVLPGTSMGCYYIAKQDLYI IVQS*
 HvMKK3-2 (5H) MP SLDEIDIDIPSKRVGQFREQFTVHPGTSMGCYYIAKQDLYI IQS*
 BAU62004.1 MP SLDEIDIDIPSKRVGQFREQFTVHPGTSMGCYYIAKQDLYI IQS*
 TaMKK3-2 (5BL) MP SLDGIDIDIPSKRVGQFREQFTVHPGTSMGCYYIAKQDLYI IVQS*
 TsMKK3-2 (B) MP SLDGIDIDIPSKRVGQFREQFTVHPGTSMGCYYIAKQDLYI IVQS*
 AetMKK3-2 MP SLDEINIDIPSKRVGQFREQFTVLPGTSMGCYYIAKQDLYI IVQS*
 TaMKK3-2 (5DL) MP SLDEINIDIPSKRVGQFREQFTVLPGTSMGCYYIAKQDLYI IVQS*

MKK4 continued

```
AK374401.1      RGIYE-----ER*
TsMKK4(U)       PQQQPQVLAAPPC*-----
HvMKK4(6H)     PQ-QQPQVLAAPPCQPPATINQVGMERX
TaMKK4(6AL)    PP-QQPQALAAPPC*-----
TaMKK4(6DL)    PQ-QQPQALAAPPC*-----
ScMKK4          PQ-QQPQVLAAPPC*-----
TaMKK4(6BL)    PQ-QQPQVLAAPPC*-----
TuMKK4         P-PQPQALAAPPC*-----
AetMKK4        PPPQPQALAAPPC*-----
                :
```


MKK6

TuMKK6 MRGKKPLKEL--SVPAQETPVDFKFLTASGTFKDGELRLNQRGLQLI SEENGDEHQSTKMKVEDVQLSMDDLEMIQV **GxGxxG** IGKGGGGVQVLRHKWVGTFFYALKGIQMNIQESVRKQIVQELKI
AK333543.1 MRGKKPLKELTSLVPAQETPVDFKFLTASGTFKDGELRLNQRGLQLI SEENGDEHQSTKMKVEDVQLSMDDLEMIQV IGKGGGGVQVLRHKWVGTFFYALKGIQMNIQESVRKQIVQELKI
TaMKK6 (4BL) MRGKKPLKELTSLVPAQETPVDFKFLTASGTFKDGELRLNQRGLQLI SEENGDEHQSTKMKVEDVQLSMDDLEMIQV IGKGGGGVQVLRHKWVGTFFYALKGIQMNIQESVRKQIVQELKI
ScMKK6 MRGKKPLKELTSLVPAQETPVDFKFLTASGTFKDGELRLNQRGLQLI SEENGDEHQSTKMKVEDVQLSMDDLEMIQV IGKGGGGVQVLRHKWVGTFFYALKGIQMNIQESVRKQIVQELKI
AK250233.1 MRGKKPLKELTSLVPAQETPVDFKFLTASGTFKDGELRLNQRGLQLI SEENGDEHQSTKMKVEDVQLSMDDLEMIQV IGKGGGGVQVLRHKWVGTFFYALKGIQMNIQESVRKQIVQELKI
HvMKK6 (4H) MRGKKPLKELTSLVPAQETPVDFKFLTASGTFKDGELRLNQRGLQLI SEENGDEHQSTKMKVEDVQLSMDDLEMIQV IGKGGGGVQVLRHKWVGTFFYALKGIQMNIQESVRKQIVQELKI
TsMKK6 (R) MRGKKPLKELTSLVPAQETPVDFKFLTASGTFKDGELRLNQRGLQLI SEENGDEHQSTKMKVEDVQLSMDDLEMIQV IGKGGGGVQVLRHKWVGTFFYALKGIQMNIQESVRKQIVQELKI
TaMKK6 (4AL) MRGKKPLKELTSLVPAQETPVDFKFLTASGTFKDGELRLNQRGLQLI SEENGDEHQSTKMKVEDVQLSMDDLEMIQV IGKGGGGVQVLRHKWVGTFFYALKGIQMNIQESVRKQIVQELKI
TaMKK6 (4DL) MRGKKPLKELTSLVPAQETPVDFKFLTASGTFKDGELRLNQRGLQLI SEENGDEHQSTKMKVEDVQLSMDDLEMIQV IGKGGGGVQVLRHKWVGTFFYALKGIQMNIQESVRKQIVQELKI
AetMKK6 MRGKKPLKELTSLVPAQETPVDFKFLTASGTFKDGELRLNQRGLQLI SEENGDEHQSTKMKVEDVQLSMDDLEMIQV IGKGGGGVQVLRHKWVGTFFYALKGIQMNIQESVRKQIVQELKI

