

Supplementary material

Supplementary material 1.



Figure S1. *H. patens* micropropagated plants used for the elicitation experiments.

Table S1. Downloaded files of transcriptomes and gene sequences of MIA-producing plants.

Plant species	Prefix	Family	Accession number	Transcriptome source	Ref
FASTA files					
<i>Amsonia hubrichtii</i>	Ahu	Apocynaceae	SPRX096091	PhytoMetaSyn (www.phytometasyn.ca)	[52]
<i>Cinchona ledgeriana</i>	Cle	Rubiaceae	-	PhytoMetaSyn (www.phytometasyn.ca)	-
<i>Vinca minor</i>	Vmi	Apocynaceae	-	PhytoMetaSyn (www.phytometasyn.ca)	-
<i>Tabernaemontana elegans</i>	Tee	Apocynaceae	SPRX096093	PhytoMetaSyn (www.phytometasyn.ca)	[52]
<i>Rauwolfia serpentina</i>	Rsa	Apocynaceae	-	http://medicinalplantgenomics.msu.edu/	[53]
<i>Camptotheca acuminata</i>	Caa	Nyssaceae	-	http://medicinalplantgenomics.msu.edu/	[53]
<i>Ophiorrhiza pumila</i>	Opa	Rubiaceae	-	http://ngs-data-archive.psc.riken.jp/pub/ophiorrhiza_pumila/download/	[54]
<i>Catharanthus roseus</i>	Cro	Apocynaceae	-	http://medicinalplantgenomics.msu.edu/	[53]
Short Read Archive (SRA) files					
<i>Rhazya stricta</i>	Rsi	Apocynaceae	SRP028239	Genbank NCBI (www.ncbi.nlm.nih.gov)	[55]
<i>Hamelia patens</i>	Hpa	Rubiaceae	SRP079620	Genbank NCBI (www.ncbi.nlm.nih.gov)	[49]
<i>Uncaria rhynchophylla</i>	Ury	Rubiaceae	SRX362039	Genbank NCBI (www.ncbi.nlm.nih.gov)	[56]

<i>Mitragyna speciosa</i>	<i>Msp</i>	Rubiaceae	SRX2855178	Genbank NCBI (www.ncbi.nlm.nih.gov)	[57]
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Table S2. MIA-biosynthesis gene sequences

Species	Gene	Code	Accession N° GenBank	Bibliography
<i>Catharanthus roseus</i>	Loganic Acid Methyl-Transferase	<i>CroLAMT</i>	ABW38009.1	[12]
	Tryptophan decarboxylase	<i>CroTDC</i>	CAA47898.1	[58]
	Strictosidine synthase	<i>CroSTR</i>	CAA43936.1	[59]
	Strictosidine beta-glucosidase	<i>CroSGD</i>	AAF28800.1	[17]
	Tetrahydroalstonine synthase	<i>CroTHAS</i>	AKF02528.1	[16]
	Heteroyohimbine synthase	<i>CroHYS</i>	ANQ45225.1	[18]
	Nitrate/Peptide Family Transporter	<i>CroNPF2.9</i>	AQM73449.1	[14]
	Elongation factor 1 -alpha	<i>CroEF1-α</i>	ABV58644.1	[49]
<i>Mitragyna speciosa</i>	Strictosidine synthase	<i>MspSTR</i>	EU288197.1	-
<i>Ophiorrhiza pumila</i>	Strictosidine synthase	<i>OpuSTR</i>	AB060341.1	[54]
<i>Ophiorrhiza japonica</i>	Strictosidine synthase	<i>OjaSTR</i>	EU670747.1	[60]
<i>Uncaria rhynchophylla</i>	Strictosidine synthase	<i>UrySTR</i>	OL310251.1 ON125563.1	-

Table S3. Degenerated primers for *H. patens* genes amplification

Gene	Primer name	Primer Sequence (5'→3')
<i>LAMT</i>	LAMT-F1deg	THGYDGYTTNGGNTGYTCNDBHGG
	LAMT-R2deg	ADNRTANDNNHHNAHGTTGAANGARTC
<i>TDC</i>	TDC-F1deg	GARAVHTWYCCDGTYYTTBAGCSAAG
	TDC-R2deg	AYTTGCCARTYYTTRWARTCNABNAC
<i>SGD</i>	SGD-F1deg	DKCNKCHTWYCARDYDYGARGG
	SGD-R1deg	GHDSWRTARTRRTNANNCCNABRWARTC
<i>THAS1</i>	THAS1-F2deg	AARJJYAARGYHGGDGAYRNRGTNG
	THAS1-R2deg	GCDGMVAANTCNANCATYTCYTG
<i>THAS2</i>	THAS2-F2deg	TDRBHD TNARRDTBVYNAARGCNTTHGG
	THAS2-R2deg	TKHKBNGCDGCRAANTYNANCATYTC
<i>NPF2.9</i>	NPF-Fdeg	GGTTTCTCTTYRTVTGGAATGCTGCTTC
	NPF-Rdeg	GCTTGTCCYGGAAAATGRAATGCTTCTC

Table S4. Primers used for RACE

Primer	Sequence 5'----3'
RACE 3'	
GeneRacer TM 3' Primer	5'-CGCTACGTAACGGCATGACAGTG-3'
<i>HpTHASR-F1</i>	5' GAC GGA ACC CCC ACA TAT GGA GG 3'
<i>HpTHASR-F2</i>	5' ACC TTA GCA TAG GAA GGA AAA TTG 3'
<i>HpTDCR-F1</i>	5' CTC AAT GAG TTT CAG CCC TCA TAA ATG G 3'
<i>HpTDCR-F2</i>	5'TGC TGG TCA AGG CAC TAA GTA CTA AC 3'
<i>HpLAMT-F</i>	5' CTT CAG ATC TCT CCC GCC AAA CAG G 3'
RACE 5'	
GeneRacer TM 5' Primer	5'-CGACTGGAGCACGAGGACACTGA-3'
<i>HpLAMT-R</i>	5' GAG AGC CAG TGA AGT GCA TAA GAG C 3'

Table S5. Primers used for RT-qPCR

Gene	Primer name	Primer Sequence	Amplicon size (bp)	Mean PCR efficiency
Elongation factor 1- α	EF1- α -F	5' CTG AAG TTA AGT CTG TTG AGA TGC ACC 3'	200	1.77
	EF1- α -R	5' GCC AGG GTG GTT CAT GAT GAT GAC C 3'		
Loganic Acid Methyltransferase	LAMT-F	5' CTT CAG ATC TCT CCC GCC AAA CAG G 3'	126	1.85
	LAMT-R	5' GAG AGC CAG TGA AGT GCA TAA GAG C 3'		
Tryptophan decarboxylase	TDC-F	5' GTGGATTCATGTTGATGCTGCTTATGC3'	90	1.82
	TDC-R	5' GAGTCAACTCTCTCAACCCCATCC3'		
Strictosidine β -D-glucosidase	SGD-F	5' CAC ACA ATC AGC TTC TAG CCC ATG C 3'	96	1.81
	SGD-R	5' ACA CGA GTG TAA TCC CAA TCT TGC C 3'		
Tetrahydroalstonine synthase 1	THAS1-F	5' GGA GTT GGT TGC CTC GTA GGA TC 3'	87	1.93
	THAS1-R	5' CGT GAA TAT TTG GGC AGG GCA GTA G 3'		
Tetrahydroalstonine synthase 2	THAS2-F	5' CTC CCC TTC TCT GTG CTG GGA TC 3'	97	1.91
	THAS2-R	5' CCA CCA AGG CCA ACC ACA CC 3'		
Nitrate/Peptide Strictosidine Transporter	NPF-F	5' CGTAATCTCTGGTGCCATCTCTCTC3'	103	2.08
	NPF-R	5' CCTAATCGTTGGAGGGGTGTTGG3'		
Strictosidine synthase	STR-F	5' GTKAGCABMRWMTATGATGACAGAGGTGT3'	131	2.04
	STR-R	5' CCTGGTAYATTYARYCCWTTTCATCAAAACT3'		

Supplementary material 2.

