

**Revealing a Cluster of Homologous Proteins Provides New Insights Into the Evolutionary
Transition from hydroxycinnamoyl-CoA: shikimate/quinate hydroxycinnamoyl transferase to
rosmarinic acid synthase**

Jiali Zhou¹, Xiaofang Zou¹, Zixin Deng¹, Lian Duan^{1*}

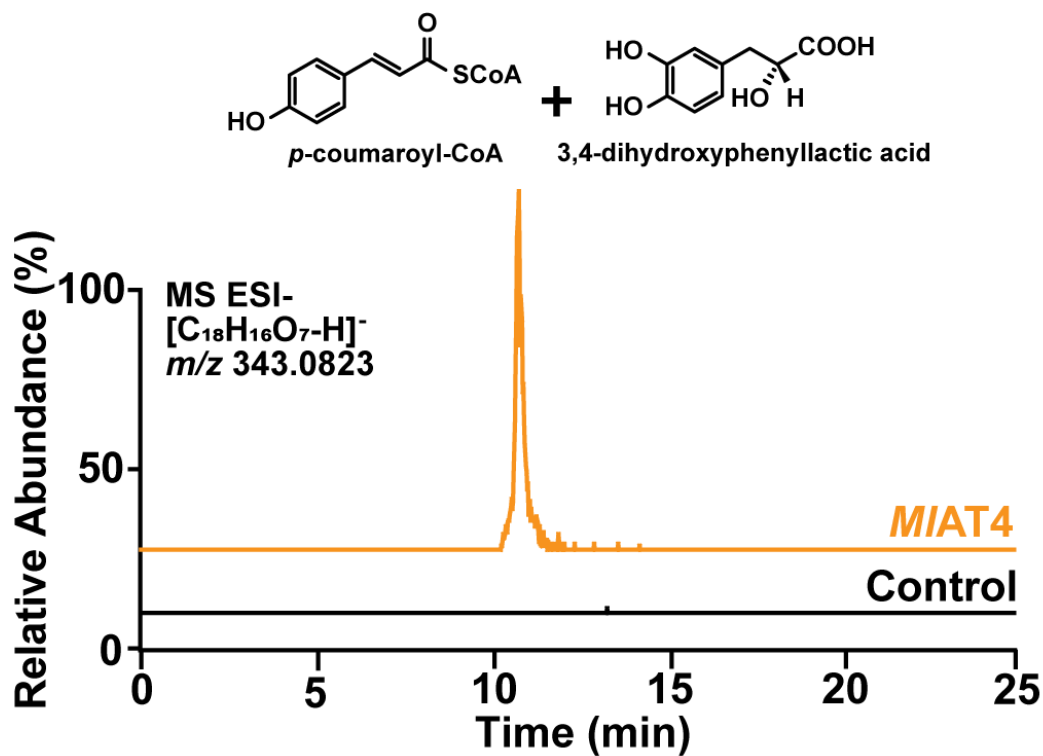


Figure S1. *MIAT4* has RAS catalytic potential. *MIAT4* has the ability to catalyze the production of a small quantity of *p*-coumaroyl-3', 4'-dihydroxyphenyllactate or its isomer by converting *p*-coumaroyl-CoA and salvianolic acid A (3,4-dihydroxyphenyllactic acid). The product was identified through mass spectrometry, with molecular ion peaks extracted while operating in negative ion mode.

