SUPPORTING INFORMATION

TITLE

INFLORESCENCE DEFICIENT IN ABSCISSION-like is an abscission-associated and phytohormone-regulated gene in flower separation of Lupinus luteus

JOURNAL NAME

Plant Growth Regulation

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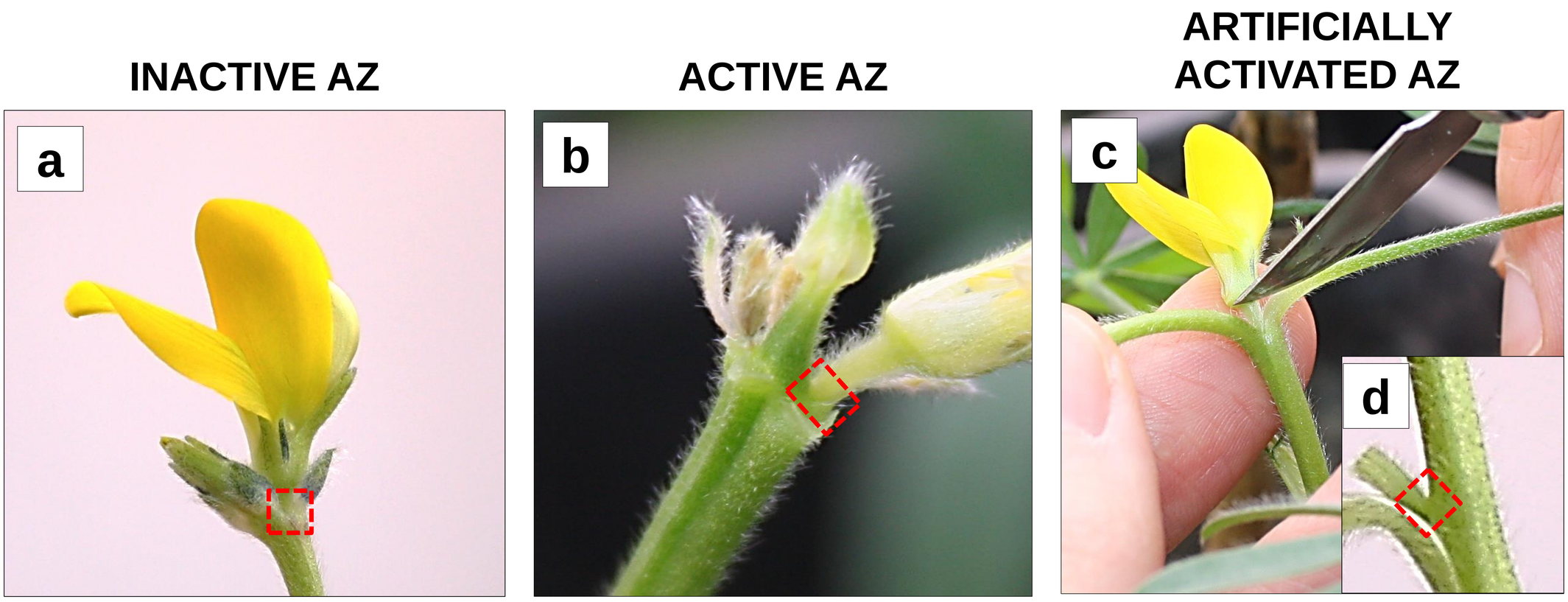
Supplementary Fig. 1 Flowers of *Lupinus luteus* L

Non-abscised (a) and naturally abscised (b) flowers. The procedure of artificial flower AZ activation (c, d). Tissue sections (indicated by white boxes) containing AZ were collected for analyses. Floral AZ was artificially activated by organ removal (c) and proper fragments (d) were sampled after 2 h, 4 h, 6 h, 8 h, 16 h and 24 h.



Supplementary Table 1 Specific primers and probes used in PCR reactions

All primers were synthesized by “Genomed S.A.” (Warsaw, Poland). Degenerated primers were constructed on the basis of conserved sequences encoding *IDL* in *Vigna angularis* (GenBank acc. no. XM_017567224), *Cicer arietinum* (GenBank acc. no. XM_012716473), *Theobroma cacao* (GenBank acc. no. XM_007048232), *Citrus sinensis* (GenBank acc. no. XM_006464542) and *Vitis vinifera* (GenBank acc. no. XM_010651162).

