

Figure S1: Cloning strategy in pGreen 0179 for expression of the fusion protein pre-pro-3xHA-mCherry-AtCEP2-KDEL under control of the endogenous AtCEP2 promoter.

DNA sequence:

GGTACCagtagagtcacttccaagaaactagggaaacatcaaaccacgctcggttcattttggggatccttatgaaat
acacaagccttatacaaaaaaaaaatattataaaaaaaaaatgaacgatatattaattcgtaattacataggccttaaaacc
aagataagatcgggtacatggtgaaaatgaaaattattcaatctcctaataagaggtgagacaattatcaattcgaa
actcatacatcaatcataaaagctacaatatttttctcaactccatcaattatccggtgggagtcatacaaaaaaaaa
aattaaaaaaaaattattacatatatatgtatttttttttcagaaaagtgaatctctttcgaacatatgaaattat
gaatattcatcaattggcctaggattacgagatcaacgtaaattatttaatacaaaaaataaaaaatagtgttc
cttgcattaggaagcattatccaaccacgacgcccgggtattaagccaagatccattccaattattcattcat
atctactacctaanaacgacattagctttttataaagaaagtcttaaccacgacggtgttcataatttaaatatt
acatttggttgtaaacaccaatggtatgcctaacaacttaataaaaaccgccataattgttttttattgtgtttt
tgaaaaactacttgcccgttggttatcttgtggcctgagtttttttctcttttgtttttaatatatgtagtatga
aaccacgtttcaacaaatgggctgcgccaatggtcacgcatcttgcccttgagaattttgaaatacaactaatta
gagattaaggtatggaaatgtacaaaaatcgccacgagatcccttcgtagatccacatgggtattaccgggataca
tggagaaacatgttttcttaagatcagtacattactcattaatgggtcgatattagtaaattatttttgtacgta
attgctcgggtgcatggtttaagacgtgtgttcttaaaagctactccaattaataatgatgctttcatgtgggtgtg
gaattaaaagttttggatgctgtagtggtcaatcaaaaaatcataaagttcatagtttaagcttcgaaaaatgcaa
tagcttggggatacaaaagctatctttacaaaaatcttagaaatgggtggagtcctacataatcacgtgtgtgatc
caaattatagatgtaatagaagaaatttttcttgtattttcatgtattatatgcatcgctttatcgtctacaca
tgaccaaaatttttccattttccatttttaactatacaaaaagaagtttttttattgtacaaggcattag
gtcaacaatgccatggtgtggaacaacttgtctccacatttttggggacataatcctaattatcgttttca
ttacttccctaagcaacaagttgcttcatcttaattttccatttttgggtataaaaactatccatcaaccctgacaa
atttaaacgatgaaagcctgaattattgataatgatattgatattcatccaaacgatgaaagcctgaatt
attcagttttaaaaggatattcagttttctctcactgtcagctaaacttagtcaaatcaaacattcataaataat
attacacaacatatagatctataagcatgacatttataaaacatatattataaatcttatgatttattatccta
aactatttagaaagaatgatggttctcttattctctcaaatgctgtcctagaagttccacaagtctaacca
agacgtatacacaatgatacacaataataatcattttccaaacggttgatggtatttgagtaatttcaaatctct
acagaaaaatatttctctttccctatatatatccgataccatctcattgcactttcaacctcaacaaataacca
atcaaccaaaaaaaaaaaaaaaaa**ATGAAGAACTTCTTTTGATATTTCTCTTTTCTCTTGTCATTCTCAAACCTGC**
TTGTGGATTTCGATTACGACGACAAGGAAATAGAAAAGCGAAGAGGGCTTATCAACGCTTTATGATAGATGGAGGAG
CCACCCTCCGTTTCTTAGGAGTCTAAATGAAAGGGGAGAAGAGATTCAACGTTTTTCAGACACAATGTCATGCATGT
CCACAATACCAACAAGAAGAACCGATCCTACAAACTTAAGCTCAACAAGTTTGCAGATTTAACAATTAATGAGTT
CAAGAATGCATACACCGGTTCCAACATCAAGCATCACAGAATGTTGCAAGGACCAAAAACGCGGCTCAAAAACAGTT
CATGTATGATCATGAGAATTTATCCAAATTACCGTCCCTCGAGT**accacatacgcagcttccctgactatgctgact**
ctaccctatgacgtaccggattatgcatccctatatccgtagatggttccagattacgcttctctacgttcctc
tagaggcgtccaccatgatGTCGAC**atggttgagcaagggcgaggaggataacatggccatcatcaaggagttcat**
gcgcttcaaggtgcacatggagggtccggtgaacggccacgagttcgagatcgaggcgaggcgaggcgccccc
ctacgagggcaccagaccgccaagctgaaggtgaccaaggggtggccccctgccttcgctgggacatcctgtc
ccctcagttcatgtaccgctcaaggcctacgtgaagcaccgccgacatccccgactacttgaagctgtcctt
ccccgagggcttcaagttgggagcgcgtgatgaacttcgaggacggcggtggtgaccgtgaccaggactcctc
cctgcaggacggcgagttcatctacaaggtgaagctgcgcggcaccaactccccctccgacggccccgtaatgca
gaagaagaccatgggctgggaggcctcctccgagcggatgtaccccgaggacggcgccctgaagggcgagatcaa
gcagaggctgaagctgaaggacggcgccactacgacgctgaggtcaagaccactacaaggccaagaagccggt
gcagctgccccggcctacaacgtcaacatcaagttggacatcacctcccacaacgaggactacaccatcgtgga
acagtacgaaacgcgcccaggggcccactccacggcgccatggacgagctgtacaadGGATCC**TTACCGTCTC**
CGTTGATTGGAGAAAGAAAGGTGCTGTCACTGAAATCAAGAATCAAGGAAAATGTGGAAGTTGTTGGGCATTCTC
TACCGTAGCAGCTGTTGAGGGAATCAACAAGATCAAGACTAACAACTGGTCTCACTGTCTGAACAAGAACTAGT
GGATTGTGATACTAAGCAGAATGAAGGTTGTAACGGAGGTCTTATGGAGATTGCATTTGAATTCATCAAGAAGAA
CGGTGGTATCACCCTGAAGATAGCTATCCTTATGAAGGTATCGATGGAAAATGCGACGCTTCAAAGGATAACGG
CGTGCTTGTGACGATAGATGGGCATGAAGATGTACCCGAAAACGACGAAAATGCTCTTCTTAAGGCTGTTGCAAA
CCAACCTGTATCTGTTGCAATTGATGCTGGAAGTTCAGATTTCCAGTTTTATTTCAGAGGGAGTGTTTACGGGATC
TGTAAGTTCAGAGGGGAGGAGGCTATATAAAGATTGAAAGAGAGATTGATGAACCGGAAGG
CGCTTCCGGTATTGCGATGGAGGCATCGTATCCGATCAAGCTATCGTCGTCTAATCCTACCCGAAAGACGGTGA
TGTCCAAAGATGAGCTCTAG**atattgtgtacacattgtgtgtaaaacatatcaaggtgatccaattccttg**
ttgattcatggtttagtttctccttcatgatttgattttggttggttttgaatttgaataaaaat
gtctcgtgttttctcGCGGCCG****

