Supporting Information

Cytochrome P450 and *O*-methyltransferase catalyze the final steps in the biosynthesis of the anti-addictive alkaloid ibogaine from *Tabernanthe iboga*

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Table of Contents:

Table S1. Primers used for gene amplification and colony PCR.

Table S2. Primers used for RT-qPCR.

Table S3. NMR spectra of Coronaridine.

Figure S1. Amino acid sequence alignment of I10H with characterized and uncharacterized P450s.

Figure S2. Amino acid sequence alignment of N10OMT with characterized and uncharacterized OMTs.

Figure S3. Phylogenetic trees of I10H and N10OMT.

Figure S4. SDS-PAGE of recombinant OMTs produced in Escherichia coli.

Gene	Strand	In-Fusion Site	Primer Sequence (5'-3')
I10H	Forward	ACCCTCACTAAAGGGCGGCCGCAACC	ATGGAGCTGATCGTCTCCTTC
I10H	Reverse	GTCATCCTTGTAATCCATCGATAC	TGCTTCATCCATCATTACC
P450-2	Forward	ACCCTCACTAAAGGGCGGCCGCAACC	ATGGAGTTAGTCACTGCC
P450-2	Reverse	GTCATCCTTGTAATCCATCGATAC	CACAGAAGAATGACTATAAGGAATTG
P450-3	Forward	ACCCTCACTAAAGGGCGGCCGCAACC	GAGCTCATCTTCTTTGTCTG
P450-3	Reverse	GTCATCCTTGTAATCCATCGATAC	TTGTAGATAAGAACGGGAGTG
P450-4	Forward	ACCCTCACTAAAGGGCGGCCGCAACC	ATGGAGCTCATCTTTCTCTTCTG
P450-4	Reverse	GTCATCCTTGTAATCCATCGATAC	GATCGCTTTTTTCAAAGAAGAAC
P450-5	Forward	ACCCTCACTAAAGGGCGGCCGCAACC	ATGGAGTTCATTCTTTTCCTTTGCATTC
P450-5	Reverse	GTCATCCTTGTAATCCATCGATAC	CTCCAGTTTTAGGAAAGAACC
N100MT	Forward	AAGTTCTGTTTCAGGGC	CCGGACGCGAAATCTGCCGAAC
N10OMT	Reverse	ATGGTCTAGAAAGCTTTA	AGGATACACTTCAATGAGACTCC
OMT-2	Forward	AAGTTCTGTTTCAGGGC	CCGGCAATGGTTGAGAAATCTGC
OMT-2	Reverse	ATGGTCTAGAAAGCTTTA	AGGATAGACCTCAATGAGAC
OMT-3	Forward	AAGTTCTGTTTCAGGGC	CCGGGAGAAGCCCAGGCTCAG
OMT-3	Reverse	ATGGTCTAGAAAGCTTTA	AGGGTAGGCTTCAATGACAG
OMT-4	Forward	AAGTTCTGTTTCAGGGC	CCGAGTGTAGCTTTGAATGGTG
OMT-4	Reverse	ATGGTCTAGAAAGCTTTA	ATAATAAACCTCAATAAGAGATCTC
OMT-5	Forward	AAGTTCTGTTTCAGGGC	CCGGCAGGAGAAGAGGAAGCTTG
OMT-5	Reverse	ATGGTCTAGAAAGCTTTA	TTTAAGCAATTCCATAATCCAACTGTTG
OMT-6	Forward	AAGTTCTGTTTCAGGGC	CCGGATTCTTCCCCCACAATCC
OMT-6	Reverse	ATGGTCTAGAAAGCTTTA	CTTGTAGAACTCCATGATCCAC
		Primers used for Colony PCR	
Name	Strand	Vector	Primer Sequence (5'-3')
GAL10-F	Forward	pESC-leu2∆	GGTGGTAATGCCATGTAATATG
GAL10-R	Reverse	pESC-leu2∆	GGCAAGGTAGACAAGCCGACAAC
T7-F	Forward	pOPINF	TAATACGACTCACTATAGGG
pOPINF-R	Reverse	pOPINF	TAGCCAGAAGTCAGATGCT

Table S1: Primers used for Full-length Gene amplification and colony PCR

Gene	Strand	Primer Sequence (5'-3')
I10H	Forward	AGGCCTCCCTCACTGTGTCCT
I10H	Reverse	TGGATGGTCTGTCGGCAAAGA
N100MT	Forward	AAGTGCGCTTACGATGCT
N10OMT	Reverse	TCTTCATTCTGGAACCACTCAC
N2227	Forward	GTGAACGTGACCAGTGCTATAA
N2227	Reverse	CAAGCAGGTGGACTCTCTTTAC