Gene	GeneBank accession no.	Primer sequence 5’-3’	UPL probe no.
LlIDL	KT716180	degenerated F: ACTGYCATGGCTCMAGAACCA R: CCAATGTCATTGTGTTTCYTTGARGGA	-
		RACE-PCR F: CCATGGCTCAAGAACCACTACTGC R: TGTGTTTCCTTGAGGGAGTGGA	-
		qRT-PCR F: ACAGCACCATGGTCACTTTTC R: TTGTGTTTCCTTGAGGGAGTG	137
LlACT	KP257588	qRT-PCR F: TAATGGTTGGGATGGGTCAG R: CAAGGTGAGAATACCCCTCT	165

Supplementary Fig. 2 Certificate of EPIP synthetic peptide analysis

Certificate of Analysis

Custom peptide synthesis

Peptide sequence: HFSGFLPKRTHMPYSTPSRKHN

Appearance: white powder

Molecular Formula: $C_{118}H_{177}N_{37}O_{30}S$

Molecular Weight: 2626.02

Mass : Consistent

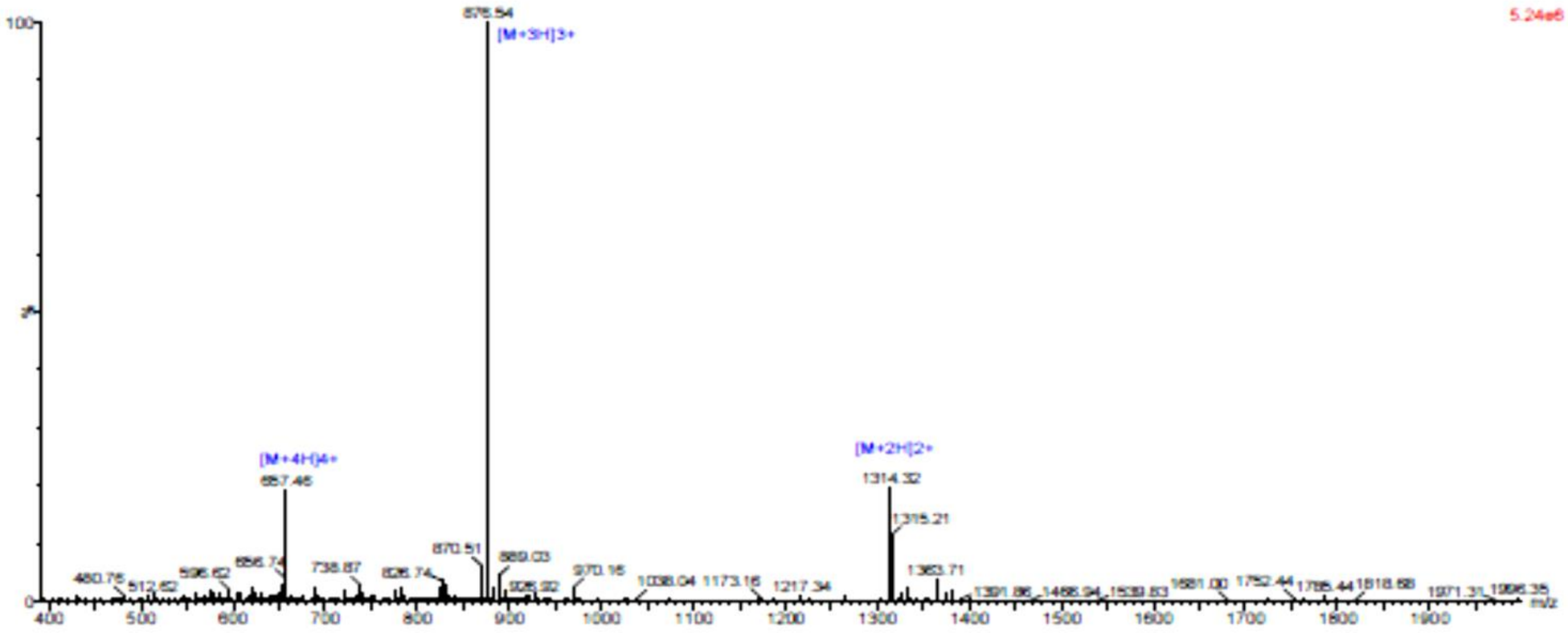
Quantity: 10.2mg

Purity(HPLC): 90.30%

Lot Number: 170302-P013322

Store at: Cool dry place

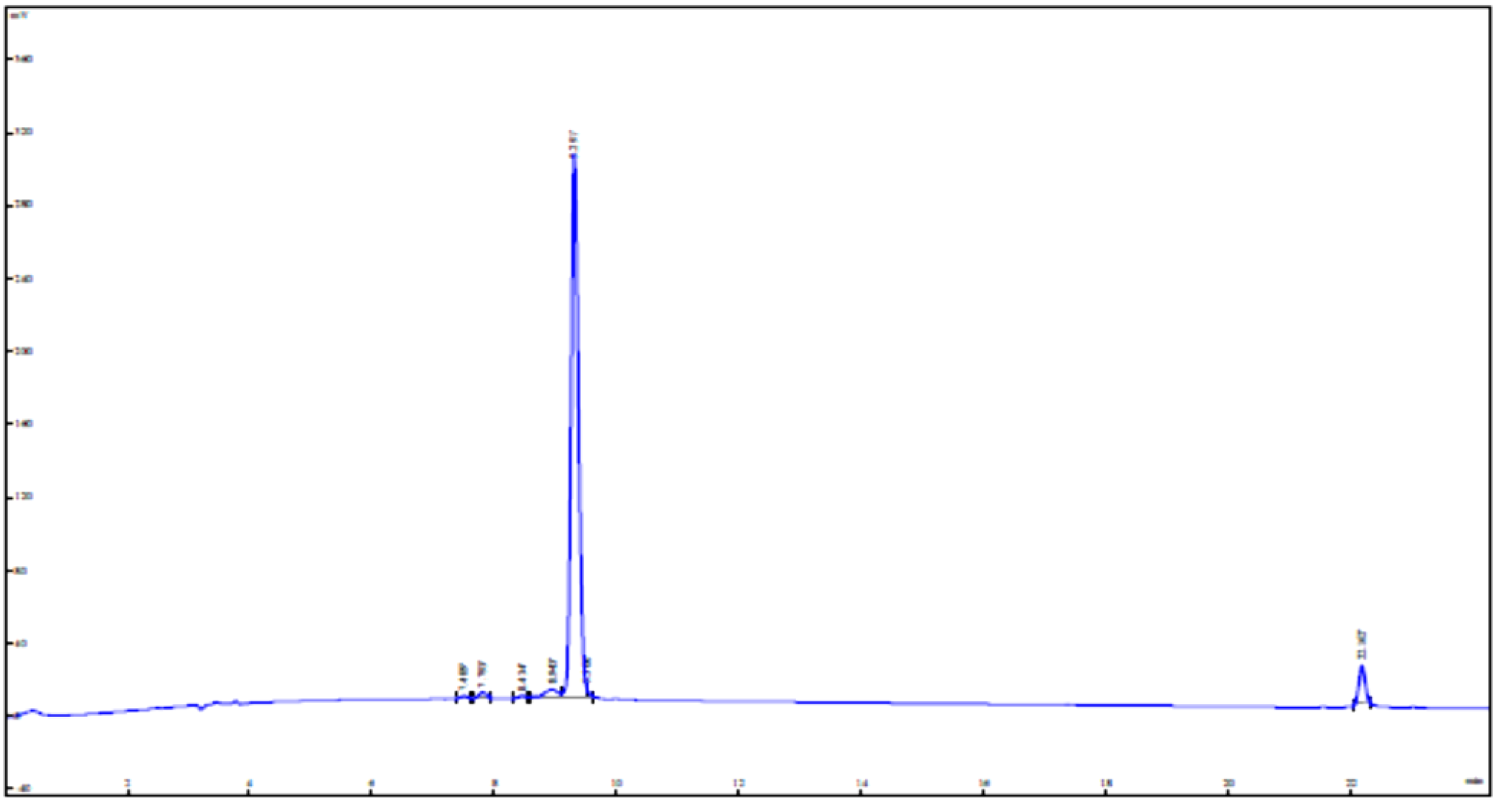
Mass Spectrometry Report



Sample: HFSGFLPKRTHMPYSTPSRKHN MW: 2626.02

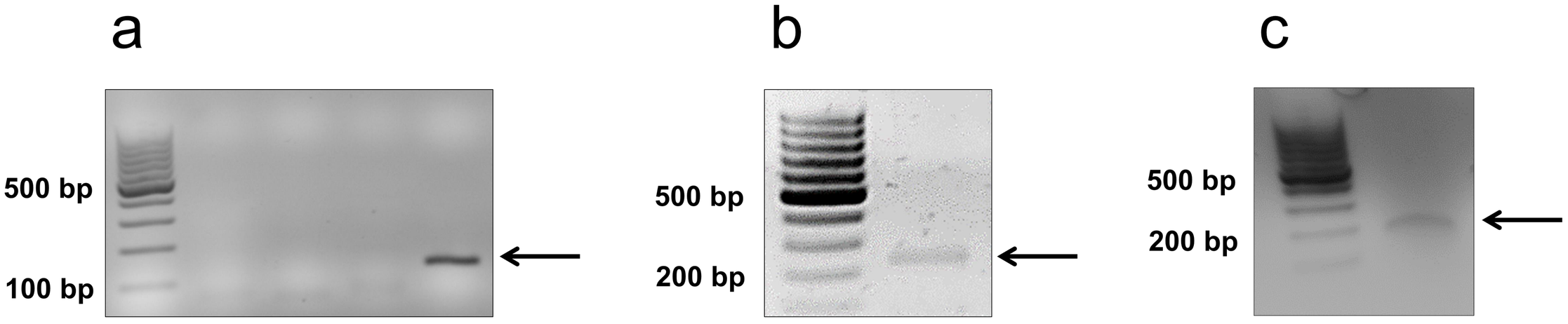
HPLC REPORT

Product Name	:	HFSGFLPKRTHMPYSTPSRKHN		
LOT NO	:	170302-P013322		
Column	:	4.6mm*250mm,Inertsil ODS-SP		
Solvent A	:	0.1%Trifluoroacetic in 100% Acetonitrile		
Solvent B	:	0.1%Trifluoroacetic in 100% Water		
Gradient	:		A	B
		0.0min	18%	82%
		25.0min	43%	57%
		25.1min	100%	0%
		30.0min	Stop	
Flow rate	:	1.0ml/min		
Wavelength	:	220nm		
Volume	:	10ul		