Primers used for PCR amplification and cloning:

Primer pair 1 for amplification of the promoter and the pre-pro-sequence (2362 bp):

Sense: 5'-cattgGGTACCagtagagtcacttccaag-3'
Tm ges.: 66°C Tm: 51°C

Antisense: 5'-gtaCTCGAGggacggttaatttgataaa-3'
Tm ges.: 65°C Tm: 53°C

Primer pair 2 for amplification of the 3xHA tag (132 bp):

Sense: 5'-aaaCTCGAGtaccatacagacgttcctg-3'
Tm ges.: 66°C Tm: 54°C

Antisense: 5'-catGTCGACcatatggtggacgcctct-3'
Tm ges.: 65°C Tm: 52°C

Primer pair 3 for amplification of mCerry (714 bp):

Sense: 5'-atgGTCGACatggttgagcaagggcgag-3'
Tm ges.: 65°C Tm: 52°C

Antisense: 5'-taaGGATCCcttgtacagctcgtccatg-3'
Tm ges.: 66°C Tm: 54°C

Primer pair 4 for amplification of AtCEP2 (846 bp):

Sense: 5'-aagGGATCCttaccgtcctccggttgat-3'
Tm ges.: 65°C Tm: 52°C

Antisense: 5'-gtgGCGGCCGCgagaaaacacgagacatt-3'
Tm ges.: 68°C Tm: 51°C

Protein sequence:

MKKLLLIFLFLSVILQACGF^{DYDDKEIESE}EGLSTLYDRWRSHHSVPRSLNEREKRFNVFRHNMHVHNTNKKN
RSYKLLKLNKFADLTINEFKNAYTGSNIKHHRLQGPKRGSKQFMYDHENLSK^{LPS}LEYPYDVPDYASLYPYDVPD
YASLYPYDVPDYASL^{RSSRGVHHMVD}MLSKGEEDNMAI^IKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTA
KLKVTGGGLPFAWDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFI
YKVKLRGTNFPDGPVMQKKTMGWEASSERMPEDGALKGEIKQRLKLDGGHYDAEVKTTYKAKKPVQLPGAYN
VNIKLDITSHNEDYTI^{VEQYERA}EGRHSTGGMDELYK^{GS}LPSVVDWRKKGAVTEIKNQKCGSCWAFSTVAAVEG
INKIKTNKLVSLSEQELVDCDTKQNEGCNGLMEIAFEFIKKNGGITTEDSYPYEGIDGKCDASKDNGVLVTIDG
HEDVPENDENALLKAVANQPVSVAIDAGSSDFQFYSEGVTGSCGTELNHGVAAVGYGSERGKKYWIVRNSWGAE
WEGGYIKIEREIDPEGRCGIAMEASYPIKLSSSNPTPKDGDV^{KDEL}

Pre - Pro - 3xHA - mCherry - AtCEP2 - KDEL

Amino acids shaded in white were introduced due to cloning strategy

Figure S2: Cloning strategy in pGreen 0179 for expression of the non-functional fusion protein pre-pro-3xHA-mCherry-KDEL under control of the endogenous AtCEP2 promoter.