H. patens cloned sequences.

>HpaLAMT (complete CDS)

ATGGCTCCAACAATGGACACCATCCCAACTGTAGACATCAAGGAAATGCC
AGAAGAAGCACACCCCATGAAAGGTGGAGATGATTTCAATAGCTATTCTC
AAAATTCTTGCTATCAGAGGGGAGTTATAGATGCCGCAAAGCTATCATTT
TTGAAGCAGTAAATGAGAATCTAGAACTTGAGAATAACAAATCTACTTTTCG
ATCCATCTAAGCCTTTTCGCATTGCTGATTTTGGTTGCTCAACCGGGCCTAA
CACATTTTTAGCTATGCAAAATATCGTGGAAGCCGTGGAGCAAAAGCACA
AATCTCTACAAGAAAAAACCAACCCAGAATTCCACGTATTTTTCAATGACC
ATGTCAACAACGATTTCAACATTCTCTTCAGATCTCTCCCGCCAAACAGGG
ATTACTTTGCTGCTGGGGTGCCCGGATCGTTTTACACGAGGGTGTACCTAG
GGCCTGTTTGCATTTTGCTCATTGCTCTTATGCACTTCACTGGCTCTCTAAGG
TTCCTAAGGAGGTTCAAGACAAGAATTCTCCCGCCTTCAACAAGGGGAGG
ATTCATTACACCGGGACTGAAAAGCATGTTGTGAAAGCTTACTTTGGTCAG
TTCCAAAAGGATATGGACGCATTTCTGAAAGCTAGAGCTCAAGAAATTGTG
GGAGGAGGGTTGATGGTGATTCAAATTCCTGGTCTTCCTAGTGGTGAGGTC
CTCTTCTCTAGGACTGGTGCTGGAATGCTTCATGCTCTTCTGGGCTCGTCCTT
GATGGAACCTCGTAACTTTGGGAGTAATAAGTGAAGAAAGTGTGGATTCCTT
CAACTTGCCTCAATACCATCCATCAATTGAGGAACTAGAAATGGTGATAGA
GATGAACAAAAGTTTTAGCCTTGAAAAAATTGGAGCATTGAATCATCCTAT
GAAGAACTTGCCATTTGATGTTCAAATGACTTCGCTACAAGTAAGAGCTAT
CATGGAGGGGATTCTAACCGACCATTTTGGAGACAAAATCTTGGACCAATT
GTTGCAAATCTACACCAAGAACTGCAAGAGAATTACAATGTTTTTGACAA
GGAAATCCGAAGAGATGCGGATTTGTTTCTTAAACGCAAGTGCAA
TTGA

>HpaTDC (partial)

GAGACATTCCCTGTCTTTAGCCAAGTTGAGCCCGGATATCTCCGTACCTCTC
AGCCCGAAACCGCCCCTTATCTGCCCGAAAAATTTGATGACATTTTGCATG
ATATTGAAAAAGATATAATCCCTGGAATGACCAACTGGCTAAGCCCTAATT
TTTATGCATATTTTCCAGCTACTGTTAGCTCAGCTGCTTTTCTTGGAGAAATG
TTGTGCACCGGTTTCAACTCTGTAGGGTTCAACTGGCTAGCCTCCCCGGCA
GCGACCGAGCTCGAGATGGTGGTGATGGATTGGCTGGCTCACATGCTTAAG
CTCCCCAAGTCCTTTATGTTCTCAGGCACTGGTGGTGGTGTCTCCAGGGAA
CCACCAGCGAGTCTATTCTTTGCACCCTCATCGCCGCCCCGCGACCGGGCTTT
CGAGGAAATCGGCGTGGAGAATATTGGGAAGCTTGTTGTCTATGGATCCGA

TCAGACACATTCATTTTTTCGTCAAAACTTGCAAACTGGCAGGTATTTTCCCT
TGCAACATAAAAAATTATCCCTACTACTGTTGAGGCCAACTTTTCCATGTCCC
CCGGTGCTCTACGTAAACAAATCGAAGCTGACGTGGCAGATGGGCTGGTC
CCACTTTTTGTATGTGCTACTGTGGGAACCACATCCACCCTGCCGTTGACT
CAGTGAGTCAGATAGCTGATGTAGCAAATGAATTCAAGATGTGGATTCATG
TTGATGCTGCTTATGCTGGTAGTGCATGCATATGTCCTGAGTTTAGGCAGTA
CTTGATGGGGTTGAGAGAGTTGACTCAATGAGTTTCAGCCCTCATAAATG
GCTACTTTGTTATTTGGATTGTTGTTGCTTGTGGGTCCAGAGACCTGACTTGC
TGGTCAAGGCACTAAGTACTAACCCTGAATACTTGAAAAATAAAAGAAGT
GAGCTTGGCTCTGTCATGGACTACAAAGACTGGCAAATTGGTACGGGAAG
ACGATTTAGAGCACTCCGATTATGGCTTATTATGCGCAGTTACGGCCTTAA
AAATCTCCAAAGCCACATCCGGTCCGACGTCCAAATGGCCAAAATGTTTCG
AAGGGTTCGTGAAATCTGATCCACGGTTTGAAATGATTGTACCGCGTGCAT
TTTCACTTGTGTGTTTTAGGCTTAATCCAAGGAGATTGGGTGAAAGTCATGC
AATTGATTTGGAGCTCTTGAACAAGAAGCTACTCGAGTCGATCAACTCAAC
TGGGCGAGTTTACATGACTCACACCAAGGTTGGTGGGGTATACCTGTTGAG
ATTTGCAGTGGGGGCCCTCGTTAACAGAGGATCGCCATGTGTGTGCCGCCTG
GGAGTTGATAAAAGAATGCACCGATAATTTGCTTAAAGAAAATAATTAG

>HpaSGD (partial)

GCGGCCTATCAATATGAAGGTGGAGCAAGTGAAGGCGGTAAAGGTCCCAG
TATATGGGATACTTTCACCCATAGACGGCCTGGTTTGATAATGGGTGGAGG
CAATGGAAACCTGGCCATTGATTCATATCATCAGTACAAGGAAGATGTCA
AGATGTTGAAGAACATGGGGTTGGATGCCTATCGGTTTTCAATATCATGGT
CAAGAGTCCTGCCAGGTGGGAATTTAAATGGTGGTGTAAATAAGGAAGGA
GTTGACTACTACAACAATCTCATAGATGAGCTCCTAGACAATGGTATCGAG
CCATATATAACTCTATTTCAATTGGGATGTTCCCCAAGCCTTGGAAGATAAAT
ATGGTGGTTTTTTAAGTCCAAAAATTGTGGACGACTTCGTGGAGTACGTAG
AGCTTTGCTTTTGGGAATTCGGAGATCGAGTGAAGAACTGGATAAACTGA
ATGAACCCTGGAGCTTTAGCACTGGTGGATATGTAAACGGTACCTTTGCAC
CCGGCCGAGGTGCCTCCGCCTCTGAGCAAGTAAATCACGATCACATTGTAC
CAAGCAGATGTTCTGCACATGTACGACAATGTATTTCTAGCAATGGAAATC
CAGGCACGGAGCCTTATTTGGTCACACACAATCAGCTTCTAGCCCATGCTG
CTGCTGTAAAACTATACAAAAGCAAATTTAGAAACCACAAGAAGGCAAG
ATTGGGATTACACTCGTGTCTCAATGGTTGGAACCATTGGATGAAAACAAT
GATGCCGATGTCCAAGCGTCCAAAAGAGCTCTCGATTTTCATGTTAGGATGG
TTAATGCAGCCACTTAA

>HpaNPF2.9 (partial)

GGCTCAAGCTTTTGTGAAACTCCATCACCTTTGCAATATACAAGCCTATTTT
TGGCTATAGCTCTGGCAGCTTTAGGGTGTGCAGGTACTAGTTTCACTGTTCGG
AACAAATGGGAGCAGATCAGTTGGATAATCCTGAGCATCAAGAGAATTTCTT
TAACTGGTTTCTTTTCATCTGGGATGCTGCTTCACTGATTAGTGGTACCGTA
ATTGTTTATGTTCAAGATAATGTGAGTTGGGGATTGGGGTATGGCCTATGTG
GTGCCGCTAATCTGCTAGGATTAATCAGTTTTCTGCTGGGAAGGCACTACT
ATCGCTATGTTCAACCACAAGGGAGTCCGTTCAAGGATGTAGCTCGCGTAG
TCTTTGCAGCATTCTCTAAGAGGAAGCAATTTTGTCAAAAACAAGAGAAG
ATTATTATAGTCCATTACATAACGAAGCCGATGACCAACATGACGGTGTCA
ATTATTTGGCAGCAGCAGCCTCACAACCAAAAGAAACATTCAAGTTTCTGA
ACCATGCAGCCTTGATAACCCAAGCAGACATCCAATCAGATGGATCAATC
AGGCAATCATGGAAGTTGTGCACGGTACAACATGTGGAAGATCTTAAAC
CTTAATTAGAATTGCCCAATTTGGGCAACTGTTATTTTCATAACCACCCCA
ATGAGTATGCTAGCCGCCTTCACACTCCTTCAGGCTCTAAAAATGGACACT
GGCATTGTATCCAATTTCAAATTCCCAGTAGGTTCTCTGGTAGTCTTTTTCG
TAATCTCTGGTGCCATCTCTCTCACCATATTAGACAGATTGATATTCCCTTT
ATGGCAAAAAATATTCGGCAAATTTCCAACACCCCTCCAACGATTAGGCA
CAGGTCATGTCATAAATGTGCTTAGCATAGTCGTTGCAGCCTTGGTGGAAT
CAAAGAGGCTGCAATTAGCTCGAGCCCACAATGTTCAAGATTTCGAGAATTT
CCATCATGCCAATGTCTGTTATGTGGTTAGTACCTCAGTTGGCACTTATGGG
AATAGGAGAAGCATTCCATTTTCCAGGACAAGC

>HpaTHAS1 (partial)