TuMKK6 NQATQSPHIVLCHQSFYHNGVIYLVLEYMDRGLADI IKQVKTILEPYLAVLCKQVLEGLLYLHHERH **DWK** VIHRDIKPSNLLVNHKGEVKITDFGVSAVLASSIGQRDTFVGTYNMAPERI
AK333543.1 NQATQSPHIVLCHQSFYHNGVIYLVLEYMDRGLADI IKQVKTILEPYLAVLCKQVLEGLLYLHHERH VIHRDIKPSNLLVNHKGEVKITDFGVSAVLASSIGQRDTFVGTYNMAPERI
TaMKK6 (4BL) NQATQSPHIVLCHQSFYHNGVIYLVLEYMDRGLADI IKQVKTILEPYLAVLCKQVLEGLLYLHHERH VIHRDIKPSNLLVNHKGEVKITDFGVSAVLASSIGQRDTFVGTYNMAPERI
ScMKK6 NQATQSPHIVLCHQSFYHNGVIYLVLEYMDRGLADI IKQVKTILEPYLAVLCKQVLEGLLYLHHERH VIHRDIKPSNLLVNHKGEVKITDFGVSAVLASSIGQRDTFVGTYNMAPERI
AK250233.1 NQATQSPHIVLCHQSFYHNGVIYLVLEYMDRGLADI IKQVKTILEPYLAVLCKQVLEGLLYLHHERH VIHRDIKPSNLLVNHKGEVKITDFGVSAVLASSIGQRDTFVGTYNMAPERI
HvMKK6 (4H) NQATQSPHIVLCHQSFYHNGVIYLVLEYMDRGLADI IKQVKTILEPYLAVLCKQVLEGLLYLHHERH VIHRDIKPSNLLVNHKGEVKITDFGVSAVLASSIGQRDTFVGTYNMAPERI
TsMKK6 (R) NQATQSPHIVLCHQSFYHNGVIYLVLEYMDRGLADI IKQVKTILEPYLAVLCKQVLEGLLYLHHERH VIHRDIKPSNLLVNHKGEVKITDFGVSAVLASSIGQRDTFVGTYNMAPERI
TaMKK6 (4AL) NQATQSPHIVLCHQSFYHNGVIYLVLEYMDRGLADI IKQVKTILEPYLAVLCKQVLEGLLYLHHERH VIHRDIKPSNLLVNHKGEVKITDFGVSAVLASSIGQRDTFVGTYNMAPERI
TaMKK6 (4DL) NQATQSPHIVLCHQSFYHNGVIYLVLEYMDRGLADI IKQVKTILEPYLAVLCKQVLEGLLYLHHERH VIHRDIKPSNLLVNHKGEVKITDFGVSAVLASSIGQRDTFVGTYNMAPERI
AetMKK6 NQATQSPHIVLCHQSFYHNGVIYLVLEYMDRGLADI IKQVKTILEPYLAVLCKQVLEGLLYLHHERH VIHRDIKPSNLLVNHKGEVKITDFGVSAVLASSIGQRDTFVGTYNMAPERI