 Table S2: Primers used for RT-qPCR

Number	This Study		Reference (22)	
	¹ H (<i>J/</i> H)	¹³ C	$^{1}\mathrm{H}\left(J/\mathrm{Hz}\right)$	¹³ C
2	-	138.5	-	136.6
3	2.79 (2H, ddd, 8.5, 1.7, 1.7), 2.94 (2H, ddd, 2.5, 3.7, 8.5)	54.3	2.81 (1H, brd), 2.89-2.92 (1H,m)	51.6
5	3.40 (1H, m), 3.00-3.16 (1H, m)	54.7	3.36-3.42 (1H, m), 3.15-3.23 (1H, m)	53.1
6	3.00-3.16 (2H, m)	22.8	2.98-3.04 (1H, m), 3.15-3.23 (1H, m)	22.1
7	-	110.7	-	110.3
8	-	137.6	-	128.8
9	7.40 (1H, ddd, 7.8, 1.0, 1.0)	118.7	7.47 (1H, brd)	118.4
10	7.02 (1H, ddd, 7.6, 7.6, 1.2)	122.2	7.08 (1H, ddd)	119.2
11	6.96 (1H, ddd, 7.5, 7.5, 1.1)	119.5	7.14 (1H, ddd)	121.9
12	7.24 (1H, ddd, 7.9,1.0, 1.0)	111.5	7.24 (1H, dd)	110.3
13	-	129.6	-	135.5
14	1.85 (1H, m)	29.0	1.88 (brs)	27.4
15	1.12 (1H, m), 1.76 (1H, m)	33.2	1.13 (1H, ddt), 1.73 (1H, m)	32.0
16	-	56.4	-	55.1
17	1.92 (1H, m), 2.72 (1H, ddd, 13.1, 2.1, 2.1)	37.0	1.9 (1H, ddd), 2.58 (1H, dd)	36.5
18	0.91 (3H, t, 7.4)	12.1	0.9 (3H,t)	11.6
19	1.34-1.49 (1H, m), 1.50-1.62 (1H, m)	28.0	1.4-1.47 (1H, m), 1.53-1.60 (1H, m)	26.7
20	1.34-1.49 (1H, m)	40.1	1.32-1.35 (1H, m)	39.1
21	3.62 (1H, brs)	57.9	3.56 (1H, brs)	57.5
22	-	176.3	-	175.7
CO_2CH_3	3.69 (3H, s)	52.9	3.71 (1H, s)	52.5

 Table S3: NMR spectra of Coronaridine



Figure S1: Amino acid sequence alignment of I10H with characterized and uncharacterized P450s. Asterisk indicate absolutely conserved cysteine residue for coordination of iron. I10H is highlighted in red.