DNA sequence:

GGTACCagtagagtcacttccaagaaaactaggaacatcaaaccacgtcgttgcatTTTTGGGGatcttatgaaat
acacaagcttatacaaaaaaaaaatattataaaaaaaaaatgaacgtatattaattcgttaattacataggcttaaaacc
aagataagatcgggtacatggttgaaaatgaaaattattcaatctcctaataagaggtgagacaattatcaattcgaa
actcatacatcaatcataaaaagctacaatattttctcaactccatcaattatccgtgggagtcatacaaaaaaaaa
aattaaaaaaaaattattacatatatatgtattttttttcagaaaagtgaaatctctttcgaacatatgaaattat
gaaatttcatcaattggcctaggattacagagatcaacgtaaaatttttaatacaaaaaataaaaaatagtttc
cttgcattaggaagcatcattatccaaccacgacgcgggtattaagccaagatccattccaattattcattcat
atctactacctaanaacgacattagctttttataaagaaagtcttaaccacgacgtggtggtcatattttaaatt
acatttgttgttaaacaccaatggtatgcctaacaacttaataaaaccgccataattgttttttattgtgtttt
tgaaaaactacttgccggtgttatcttggcctgagttttttctctttgttttaataatgtagtatga
aaccagtttcaacaaatgggctgcgccaatggtcacgcatcttgcccttgagaattttgaataacaactaatta
gagattaaggatggaatgtacaaaaatcgccacgagatcctttcgtagatccacatggtattaccgggataca
tgagaaaacatgttttcttaagatcagtagactcattaaatggtcgtatattagtaaattattttgtacgta
attgctcgggtgcatggtttaagacgtgtgttcttaaaagctactccaattaataatgatgctttcatgtggtgtg
gaattaaaagttttggatgctgtagtggtcaatcaaaaaatcataaagttcatagtttaagcttcgaaaatgcaa
tagcttggggatacaaaagctatctttcaaaaaatcttagaaatggtggagtcctacataatcacgtgtgtgatc
caaattatagatgtaatagaagaaatTTTTCTgtattttcatgtattatgcatcgcctttatcgtctacaca
tgaccaaaatTTTTTcccattttcccatttttaatacctatacaaaagaagtTTTTTTattgtacaaggcattag
gtcaacaatgccatggtgtgaaacaactttgtctccacatTTTTGGGGacatatcttaattcaattatcgccttca
ttacttccctaagcaacaagtgtgcttcatcttaattttcccattattgtataaaactatccatcaaccctgacaa
atTTaaacgatgaaagcctgaattattgataatgatattgatattcattatcatccaacgatgaaagcctgaatt
atccagttttaaaggatattcagttttctctcactgctcagctaaacttagtcaaatcaaacattcataaatat
attacacaacatatagatctataagcatgacatttataaaaccatataattataaattcttagatttattattccta
aactatttagaagaatgatgaggttcccttattctctcaaatgctgtgctcctagaagttccacaagtccaacca
agacgtatacacaatgatacacaataataattcattttccaaacggttgatggtatttgagtaatttcaaatctct
acagaaaaatatttctctttccctatatatatccgataccatctcattgcactttcaacctcaaaacaaataacca
atcaaccaaaaaaaaaaaaaaaaa**ATGAAGAACTTCTTTTGATATTTCTCTTTCTCTTGTCAATTCTCCAAACTGC**
TTGTGGATTTCGATTACGACGACAAGGAAATAGAAAGCGAAGAGGGCTTATCAACGCTTTATGATAGATGGAGGAG
CCACCCTCCGTTCCCTAGGAGTCTAAATGAAAGGGAGAAGAGATTCAACGTTTTTCAGACACAATGTCATGCATGT
CCACAATACCAACAAGAAGAACCGATCCTACAAACTTAAGCTCAACAAGTTTGCAGATTTAACAATTAATGAGTT
CAAGAATGCATACACCGGTTCCAACATCAAGCATCACAGAATGTTGCAAGGACCAAAACGCGGCTCAAAACAGTT
CATGTATGATCATGAGAATTTATCCAAATTACCGTCC**CTCGAG**taccatacgcagcttccctgactatgctcact****
ctacccttatgacgtaccggattatgcatccctatatccgtatgatgttccagattacgcttctctacgttcctc****
tagaggcgtccaccatgatGTCGAC**atggtgagcaagggcgaggaggataacatggccatcatcaaggagttcat**
gcgcttcaaggtgcacatggagggtccgtgaacggccacgagttccagatcgaggggcgaggggcgaggccgccc
ctacgagggcaccagaccgccaagctgaaggtgaccaaggtggccccctgcccttcgctgggacatcctgtc
ccctcagttcatgtacggctccaaggcctacgtgaagcaaccccgccgacatccccgactacttgaagctgtcctt
ccccgagggcttcaagtgggagcgcgtgatgaacttcgaggacggcggcgtggtgaccgtgaccaggactcctc
cctgcaggacggcgagttcatctacaaggtgaagctgcgcggcaaccaacttcccctccgacggccccgtaatga
gaagaagaccatgggctgggaggcctcctccgagcggatgtaccccaggacggcgcctgaagggcgagatcaa
gcagaggctgaagctgaaggacggcggcactacgacgctgaggtcaagaccctacaaggccaagaagcccgt
gcagctgcccggcctacaacgtcaacatcaagttggacatcacctcccacaacgaggactacaccatcgtgga
acagtacgaacggcggcggggccgcccactccaccggcggcatggacgagctgtacaadGGATCCGGTGATGTCAA****
AGATGAGCTCTAGatattgtgtacacattgtgtaaaaccatatacaaggtgatcccaattccttgttgat
tcatgttgttagtttctccttcatgatttgattttgttggtttgaatttgaataaaaaatgtctc
gtgttttctc**GCGGCCGC**