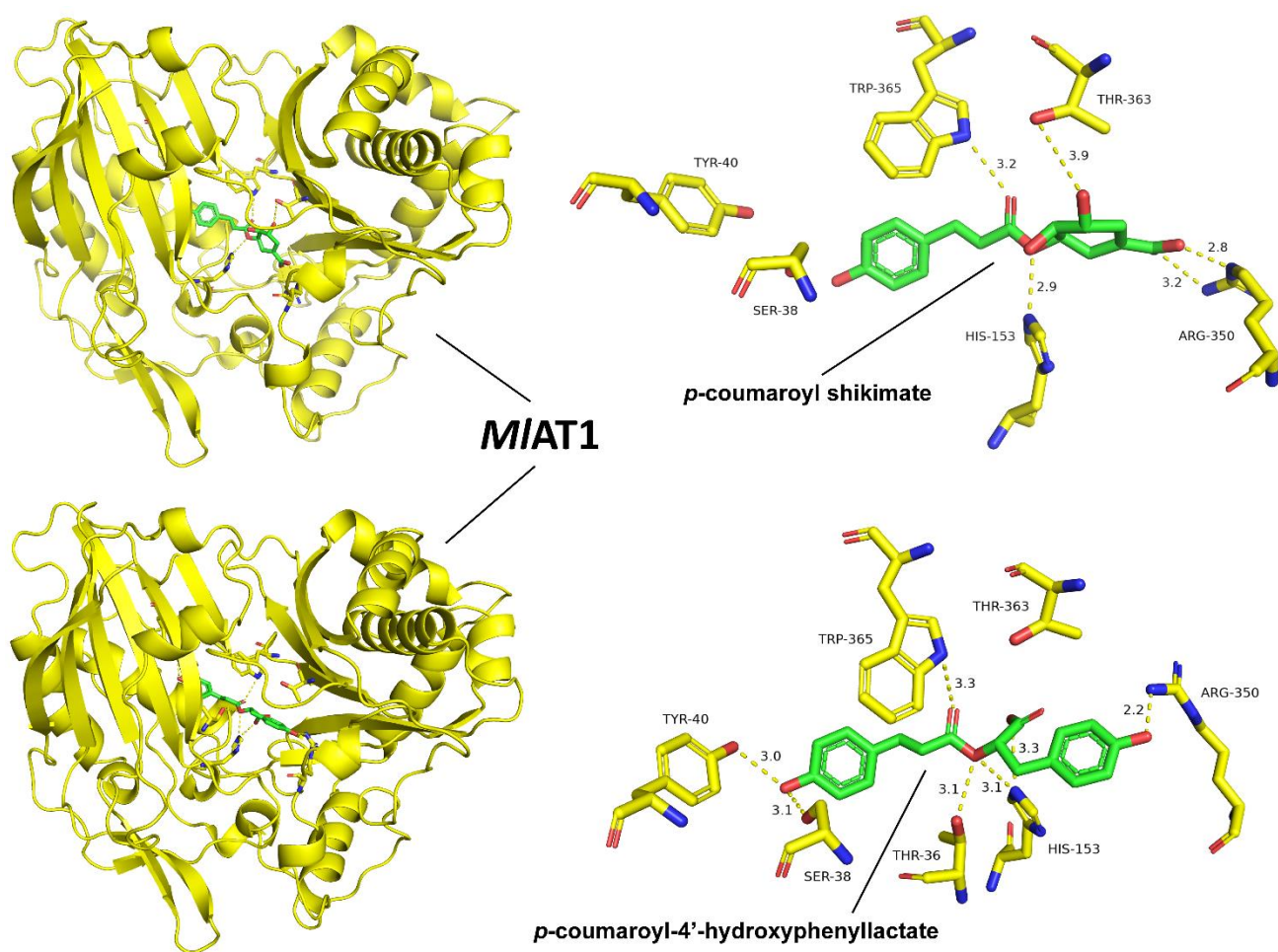


Figure S2. The homology model of *MIAT1*. The binding mode between the enzyme and *p*-coumaroyl shikimate resembles that observed in other HCTs. Additionally, active residues in its catalytic cavity might non-specifically guide the binding of 4-hydroxyphenyllactate, resulting in promiscuous activity. Thr-36, Arg-350, and Thr-363 may all potentially provide binding sites for the 4-hydroxyphenyllactate molecule. Ligand molecules are labeled in green, and residues are displayed in yellow.