	MGSSIDAETHEVDIKDOAOLMNIIYGYADSLVLRCTVEIGIADIIKNNN-GSITLSELVSKLPLSNVNSDNLYRLLRYLVHLNILGOOTCAAGVDRVYSLKPVGTLLLKDSE
40MT2_PAPSO:	: MGSLDARPAAATQEVSIKDQAQLMNIIYGPADSLVLRCAVEIGIADIIKNNDGAITLAQLAAKLPITNVSSDYLYRMVRYLVHLNIIEQETCNGGVEKVYSLKPVGTLLLRDAE
40MT_COPJA:	MAFHGKDOVLDIKAQAHVWKIIYOFADSUVLRCAVELGIVDII-DUNAQPMALADLASKLPV8DVNCDNLYRILRYLVKWEILRVEK8DDGQKKYALEPIATLLSRNA
60MT_COPJA:	MEVREDALSQARKUNFIYGFAESUVERCAVQLDLANII-HHSG-TSMTLSELSSRL-PSQPVNEDALVRVMKVLVHKLFTKASDGELRYGLAPPARVLVKKMD
NONT PAPSO:	
N/ONI_PAPSO:	. MEV
TONIC MEDSA:	
TOMTS MEDSA.	- RDS CANGERGEITERGENEITERTENDUBLERGEVENTETETER UND RESELUCIONE DE QUEE SENGUERENTE INDESE IN AUGUST AUGUST AUGUST. AUGUST AUGUST AUGUST. AUGUST AUGUST AUGUST. AUGUST AUGUST. AUGUST AUGUST. AUGUST AUGUST. AUGUST AUGUST AUGUST. AUGUST. AUGUST. AUGUST. AUGUST AUGUST. AUGUST. AUGUST AUGUST. AUGUST AUGUST. AUGUST AUGUST. AUGUST
DTOMT GLYEC:	MASSINGRKFSEIFOGOALLYRHIYAFIDSMCLKWIVELDIPNIIHNHGEPITVSELV3ILEVFQTKAGNVORIMRYMAHNGFFERVRIOEEOEENEAYALTAASELLVKGSE
SOMT2_SOYEN:	MASPLNNGRKASEIFQGQALLYKHLLGFIDSKCLKMMVELDIPDIIHSHSHGQPIFFSELVSIL-QVPPTKTRQVQSLMRYLAHNGFFEIVRIHDNIEAYALTAASELLVKSSE
I4OMT_GLYEC:	: MAFSTNGSEEIELYHAQIHLYKHVYNFVSSMALKSAMELGIADVIHNHGKPITLPELASALKLHPSKVGILYRFLRLITHNGFFAKTTVPSQ-NGKDGEEEEETAYALTPPSKLLVKGKP
I4OMT_MEDTR:	: MAFSTNGSEESELYHAQIHLYKHVYNFVSSMALKSAMELGIADAIHNHGKPMILSELASSLKLHPSKVNILHRFLRLIHNGFFAKTIVKGKEGDEEEEIAYSLTPPSKLLISGKP
M3OM1_PEA:	MDFSTNGSEESELYHAQIHLYKHVYNFVSSMALKSAMELGIADAIHNHGKFMTLPELSSSLKLHPSKVNILYRFLRLITHNGFFAKTTVKSNEGEEETAYVLTPSSKLLVSGKS
M3OM2_PEA:	MDFSTNGSEESELYHAQIHLYKHIYNFVSSMALKSAVELGIADAIHNHGKPMTLPELASSLKLHPSKVNILYRFLRLITHNGFFAKTTVKSNGEEEETAYVLTPSSKLLVSGKS
I40MT_LOTJA:	DDFSSNGSEDTELSQAQIHVYRVYNFYSSMALKSAMELGIADUI-HSHGKPITLPELATALNLRFSKIGVHRFLRLITHRGFFAKTTVSRGG-AEEETAYGLTPPSKLUVKNS AND AND AND AND AND AND AND AND AND AND
CVMT1_OCIBA:	MALQNMDISLSTEQLIQAQAHWWNNMAFANSKEKCAIQUGIPDILHWNISQLEKAIPIKKEKSQSFQKIMKAINNNFTIEENSNNQEVCYWLTRASKLLKKAP
G=OMT-	RAL (UNIDEDIDGEDGEDGEDGEDGEDGEDGEDGEDGEDGEDGEDGEDGED
Ti N100MT:	M
Ti OMT 2:	MAMVEKSAEILKAQARVWNQLFCFKNSASLKCAVQLGIPDAIENHGKAMTLSELTDALPLNFSEACYIHHLMRILVNAGFFVEERLDDGKEEKAYALAPPGHLLLKNNF
MOMT_CATRO:	MELQSSEIRNAQAHFFTQVF3FT3MSSLKCAVQLGIFDAIH3HGKPMALSDLTNSLPINPSKAPYIYRLMRILVAAGYF3EEEKNVYSLTPFTRLLLKNDP
HTOMT_CATRO:	: MDVQSEEFRGAQAQIWSQSCSFITSASLKCAVKLGIPDTIDNHGKPITLSELTNALVPPVHPSKAPFIYRLMRVLAKNGFCSEEQLDGETEPLYSLTPSSRILLKKEP
OMT3_HUMLU:	MEKLKSFRHLNNNIDLILNEENSTEILGAQAHIMNQIFNFINSMSLKCAIQLGIPDIINNHGKPMTISQLTLALPINRKKSPCVYRLMRILIHSGFFALQKAEVGEEGGGEEEGYVITDASKLLLKDNP
Ti_OMT_4:	MSVALNGETSELLQANAHIWNNIFNFINSMSLKCAVQLGIPDIIHNNGKBMLSELIKAMKINDSKAPYVYRLMKILIHSGFFVKAKTAGEKREAYILTPASKLLLKNDP
ROMT_VITVI:	
ASMT1 OPVS.T.	RAL
OMTS SORBI:	NVL
ZRP4 MAIZE:	MELSPUNSTDOSLLDAQLELWHTTFAFMKSMALKSAIHLRIADAIHLHG-GAASLSQILSKVHLHPSRVSSLRRLMRVLTTTNVFGTQPLGGGSD-DDSEFVY1LFVSRLLIGSQSS
Ti_OMT_3:	MGEAQAQIDIWRYVFGF8EMAVVKCAIELGIADVLETQEGPNTLDDL\$3SLGC8FSPLYRIMRFLTYRGIFKEVAVT\$YAQTPLSRLLMRDGE