Primers used for PCR amplification and cloning :

Primer pair 1 for amplification of the promoter and the pre-pro-sequence (2362 bp):

Sense: cattgGGTACCagtagagtcacttccaag
Tm ges.: 66°C Tm: 51°C

Antisense: gtaCTCGAGgggacggtaatttggataaa
Tm ges.: 65°C Tm: 53°C

Primer pair 2 for amplification of the 3xHA tag (132 bp):

Sense: aaaCTCGAGtaccatacagacgttctctg
Tm ges.: 66°C Tm: 54°C

Antisense: catGTCGACcatatggtggacgcctct
Tm ges.: 65°C Tm: 52°C

Primer pair 3 for amplification of mCerry (714 bp):

Sense: atgGTCGACatggttgagcaagggcgag
Tm ges.: 65°C Tm: 52°C

Antisense: taaGGATCCcttgtacagctcgtccatg
Tm ges.: 66°C Tm: 54°C

Primer pair 4 for amplification of the KDEL-3'UTR (178 bp):

Sense-kdel aagGGATCCGGTGATGTCAAAGATGAGC
Tm ges.: 65°C Tm: 54°C

Antisense: gtgGCGGCCGcagaaaacacgagacatt
Tm ges.: 68°C Tm: 51°C

Protein sequence:

MKKLLLIFLFLVILQTACGFDYDDKEIESEEGSLTLYDRWRSHHSVPRSLNEREKRFNVFRHNVMHVHNTNKKN
RSYKLLKLNKFADLTINEFKNAYTGSNIKHHRLQGPKRGSKQFMYDHENLSKLPSELYPYDVPDYASLYPYDVPD
YASLYPYDVPDYASLRSSRGVHHMVDMLSKGEEDNMAIIEKFMRFKVHMEGVSVNGHEFEIEGEGEGRPYEGTQTA
KLKVTGGGLPFAWDILSPQFMYGSKAYVKHPADIPDYKLSFPEGFKWERVMNFEEDGGVVTVTQDSSLQDGEFI
YKVKLRGTNFPDGPVMQKKTMGWEASSERMPEDGALKGEIKQRLKLDGGHYDAEVKTTYKAKKPVQLPGAYN
VNIKLDITSHNEDYTIQEYERAEGRHSTGGMDELYKSGSDVKDEL

Pre - Pro - 3xHA - mCherry - KDEL

Amino acids shaded in white were introduced due to cloning strategy

Figure S4: Antibodies directed against the mature subunit of AtCEP1 cross-react with AtCEP2

A: Cloning strategy. M, L and E (shaded in green) and the His-tag (yellow) were added by cloning.

AtCEP1 (636bp)

```
GGAGCCGTCACCTCCTGTCAA AAAACCAAGGCCAATGCGGGAGTTGTTGGGCGTTTTTCAACAGTTGTTGCGGTGGAA
GGGATCAACCAAATAAGA AACTAAAAAGCTGACATCACTCTCAGAGCAAGAGCTAGTAGATTGTGATACAAACCAG
AACCAAGGATGCAATGGAGGTCTAATGGACCTTGCTTTTGAGTTCATCAAGGAGAAAAGGAGGACTCACAAAGTGAG
CTAGTGTACCCTTACAAGGCTTCTGATGAAACTTGTGACACAAAACAAAAGAAAATGCTCCGGTAGTTTCAATCGAT
GGACACGAAGATGTTTCTAAGA ACAGCGAGGATGATCTAATGAAAGCTGTTGCTAATCAGCCTGTTTCTGTTGCT
ATTGATGCTGGAGGCTCAGACTTTCAATTCTACTCCGAGGGAGTGTTTACCGGGAGATGCGGAACAGAGCTAAAC
CATGGAGTTGCGGTAGTAGGGTATGGAACAACGATAGACGGAACAAAGTATTGGATTGTTAAGAATTCATGGGGA
GAGGAATGGGGAGAGAAAAGGATACATAAGAATGCAGAGAGGGATTTCGTCATAAAGAAGGACTTTGTGGTATTGCA
ATGGAAGCTTCTTATCCTCTCAAGAACTCCAACACT
```