AAAGTTAAAGTTGGGGACGAGGTGGGAGTTGGTTGCCTCGTAGGATCATGT
CGAAATTGTAACAGGTGCAACGAAGACCTTGAAAACACTGCCCCTGCCCA
AATATTCACGTATGGCTCCCCAGACACCGACGGAACCCCCACATATGGAG
GCTATTCAGATATCATGGTTGTGGACGAGCACTTCGTTGTTTCGTTGGCCTGA
AAACTTCCCTCTTGATGCCGGTGCACCCCTTCTCTGTGCTGGAATCACTACA
TATAGCCCGTTGAGATATTTTGGACTTGACAAACCTGGAATTCATATTGGTG
TGGTTGGCCTTGGTGGGCTTGGTCATGTGGCCGTGAAATTCGCCAAGGCAT
TTGGGGCAAAGGTGACCTTGATCAGCACTTCCGCTAGTAAAAAACAGGAT
GCCATCGAAAAACTAGGGGCTGATTCATTTATACTTAGTAATGACCCTAAG
GAAATGGAGGCTGCATTTGGAACATATGGATGGTATTATTGATACTGTCTCT
GCTGTTCAATTCATTCTGCCTTTGATTGATTTGTTAGCATTTGATGGGAAGCT
TGTTGAGGTTGGTATACCAGCAAAGCCACTTGAAGTGGCCATATATAACCT
TAGCATAGGAAGGAAAATTGTGGGAGCGACTACTATTGGAGGCTTGAAGG
AAACGCAAGAAATGATTGATTTTGCAGTAAAGCACAATATAGTACCTGAT

GTGGAGATCATCCCAATTGATTATGTGAACACCGCAATGGAGCGCCTTGAG
AGGGGTGAAGTCAAGTACCGATTTGTGATAGATGTGGGGAATACTAAA
GTCTACTTAG

>HpaTHAS2 (partial)

GGTAAAGTTGGAGATGTGGTAGGAGTGGGTTGCCTAGTTGGATCATGTTCGC
AACTGTGACATGTGTTCCAAAGATCTCGAGAACTACTGTCCTGGGCAGATA
CTCACATACAGCGCCGCTTATACCGATGGTACAATCACATATGGAGGCTAC
TCTGATCTTATGGTTGCTGATGAGCACTTTGTGATCCGCTGGCCCGAGAACT
TTCCTCTTGATGCTGGTCGTCCCCTTCTCTGTGCTGGGATCACTACTTACAGC
CCCTTGAGATACTTTGGACTTGATAAGCCTGGAACCCATGTTGGTGTGGTTG
GCCTTGGTGGGCTTGGTCACGTTGCTGTGAAATTTGCCAAGGCTTTTGGGGC
AAAGGTGACTGTGATCAGTACCTCTGAGGGGAAAAAGAAGGAGGCCATTG
AAAAACTTGGAGCAGACGCGTTCTTAAATAGCCGGGACCCTGAGCAGATG
CAGGCTGCACGTGGTACAATAGATGGTATTATTGATACTGTTTCCGCAACA
CATCCTGTTATTCCATTGATCAATTTGGTGAAGTCTCATGGGAAGATAATAC
TGRRRGTTGCAGGCGAAAAGCCACTTGAGGTTCCYGCATTTCCGCTTTTGA
TCGGGAGGAAGACGCTTACTGGGAGTGCTATTGGCAGGTCTGAAGGAAAC
TCAGGAGATGCTGGACTTCGCAGC

Supplementary material 3.

Accession numbers of amino acid sequences used for phylogenetic analysis.

Loganic acid O-methyltransferase (LAMT)

Ophiorrhiza pumila (OpuLAMT) -QWX38535.1

Mitragyna speciosa (MspLAMT)-[37]

Mitragyna speciosa (MspLAMT2)- [37]

Catharanthus roseus (CroLAMT)- AGX93063.1

Uncaria tomentosa (UtoLAMT)- QDD67562.1

Tryptophan decarboxylase (TDC)

Catharanthus roseus (CroTDC)- AYA72254.1

Rauwolfia tetraphylla (RteTDC)-WMM65729.1

Rauwolfia verticillata (RveTDC)- ABP96805.1

Vinca minor (VmiTDC)- AEY82397.1

Tabernaemontana elegans (TelTDC)- AEY82396.1

Ophiorrhiza pumila (OpuTDC2)- QLQ34389.1

Mitragyna speciosa (MspTDC)- AEQ01059.1

Ophiorrhiza prostrata (OprTDC)- ABU40982.1

Ophiorrhiza pumila (OpuTDC)- BAC41515.1

Uncaria tomentosa (UtoTDC)- QDD67561.1

Uncaria guianensis (UguTDC)- ASY03221.1

Camptotheca acuminata (CacTDC)- AAB39708.1

Camptotheca acuminata (CacTDC2)-AAB39709.1

Uncaria rhynchophylla (UryTDC)- [56]

Tetrahydroalstonine synthase (THAS)

Uncaria tomentosa (UtoHYS)-QDD67564.1

Uncaria tomentosa (UtoTHAS)- QDD67563.1

Catharanthus roseus (CroHYS)-ANQ45225.1

Catharanthus roseus (CroTHAS1)-KM524258.1

Catharanthus roseus (CroTHAS2)- ANQ45223.1

Catharanthus roseus (CroTHAS3)- ANQ45222

Catharanthus roseus (CroTHAS4)- KU865324

Rauwolfia tetraphylla (RteTHAS)-MH010799.1

Rauwolfia tetraphylla (Rtiso1THAS)-ASR92154.1

Mitragyna speciosa (MspTHAS)-WNF20697.1

Rauvolfia tetraphylla (RteTHAS3)- OR514625
Rauvolfia tetraphylla (RteTHAS4A)- OR514623
Rauvolfia tetraphylla (RteTHAS4B)- OR514624
Rauvolfia tetraphylla (RteTHAS5)- OR514622
Rauvolfia tetraphylla (RteYOS)- OR514626
Rauvolfia tetraphylla (RteAMS)- OR514628
Rauvolfia tetraphylla (MSTRG.5534)-OR514630
Rauvolfia tetraphylla (MSTRG.5531)-OR514631
Rauvolfia tetraphylla (MSTRG.5530)-OR514632.

Strictosidine beta-glucosidase (SGD)

Mitragyna speciosa (MspSGD1) - WNF20694.1
Rauvolfia verticillata (RveSGD)-AFI71457.1
Rauvolfia serpentina (RseSGD)- CAC83098.1
Catharanthus roseus (CroSGD)-AAF28800.1
Catharanthus roseus (CroSGDs)- AVH80943.1
Uncaria tomentosa (UtoSGD)- AFN69080.1

Loganic acid O-methyltransferase (LAMT)

