FigS1

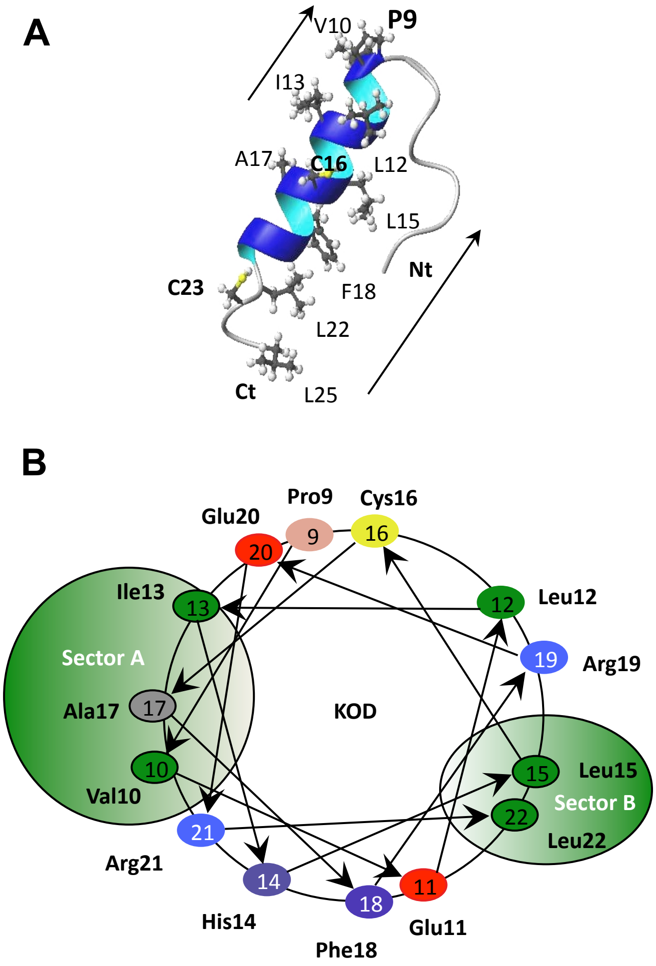

Fig. S1. A) **Model of the alpha-helix based on NMR data**, with two hydrophobic ridges of 6 residues (P9, V10, L12, I13, C16, A17) and 4 residues (L15, F18, L22, L25). B) **Helical wheel representation of the carboxy-terminal segment of KOD (aa 9-22)**. Pro-9 was not excluded to indicate the anchor amino acid of the alpha-helix (aa 10-22). The representation reveals the organization of highly hydrophobic amino acids in two opposite sectors (sector A and sector B) framed by polar amino acids of opposite charges. The amphiphillic nature of this helix and the symmetric distribution of charges may have a functional relevance. RasMol amino acid color code.

FigS2

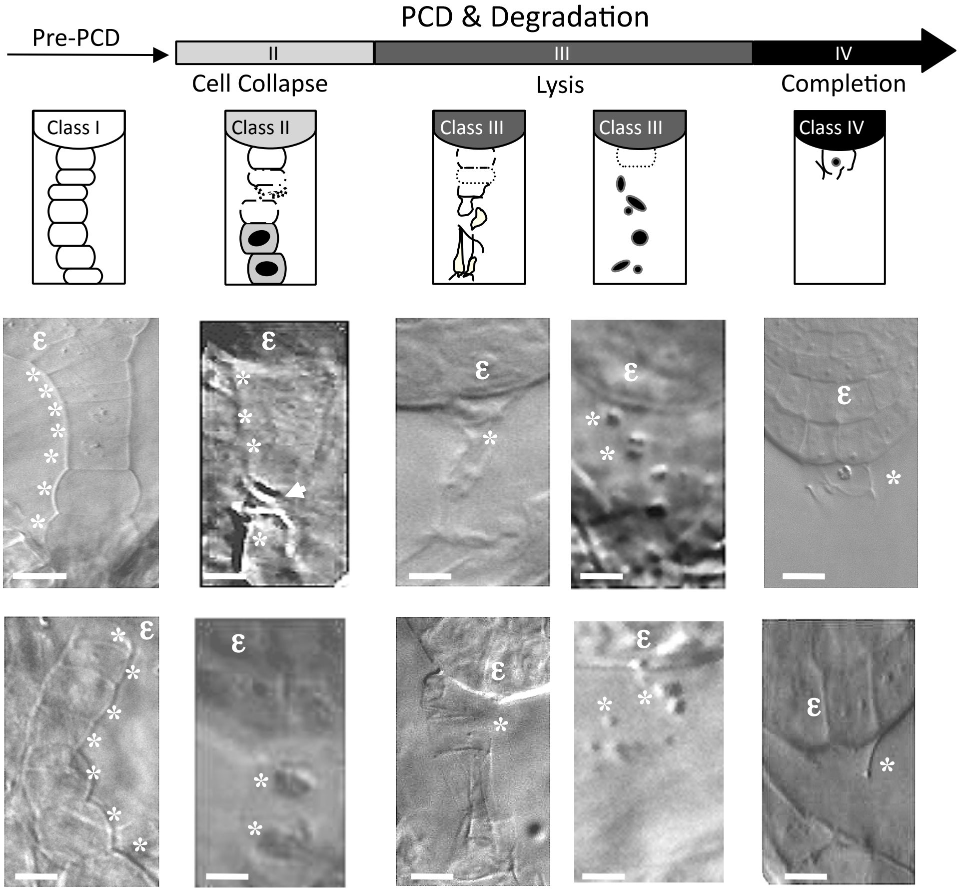

Fig. S2. PCD stages of *Arabidopsis* Col-0 suspensors at the bent-cotyledon embryo stage. ε, embryo proper; *, suspensor cells; arrowheads point to breaks in the suspensor cell file.