CEP1 sense 5' -agaCATATGGGAGCCGTCACCTCCTGTCAA-3'`
 CEP1 anti-sense 5' -agaCTCGAGAGTGTGGAGTTCTTGAGAGG-3'

Protein:

MGAVTPVKNQGCWSCWAFSTVVAVEGINQIRTKKLSLSEQELVDCDTNQNQGCNGLMDLAFEFIKKGLTSELVYPYKA
 SDETCDTNKENAPVVSIDGHEDVPKNSDDLKAVANQPVSVAIDAGGSDFFQFYSEGVTGRCGTELNHGVAVVGYGTTIDG
 TKYWIVKNSWGEEWGEKGYIRMQRGIRHKEGLCGIAMEASYPLKNSNT**LE**HHHHHHH*

AtCEP2 (630bp)

```
GGTGCTGTCACTGAAATCAAGAATCAAGGAAAATGTGGAAGTTGTTGGGCATTCTCTACCGTAGCAGCTGTTGAG
GGAATCAACAAGATCAAGACTAACA AACTGGTCTCACTGTCTGAACAAGA AACTAGTGGATTGTGATACTAAGCAG
AATGAAGGTTGTAACGGAGGTCTTATGGAGATTGCATTTGAATTCATCAAGAAGAACGGTGGTATCACCCTGAA
GATAGCTATCCTTATGAAGGTATCGATGGAAAATGCGACGCTTCAAAGGATAACGGCGTGCTTGTGACGATAGAT
GGGCATGAAGATGTACCCGAAAACGACGAAAATGCTCTTCTTAAGGCTGTTGCAAACCAACCTGTATCTGTTGCA
ATTGATGCTGGAAGTTCAGATTTCCAGTTTTTATTTCAGAGGGAGTGTTTACCGGATCTTGTGGAACAGAGCTGAAC
CATGGTGTGGCAGCGGTTCGGGTATGGATCTGAGAGGGGGAAAAAGTATTGGATAGTGAGAAA AACTCATGGGGAGCT
GAATGGGGAGAGGGAGGCTATATAAAGATTGAAAGAGAGATTGATGAACCGGAAGGGCGTTGCGGTATTGCGATG
GAGGCATCGTATCCGATCAAGCTATCGTTCG
```

CEP2 sense 5' -agaCATATGGGTGCTGTCACTGAAATCAAGA-3'`
 CEP2 anti-sense 5' -agaCTCGAGCGACGATAGCTTGATCGGAT-3'

Protein:

MGAVTEIKNQKCGWSCWAFSTVAAVEGINIKIKTNKLVSLSEQELVDCDTKQNEGCNGLMEIAFEF IKKNGGIT
 EDSYPYEGIDGKCDASKDNGVLVTIDGHEDVPENDENALLKAVANQPVSVAIDAGSSDFQFYSEGVTGSCGTEL
 NHGVAAVGYGSEKGYIWRNSWGAEWGEGGYIKIEREIDEPEGRCGIAMEASYPIKLSS**LE**HHHHHHH*

B: Westernblot analysis

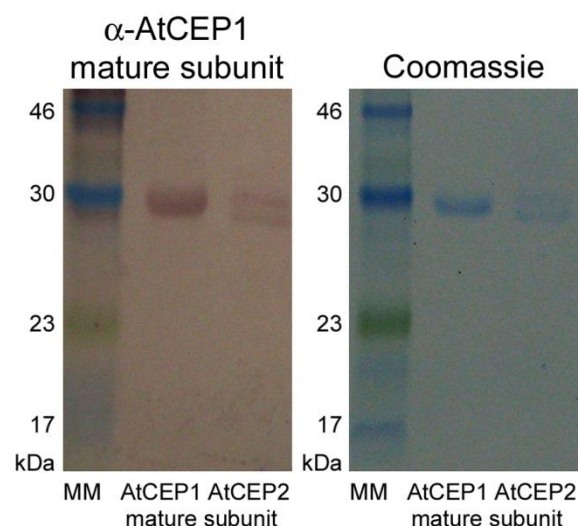


Figure S5: AtCEP2 accepts proline near the cleavage site thus exhibiting the broad substrate specificity typical for KDEL-CysEPs.

Amino acids of the entire beta-casein sequence (224 aa) including the pre-sequence (amino acid residues 1-15) and the mature beta-casein (amino acid residues 16-224) with the cleavage sites indicated by arrows; proline residues are shown in red.