Consensus	Sequence	Position
CroLAMT	-----M V A T I D S I E M-----P A L P T A V E A H P M K G G D D S H S Y S Q N S C Y Q K G V I D A A K A V I E A V N E	55
OpuLAMT	-----M A P T M D N N T T T I T T V E I I K E M P E E A H P M K G G D D L N S Y S Q N S C Y Q K G V I E A A K A V I E A V H E	61
HpaLAMT	-----M A P T M D T I-----P T V D I K E M P E E A H P M K G G D D F N S Y S Q N S C Y Q R G V I D A A K A I F E A V N E	56
MspLAMT2	M A P T V K T P T P I P T P N P N-----P S L D I K V M P E E A H P M K G G D D L N S Y S Q N S C Y Q K G V I D A A K S V I I E A V T E	65
MspLAMT	-----M A P T L D T I-----P T V D V K E M P E E A H P M K G G D D F N S Y S Q N S C Y Q R G V I D A A K V V I E A V N E	56
UtoLAMT	-----M A P T M D T V-----P T V D V K E M P E E A H P M N G G D D L N S Y S Q N S C Y Q K G V I D A A K T V I L E A V T E	56
Consensus	K L D L E N N I--XX F D P S K P F R I A D F G C S T G P N T* F A M Q N I V E A V*XX K Y K S L*XX K Q P E F H V F F N D H V N D F N	
CroLAMT	K L D L E N N I--P I F D P I K P F R I A D F G C S T G P N T F H A M Q N I V E S V E T K Y K S L Q K--T P E F H V F F N D H V N D F N	121
OpuLAMT	K M D L E N N I I T T F D P S K P F R I A D F G C S T G P N T F F A M Q N I V E V D N R Y K S L L K N Q Q V E F H V F F N D H A N D F N	131
HpaLAMT	N L E L E N N K--S T F D P S K P F R I A D F G C S T G P N T F F A M Q N I V E A V E Q K H K S L Q E K T N P E F H V F F N D H V N D F N	125
MspLAMT2	K L D L E N N I--T T F D P A K P F R I A D F G C S T G P N T Y F A M Q N V E A V E L K Y K S L--K K D Q P E F H V F F N D H V N D F N	133
MspLAMT	K L D L K N N--A N F D P S K P F H I A D F G C S T G P N T Y F A V Q N I V E A V D Q K H K S L H E K I Q P E F H V F F N D H V N D F N	124
UtoLAMT	K L D L E N N--A N F D P S K P F R I A D F G C S T G P N T Y F A M Q N I V E A V D Q K Y K S Q L G K S Q P E F H V F F N D H V N D F N	124
Consensus	I L F R S L P Q N R D Y F A A G V P G S F Y T R V F P K A S L H F A H C S Y A L H W L S K V P K E I Q D K N S P A N K G R I H Y T G T E K	
CroLAMT	V L F R S L P P N R E F F A A G V P G S F Y T R V F P K N S I H F A H C S Y A L H W L S K V P K E I Q D K N S L A Y N K G R I H Y T G T E K	191
OpuLAMT	M L F R S L P Q N R D Y F A A G P G S F Y S R V F P K A S L H F A H C S Y A L H W L S K V P K E I Q D K N S P A Y N K G R I H Y T G T E K	201
HpaLAMT	I L F R S L P P N R D Y F A A G V P G S F Y T R V L P R A C L H F A H C S Y A L H W L S K V P K E V Q D K N S P A F N K G R I H Y T G T E K	195
MspLAMT2	I L F R S L P Q N R D Y F A A G V P G S F Y T R V F P K A S L H F A H C S Y A L H W L S K V P K E I Q D K N S P A F N K G G I H Y T G T E K	203
MspLAMT	I L F R S L P Q D R D Y F A A G V P G S F Y T R V F P K A S V H F A H C S Y A L H W L S K V P K E I Q D K N S P A F N R G R I H Y T G T E K	194
UtoLAMT	I L F R S L P Q D R E Y F A A G V P G S F Y T R V F P K A S L H F A H C S Y A L H W L S K V P N E I Q D K N S P A Y N K G R I H Y T G T E K	194
Consensus	H V V K A Y F*Q F Q K D M*S F L K A R A Q E I V G G G L M V I Q I P G L P S G E V L F S R T G A G M L H A L L G S S L M E L V N L G*I	
CroLAMT	H V V K A Y F G Q F Q R D F E G F L K A R A Q E I V G G G L M V I Q I P G L P S G E V L F S R T G A G L L H F L L G T S L M E L V N K G I I	261
OpuLAMT	Q V V K A Y F S Q F Q K D L D G F L K A R A Q E I V G G G L M V I Q P L G P S G E V L F S R T G A G M L H A L L G S S L M D L V N M G I I	271
HpaLAMT	H V V K A Y F G Q F Q K D M A F L K A R A Q E I V G G G L M V I Q I P G L P S G E V L F S R T G A G M L H A L L G S S L M E L V T L G V I	265
MspLAMT2	H V V K A Y F G Q F Q K D M D S F L K A R A L E I V G G G L M V I Q P L G P S G E V L F S R T G A G L H A L L G A S L M E L V N L G V I	273
MspLAMT	H V V K A Y F S Q F Q K D M G S F L K A R A Q E I V G G G L M V I Q P L G P S G E V L F S R T G A G M L H A L L G S--L M D L V N L G I I	263
UtoLAMT	H V V K A Y F S Q F Q K D M G S F L K A R A Q E I V G G G L M V I Q I P G L P S G E V L F S R T G A G M L H A L L G S S L M E L V N L G V I	264
Consensus	*E E S V D S F N L P Q Y H P S I E E L E M V I E M N* S F T L E K*G A L N H P M K N L P F D V Q M T S L Q V R A I M E G I L T D H F G*	
CroLAMT	N E E S V D S F N L P Q Y H P S V E D L E M V I E M N D C F T I E R V G T L P H P M K N L P F D V Q R T S L Q V R A I M E C I L T E H F G E	331
OpuLAMT	S E E S V D S F N L P Q Y H P S I E E L E M N G S F T L E K I G A L N H P M K N L A F D A Q M T S L Q V R A I M E G I L T Q F G D	341
HpaLAMT	S E E S V D S F N L P Q Y H P S I E E L E M V I E M N K S F S L E K I G A L N H P M K N L P F D V Q M T S L Q V R A I M E G I L T D H F G D	335
MspLAMT2	S E K S V D S F N L P Q Y H P S I E E L E M V I E M N S F T L E K I G A L N H P M K S L P F D V Q M T S L Q V R A I M E G I L T D H F G E	343
MspLAMT	T E E S V D S F N L P Q Y H P S I E E L E M V I E M N S F T I E K V G A L N H P M K N L P F D V Q M T S L Q I R A V M E G I L S D H F G G	333
UtoLAMT	T E E S V D S F N L P Q Y H P S I E E M E M V I E M N N F T L E K A G A L N H P M K N L P F D V Q M T S L Q V R A V M E G I L T D H F G E	334
Consensus	K I L D Q L F E I Y T*K L Q E N Y N V F D K E I R R D A D L F L V L K R K*N	
CroLAMT	N I L D P L F E I Y T K N L Q E N F H V F D K E I R K D A D L Y L V L K R K G N	371
OpuLAMT	K I L D Q L F E I Y T N K L Q E N Y I V F D K E I R K D A D L F L I L K R K I N	381
HpaLAMT	K I L D Q L F E I Y T M K L Q E N Y V F D K E I R R D A D L F L V L K R K C N	375
MspLAMT2	K I L D Q L F E I Y T K K L Q E N Y N V F D K E I R R D A D L F L V L K R K S K	383
MspLAMT	K I L D Q L F E I Y T T K L Q E N Y N V F D K E I R R D A D L F L V L K R K S N	373
UtoLAMT	N I L D P L F E I Y T K K L Q E N Y N V F D K I R R D A D L F L V L K R K S N	374