BX7_MAIZE:	MGHQAQHGTDDTEELLAAHRQLWCHALGYVKSMALKCALDLRIPDTIDRCGGSATLGELLAASEISASNHDYLRRVMRTLTAMRIFAASHDPAKAD-DAAAISYQLTPASRLLVSSSSSVDDAAGASKENT
70MT_PAPSO:	MDTAEERLKGQAEIWEHMFAFVDSMALKCAVELGIPDIINSHGRFVTISEIVDSLKTNTPSSSPNIDYLTRIMRLLVHKRLFTSELKQESNQLLYNLTRSSKWLLKDSK
OMT2_HUMLU:	MELARNDQTEAALRGEANWKSINGIADEWWKCALELRIPDIV-HEHSAFITLAGIASUPDSPSLNLSYLSRIMALLVRKIF3QHKELDGEEVLYGFTHSSKLLSKTIFD
OMTI_CHRAE:	M
Ti OMT 6:	NRSPTILLETUNNDROUPSVINUUTSUERVUNSTUEDELLI - INVESTIVOSULUSSUERVUNSTUEDELLI - NUEVISSUERVUNSTUESUUSSUERVUNSTUESU
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40MT1 PAPSO:	RSMAPVILGLSQKDFLFVWNF-VKEGLGTG-STTAFERAM-GMDMMKYLEVNPNQSQLFDEGQAGETRLLTKTLLVDCRDTF-QGMD-SLVDVGGGNGTTIKAIHEAFPHI-KCTLYDLPHVIANSDDHPNILKVPGDMFMSVPSAQ
40MT2_PAPSO:	: R5MVFMILGMTQKDFMV5WHF-MKEGLGNG-STTAFEKGM-GMDIWKYLEGNPDQSQLFNEGMAGETRLLTKTLIEDCRDTF-QGLD-SLVDIGGGNGTTIKAIYEAFPHI-KCTLYDLPHVVANSHDLPNIEKVPGDMFKSVP5AQ
40MT_COPJA:	RSMVFMILGMTQXDFMTFWHS-MKDGL3DNGTAFEKAM-GMTIWEYLEGHPDQSQLFNEGMAGETRLLTSSLISGSRDMF-QGID-SLVDVGGGNGTTVKAISDAFFHI-KCTLFDLPHVIANSYDLPNIERIGGDMFKSVPSAQ
60MT_COPJA:	KCMVGSILAITDXDFMAP#HY-LKDGL3GE-SGTAFEKAL-GTNI#GYMAEHPEKNQLFNEAMAND3RLIM3ALVKECGNIF-NGIT-TLVDVGGGTGTAVRNIANAFPHI-KCTVYDLPHVIAD3PGYSEVHCVAGDMFKFIFKAD
60MT_PAPSO:	KSMVDSILCINCKDFLAP#HH-LGDGLTGNCDAFEKAL-GKSIWVYMSVNPEKNQLFNAMACDTRLVTSALANECKSIFSDGIS-TLVDVGGGGTGTAVKAISKAFPDI-KCTIYDLPHVIADSPEIPNITKISGDMFKSIFSAD
N7OMT_PAPSO:	2 3 MYPSYLGI DEDMFAPMHI-LKDSLTGECNIFETAL-GKSISYYMSEMPEMNQISMGAMAFDSGLYTSHLVMECKSYFGDEIK-ILVDVGGGTGTALKAISKAFPMI-KCILFDLPMVIADSPEIPTITKYSGMMKKSIPSAD
TOMTS MEDSA:	
70MT9 MEDSA:	LCLARWEEVLOPTISGSWEELKKWITED IIIGUT GGGWDELKKWEIN HORAKADDSLI KAEADDSKIT DEBLESUNDGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
D7OMT GLYEC:	LCLAPHVECVLDPTLSGSYHQ-LKKWIYEE-DLTLFGVSL-GSHFWEFLNENPEYNRSFNDAMASDSQMI-NLALRDCNSGF-EGVE-SIVDVGGGIGTTAKIICDTFPNL-KCIVFDRPKVVENLSGINNLSYVGGDMFQSVPKADD
SOMT2_SOYBN:	: L3LAPMVEYFLEPNCQGAWNQ-LKRWVHEE-DLTVFGV3L-GTPFWDFINKDPAYNK3FNEAMACD3QML-NLAFRDCNWVF-EGLE-SIVDVGGGTGITAKIICEAFPKL-KCMVLERPNVVENL3G3NNLTFVGGDMFKCIPAAD
I4OMT_GLYEC:	: tolasivgalhpssldmmrs-sexwfkedkeltlpesat-gesfwdplnkdsesgtlsmpqeamaadsqmf-klalkecrhvf-egle-slvdvgggtggvtklheepphl-kctvpdqpqvvgnlsgnenlkfvggdmfksippad
I4OMT_MEDTR:	: TCLSSIVKGALMSSBLDMSS-SKWENEDKE
M3OM1_PEA:	TCLSSUVKGALHSSLDMKGV-SKKWFHDIKE
TAOMT LOTIA	ICLSOVY KOLT HOR LOW SAME TELEKE
CVMT1 OCIBA:	LTVAPLVOVULDFTFINPWHY-MSENFKHE-NHATOFEAAN-GCTFWEKLANKPSMGRFFDEAMSCDSRLVAHULTKDYKHVI-DGIR-TLVDVGGGNGTMAKAIVEAVFTM-KCTVLDLPHUVAGLESTDKLSYIGGDMFOSIPSAD
EOMT1_OCIBA:	: LTVTFLVQVVLDFFFTNFWHH-MSEWFTHE-KHATQFEAAN-GCTFWEKLANEPSKGRFFDEAMSCDSRLIAHVFTKDYKHVI-EGIR-TLVDVGGGNGTMAKAIVEAMPTI-KCTVIDLPHVVAGLESTDNLNYIGGDMPQSIPSAD
GBOMT:	FNERGSVLMTLDPVMVKPWFT-LGEWFQND-DPSPFHTAH-GKSFWEHTAEEPGFGKLFDEVMAND3QFIKHVLINDYKFVF-EGLI-SLVDVGGGTGTVARAIAETFPKL-KCTVYDLPQVVANLQGSE-NFEFVAGDMFKEIFTAN
Ti_N100MT:	L5LRASALTMLDPVTVKTWNA-L5EWFQNE-DQTAFETAH-GKNMWDFFAEDPGL5KKFNE5MASD5QLVTEVLVTKCKFVF-EGLT-5MVDVGGGGTGTVAGAIAKTFP5L-RCTVFDLPHVVANLEPTENLDFVAGDMFGKIPPAN