MKVLILACLVALALA-
 REL↓E↓ELN↓VPGEIVESLSSEESITRINKK↓IE↓KFQ↓S↓EEQQQTEDELQ↓DKIH↓PFA↓Q↓TQS↓LV↓YP↓F
 PGP↓IP↓N↓S↓L↓PQ↓NIPPLT↓Q↓TPVV↓V↓PPFL↓QPEVM↓G↓VS↓KVK↓E↓A↓MAPKH↓K↓E↓MPFPK↓YPVE
 PFT↓ES↓QS↓LT↓LT↓DVENLH↓LPLPL↓Q↓SWM↓H↓QPH↓QPLPPTVM↓FPPQSVLS↓LS↓Q↓SKV↓LPVPQ↓
 K↓A↓VPYQ↓R↓D↓MPIQ↓AF↓L↓L↓Y↓Q↓EPVL↓GPVR↓GFPPIIV

Cleavage sites in beta-casein ↓ identified by amino acid sequencing alone or in combination with MALDI-TOF and summary of amino acids found in positions P2, P1, P1' and P2'

MKVLILACLVALALA		KHKE↓MPFP		P2	P1	P1'	P2'
-REL↓EELN		PFPK↓YPVE		L (14x)	Q (11x)	Q (9x)	P (20x)
RELE↓ELNVP		EPFT↓ESQS		V (8x)	S (8x)	L (9x)	S (7x)
EELN↓VPGEIVESLSSEESITR		FTES↓QSLT		K (6x)	L (7x)	E (7x)	E (6x)
INKK↓IEKF		ESQS↓LTLT		P (6x)	K (5x)	K (4x)	V (5x)
KKIE↓KFQS		QSLT↓LTDV		Q (5x)	H (4x)	V (4x)	Q (4x)
EKFQ↓SEEQ		LTLT↓DVEN		F (5x)	E (4x)	S (4x)	T (4x)
KFQS↓EEQQQTE		ENLH↓LPLP		I (3x)	T (4x)	M (3x)	L (4x)
DELQ↓DKIH		LPLL↓QSWM		E (3x)	V (4x)	A (3x)	M (3x)
HPFA↓QTQS		PLLQ↓SWMH		M (2x)	A (3x)	G (3x)	A (3x)
PFAQ↓TQSL		QSWM↓HQPH		Y (2x)	M (3x)	Y (3x)	F (2x)
QTQS↓LVYP		SWMH↓QPHQ		S (2x)	P (2x)	D (3x)	Y
QSLV↓YFPF		HQPH↓QPLP		A (2x)	N (2x)	P (2x)	K
LVYP↓FPGP		PTVM↓FPPQ		W	R (2x)	F (2x)	D
GPPI↓NSLPQ		SVLS↓LSQS		H		T (2x)	I
PIPN↓SLPQ		LSLS↓QSKV		R	F	N (2x)	W
IPNS↓LPQN		SLSQ↓SKVL		T	Y	I	
PNSL↓PQNI		QSKV↓LPVP		N	G	R	
SLPQ↓NIPP		PVPQ↓KAVP				H	
PPLT↓QTPV		VPQK↓AVPY					
PLTQ↓TPVV		PQKA↓VPYP					
TPVV↓VPPF		PYPQ↓RDMP					
PVVV↓PPFL		YPQR↓DMPI					
PPFL↓QPEV		PQRD↓MPIQ					
PEVM↓GVSK		MPIQ↓AFLL					
EVMG↓VSKV		IQAF↓LLYQ					
MGVS↓KVKE		QAFL↓LYQE					
SKVK↓EAMA		AFLL↓YQEP					
KVKE↓AMAP		FLLY↓QEPV					
VKEA↓MAPK		LLYQ↓EPVL					
APKH↓KEMP		EPVL↓GPVR					
PKHK↓EMPF		GPVR↓GFPPIIV					

Residues in black correspond to the primary sequence, and those shown in red are replicates to illustrate the cleavage site from P4 to P4'.

distribution	P2	P1	P1'	P2'
nonpolar	65 %	32 %	38 %	62 %
basic	13 %	17 %	10 %	2 %
acidic	5 %	8 %	16 %	11 %
polar, uncharged	17 %	43 %	36 %	25 %

Figure S6: Expression of *AtCEP1* (At5g50260), *AtCEP2* (At3g48340) and *AtCEP3* (At3g48350) as visualized by the “root expression map visualizer [www.arexdb.org/]” shown in red (middle and right) and the *Arabidopsis* root template (left). The www.arexdb.org database attributes the observed expression for the KDEL peptidase(s) to *AtCEP1* (middle) and *AtCEP3* (right). No data set is available for *AtCEP2* in the ATH1 database. Comparison with our results from *P_{CEP1}::GUS*, *P_{CEP2}::GUS* and *P_{CEP3}::GUS* plants (Helm et al., 2008) and *P_{CEP2}::pre-pro-3xHA-mCherry-AtCEP2-KDEL*, however, suggests that the *AtCEP2* expression pattern has erroneously been attributed to *AtCEP1* (At5g50260, probe ID 248545_at) or *AtCEP3* (At3g48350; probe ID_252368_at).