Consensus		MGSIDXXXX-XXS SXVAFKPLXXEERFKQAHMVDFIADYYKNXEXYVPLSQVEPGYLRRLPETAP
CroTDC	68	MGSIDSTNVA--MNSNPVGEFKPLEAEERFKQAHMVDFIADYYKNVETYPVLSVEVEPGYLRKRIPETAP
VmiTDC	70	MGSIDSTNDVALSNGSSVGEFKPLEAEERFKQAHMVDFIADYYKNVESYPVLSQVEPGYLRERLPETAP
TeiTDC	68	MGSIDSTNVA--PSTPSIAEFKPLDAEERFKQAHMVDFIADYYKNVENYPVLSQVEPGYLRERLPENAP
RveTDC	68	MGSIDSTDVA--ISASPAVEFKPLEAEERFKQAHMVDFIADYYKNVESYPVLSQVEPGYLRERLPETPP
RteTDC	68	MGSIDSTDVA--FSASAVAEFKPLEAEERFKQAHMVDFIADYYKNVESYPVLSQVEPGYLRERLPESPP
CacTDC	68	MGSIDSNYD--TESPASVGGFNLPDPEERFKQAHMVDFIADYYKNIESYPVLSQVDPGVRHSRLGKNAP
CacTDC2	65	MGSIDSNVA--PSTPSIAEFKPLDAEERFKQAHMVDFIADYYKNIESYPVLSQVEPGYLRERLPETAP
OpuTDC	67	MGSISENC---DDISISLAAPFRPLEPEERFKQAHMVDFIADYYKNINENYPVLSQVEPGYLRNRLPETAP
OprTDC	67	MGSISENC---DDISISLAAPFRPLEPEERFKQAHMVDFIADYYKNINENYPVLSQVEPGYLRNRLPETAP
HpaTDC	23	-----ETFPVFSQVEPGYLRTSQPETAP
OpuTDC2	70	MGSIDANNINGAYPSSSPVAPFKPLDPEERFKQAHMVDFIADYYKNIEKYPVLSQVEPGYLRTRLPETAP
UtoTDC	22	-----RQPVLSQVEPGYLRKHLPETAP
MspTDC	69	MGSIDTSDGDAYANSAPVAFKPLDPEERFKQAHMVDFIADYYKNINENYPVLSQVEPGYLRQLSQTAP
UryTDC	69	MGSIDTNDDAAYANSAPVAFKPLDPEERFKQAHMVDFIADYYKNINENYPVLSQVEPGYLRARLPETAP
UguTDC		-----
Consensus		YLPExFEXILDIQKDIIPGMTNWLSPNFFAFPATVSSAAFLGEMLCTFNSVGFNWLASPAATELEMV
CroTDC	13	YLPPELDDIMKDIQKDIIPGMTNWMSPNFFAFFPATVSSAAFLGEMLSTALNSVGFTWVSSPAATELEMI
VmiTDC	14	YLPESLDKIMSDIQKDIIPGMTHWMSPNFFAFFPATVSSAAFLGEMLSTALNSVGFTWVSSPAATELEMI
TeiTDC	13	YLPESLDMIINDIQKDIMPGMTNWMSPNFFAFFPATVSSAAFLGEMLSTALNSVGFTWVSSPAATELEMI
RveTDC	13	YLPDSLDKIIDDIQKDIIPGMTNWMSPNFFAFFPATVSSAAFLGEMLSTALNSVGFTWVSSPAATELEMI
RteTDC	13	HLPESLDKIIDEIQKDIIPGMTNWMSPNFFAFFPATVSSAAFLGEMLSTALNSVGFTWVSSPAATELEMI
CacTDC	13	YRSEPFESILKDVQKDIIPGMTHWMSPNFFAFFPATVSSAAFLGEMLCTCFNSVGFNWLASPAATELEMV
CacTDC2	13	YRPEPFESILKDVHKDIIPGVTHWLSPNFFAFFPATVSSAAFLGEMLCTCFNAVGFNWLASPAATELEMV
OpuTDC	13	HLPESEFETILKDIKKDIVPGMTNWLSPNFFAFFPATVSSAAFLGEMLCTGFNSVGFNWLASPAATELEMV
OprTDC	13	HLPESEFETILKDIKKDIVPGMTNWLSPNFFAFFPATVSSAAFLGEMLCTGFNSVGFNWLASPAATELEMV
HpaTDC	93	YLPEKFDLILHDIEKDIIPGMTNWLSPNFFAFFPATVSSAAFLGEMLCTGFNSVGFNWLASPAATELEMV
OpuTDC2	14	YLPEPFENILQDIQKDIIPGMTNWLSPNFFAFFPATVSSAAFLGEMLCTGFNSVGFNWLASPAATELEMV
UtoTDC	92	YLPEPFENILHDIEKDIIPGMTNWLSPNFFAFFPATVSSAGFLGEMLCTGFNSVGFNWLASPAATELEMV
MspTDC	13	YLPEPFENILQDIQKDIIPGMTNWLSPNFFAFFPATVSSAAFLGEMLCTGFNSVGFNWLASPAATELEMV
UryTDC	13	YLPEPFENIMQDIHKDIIPGMTNWLSPNFFAFFPATVSSAAFLGEMLCTGFNSVGFNWLASPAATELEMI
UguTDC		-----
Consensus		VMDWLA MLKLPKFSMFSGTGGGVIQGTTSEAILCTLIAARDRALEKXGVXNIGKLVVYGSQDQTHSFXK
CroTDC	20	VMDWLAQILKLPKFSMFSGTGGGVIQNTTSEILCTIIAARERALEKLGPD SIGKLVCYGSQDQTHMFPK
VmiTDC	21	VMDWLAKMLKLPKFSMFSGTGGGVIQNTTSEILCTIIAARERALEKLGPD SIGKLVCYGSQDQTHMFPK
TeiTDC	20	VMDWFAQMLKLPKFSMFSGTGGGVIQNTTSEILCTIIAARERALEKLGPD SIGKLVCYGSQDQTHMFPK
RveTDC	20	VMDWLAQMLKLPKFSMFSGTGGGVIQNTTSEILCTIIAARERALEELGVD SIGKLVCYGSQDQTHMFPK
RteTDC	20	VMDWLAQMLKLPKFSMFSGTGGGVIQNTTSEILCTIIAARERALEELGVD SIGKLVCYGSQDQTHMFPK
CacTDC	20	VIDLWANMLKLPKFSMFSGTGGGVILQGTTSAILCTLIAASPMHFEIVGVKTSFVVYGSQDQTHSTYAK
CacTDC2	20	VMDWLASMLKLPKNSFTFLGTGGGVIQGTTSEAILCTLIAARDRALESGVDSIHKLVVYGSQDQTHSTYAK
OpuTDC	16	VIDLWANMLKLPKFSMFHGTGGGVILQGTTSAILCTLIAARDGALEKIGMENVGKLVVYGSQDQTHSFFQK
OprTDC	16	VIDLWANMLKLPKFSMFHGTGGGVILQGTTSAILCTLIAARDGALEKIGMENVGKLVVYGSQDQTHSFFQK
HpaTDC	21	VMDWLAHMLKLPKFSMFSGTGGGVILQGTTSAILCTLIAARDRAFEIIGVENIGKLVVYGSQDQTHSFFHK
OpuTDC2	16	VIDLWANMLKLPKFSMFSGTGGGVILQGTTSAILCTLIAARDHVLNKIGVKNIGKLVVYGSQDQTHFFIK
UtoTDC	16	VMDWLADMLKLPKFSMFSGTGGGVILQGTTSAILCTLIAARDRAFEIIGVENIGKLVVYASDQTHSFFVK
MspTDC	20	VMDWLANMLKLPKFSMFSGTGGGVILQGTTSAILCTLIAARDRAFEIIGVENIGKLVVYASDQTHSFFVK
UryTDC	20	VMDWMANMLDLPKFSMFSGTGGGVILQGTTSAILCTLIAARDRAFEKFGADNIGKLVVYASDQTHSFFVK
UguTDC		-----

Consensus	TCKLAGIFPCNIR×IPTT×E×NFSMSP×ALR×QIEADVA×GLVPLFLCATVGGTSTTAIDPVS×LA×VAN	
CroTDC	TCKLAGIYPNNIRLIPPTTETDFGISPQVLRKMVEDDVAAGYVPLFLCATLGTTSTTATDPVDSLSEIAN	278
VmiTDC	TCKLAGIFPDNIRLIPPTLETDFSIDPHVLRVMKADVADAGLIPLFLCATLGTTSTTATDPVSSLSEITN	280
TelTDC	TCRLAGIFPSNIRLVPPTAETDFSIAPEVLRKMVEADVAAGLTPLFLCATLGTTSTTATDPVNALAEIAN	278
RveTDC	TCKLAGISPKNIRLIPPTAETDFGIAPEVLRGMVEADIAAGLVPLFLCATLGTTSSSTATDPVDSLSEIAN	278
RteTDC	TCKLAGISPNNIRLVPPTAETDFGIAPEVLRRMVEADVAAGLVPLFLCATLGTTSSSTATDPVDTLSEIAN	278
CacTDC	ACKLAGILPCNIRSIPTTADSNFSVSPLLRRRAIEADKAAGMVPLYICATVGGTSTTAIDPLSSLADVAN	278
CacTDC2	ACNLAGILPCNIRSIRTEAVANFSLSPDSLHREIEADVAAGMVPLYLCATVGGTSTTAIDSLSPADVAN	275
OpuTDC	TCKVAGIFPCNIKLIPTTREDNFSMSPIALREQIEADVADGLVPIFLCTTVGGTSTAAIDPVSEVAKVAN	277
OprTDC	TCKVAGIFPCNIKLIPTTREDNFSMSPIALREQIEADVADGLVPIFLCATVGGTSTAAIDPVSEVAKVAN	277
HpaTDC	TCKLAGIFPCNIKLIPTTVEANFSMSPGALRKQIEADVADGLVPLFVCATVGGTSTTAVDSVSQLADVAN	233
OpuTDC2	TCKLAGIFPCNIKLIPTTSEANFSMSPHALRKQIESDVAGGLVPIFLCATIGTTSTTAIDPVSGLAKVAN	280
UtoTDC	TCKLAGIFPCNIRIIPTTAEANFSMSPVALRQQIEADAADGLVPLFLCATVGGTSTTAVDPVSQLAHVAN	232
MspTDC	TCKLAGIFPCNIRIIPTTADDNFSMSPDALRKQIEADVEDGLVPLFICATVGGTSTTAIDPVSELADVAN	279
UryTDC	TCKLAGIFPRNIRIIPTTVENYFSMSPEAVRKQIQADVENGVLVPLFLCATVGGTSTTAIDSVSQLADIAN	279
UguTDC	-----MSPEAVRKQIQADVKNGLIPLFLCATVGGTSTTAIDSVSQLADIAN	46






Consensus	EFN×WIHVDAAYAGSACICPEFR×YLDGIERVDSLSLSPHKWLL×YLDCCCLWVKKP×LLVKAL×TNPEY	
CroTDC	EFGIWIHVDAAYAGSACICPEFRHYLDGIERVDSLSLSPHKWLLAYLDCTCLWVKQPHLLLRALTNNPEY	348
VmiTDC	EFNIWMHVDAAYAGSACICPEFRHYLDGIERVDSLSLSPHKWLLAYLDSTCLWVKNNPNNLLRALTNNPEY	350
TelTDC	EFDIWIHVDAAYAGSACICPEFRHYLDGIERVDSLSISPHKWFLAYLDCTCLWVKKPQLLLRALTNNPEY	348
RveTDC	EFNIWMHVDAAYAGSACICPEFRHYLDGIERVDSLSISPHKWLLAYLDCTCLWVKKPHFILRALTNNPEY	348
RteTDC	EFNIWMHVDAAYAGSACICPEFRHYLDGVERVDSLSLSPHKWLLAYLDCTCLWVKKPYLLLRALTNNPEY	348
CacTDC	DYGVWFHVDAAYAGSACICPEFRHYLDGIERADSLSLSPHKWLLSYLDCCCLWVKSPSLLVKALSTDPEY	348
CacTDC2	DYGLWFHVDAAYAGSACICPEFRHYLDGIERADSLSLSPHKWLLSYLDCCCLWVKRPSVLVKALSTDPEY	345
OpuTDC	DFNIWMHVDAAYAGSACICPEFRQYLDGIELVDSFSLSPHKWLLCFLDCCCLWLKKPHLMVKALSTNPEY	347
OprTDC	DFNIWMHVDAAYAGSACICPEFRQYLDGIELVDSISLSPHKWLLCFLDCCCLWLKKPHLMVKALSTNPEY	347
HpaTDC	EFKMWIHVDAAYAGSACICPEFRQYLDGVERVDSMSFSPHKWLLCYLDCCCLWVQRPDLLVKALSTNPEY	303
OpuTDC2	DFSVWIHVDAAYAGSACICPEFRKYLDGVELVDSLSLSPHKWLLCYLDCCCLWVKKPALMVKALSTNPEY	350
UtoTDC	EFNVWIHVDAAYAGSACICPEFRQYLDGIERADSLSLSPHKWLLCYLDCCCLWVKKPDLMVKALSTNPEY	302
MspTDC	DFNVWIHVDAAYAGSACICPEFRQYLDGIERVDSLSLSPHKWLLCYLDCCCLWVKKTDLLVKALATNPEY	349
UryTDC	EFNVWIHVDAAYAGSACICPEFRQYLEGVERVDSLSLSPHKWLLCYLDCCCLWVKKTDLLVKALATNPEY	349
UguTDC	EFNVWIHVDAAYAGSACICPEFRQYLEGVERVDSLSLSPHKWL-----	89