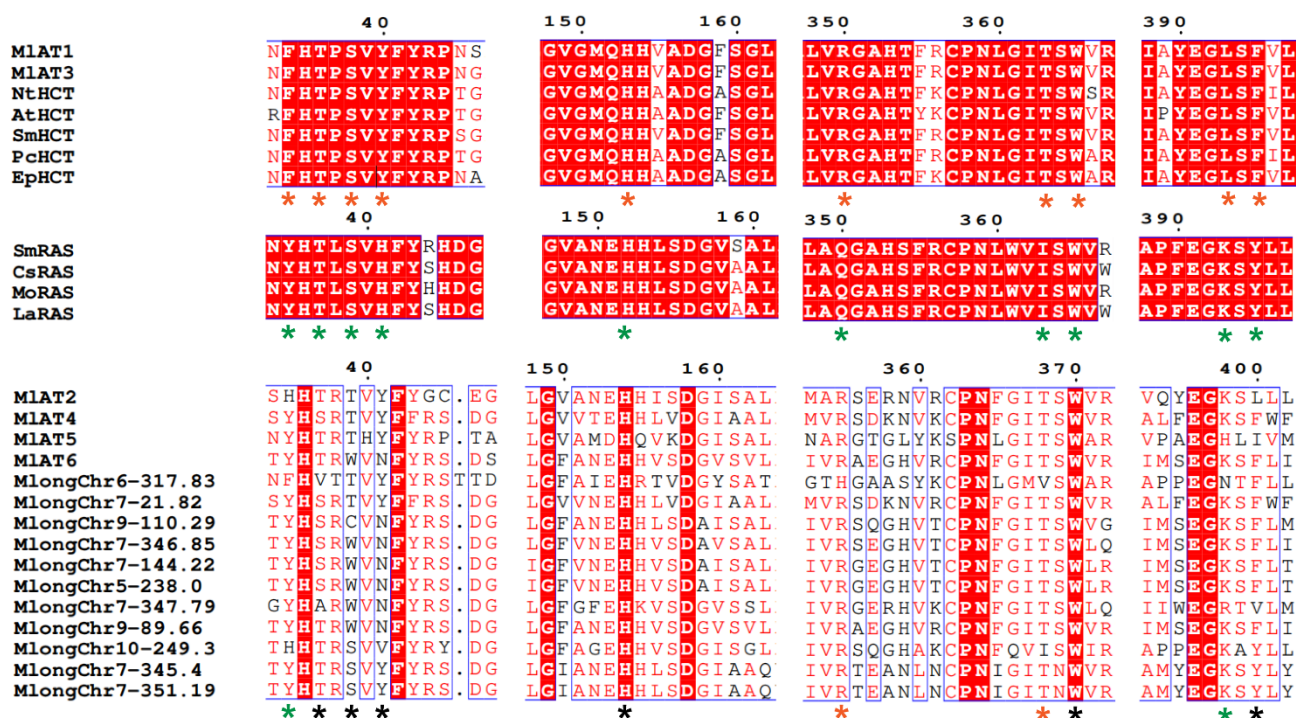
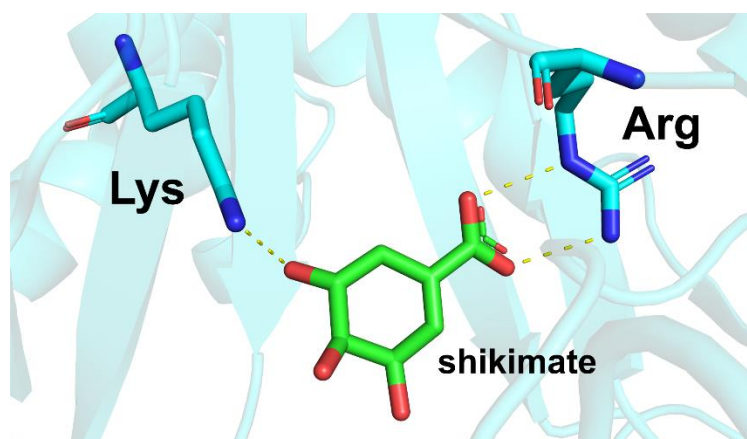


Figure S3. The multiple sequence alignment of HCTs, RAS-homo proteins in *Menta longifolia*, and Lamiaceae RASs. Active residues in the catalytic pocket were indicated by asterisks. Orange asterisks denote active residues conserved in HCT, while green asterisks represent active residues conserved in RAS. The residues associated with acyl acceptor binding in RAS-homo exhibit significant dual characteristics of both HCT and RAS.