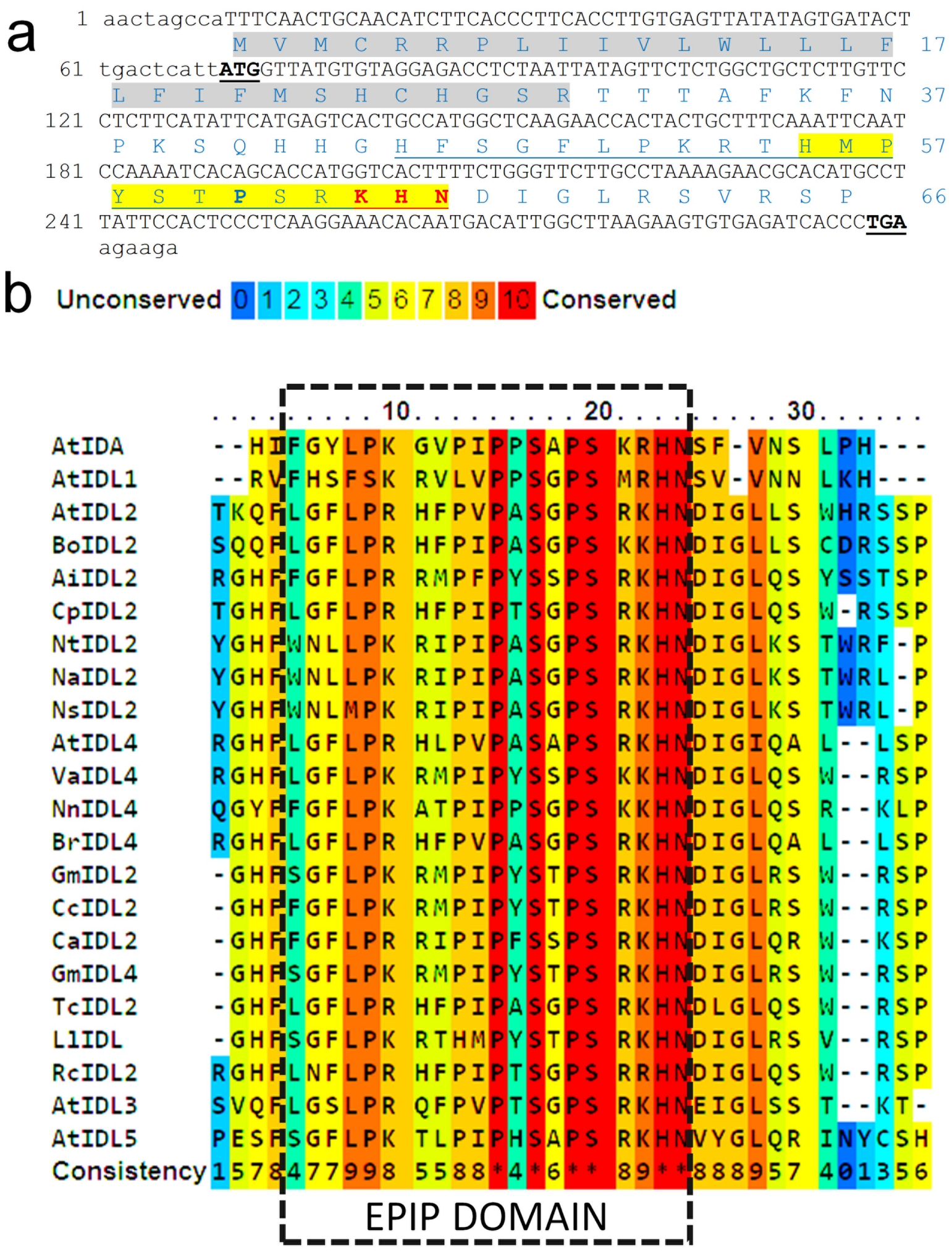


Rank	Time	Conc.	Area	Height
1	7.489	0.3658	10219	1478
2	7.793	0.9687	27062	3261
3	8.434	0.3672	10260	1644
4	8.943	2.2788	63662	4317
5	9.291	90.3019	2522776	300296
6	9.500	0.4398	12286	4409
7	22.162	5.2778	147446	21164
Total		100	2793711	336569

Supplementary Fig. 3 Products of PCR with degenerated primers for *LlIDL* (a), 5'-RACE-PCR (b), 3'- RACE-PCR (c)



Supplementary Fig. 4 The coding sequence of *LlIDL* and its deduced amino acid sequence (a). Subsequent nucleotide positions are marked on the left side of the figure and amino acid positions on the right. The translation initiation point (the start codon) and termination point (the stop codon) are bolded and underlined. Small letters are used for regions not subject to translation. The N-terminal signal peptide characteristic for IDA/IDL is marked dark gray. Additionally, EPIP domain is underlined: C-terminal PIP motif is indicated light gray, (P) – Pro residue highly conserved for the IDA/IDL is bolded. The conserved KHN motif responsible for co-receptor recognition is also bolded. Alignment of the EPIP domain of predicted LlIDL proteins with other plant EPIP domains (b). Accession numbers of the amino acid sequences used to build the alignment were as follows: AtIDA (NP_564941.1), AtIDL1 (NP_566774.1), AtIDL2 (NP_001078796.1), BoIDL2 (XP_013610915.1), AiIDL2 (XP_020969157.1), CpIDL2 (XP_021899937.1), NtIDL2 (XP_016454757.1), NaIDL2 (XP_019236937.1), NsIDL2(XP_009761582.1), AtIDL4 (NP_001319583.1), VaIDL4 (XP_017422713.1), NnIDL4 (XP_010245269.1), BrIDL4 (XP_009135593.1), GmIDL2 (KHN34057.1), CcIDL2 (KYP67833.1), CaIDL2 (XP_012571927.1), GmIDL4 (KHN29158.1), TcIDL2 (XP_007048294.2), LlIDL (AMH85930.1), RcIDL2 (XP_015583407.1), AtIDL3 (NP_001318520.1), AtIDL5 (NP_001319392.1). The conservation scores were determined by the PRALINE program. The scoring scheme works from 0 for the least conserved alignment position, up to 10 for the most conserved alignment position



Supplementary Fig. 5 Alignment of the predicted LlIDL proteins with other IDA/IDL constructed using the Phylogeny.fr. Accession numbers of the amino acid sequences used to build the alignment were as follows: AtIDL1 (NP_566774.1), AtIDA (NP_564941.1), NnIDL4 (XP_010245269.1), AtIDL5 (NP_001319392.1), VaIDL4 (XP_017422713.1), CcIDL2 (KYP67833.1), LlIDL (AMH85930.1), GmIDL2 (KHN34057.1), GmIDL4 (KHN29158.1), AiIDL2 (XP_020969157.1), CaIDL2 (XP_012571927.1), NaIDL2 (XP_019236937.1), NtIDL2 (XP_016454757.1), NsIDL2(XP_009761582.1), AtIDL3 (NP_001318520.1), RcIDL2 (XP_015583407.1), CpIDL2 (XP_021899937.1), BoIDL2 (XP_013610915.1), TcIDL2 (XP_007048294.2), AtIDL4 (NP_001319583.1), BrIDL4 (XP_009135593.1), AtIDL2 (NP_001078796.1).