Consensus	LKNK×SE×D×VVDFKDWQIGTGR×FRALRLWL×MRSYGV×NLQSHIRSDV×MAKMFEFV×SDPRFE×VV	
CroTDC	LKNKQSDLDKVVDFKNWQIATGRKFRLSLKLWLILRSYGVVNLQSHIRSDVAMAKMFEFVRSRFEIIV	418
VmiTDC	LKNKQSDLDKVVDFKNWQIATGRKFRLSLKLWLILRSYGVANLQTHIRSDVAMAKMFEFVRSRPFEEVV	420
TelTDC	LKNKQSELDKVVDFKNWQIATGRKFRLKLWFLILRSYGVANLQSHIRSDVAMAKMFEFVRSRPFEEVV	418
RveTDC	LKNKQSELDKVVDFKNWQIATGRKFRLKLWILILRSYGVSNLQSHIRSDVAMAKMFEDFARSRPFEEVV	418
RteTDC	LKNKQSELDKVVDFKNWQIATGRKFRLKLWILILRSYGVENLQSHIRSDVAMAKMFEDFVRSRPFEEVV	418
CacTDC	LKNQPSSEKSVVDYKDWQVGTGRRFKALRLWFMRSYGVANLQSHIRTDVQMAKMFEFVKS DPRFEILV	418
CacTDC2	LKNKPSSESNVVDYKDWQVGTGRRFKALRLWFMRSYGVANLQSHIRSDIQMAKMFEFVNS DPRFEIIV	415
OpuTDC	LRNKRSEFDGVDFKDWQIGTGRRFKALRLWLMRSYGVENLKRHILSDVQMAKMFEGLVKS DPRFEIIV	417
OprTDC	LRNKRSEFDGVDFKDWQIGTGRRFKALRLWLMRSYGVENLKRHILSDVQMAKMFEGLVKS DPRFEIIV	417
HpaTDC	LKNKRSELGSVMDYKDWQIGTGRRFRALRLWLIMRSYGLKNLQSHIRSDVQMAKMFEFVKS DPRFEMIV	373
OpuTDC2	LRNKRSEFDSVVDYKDWQIGTGRRFRALRLWLIMRSYGVANLQRHIRSDVEMAKMFEFVKS DPRFEEVV	420
UtoTDC	LRNKRSEFDSVMDYKDWQV-----	321
MspTDC	LRNKRSEFDSVVDYKDWQIGTGRRFRALRLWLMRCYRVANLQSHIRSDVQMAKMFEFVKS DPRFEMIV	419
UryTDC	LRNKRSEFDSVVDYKDWQIGTGKFRSLRLWLVMRCYGVANLQSHIRSDVQMAKMFEFVKS DPRFEIIV	419
UguTDC	-----	89

Consensus	PR×FSLVCFRLNP××-G×××××D×E×LNKKLLD××NSTGRVYMTHTKVGGIYMLRFAVG××LTEE×HV×A	
CroTDC	PRNFSLVCFRLKPDVSS----LHVEEVNKKLLDMLNSTGRVYMTHTIVGGIYMLRLAVGSSLTEEHHVRR	484
VmiTDC	PRNFSLVCFRLKPLP-G----SDVEILNKKLLNDMLNSTGRVYMTHTIVGGIYMLRLAVGSSLTEEHHVRA	485
TeiTDC	PRAFSLVCFRLKPPF-G----SDVEALNKKLLDKLNSTGRVYMTHTIVGGIYMLRLAVGSSLTEEHHVRA	483
RveTDC	PRNFSLVCFRLKALP-G----SDVEALNKKLLDMLNSTGRVYMTHTIVGGIYMLRLAVGSSLTEEHHVRA	483
RteTDC	PRNFSLVCFRLKALP-G----SDVETLNKKLLDMLNSTGRVYMTHTIVGGIYMLRLAVGSSLTEEHHVRS	483
CacTDC	PRVFSLVCFRLNPIS--GSDPTGTEALNRKKLLDWVNSTGRVYMTHTKVGGIYMLRFAVGATLTEKRHVSS	486
CacTDC2	PRVFSLVCFRLNPFPS--KSDPCNTELLNRKKLLEWVNSTGQVYIHTTKVGGVYMLRFAVGATLTEEHHVSA	483
OpuTDC	PRAFALVCFRLNPGK-GYDDEIDKEILNKKELLDLINSTGRAYMTHTKAGGIYMLRFAVGTTLTEEHHVYA	486
OprTDC	PRAFALVCFRLNPGK-GYDDEIDKEILNKKELLDLINSTGRAYMTHTKAGGIYMLRFAVGTTLTEEHHVYA	486
HpaTDC	PRAFSLVCFRLNPRRLGESHAIDLELLNKKLLESINSTGRVYMTHTKVGGVYLLRFAVGASLTEDRHVCA	443
OpuTDC2	PRTFSLVCFRLNPFGRSNNATYVELLNEKKLLDLVNSTGRAYMTHTKVGGVYMLRFAVGATLTEERHVNA	489
UtoTDC	-----	321
MspTDC	PRAFSLVCFRLNPSG-GSNEA-DLELLNKKLLDRVNSTGRTYMTHTKAGEVYLLRFAVGATLTEDRHVYA	487
UryTDC	PRAFSLVCFRLNPSE-GSSEA-HLELLNKKLLERVNSTGRAYMTHTKAGEVYLLRFAVGATLTEDRHVYA	487
UguTDC	-----	89

Consensus	AWELIKE××D×LLKE×-----	
CroTDC	VWDLIQKLTDDLKEA-----	500
VmiTDC	VWELIKKLADDLLKEA-----	501
TeiTDC	VWELIKELANDSLKEA-----	499
RveTDC	VWELIKELANDLLKEA-----	499
RteTDC	VWELIKELTSDLLKEA-----	499
CacTDC	AWKLIKEGADVLLKED-----	502
CacTDC2	AWKLIREGADALLCS-----	498
OpuTDC	AWELIKECTDASLTKTNIIE-----	506
OprTDC	AWELIKECTDASLTKTNIIESRANPQ	512
HpaTDC	AWELIKECTDNLLKENN*-----	461
OpuTDC2	AWELIKECTAALLKENNHQCIDI----	511
UtoTDC	-----	321
MspTDC	AWELIKQCADAVLLKENVLD-----	506
UryTDC	AWELIKACADAVIKENLLD*-----	507
UguTDC	-----	89

Strictosidine beta-glucosidase (SGD)

	
Consensus	MXXXXXXXXLVVAIXXXXXXXXXX-----XXXXXPKXXKXXVHRRDFPXDFFFGAGGSAYQCEGAY
UtoSGD	-----MSTPATKFSGTVSRSDFPPEGFLFGSASSAFQYEGAH36
HpaSGD	-----AAYQYEGGA9
MspSGD1	-----MEAQRTATVVSNDASKINRGDFAEDFIFGAASSAYQTEGGA41
CroshSGD	MGSKDDQSLVVAISPAAEPNGNHSVIPFAYPSIPIQPRKHNKPIVHRRDFPSDFILGAGGSAYQCEGAY70
CroSGD	MGSKDDQSLVVAISPAAEPNGNHSVIPFAYPSIPIQPRKHNKPIVHRRDFPSDFILGAGGSAYQCEGAY70
RseSGD	MDNTQAEP LVVAIVPKPNASTEHT-----NSHLIPVTRSKIVVHRRDFPQDFIFGAGGSAYQCEGAY62
RveSGD	MESNQGEPL LVVAIVPKPNASTEQK-----NSHLIPATRSKIVVHRRDFPQDFVFGAGGSAYQCEGAY62
	
Consensus	NEGNRGPSIWDFTFXRPAKIXDGSNGNQAINSYHXKEDIKIMKQXGLEXYRFSISWSRVLPGGNLX--
UtoSGD	NVDGRLPSIWDFTFLVETHPDIV-AANGLDAVEFYRYKEDIKAMKDIGLDTFRFSLSWPRILPNGRRTRG105
HpaSGD	SEGGKGPSIWDFTTHRRPGLIMGGGNGNLAIDSYHQYKEDVKMLKNMGLDAYRFSISWSRVLPGGNLN--77
MspSGD1	SEGGKGPSIWDFTTQRRPGMIKEGGNGNMAVDSYHQYKEDVKILKNMGLDAYRFSISWSRVLPGGNLN--109
CroshSGD	NEGNRGPSIWDFTFNRYPAKIADGSNGNQAINSYNLYKEDIKIMKQTGLESYRFSISWSRVLPGGNLS--138
CroSGD	NEGNRGPSIWDFTFNRYPAKIADGSNGNQAINSYNLYKEDIKIMKQTGLESYRFSISWSRVLPGGNLS--138
RseSGD	NEGNRGPSIWDFTTQRSPAKISDGSNGNQAINCYHMYKEDIKIMKQTGLESYRFSISWSRVLPGGRLA--130
RveSGD	NEGNRGPSIWDFTTQRTPAKISDGSNGNQAINCYHMYKEDIKIMKQAGLEAYRFSISWSRVLPGGRLA--130
	