Ti_OMT_2:	ONLEELYFLYLOPWALRPMNY-LSEWFOND-DQTAFETAH-GKKLMOVISEEPFFCROFFNEAWVSDSKIISELLISELFFFF-BGLE-SMVDVGGGTGTVSMAIAMFFCL-RCTFVDLFMVADLEGTENLDFFGCMMERIFFAN
MOMI_CAIRO:	LISIS U LEVRUIR LIKARNA WOLMU UNE LIRE LIRE GUN GREUFALERUE U GUN ER LISIS U LORRITE EN LIE-LOUD STUDY OGGI GI I KAKAKAGE PL-RUIY D LEVY AN LES LE-RUEY OG DNE EKTESAN
WTOMT CLTDO.	INIDCITITY ADDUCT VARE G = I GDEVONE = D = = D G GT A FFT A = C VERY CV G F SUP A GD OCT TOVI I TOVI TOVI TOVI TOVI TOVI TOVI T
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HTOMT_CATRO: OMT3_HUMLU: Ti OMT 4:	INIGUIDINADFULTAMES-LSDWUGNEDDSSTAFETAM-GRUFWUSSERHERAEFFNEMASBOGLISKLICENTL-FGLA-SLUDIGGGTGTIAKIANNFQL-KUTVDLEHWUNALESKE-WUSTVAGUMFENISBAL MSVTPFLLALLDFWITKFWGD-LSNWFQNG-DPSFPTAM-GRAFWUSSERHENARFFNEMASBORLUTSVVIEKCKUT-EGU-SLUDVGGGTGTVASSIAAFFHI-QUTVDLEHWUNALESKE-WUSVFNGGMVFDVPATE LSVSFFLAALDFLITFWNG-1SENFUNST-OPFVTSH-GSLUDKGEPRINYFINEGAASBORLUTSVVIEKCKUT-EGU-SLUDVGGGTGTVASSIAAAFFHI-QUTVDLEHWUNALESKE-WUSVFNGGMVFDVPATE LSVSFFLAALDFIITFWNG-1SENFUNST-OPFVTSH-GSLUDKGEPRINYFINEGAASBORLUTSVVIEKCKUT-EGU-SLUDVGGGTGTVASSIAAAFFHI-QUTVDLEHWUNALESKE-WUSVFNGGMVFDVPATE LSVSFFLAALDFIITFWNG-1SENFUNST-OPFVTSH-GSLUDKGEPRINYFINEGAASBORLUTSVVIEKCKUT-EGU-SLUDVGGGTGTVASSIAAFFHI-QUTVDLEHWUNALESKE-NUSVFNGGMVFDVPATE LSVSFFLAALDFIITFWNG-1SENFUNST-OPFVTSH-GSLUDKGEPRINYFINEGAASBORLUTSVVIEKCKUT-EGU-SLUDVGGGTGTVASSIAAFFHI-QUTVDLEHWUNALESKE-NUSVFNGGMVFDVFAGUMVFDVFACU LSVSFFLAALDFIITFWNG-1SENFUNST-OPFVTSH-GSLUDKGEPRINYFINEGAASBORLUTSVVIEKCKUT-GSLUDSVIEKCKUT-SUDVGGGTGTVASSIAAFFHI-QUTVDLEHWUNGLEGTFT-NUSVFGGMVFDVFACU LSVSFFLAALDFIITFWNG-1SENFUNST-OPSUDVEGAASBORLUTSVVIEKCKUT-GSLUDSVIEKCKUT-SUDVGGGTGTVASSIAAFFHI-QUTVDLEHWUNGLEGT-NUSVFGGUNGTVASSIAAFFHI-QUTVDLEHWUNGLEGT-NUSVFGGUNGTVASSIAUAFFHI- SUDVGGUNGTVAKANAASAAAFFHI-QUTVALESKE LSVSFFLAAGGUNGT-SUDVGGUNGTVASSIAAFFHI-QUTVALESKUTSVVIEKCKUT-SUDVGGUNGTVASSIAAFFHI-QUTVDLEHWUNGLEGT-NUSVFGUNGTVAS LSVSFFLAAFFHI-QUTVASSIAFFHI-QUTVASSIAFFHI-QUTVASSIAFFHI-QUTVASSIAFFHI-QUTVASSIAFFHI-QUTVASSIAFFHI-QUTVASSIAFFHI- NUSVFFLAAFFHI-QUTVASSIAFFHI-
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HTOMT_CATRO: OMT3_HUMLU: Ti_OMT_4: ROMT_VITVI: QSOMT_MENPI: ASMT1_ORY3J: OMT3_SORBI: ZRP4_MAIZE: T: OMT 2:	INTROLUCED PUTCHENE - LOW ONE
HTOMT_CATRO: OMT3_HUMLU: Ti_OMT_4: ROMT_VITVI: QSOMT_MENPFI: ASMT1_ORYSJ: OMT3_SORBI: ZRP4_MAIZE: Ti_OMT_3: BX7_MAIZE:	INIAGUUTINADFVQLAMAE-L5UVYQNE-0DSTATEIAM-CKNFKVJSENKUA-EFFNEAMABJQLISKLIJCENTLI-GLA-SUVJGGGGTIAMAIANFPQL-KUVTDLENVAALESEE-NVITAGUMETAIPSAN MSTFFLIAMLDFLITPKNFKDS-0FFFTJAM-GANFKVJSENKUA-FFNEAMABJALISVIIKCKAVF-GGU-SUVVGGGTGTAMAIANFH-KUVDLENVAGLGGS-NUNFAGGAGGS-NUNFAGGS-NUNF
HTOMT_CATRO: OMT3_HUMLU: Ti_OMT_4: ROMT_VITVI: Q8OMT_MENFI: ASMT1_ORV51: OMT3_BORBI: ZRP4_MAIZE: Ti_OMT_3: BX7_MAIZE: 70MT PAPS0:	I MIABUVITMADFVQLAKAS-ISDVQKE-DDSTATETAM-CKRTKVSSENKLA-EFTERAMABOQLISKLIDETKI-FGLA-SLVDIGGGTGTIAKIANFKQL-KUVTDLEKWAALESE-NVFT4AGUMETKIFSAN MWYTFFLLAMLDFILTERWIG-DFFFTAM-GATKFVGSSENKLA-FFERDAMABABLVISVIEKKKVF-GGU-SLVDVGGGTGTAKAIAAFHL-KUVDLEKWAALESE-NVFT4AGUMETKIFSAN LSVRFTFLLAMLDFILTERWIG-LSKFQK-OFFFTAM-GATKFVGSSENKLA-FFERDAMABABLVISVIEKKKVF-GGU-SLVDVGGGTGTAKAIAAFHL-KUVDLEKWAQUGGS-NIAFKGGAGG LSVRFVLAMLSFTUD-SLVFQKVFFTAM-ESTFFVGSSENKLA-FFERDAMABABLVISVIEKKKVF-GGU-SLVDVGGGTGTAKAIAAFHL-KUVDLEKWAQUGGS-NIAFKGGAGG LSVRFVLAMLSFTUD-SLVFQK