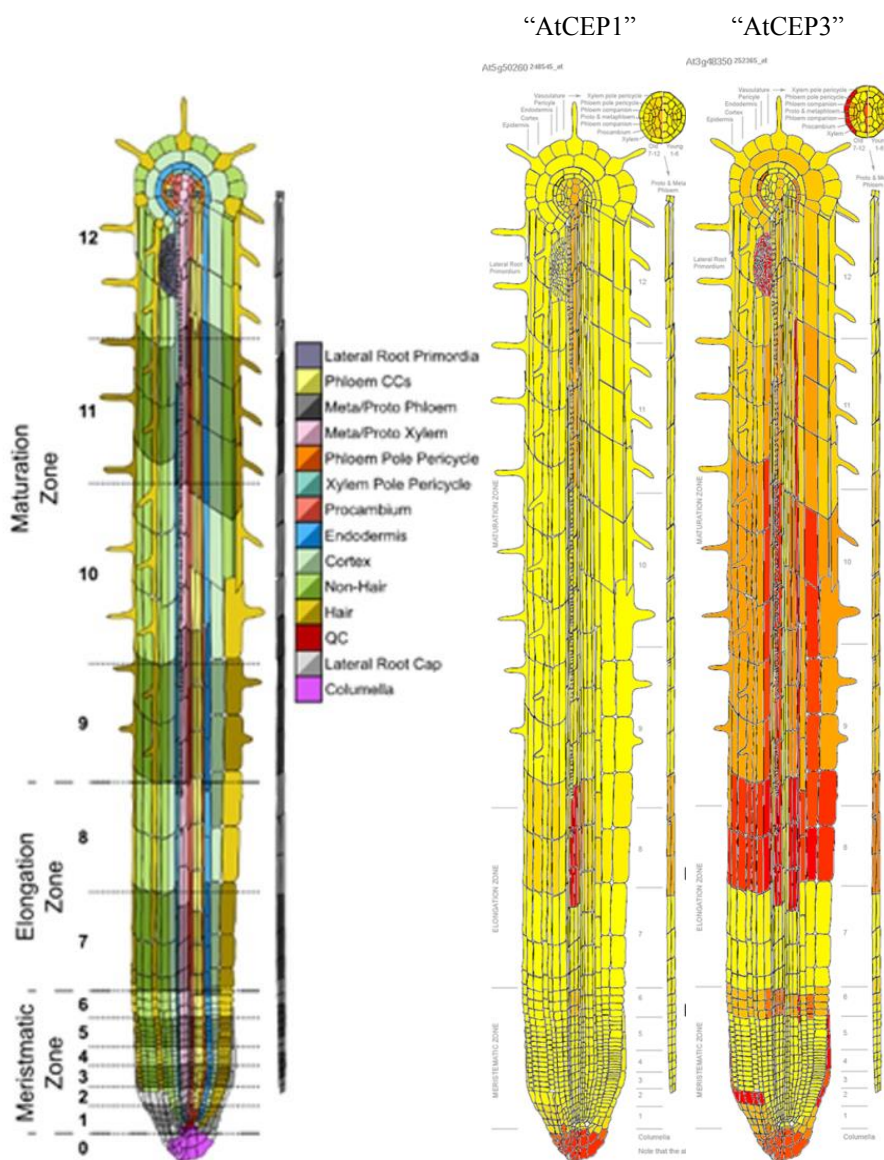


Figure S7: *AtCEP1* and *AtCEP3* transcripts are slightly up-regulated in *cep2*. Relative gene expression of *AtCEP1*, *AtCEP2* and *AtCEP3* in wild-type (WT) and *cep2* seedlings. Total RNA was extracted from 7-day-old seedlings. Expression levels were normalized to the reference gene *ACT8* and the expression in wild type was set to 1 in each experiment. Error bars: SEM.