<i>p</i> -coumaroyl shikimates	
<i>MIAT6</i>	100%
R355A	0%
K398L	0%
R355A+K398L	0%

Figure S4. Validation of two key active residues. Mutation of either of two active residues (the arginine residue Arg-355 and the lysine residue Lys-398) in *MIAT6* results in complete deactivation of the enzyme. These two residues potentially influenced enzyme activity by participating in shikimate binding.

Table S1. Enzymes used for the phylogenetic tree.

Enzyme	Species	ACCESSION	Enzyme	Species	ACCESSION
NtHCT	<i>Nicotiana tabacum</i>	Q8GSM7	NtHQT	<i>Nicotiana tabacum</i>	CAE46932.1
ArHCT1	<i>Actaea racemosa</i>	D4NUX0	NtTHT	<i>Nicotiana tabacum</i>	P80969
AsHHT1	<i>Avena sativa</i>	Q7XXP3	OsAHT1	<i>Oryza sativa</i> Japonica Group	Q7XPK7
AsHHT4	<i>Avena sativa</i>	A0A4Y5UJ70	OsHCT1	<i>Oryza sativa</i> subsp. japonica	Q0JBZ8
AtHCT	<i>Arabidopsis thaliana</i>	Q9FI78	OsHCT2	<i>Oryza sativa</i> subsp. japonica	Q6K638
AtSHT	<i>Arabidopsis thaliana</i>	O64470	OsHCT4	<i>Oryza sativa</i> subsp. japonica	Q5SMM6
CcHCT	<i>Coffea canephora</i>	ABO47805.1	OsPHT1	<i>Oryza sativa</i> subsp. japonica	Q5SMM8
CcHQT	<i>Cynara cardunculus</i> var. <i>scolymus</i>	CAM84302.2	OsSHT1	<i>Oryza sativa</i> Japonica Group	Q2QRK9.1
CiHCT	<i>Cichorium intybus</i>	ANN12609.1	OsSHT2	<i>Oryza sativa</i> Japonica Group	Q0ING3.1
CkHCT	<i>Caragana korshinskii</i>	AHK05938.1	OsTBT1	<i>Oryza sativa</i> Japonica Group	Q2R0K3.1
CsHCT	<i>Coleus scutellarioides</i>	CBI83579.1	OsTHT1	<i>Oryza sativa</i> Japonica Group	Q338X7.1
CsRAS	<i>Coleus scutellarioides</i>	A0PDV5.1	PcHCT	<i>Phacelia campanularia</i>	QDF44405.1
DcHCBT1	<i>Dianthus caryophyllus</i>	O24645	PcRAS	<i>Phacelia campanularia</i>	QDF44407.1
EpHCT	<i>Echinacea purpurea</i>	AXY97959.1	PvHCT2	<i>Panicum virgatum</i>	5FAL
EpHQT	<i>Echinacea purpurea</i>	QRI59127.1	SbHCT	<i>Sorghum bicolor</i>	4KEC_A
EsHCT	<i>Eleutherococcus senticosus</i>	UWM25202.1	SIHQT	<i>Solanum lycopersicum</i>	CAE46933.1
LaRAS	<i>Lavandula angustifolia</i>	AEA36976.1	SmHCT	<i>Salvia miltiorrhiza</i>	ACA64049.1
LjHQT	<i>Lonicera japonica</i>	ACZ52698.1	SmRAS	<i>Salvia miltiorrhiza</i>	ADA60182.1
MoRAS	<i>Melissa officinalis</i>	G0LD36	SnHCT	<i>Solanum nigrum</i>	QIC52996.1
NpHCT	<i>Narcissus pseudonarcissus</i>	A0A2H5AIZ1			

Table S2. PCR primers used for protein expression.

[illegible]

Information S1. The CDS sequences of *MIAT1-MIAT7*.

>MIAT1

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>MIAT2

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>MIAT3

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>MIAT4

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>MIAT5

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>MIAT6

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>MIAT7

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Information S2. The optimized sequences of *MIAT1*, *MIAT2*, *MIAT4* and *MIAT6*.

>MIAT1

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>MIAT2

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>MIAT4

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>MIAT6

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Information S3. The nucleotide sequences of *MIAT6* mutants.

>*MIAT6* R355A

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>*MIAT6* K398L

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>MIAT6 R355A+K398L

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