HTOMT_CATRO: OMT3_HUMLU: Ti_OMT_4: ROMT_VITVI: QSOMT_MENFI: ASMT1_ORYSJ: OMT3_SORBI: ZRP4_MAIZE: Ti_OMT_3: BX7_MAIZE: 70MT_PAFSO: OMT2_HUMLU:	INIAGUUTINADFVQLTAMES-L5UVYQNE-0DSTATETAM-CHTFEVJSEINUM- EFFNEAMABDQLISKLIDETKI-FGLA-SLVDGGGGTIAMIANINFU-KUVTDLEHVVAALESE-NVIFTAGUHEKI-SUV MUSTFELLALDFUTTENTKENGE-0FFFTJAM-GARFHOSSEINUA-FFNEAMABDALIVSVIEKKEVF-GGU-SLVDVGGGTAMAIANAFH-KUVDLEHVVAALESE-NVIFTAGUHEKIFFABA LSTPELLALDFITIENTG-15ENFONFFFTJAM-GARFHOMABDALIVSVIEKKEVF-GGU-SLVDVGGGTAMAIANAFH-KUVDLEHVVAALESE-NVIFTAGUHEKIFFABA LSTPELLALDFITIENTG-15ENFONVFFTJAM-GARFHOMABDALIVSUIEKKEVF-GGU-SLVDVGGGTAMAIANAFH-KUVDLEHVVAALESE-NVIFTAGUHEKIFFABA LSTPELLALDFITIENTG-15ENFONVFFTJAM-GARFHOMABDALIVSUIEKKEVF-GGU-SLVDVGGGTAMAIANAFH-KUVDLEHVVAALESE-NVIFTAGUHEKIFFABA LSTPELLAUSDFVTTENH-15ENFONVFFTJAM-GARFHOMABDALIVSUIEKKEVF-GGU-SLVDVGGGTAMAIANAFH-KUVDLEHVVAALESE-NVIFTAGUHEKIFFABA LSTPELLAUSDFVTTENH-15ENFONVFFTJAM-GARFHOMABDALIVSUIEKKEVF-GGU-SLVDVGGGTAMAIANAFH-KUVDLEHVVAALESE-NVIFTGGUHEKIFFABA LSTPELLAUSDFVTTENH-15ENFONVFFTJAM-GARFHANDESCH-VFFTIAM-CETTERADABDALIVSUIEKKEVF-GGU-SLVDVGGGTAMAIANAFH-KUVDLEHVVAALESE-NVIFTGGUHEFIFFADA LSTPELLAUSDFVTTENH-15ENFONVFFTAM-CETTERVGARDABINVLFTGGGGTAMAINAFH-SLVDVGGGTAMAINAFH-KUVDLEHVVAALESE-NVIFTGGUHEFIFFADA LSTPELLAUSDFVTTENH-15ENFON
HTOMT_CATRO: OMT3_HUMLU: Ti_OMT_4: ROMT_VIIVI: QSOMT_MENPI: ASMT1_ORYSJ: OMT3_SORBI: ZRP4_MAIZE: Ti_OMT_3: BX7_MAIZE: TOMT_PAPSO: OMT2_HUMLU: OMT1_CMRAE:	INISOUUTIADPYQLAMES-LSDWQIM-DDSTATEIAM-CKREWGYSSERIAEFFEMAASSQLISKLIGETKI-FGLA-SUVGGGGGTIAAIANFEQ-KCUVDLEHWAALESENUFTAGUHEKI-SU MUSTFFLIAMLOFUTIKEMU-LSENFQNDFFETAM-GARENGYSSERIAYEITBOMASDALVSTVIEKCKVF-GUT-SLUVGGGGTAAAIANFHL-KCUVDLEHWAALESENUFTAGUHEKIFDA LSTREVIALDFILTEMU-LSENFQNDFFETAM-GARENGN-NETHBOMASDALVSTVIEKCKVF-GUT-SLUVGGGGTAAAIANFHL-KCUVDLEHWAALESENUFTAGUHEKIFDA LSTREVIALDFILTEMU-LSENFQNDFFETAM-SERIEN-YEITBOMASDALVSTVIEKCKVF-GUT-SLUVGGGGTAAAIANFHL-KCUVDLEHWAALESENUFTAGUHEKIFDA LSTREVIALDFILTEMU-LSENFQNDVFETAM-SERIEN-YEITBOMASDALVSTVIEKCKVF-GUT-SLUVGGGGTAAAIANFHL-KCUVLDEHWAALESENUFTAGUHEKIFDA LSTREVIALDFUTIKENFU-LSENFQNDVAIFUKK-GHTFEYANDDALNVLIEMACAGUVSIISLITELGE-SUUVGGGTAAAANAFHL-KCUVLDEHWAALESENUFTAGUHESIFF NGLGGWAVWUFVIANSOF-LSENFUNDVAIFUKK-GHTFEYANDDALNVLIEMACAGUVSIISLITELGE-SUUVGGGGTAAAANAFHE-KCUVLDEHWAALESENUFTGGGG ALGUGGWAVWUFVIANSOF-LSENFUT-SAANJIETVA-GUTEKIADSGDALNALFINMAANSILULESSUVF-GUT-SUUVGGGGTAAAAVVAAFDF-KCUVLDEHWAALESSI-NUFTGFF ALGUGWAVWUFVIANSOF-LSENFUT-SAANJIETVA-GUTEKIADSGDALNALFINMAANSILUUTIKESSUVF-GUT-SUUVGGGGAAAAJSAAFHE-KCUVLDEHWAALESSIGNUOTOGGGEFSIFEN ALGUGWAVWUFVIANSOF-LSENFUT-SAANJIETVA-GUTEKIADSGDALNALFINMAANSILUUTIKESSUVF-GUT-SUUVGGGGAAAAJSAAFHE-KCUVLDEHWAALESSIGNUOTOGGGEFSIFEN LAQTELANULDEFNGLE-LSENFUT-SAANJIETVA-GUTEKIADATOALVINGLASSOLUVVIA