

Table 1 Suppl. The detection of terpenes in *A. lancea* leaves

RT	Compound	Formula
12.54	citral	C ₁₀ H ₁₆ O
14.16	farnesene	C ₁₅ H ₂₄
15.40	linalool oxide	C ₁₀ H ₁₈ O ₂
16.44	nerolidol	C ₁₅ H ₂₆ O
38.56	squalene	C ₃₀ H ₅₀
43.25	α-amyrin	C ₃₀ H ₅₀ O

Table 2 Suppl. Terpene synthases (TPS) used in phylogenetic analysis.

Protein name	Note	Plant species	Accession number
AaLIS	linalool synthase	<i>Arabidopsis thaliana</i>	AAO85533
AaLIM1	(3R)-linalool synthase	<i>Artemisia annua</i>	Q9SPN1
AaTPS	sesquiterpene synthase	<i>Artemisia annua</i>	PWA60940.1
AgLIS	(-)-4S-limonene synthase	<i>Abies grandis</i>	O22340
AgMER	myrcene synthase	<i>Abies grandis</i>	O24474
AgPIN1	pinene synthase1	<i>Abies grandis</i>	O24475
AgaTPS	sesquiterpene synthase	<i>Ageratina adenophora</i>	AYV65217.1
AmNES/LIS-2	nerolidol/linalool Synthase 2	<i>Antirrhinum majus</i>	ABR24418
AtLIS	linalool synthase	<i>Arabidopsis thaliana</i>	AAO85533.1
AtTPS10	myrcene/ocimene synthase	<i>Arabidopsis thaliana</i>	NP_179998.2
AtTPS2	terpene synthase 2	<i>Arabidopsis thaliana</i>	NP_193406.3
AtTPS14	terpene synthase 14	<i>Arabidopsis thaliana</i>	NP_001185286.1
CiGER	germacrene A synthase	<i>Cichorium intybus</i>	Q8LSC3
CILIS	(+)-limonene synthase	<i>Citrus limon</i>	Q8L5K3
CmCPS1	copalyl-diphosphate synthase 1	<i>Cucurbita maxima</i>	AAD04292
CsTPS	ent-kaurene oxidase, chloroplastic-like	<i>Citrus sinensis</i>	XP_006492559.1
AtLIS	linalool synthase	<i>Arabidopsis thaliana</i>	AAO85533.1
FaNES2	nerolidol synthase 2	<i>Fragaria × ananassa</i>	P0CV95.1
FhTPS1	linalool synthase	<i>Freesia hybrid cultivar</i>	AFP23421.1
FhTPS2	linalool synthase	<i>Freesia hybrid cultivar</i>	AQM50913.1
HcTPS7	monoterpene synthase	<i>Hedychium coronarium</i>	AHJ57305.1
HcTPS8	terpene synthase	<i>Hedychium coronarium</i>	AGY49283.1
LeCPS	copalyl diphosphate synthase	<i>Lycopersicon sculentum</i>	BAA84918
LaCARS	B-caryophyllene synthase	<i>Lavandula angustifolia</i>	AGL98419.1
LaGERDS	germacrene-D synthase	<i>Lavandula angustifolia</i>	AGL98420.1
LaLINS	R-linalool synthase	<i>Lavandula angustifolia</i>	Q2XSC5.1
McvrTPS1	sesquiterpene synthase 1	<i>Matricaria chamomilla</i> var. <i>recutita</i>	AIG92846.1
MtTPS23	α-farnesene synthase	<i>Medicago truncatula</i>	XP_003621227.1
MtTPS23	(3S,6E)-nerolidol synthase 1	<i>Medicago truncatula</i>	003619707.1
SIGER	germacrene C-synthase	<i>Solanum lycopersicum</i>	NP_001234055
SITPS24	diphosphate synthase	<i>Solanum lycopersicum</i>	NP_001234008.2
SITPS5	linalool synthase	<i>Solanum lycopersicu</i>	NP_001233805.1
SITPS8	1,8-cineole synthase	<i>Solanum lycopersicu</i>	XP_004231365.1
SITPS40	copalyl-diphosphate synthase	<i>Solanum lycopersicu</i>	NP_001234008.2
TcTPS	terpene synthase	<i>Taiwania cryptomerioides</i>	AIO10963.1
VGwGers	germacrene A synthase	<i>Vitis vinifera</i>	ADR66821.1
VvGwTPS	terpene synthase	<i>Vitis vinifera</i>	ADR74202.1
VvGwBer	(E)-α-bergamotene synthase	<i>Vitis vinifera</i>	ADR74195.2
VvGwqCad	γ-cadinene synthase	<i>Vitis vinifera</i>	ADR74199.1
XsTPS	sesquiterpene synthase	<i>Xanthium strumarium</i>	AMP42991.1