Consensus	-----XGVNKDGVKFYHDFIDELLANGIKPXXTLFHWDLPPQALEDEYGGFLSXRIVDFFXEYAEFCFWEF
UtoSGD	PNNEEQGVNKLAIIDFYNKVINLLENGIEPSVTLFHWDPVQALETEYLGFLSEKSVEDFVDYADLCFREF175
HpaSGD	-----GGVNKEGVYYNNLIDELLNGIEPYITLFHWDPVQALEDKYGGFLSPKIVDDFVEYVELCFWEF142
MspSGD1	-----AGVNKEGINYYNNLIDELLANGIEPYVTLFHWDPVQALEDKYGGFLSPQIVDDFREYVELCFWEF174
CroshSGD	-----GGVNKDGVKFYHDFIDELLANGIKPFATLFHWDLPPQALEDEYGGFLSDRIVEDFTEYAEFCFWEF203
CroSGD	-----GGVNKDGVKFYHDFIDELLANGIKPFATLFHWDLPPQALEDEYGGFLSDRIVEDFTEYAEFCFWEF203
RseSGD	-----AGVNKDGVKFYHDFIDELLANGIKPSVTLFHWDLPPQALEDEYGGFLSHRIVDDFCEYAEFCFWEF195
RveSGD	-----AGVNKDGVKFYHDFIDELLANGIKPFATLFHWDLPPQALEDEYGGFLSHRIVDDFCEYAEFCFWEF195
	
Consensus	GDKVKXWTTFNEPHTFXXXGYAXGEFAPGRGXXX-----XXGXPGTGE
UtoSGD	GDRVKYWMTFNETWSYSLFGYLLGTFAFGRGSTNEEQRKAIAEDLPSSLGKSRQAFASRTPRAGDPSTE245
HpaSGD	GDRVKNWITLNEPWSFSTGGYVNGTFAPGRGASASEQV-NHDHIVPSRCS---AHVRQCISSNGNPSTE207
MspSGD1	GDRVKHWITLNEPWSFVGGYVNGTFAPGRGASSDQENDHPAALPSRCS---PWQSQSISSNGNPSTE240
CroshSGD	GDKVKFWTTFNEPHTYVASGYATGEFAPGRGGAD-----GKGNPGKE245
CroSGD	GDKVKFWTTFNEPHTYVASGYATGEFAPGRGGAD-----GKGEPPKE245
RseSGD	GDKIKYWTTFNEPHTFAVNGYALGEFAPGRGGKG-----DEGDPAIE237
RveSGD	GDKIKYWTTFNEPHTFTANGYALGEFAPGRGKNG-----KGDPATE236
	
Consensus	PYXVTHNXXLLAHKAAVEXYRXXFQK---CQXGEIGIVLNSXWMEPLNEX-ADIDAXXKRALDFMLGWFXE
UtoSGD	PYIVTHNQLLAHAAAVKLYRFAYQNAQNAQKGKIGIGLVSIWAEPHNDT-TEDRDAARQLDFMLGWLFQ314
HpaSGD	PYLVTHNQLLAHAAAVKLYKSKFQK---PQEGKIGITLVSQWLEPLDENNDADVQASKRALDFMLGWLQ274
MspSGD1	PYVVTHNQLLAHAAAVELYKSNFQK---SQNGKIGITLVSQWMEPLDENSKADVEAAKRALDFMLGWFM2307
CroshSGD	PYIATHNLLLSHKAAAEVYRKNFQK---CQGGIEIGIVLNSMWMEPLNET-KEDIDARERGLDFMLGWFI2311
CroSGD	PYIATHNLLLSHKAAAEVYRKNFQK---CQGGIEIGIVLNSMWMEPLNET-KEDIDARERGLDFMLGWFI2311
RseSGD	PYVVTNILLAHKAAVEEYRNKFQK---CQEGIEIGIVLNSMWMEPLSDV-QADIDAQKRALDFMLGWFL2303
RveSGD	PYLVTHNILLAHKAAAEAYRNKFQK---CQEGIEIGIVLNSTWMEPLNDV-QADIDAHKRALDFMLGWFI2302

YpkA

Consensus: PLTTGYPKSMRVLGRLPFSXSEKLGCYDFIGMNYTXYVNAKXS--XXXXYETDXXX--X

UtoSGD 373
HpaSGD 276
MspSGD1 375
CroshSGD 379
CroSGD 379
RseSGD 371
RveSGD 370

YpkB

Consensus: FXXXXDXXVPIGXXYGWQHVPVGLYKLLVYTKEYHVPVIYVTEGXVEENXTXI-----L

UtoSGD 431
HpaSGD 276
MspSGD1 433
CroshSGD 449
CroSGD 449
RseSGD 428
RveSGD 431

YpkC

Consensus: LEARDXRXDYQXHLASVRDAIXDGVNVKGYFVWSFDNFEWXXGXXRXG IHVDYXFXRYPKX



UtoSGD 501
HpaSGD 276
MspSGD1 503
CroshSGD 475
CroSGD 518
RseSGD 497
RveSGD 500

YpkD

Consensus: SAIWKNFXXXXXXXXX-XXXXXXXXX-LVKXXXXX-----

UtoSGD 553
HpaSGD 276
MspSGD1 539
CroshSGD 475
CroSGD 555
RseSGD 532
RveSGD 536

[illegible]

		
Consensus	CXXXEXYCPXXXXTDGXXXXDG-----XXYGGXSNIMVXXEXFVVRWPENLPLDGV	
RteTHAS5	-----PMGAYAEEQILPADRAVPVPSPSIDPIVGA	119
CroTHAS2	CNEGLEPYCPKVIYTDGTAFSDENNTVYGDVSGD---GEDRIYGGYSNIMVANEYVVRWPENLPLAAGV	173
CroTHAS3	CKEGEDSYCPSLITGDGTSFSDGNDVFFYDPNDNTKETTKTYGSYSNFTVVDEYYVIRWPENFPLAAGV	179
RteTHAS2	CKEGLDSYCPNLITGDGTSFSDGNDLYFHDPNDTE---SKIYGGFSNITVVEEYVVRWPENFPLAAGV	173
RteTHAS	CKEGFDSYCPNLITADGTSFSDGNDIYFHDPNDTE---SKIYGGFSNITVVDEYYVVRWPENFPLAAGV	173
RteTHAS3	CKEGFDSYCPNLITADGTSFSDGNDLYFHDPNDTE---SKIYGGFSNITVVDEYYVVRWPENFPLAAGV	173
RteTHAS4A	CADEVEQYCPKAVATDG---FMG-----SGQYGACSDIMVADEDFLLVLPENLPLDSGV	191
RteTHAS4B	CANEVEQYCPKAVATDG---FMG-----SGQYGSCSDIMVADEDFLLVLPENLPLDCGV	160
CroTHAS1	CTNEVENYCPPEAGSIDS-----NYGACSNIAVINENFVIRWPENLPLDSGV	158
RteYOS	CTNEVENYCPKAVSIDS---NFA-----N-NYGGCSNIMVTKENFVIHWPENLPLDSGV	159
RteAMS	CIIQAENNCPKLESTDG---HFG-----T-NYGGCSNIMVNEKFFVVLWPENLPPDSGV	163
CroHYS	CVNGVENNCSKVESTDG---HFG-----N-NFGGCCNIMVNEKYAVVWPENLPLHSGV	159
CroTHAS4	CINGVENNCPEAESTDG---FSG-----K-NFGGCCNIMVNEKYAVVWPENLPLHSGV	159
UtoHYS	-----	
UtoTHAS	CTNDLENYCPKAVLTE-----ATSGGCSNFVVADEDFVFRWPEKLPDLGA	68
MspTHAS	CSNDLEPYCPKMMMTYNSIDEDG-----IPTRGGFSNEMVNEHFVVRWPDNLPLDGGV	180
MSTRG5530(Rte-YOS)	CSADLENYCPKQVPTYSMPIYFDG-----TITYGGYSNEMVCNEHFIRFPNKIPLDAGA	163
MSTRG5531(Rte-YOS)	CRADMESYCPKMVMMAHGSPNFDG-----TITYGGFSNEMVLNEHFVIRYDPNLPLAAGA	163
HpaTHAS2	CSKDLENYCPGQILTYSAAYTDG-----TITYGGYSNEMVNEKFFVIRWPENFPLDAGR	75
HpaTHAS	CNEDLENYCPAQIFTYGSPTDG-----TPTYGGYSNIMVNEKFFVVRWPENFPLDAGA	76
MSTRG5534(Rte-YOS)	CSNDLENYCPGQILTYSATNTDG-----TTTYGGYSNIMVNEKFFVIRWPENLPLMDIGA	162
		