KQSSUVF-GUT-SUUVGGGGAAAAJSAAFHE-KCUVLDEHWAALESSIGNUOTOGGGEFSIFEN LAQTELANULDEFNGLE-LSENFUT-SAANJIETVA-GUGMACUEDAANASITEMMADISUUVGGUTAAUNATUV-GUT-SUUVGGGGAAAAJAAAVAAPTO-KGINDLANAAAFH SUUVGGGGAAAAJSAAFHOL-KCUVLDEHWAALESSIGNUGHFSIFEN LAQTELANULDEFNGLE-LSENFUT-SAANJIETVA-GUGMACUEAAAN-ASITEMAADISUUVGGUTAAUNATUVGGUGGGAAAAJAAAHAFHOL-KCUVULDEHWAALEST-GUGWGGGTIFSIFEN SUUVGGGGAAAAJAAFHOL-KCUVULDEHWAALESSIFF SUUVGGGGAAAAJAAFHOLKUVAALESSIFF SUUVGGGGAAAJAAJAAFHOLKUVAALESSIFF SUUVGGGGAAAAJAAFHOLKUVAALESSIFT SUUVGGGGAAAJAAJAAFHOLKUVAALESSIFF SUUVGGGGAAAJAAJAAFHOLKUVAALESSIFF SUUVGGGGAAAJAAJAAFHOLKUVAALESSIFT SUUVGGGGAAAJAAJAAFHOLKUVAALESSIFT SUUVGGGGAAAJAAJAFHOLKUVAALESSIFT SUUVGG
HTOMT_CATRO: OMT3_HTMLU: Ti_OMT_4: ROMT_VITVI: ASMT1_ORY3J: OMT3_SORBJ: ZRP4_MAIZE: Ti_OMT_3: BX7_MAIZE: TOMT_PAPSO: OMT1_CHRAE: Ti_OMT_5:	INIAGUVIINADFVILKARS-LSUVQUE-0USSTATETAM-CHUFFVISSENELA-ELFELMAADSQLISKLIGETKI-EGLA-SLUVGGGGTGTAKAIANTFUG-KUVTULEUVVALUSGG-VHUVALUSGGG-VHUVALUSGGG-VHUVALUSGGG-VHUVALUSGGG-VHUVALUSGGG-VHUVALUSGGG-VHUVALUSGGG-VHUVALUSGGG-VHUVALUSGGG-VHUVALUSGGG-VHUVALUSGGG-VHUVALUSGGG-VHUVALUSGGG-VHUVALUSGGG-VHUVALUSGGG-VHUVALUSGGG-VHUVALUSGGG-VHUVALUSGGGG-VHUVALUSGGGG-VHUVALUSGGGG-VHUVALUSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
HTOMT_CATRO: OMT3_HTMLU: Ti_OMT_4: ROMT_VITU1: ASMT1_ORYSJ: OMT3_SORBI: ZRF4_MAIZE: Ti_OMT_9AF80: OMT2_HTMLU: OMT2_HTMLU: OMT2_HTMLU: GMT1_CHRAE: Ti_OMT_5: Ti_OMT_6:	INIAGUUTIADPVQLAMES-L5UVQNE-0DSTATEIA-CKIFFOISSENELA-EFFEMAAB3QLISKLIDEUKLI-EGLA-SUVGGGGTIAAIANFEU-KUVDLEHVAALESE-NUT7AGUHEKIFABA MSYTFILALDFUITENTKENG-50FFFITAM-CKIFFOISSENELA-FFEMAAB3QLISKLIDEUKLI-EGLA-SUVGGGGTIAAIANFEU-KUVDLEHVAALESE-NUT7AGUHEKIFI LSYSFILALDFUITENTKENG-50FFFITAM-CKIFFOISSENELA-FFEMAAB3ALVSVIEKKKAF-GGU-SUVGGGTGAAAIAAFH-KUVDLEHVAAGSGS-NLAFFAGGGSS-NLAFFAGGGSS-NLAFFAGGGSS-NLAFFAGGGSS-NLAFFAGSSS-NLAFFAGSSS-NLAFFAGSSS-NLAFFAGSSS-NLAFFAGSSS-NLAFFAGSSS-NLAFFAGSSS-NLAFFAGSSS-NLAFFAGSSS-NLAFFAGSSSS-NLAFFAGSSSS-NLAFFAGSSSS-NLAFFAGSSSS-NLAFFAGSSSS-NLAFFAGSSSS-NLAFFAGSSSSS-NLAFFAGSSSSS-NLAFFAGSSSSS-NLAFFAGSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS
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HTOMT_CATRO: OMT3_HUMLU: Ti_OMT_4: ROMT_VITVI: QSOMT_MENPFI: ASMT1_ONY30: ZRP4_MAIZE: Ti_OMT_3. BX7_MAIZE: OMT2_HUMLU: OMT1_CHRAE: Ti_OMT_5: Ti_OMT_6:	I MIABOVULTMADFVULTAMES-LEDWIGNE-ODESTATETAM-CHIFFOYSSEMELAEFFEMAADSQLISKLIDETKI-FGLA-SLUDGGGGTIAMAIANTPU-KUVTDLEWAVANLESENUTYAGUMETAIPSAN MUSTFELLALDFILTEMEN-LEDWIGNE-OFEFETAM-GARTENGSEMELAFETEMAADSQLISKLIDETKI-FGLA-SLUDGGGGTIAMAIANTPH-KUVDLEWAVANLESENUTYAGUMETAIPSAN LSTREVLANDFILTEMEN-LEDWIGNE-OFETETAM-GARTENGSEMELAFETEMAADSQLISKIJUSVIEKKEVF-GGL-SLUDVGGGTAMAIANTPH-KUVDLEWAVGLOSS-NUSTFAGADS LSTREVLANDFILTEMEN-LEDWIGNE-OFETETAM-GARTENGAL-VIENDAGEDALVISVIEKKEVF-GGL-SLUDVGGGTAMAIANATPH-KUVDLEWAVGLOSS-NUSTFAGADS LSTREVLANDFVITEME-LEDWIGNE-OVETEMENDAGEDALVISVIEKKEVF-GGL-SLUDVGGGTAMAIANATPH-KUVDLEWAVGLOSS-NUSTFAGADS LSTREVLANDFVITEME-LEDWIGNE-OVETEMENDAGEDALVISVIEKKEVF-GGL-SLUDVGGGTAMAIANATPH-KUVDLEWAVGLOSS-NUSTFAGADS