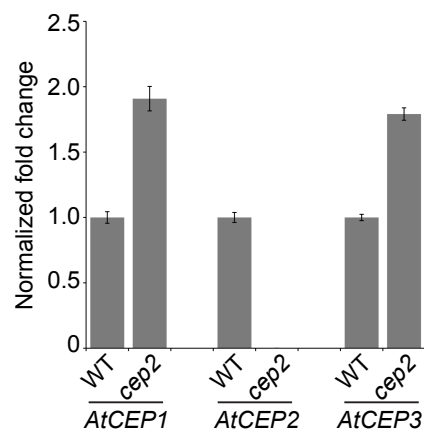


Table S1: Beta-casein peptides obtained by cleavage with AtCEP2

aa-position in beta-casein	Peptide sequence
16 - 22 N-term	- .RELEELN V
50 - 68	Q SEEQQOTEDELQDKIHPFA Q
51 - 68	S EEQQQOTEDELQDKIHPFA Q
62 - 68	Q DKIHPFA Q
62 - 69	Q DKIHPFAQ T
73 - 82	S LVYFPFGPIIP N
73 - 87	S LVYFPFGPIHNSLPQ N
73 - 93	S LVYFPFGPIHNSLPQNIPPLT Q
75 - 82	V YFPFGPIIP N
75 - 83	V YFPFGPIPN S
75 - 84	V YFPFGPIPN S
75 - 84	V YFPFGPIPN S
75 - 87	V YFPFGPIPN S
75 - 87	V YFPFGPIPN S
75 - 93	V YFPFGPIPN S
75 - 93	V YFPFGPIPN S
75 - 93	V YFPFGPIPN S
77 - 87	P FPGPIPN S
77 - 87	P FPGPIPN S
94 - 108	T QTPVVVPPFLQPEVM G
94 - 103	T QTPVVVPPFL Q
94 - 111	T QTPVVVPPFLQPEVMGVS K
95 - 103	Q TPVVVPPFL Q
100 - 108	V PPFLQPEVM G
100 - 109	V PPFLQPEVM G
100 - 109	V PPFLQPEVM G
100 - 111	V PPFLQPEVMGVS K
100 - 111	V PPFLQPEVMGVS K
110 - 135	G VSKVKEAMAPKHKEMPFPKYPVEPFT E
110 - 141	G VSKVKEAMAPKHKEMPFPKYPVEPFTESQSLT L
112 - 128	S KVKEAMAPKHKEMPFPK Y
112 - 135	S KVKEAMAPKHKEMPFPKYPVEPFT E
112 - 137	S KVKEAMAPKHKEMPFPKYPVEPFTES Q
112 - 141	S .KVKEAMAPKHKEMPFPKYPVEPFTESQSLT L
115 - 135	K EAMAPKHKEMPFPKYPVEPFT E
115 - 141	K EAMAPKHKEMPFPKYPVEPFTESQSLT L
116 - 135	E AMAPKHKEMPFPKYPVEPFT E
116 - 141	E AMAPKHKEMPFPKYPVEPFTESQSLT L
117 - 135	A MAPKHKEMPFPKYPVEPFT E
122 - 128	H KEMPFPK Y
122 - 135	H KEMPFPKYPVEPFT E
122 - 141	H KEMPFPKYPVEPFTESQSLT L
123 - 135	K EMPFPKYPVEPFT E
123 - 137	K EMPFPKYPVEPFTES Q
123 - 141	K EMPFPKYPVEPFTESQSLT L
124 - 135	E MPFPKYPVEPFT E
129 - 135	K YPVEPFT E
140 - 156	S LTLTDVENLHLPLPLLQ S
144 - 149	T DVENLH L
144 - 155	T DVENLHLPLPLL Q
144 - 166	T DVENLHLPLPLLQ S
150 - 156	H LPLPLLQ S
160 - 171	M HQPHQPLPPTVM F
160 - 179	M HQPHQPLPPTVMFPPQSVLS L
161 - 171	H QPHQPLPPTVM F
161 - 179	H QPHQPLPPTVMFPPQSVLS L
164 - 171	H QPLPPTVM F
182 - 191	S QSKVLPVPQK A
182 - 192	S QSKVLPVPQKA V
182 - 198	S QSKVLPVPQKAVPYPQR D
182 - 203	S QSKVLPVPQKAVPYPQRDMPIQ A
182 - 205	S QSKVLPVPQKAVPYPQRDMPIQAF L
182 - 206	S QSKVLPVPQKAVPYPQRDMPIQAFLL L
182 - 207	S QSKVLPVPQKAVPYPQRDMPIQAFLL Y

183 - 191	Q	SKVLPVPQK	A
186 - 203	V	LPVPQKAVPYPQRDMPIQ	A
191 - 198	Q	KAVPYPQR	D
191 - 203	Q	KAVPYPQRDMPIQ	A
192 - 198	K	AVPYPQR	D
192 - 199	K	AVPYPQRD	M
192 - 203	K	AVPYPQRDMPIQ	A
192 - 205	K	AVPYPQRDMPIQAF	L
192 - 206	K	AVPYPQRDMPIQAF	L
192 - 224 C-term	K	AVPYPQRDMPIQAFLLYQEPVLPVLRGPFPIIV	.
193 - 198	A	VPYPQR	D
193 - 199	A	VPYPQRD	M
193 - 203	A	VPYPQRDMPIQ	A
198 - 203	Q	RDMPIQ	A
200 - 224 C-term	D	MPIQAFLLYQEPVLPVLRGPFPIIV	.
204 - 224 C-term	Q	AFLLYQEPVLPVLRGPFPIIV	.
207 - 224 C-term	L	LYQEPVLPVLRGPFPIIV	.
208 - 217	L	YQEPVLPVLR	G
208 - 224 C-term	L	YQEPVLPVLRGPFPIIV	.
209 - 217	Y	QEPVLPVLR	G
210 - 217	Q	EPVLPVLR	G
214 - 224 C-term	L	GPVLRGPFPIIV	.
218 - 224 C-term	R	GPFPIIV	.