Consensus	PLLCAGITXYSPM-RXFGLDKPGHXGVGLGGLGHXAVKFAKAFGAKVTVISSSXXKKXEAIEXGADX	
RteTHAS5	SILLKGHTAQFLVRHCFKVECGHTVLVHAAAGGVGSLLCQWANALGATVIGTVSTKEAAQ-AKDDGCHH	188
CroTHAS2	PILCGGIVPYSPM-RHFGLDKPGLSIGVVGFGGRIGKLAVKFAKAFGANVTVISTISIKKQEAIEKYGVDR	242
CroTHAS3	PLLCAGTVPYSPM-RHFGFDKPGIHHIGVVGGGIGKLVVKFAKAFGVKVTVISTSIDKKHEAIEHYGAHG	248
RteTHAS2	PVLCAGTVPYSPM-RCFGFDKPEIHLGVVGLGGIGRLTVKFAKAFGAKVTVISTSIDKKQEAIEKYGADS	242
RteTHAS	PLLCAGTVPYSPM-RCFGFDKPEIHLGVVGLGGIGKLTVKFAKAFGAKVTVISTSIDKKQEAIEKYGADR	242
RteTHAS3	PLLCAGTVPYSPM-RCFGFDKAEIHLGVVGLGGIGKLTVKFAKAFGAKVTVISTSIDKKQEAIEKYGADR	242
RteTHAS4A	PLLC-GVTIYSPM-RRFGLDKPGTHIGIAGLGGFGHMAVRFKAFAGTQVTVISSSAKKKRETLEKFGADS	259
RteTHAS4B	PLLC-GVTIYSPM-RRFGLDKPGTHIGIAGLGGFGHMAVRFANAFGTQVTVISSSAKKKRETLEKFGADS	228
CroTHAS1	PLLCAGITAYSPM-KRYGLDKPGKRIGIAGLGGGLGHVALRFKAFGAKVTVISSSLKKKREAFKFGADS	227
RteYOS	PLLCAGINAYSPM-RRYGLDKTGMRVGIAGLGGGLGHVGVRFKAFGAKVTVISSSLKKKHEALEKFGADS	228
RteAMS	PLLCAGITTYSPM-RRYGLDKPGMRVGIAGLGGGLGHLAVRFKAFAGANVTVISSSLEKKREALEKFGADS	232
CroHYS	PLLCAGITTYSPL-RRYGLDKPGLNIGIAGLGGGLGHLAIRFAKAFGAKVTLISSSVKKKREALEKFGVDS	228
CroTHAS4	PLLCAGITTYSPL-RRYGLDKPGLNIGIAGLGGGLGHLAIRFAKAFGAKVTLISSSVKKKREALEKFGVDS	228
UtoHYS	-----SIRVAKAFGAKVTVISSTPGKKEEATKNFKADS	33
UtoTHAS	PLLCAGITTYSPL-KNFGLDKPGHLHVGVAAGLGGGLGHVAVKFLKAFGAKVTVISSSDNKKKEAIEKYGADA	137
MspTHAS	PLLCAGSTVYSPM-MYYGLSKPGTHLGVAGLGGGLGHVAVKFAKAFGEVTVISTSPSKKEEAINHLGADH	249
MSTRG5530(Rte-YOS)	PLLCAGITVYSTM-KHYGIAKAGNHIGVNLGGLGHHVAVKFAKAMGAKVTVISTSGSKKDEAINLLGADA	232
MSTRG5531(Rte-YOS)	PLLCAGITVYSPM-KYYGIAKPGNHIGVNLGGLGHHMAVFAKALGAKVTVISSSESKKDDSIINRLGADA	232
HpaTHAS2	PLLCAGITTYSPL-RYFGLDKPGTHVGVVGLGGGLGHVAVKFAKAFGAKVTVISTSEGKKKEAIEKLGADA	144
HpaTHAS	PLLCAGITTYSPL-RYFGLDKPGIHHIGVVGGLGGGLGHVAVKFAKAFGAKVTLISTASKKQDAIEKLGADS	145
MSTRG5534(Rte-YOS)	PLLCAGITTYSPL-RYFGLDKPGTHVGIIVGLGGGLGHVAVKFAKAFGAETVISTSESKKQEAIEKLGADA	231

[illegible]

Consensus
RteTHAS5
CroTHAS2
CroTHAS3
RteTHAS2
RteTHAS
RteTHAS3
RteTHAS4A
RteTHAS4B
CroTHAS1
RteYOS
RteAMS
CroHYS
CroTHAS4
UtoHYS
UtoTHAS
MspTHAS
MSTRG5530(Rte-YOS)
MSTRG5531(Rte-YOS)
HpaTHAS2
HpaTHAS
MSTRG5534(Rte-YOS)

--NTLK	SXX	-----
LEN	RR	TAGSVVLI
P	D	TIDQ*
330		
--NTLK	SA	-----
371		
--NS	LG	SV-----
377		
--NTLK	SA	-----
371		
--NTLK	SA	-----
371		
--NTLK	SA	*-----
372		
--NTLK	SA	*-----
389		
--NTLK	SA	*-----
358		
--NTLK	SN	-----
356		
--NTL	RS	*-----
358		
--N	CL	KA
362		
--NTLK	SP	SF-----
359		
--NTLK	SP	SF-----
359		
-----		119
-----		223
--NTL	V	ATTST-----
381		
--NTL	R	AP*-----
362		
--NTL	K	AP*-----
362		
---	L	-----
274		
--NTLK	ST	*-----
275		
--NTLK	SA	*-----
361		

Supplementary material 4.

SA concentration experiment

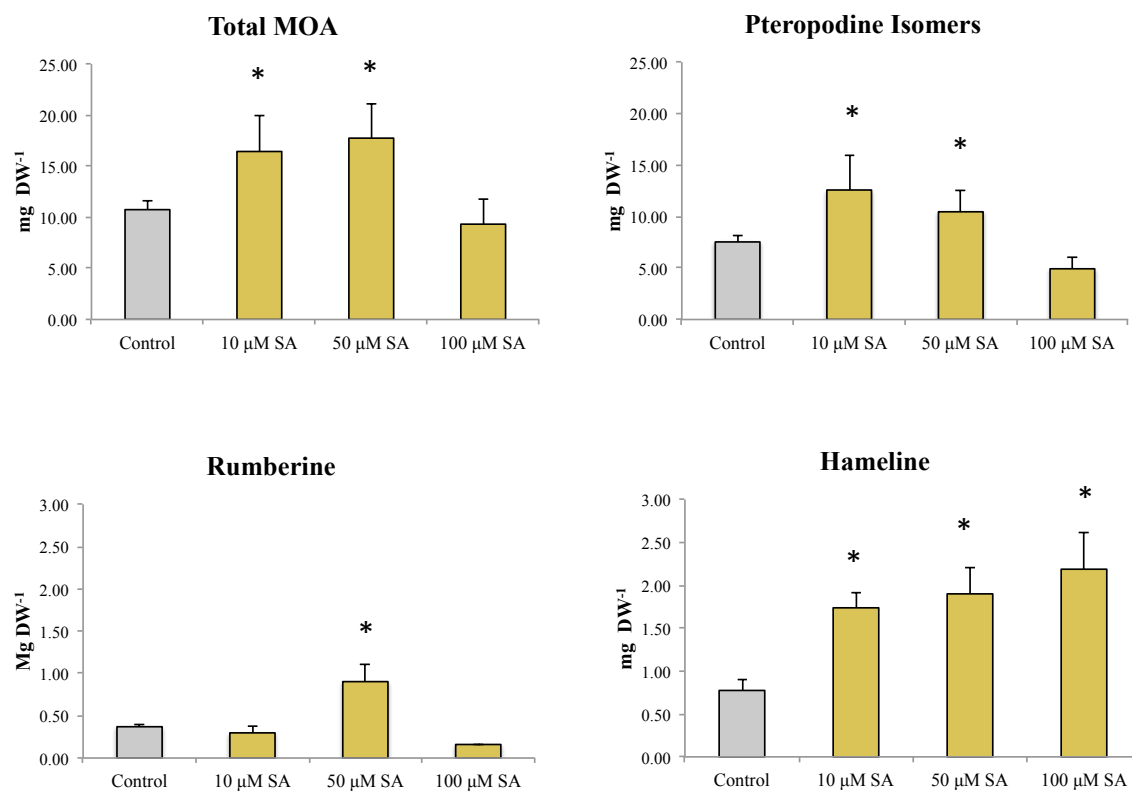


Figure S2. MOA production in 1.5-month-old *H. patens* plants, under different SA treatments after 120 h (n=3).

Supplementary material 5.

HPLC chromatogram of the *H. patens* extract indicating the retention times of each MOA.

Alkaloid detection was at 244 nm. Retention times: [1] rumberine 9.4 min, [2] speciophylline 13.5 min, [3] uncarine F 16.5 min, [4] hameline 20 min, [5] pteropodine 23.2 min, [6] isopteropodine 40.9 min.