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1   ATGTTTACTACCTCAAACCAGAAGTCTTGTATCCGTTAGAACTAACGAGACCTGCAACAAGCACGTGAACATTATTATTGCTGAGGAAGAGAATGATGTGAAA
1   M F T T S N Q K S C Y P L E T N E T C N K H V N I I I A E E E N D V K
106 CATGAAGAATTGGTGAATCATGTTCCAGAGATTAATGGCCAAAGTTAAAGATGACAGATTTGAGGATCTGATTATGGTTGATTCTCTCCAGCGACTGGCAATCGAT
36  H E E L V N H V Q R L M A K V K D D R F E D L I M V D S L Q R L A I D
211 TATCACTTCGAAGATGAGATCAACTTAATATTGAGAAGGCGTTACACACAATTTCTAAACACAGATTTATTTGAGCATCAAAATCTCTATGAGGTCTCTCTATGT
71  Y H F E D E I N L I L R R R Y T Q F L N T D L F E H Q N L Y E V S L C
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106 F R I L R Q K G F Q V S P D V F A N F K Q K D G K F K G E I A E D V K
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176 F L D E D E A I M V K N T L V H S Y Q R T P S S F M V K R F I Q H Y M
631 GGGACTACCATGTCACACTGGCAGACTTGGAGTTGGCTAACTCCAGTTGGTACATCAAACAGAAGTAGATCAAATCTCTAGATGGTGGAGGAGTTGGGTTTG
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736 GCTCAGGAGCTGAAGCTTGCAAGGAACCAACCACTGAAGTGGTACTTATGGCTATGGCTAGCCTCACAGATCCACCTTGTCGGACCAAGAATTGAGCTCACA
246 A Q E L K L A R N Q P L N W Y L W P M A S L T D P T L S D Q R I E L T
841 AAGACCATTGCTTTAATCTTTTAATTGACGACATTTTGTATGTTTGAAGTCTAGACCAACTCATCCTCTTCACAGAAGCAGTGAATAGATGGGATATTAAC
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316 T L E R L P Y H L R I C I Q A L Y D E I K E T S D K I Y N K Y G F N P
1051 ATGGAGTACTTAAAAAGAACGTGGGCAAAGCTTTGTGAAGCATTCTAGTGGAGGCAAAATGGTTTGCTTCAAGGACAATTGCCGATGGCGGAGGATTACGTGAAG
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386 N G I V S S G A H V V T M H M F F L L G G A T S K E I A S I I D D N P
1261 AGCATAACTTATTGTTTAGCGAAAATCTTCGTCTTTGGGATGATTTAGGAAGCGCCAAGGATGAGAAGCAAGATGGGCATGATGGATCATATGTGATGTATTAC
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1576 GTAAGCTCCATGTTCTAG
526 V S S M F *

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Fig. 1 Suppl. The nucleotide sequence and the deduced amino acid sequence of the *AITPSI* cDNA.

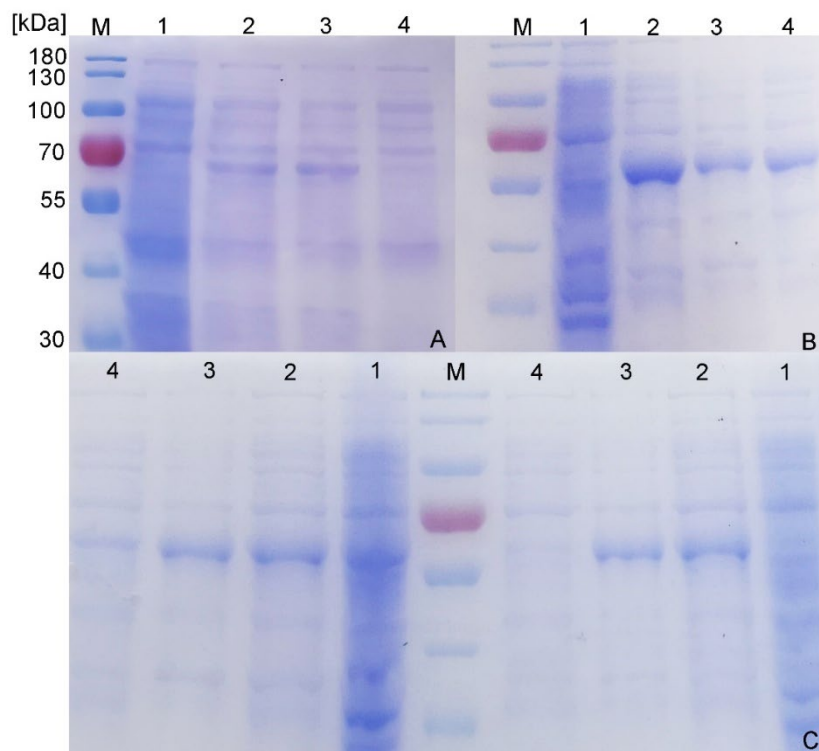


Fig. 2 Suppl. The expression of the recombinant AITPS1 protein in *Escherichia coli*. *A* - SDS-PAGE analysis of recombinant AITPS1 protein. *B* - SDS-PAGE analysis of recombinant AITPS1 protein co-expressed with molecular chaperons pGr07. *C* - SDS-PAGE analysis of recombinant AITPS1 protein co-expressed with molecular chaperons pTf16 (*left*), and pG-KJE8 (*right*). Lane 1 - the total protein extract of noninduced culture, lane 2 - total protein extract of induced culture, lane 3 - lysate pellet, lane 4 - lysate supernatant; M – Marker.