FigS3

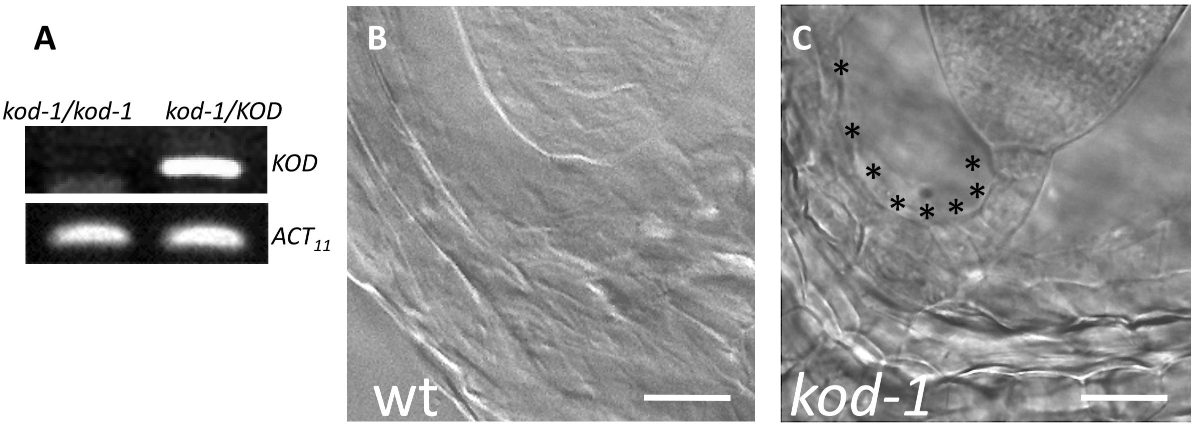

Fig. S3. *KOD* expression in the kod-1 background. (A*) KOD* transcript level in cDNA from green siliques using a 3’RACE approach to prevent amplification of genomic DNA. ACTIN11 (ACT_{11}) is used as reference gene as it is the actin family member most expressed in embryos. Expression of *KOD* was only detected in heterozygotes and WT plants. The data presented is for an heterozygote plant. (B-C) DIC images of representative suspensors at the bent-cotyledon stage in WT and *kod-1* seeds. Bars equal 10 μm.

FigS4

Fig. S4. Bax-induced PCD in detached leaves. Representative leaves of the dex-Bax line after 3 days of induction by dex. Individual leaves were kept in 1.5mL Eppendorf tubes with their petioles submerged in 30µM dex, in continuous light.

Supplementary table 1: primers used in the study

Primer	**Sequence 5'> 3'**
GUSI	TGGACTGGCATGAACTTCGG
GUS3	GTTGTCTAAGCGTCAATTG
oGUSJ	TCACGGGTTGGGGTTTCTAC
oSUPR	TACTTAGAGATGACAGAGACG
oexTi15 (K)	ATCAGTCACAGTCAAATTCGA
oTI05 (L)	CGTCTTCGAGAAAAGTGTTAG
oSUPR1	GATGACAGAGACGCTCTCG
act2.3	CAGCACCAATCGTGATGACTTGCCC
act2.5	GTTAGCAACTGGGATGATATGG
act11F	GGAACAGTGTGACTCACACCATC
act11R	AAGCTGTTCTTTCCCT
oxpo4	GTATGTCGTTGGCCAGTATCC
oxpo7	TCCCAGTGAAGTAGCAGCAC
Spep5	TCGAGATGTGGTGGCTAGTTGGACTTAGACCAGTTGAGTTGATCCATCTT
Spep3	AAGATGGATCAACTCAACTGGTCTAAGTCCAACTAGCCACCACATC
pep5	TCGAGATGTGGTGGCTAGTTGGACTTAGACCAGTTGAGTTGATCCATCTTTGCGCATTTCGAGAGCGTCTCTGTCATCTC
pep3	GAGATGACAGAGAGACGCTCTCGAAATGCGCAAAGATGGATCAACTCAACTGGTCTAAGTCCAACTAGCCACCACATC
Race-anchor	GGCCACGCGTCGACTAGTAC
Race-3	GGCCACGCGTCGACTAGTACTTTTTTTTTTTTTTTTT
18S-29F	GGTCTGTGATGCCCTTAGATGTT
18S-102R	GGCAAGGTGTGAACTCGTTGA
18S-58T (Taqman probe)	CGCACGCGCGCTACACTGATGT
KOD-267F	TATGTGGTGGCTAGTTGGACTTACA
KOD-353R	AGCTTTACTTAGAGATGACAGAGACGCT
KOD-293T (Taqman probe)	CAGTTGAGTTGATCCATCTTTGCGATTTC
Act2-123F	GAGAGATTCAGATGCCCAGAAGTC
Act2-190R	TGGATTCCAGCAGCTTCCA
Act2-148T (Taqman probe)	TGTTCCAGCCCTCGTTTGTGGGA
KOD-ATG F	ATGTGGTGGCTAGTTGG