TuMKK6 SGSSYDYKSDVWSLGLVILECAIGRFPTYTPPEGEGWLSFYELLEAIVDQPPPSAPADQFSPEFCSFISSCIQKDAERMSASELLNHAFIKKFEDKDLDRILVESLEQPMNVPE*
AK333543.1 SGSSYDYKSDIWSLGLVILECAIGRFPTYTPPEGEGWLSFYELLEAIVDQPPPSAPADQFSPEFCSFISSCIQKDAERMSASELLNHAFIKKFEDKDLDRILVESLEQPMNVPE*
TaMKK6 (4BL) SGSSYDYKSDIWSLGLVILECAIGRFPTYTPPEGEGWLSFYELLEAIVDQPPPSAPADQFSPEFCSFISSCIQKDAERMSASELLNHAFIKKFEDKDLDRILVESLEQPMNVPE*
ScMKK6 SGSSYDYKSDVWSLGLVILECAIGRFPTYTPPEGEGWLSFYELLEAIVDQPPPSAPADQFSPEFCSFISSCIQKDAERMSASELLNHAFIKKFEDKDLDRILVESLEQPMNVPE*
AK250233.1 SGSSYDYKSDVWSLGLVILECAIGRFPTYTPPEGEGWLSFYELLEAIVDQPPPSAPADQFSPEFCSFISSCIQKDAERMSASELLNHAFIKKFEDKDLDRILVESLEQPMNVPE*
HvMKK6 (4H) SGSSYDYKSDVWSLGLVILECAIGRFPTYTPPEGEGWLSFYELLEAIVDQPPPSAPADQFSPEFCSFISSCIQKDAERMSASELLNHAFIKKFEDKDLDRILVESLEQPMNVPE*
TsMKK6 (R) SGSSYDYKSDVWSLGLVILECAIGRFPTYTPPEGEGWLSFYELLEAIVDQPPPSAPADQFSPEFCSFISSCIQKDAERMSASELLNHAFIKKFEDKDLDRILVESLEQPMNVPE*
TaMKK6 (4AL) SGSSYDYKSDVWSLGLVILECAIGRFPTYTPPEGEGWLSFYELLEAIVDQPPPSAPADQFSPEFCSFISSCIQKDAERMSASELLNHAFIKKFEDKDLDRILVESLEQPMNVPE*
TaMKK6 (4DL) SGSSYDYKSDVWSLGLVILECAIGRFPTYTPPEGEGWLSFYELLEAIVDQPPPSAPADQFSPEFCSFISSCIQKDAERMSASELLNHAFIKKFEDKDLDRILVESLEQPMNVPE*
AetMKK6 SGSSYDYKSDVWSLGLVILECAIGRFPTYTPPEGEGWLSFYELLEAIVDQPPPSAPADQFSPEFCSFISSCIQKDAERMSASELLNHAFIKKFEDKDLDRILVESLEQPMNVPE*
*****:*****

MKK10 continued

TuMKK10p	REVIAQRV*-----
AetMKK10p	-----
HvMKK10(1H)p	RHVIVETM*-----
ScMKK10p	REIIVETM*-----
BAJ94499.1	AALVAEAAELGDQ*-----
HvMKK10-2(4H)	AALVAEAAELGDQ*-----
TaMKK10-2(4AS)	AALVAEAAELGDQ*-----
TsMKK10p	-----
TaMKK10-2(4BL)	AALVAEAAELGDQ*-----
TaMKK10-2(4DL)	AALVAEAAELGDQ*-----
TuMKK10-1/3	RKLIEQRC*-----
TaMKK10-1/3(4BSc1)	-----
TaMKK10-1/3(4BSc4)	RKLVADASSSL*-----
TaMKK10-1/3(4BSc5)	-----
TaMKK10-1/3(4DSc2)	RKLVADASSPSSDCRHT*
TaMKK10-1/3(4BSc3)	RKLVADASSSL*-----
HvMKK10-1/3(U)	RKLVADASSSL*-----
TaMKK10-1/3(4AL)	RKLVADASSSL*-----
TaMKK10-1/3(4BSc2)	RKLVADASSSL*-----
TaMKK10-1/3(4DSc1)	RKLVADASSPSSLECRHT*
AetMKK10-5p	REVIAQR-----
HvMKK10-5(4H)	REVIEQRQ*-----
TaMKK10-5(4DS)	REVIAQRV*-----
TaMKK10-5(4AL)	REVIAQRV*-----
TaMKK10-5(4BS)	REVIEQRV*-----
HvMKK10-4(4H)	CQVIEQRSMPISTRV*---
TaMKK10-4(3B)	REVIDQRRCR*-----
TaMKK10-4(4BS)	REAIEQRRCR*-----
TaMKK10-4(4DS)	REVIEQRRCG*-----
TaMKK10-4(4ALc2)	RKLIEQRC*-----
TaMKK10-4(4ALc1)	GEVIKQRC*-----
TuMKK10-4	GEVIKQRC*-----