LSTREVLANDSVITEME-LEDWIGNE-GARAGUETAM-VIENDAGEDAGUN-VIENDAGEDALVISVIEKKEVF-GGL-SLUVVGGGTAMAIANATPH-KUVDLEWAVGLOSS-NUSTFAGADS LSTREVLANDSVITEME-LEDWIGNE-GARAGUETAMINGSKO-SHANGKINGSVINGALVISVIEKKEVF-GGL-SLUVVGGGTAMAINATPH-KUVDLEWAVGLOSS-NUSTFAGADS LSTREVLANDSVITEME-LEDWIGNE-GARAGUETAMINGSKO-SHANGKINGSVINGALVISVIEKKEVF-GGL-SLUVVGGGTAMAINATPH-KUVDLEWAVGLOSS-NUSTFAGADS SUGLGWAVXVVERVINASG2-LEDWIGNE-GARAGUETAMINGSKO-SHANGKINGSVINGALVISVIEKGEVF-GGL-SLUVVGGGTAMAINATPH-KUVDLEWAVGLOSS-NUSTFAGADS SUGLGWAVXVVERVINASG2-LEDWIGNE-GARAGUETAMINGSKO-SHANGKINGSVINGALVANDSVINGENTI-SLUVGGGGTAMAINATPH-GUNGANGANAVARAFU SUGLGWAVXVERVINASG2-LEDWIGNE-GARAGUETAMINGSVINGANGANAVARAFUGANAVARAFUGAGANAVARAFUGAGANAVARAFUGAGANAVARAFUGAGANAVARAFUGAGANAVARAFUGAGANAVARAFUGAGANAVARAFUGAGANAVARAFUGAGANAVARAFUGAGANAVARAFU
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HTOMT_CATRO: OMT3_HMMLU: Ti_OMT_4: ROMT_VITVI: QSOMT_ICATOR ZRF4_MAI2E: ZRF4_MAI2E: ZRF4_MAI2E: GMT1_GRAPS0: OMT1_CRAPS0: OMT1_CRAPS0: 40MT1_PAPS0: 40MT1_PAPS0: 40MT1_PAPS0:	I MIAGUVILMADYVILMAS-ILDUVQME-0DESTATEIA-GRIFFONSSEMELA-EFFELMADGLISHLIGETHI-FGLA-SLUDGGGGTIAKIAANAFFU-KUVUDEKUVAALESE-NUTYAGUHEKIFUFAGU MUTTEILALDFIIIEMU-LSUFQME-0FFETAM-GRIFFONSSEMELA-EFENDAMADALVISVILKKAVF-GGU-SLUVVGGGGTAMAIAAFH-KUVUDEKUVAALESE-NUTYAGUM-HUITAFE LSUPEILALDFIIIEMU-LSUFQME-0FFETAM-GRIFFONSSEMELA-EFENDAMADALVISVILKKAVF-GGU-SLUVVGGGTAMAIAAFH-KUVUDEKUVAALESE-NUTYAGUM-HUITAFE LSUPEILALDFIIIEMU-LSUFQME-0FFETAM-GRIFFONSSEMELA-EFENDAMADALVISVILKKAVF-GGU-SLUVVGGGTAMAIAAFH-KUVUDEKUVAQUSG-NULKYGGMENSIFTU LSUPEILAUDFVILEMU-LSUFQME-0
HTONT_CATRO: ONT_HUMLU: Ti_ONT_4: RONT_VITVI: CRONT_VITVI: CRONT_MENPE: SANT1_ORX53: ONTSTATA EX7_MAIZE: TI_ONT_2 EX7_MAIZE: TI_ONT_2 HAMLU: ONT1_CHARA: TI_ONT_6: TI_ONT_6: ONT1_CAPAFO: ONT1_CAPAFO: ONT1_CAPAFO: ONT1_CAPAFO: ONT1_COFJA:	<pre>NINGOVULTADAYQUTAMES-LEWYQRE-0DSTATETAM-CHNFWYSSERHAEFFEAMABOQLISHLIGETH-FGLA-SLUDGGGGTAAMAIAANFH-CUVTULEHVVAALESENUTYGGEN-NINTGGGANG-NINTGGANGAGAN- WATTETLALLOFITTENN-LEWYQR-0FFETTAM-CHNFWSSERHAEFFEAMABOQLISHLIGETH-FGLA-SLUDGGGGTAAMAIAAFH-CUVULEHVVAALESENUTYGGEN-NINTGGGANG-NINTGGANGAGAN- WATTETLALLOFITTENN-LEWYQR-0FFETTAM-CHNFWSSERHAFFENDAMBOALVSUULEKTUR-GUN-SLUDGGGGTAAMAIAAFH-CUVULEHVVAALESENUTYGGEN-NINTGGGANG-NINTGGANGAGAN- WATTETLALLOFITTENN-LEWYQR-0FFETTAM-CHNFWSSERHATUTHEGAABOALVSUULEKTUR-GUN-SLUDGGGGTAAMAIAAFH-CUVULEHVVAALESENUTYGGEN-NINTGGANGAGAN- LISTREVIALUSUULEKTUR-LEWYQR-0FFETTAM-CHNFWAXEENIFUTHEGAABOALVSUULKSUUTEKTUR-GUN-SLUDGGGGTAAMAIAAFH-CUVULEHVVAALESENUTYGGEN-NINTGGANGAGAN- LISTREVIALUSUULEKTUR-LEWYQR-0FFETTAM-CHNFWAXEENI-TUTHEGAABOALVSUULKSUUTEKTUR-GUN-SUUTGGGGTAAMAIAAFH-CUVULEHVVAALESENUTYGGGAN-NINTGGANGAGAN- LISTREVIALUSUULKSUULEKTUR-LEWYDR-COM-FFETTAM-DENTEN-BANGKUSSUULKSUUTEKSUUTEGUN LISTREVIALUSUULKSUULEKUULEKUULEKUULEKUULEKUULEKUU</pre>
HTOMT_CATRO: OMT3_HMMLU: Ti_OMT_4: ROMT_VITVI: QCOMT_MEMPE: 2RP4_MAILE: 2RP4_MAILE: BX7_MAILE: DMT2_CHRAE: Ti_OMT_S: Ti_OMT_S: Ti_OMT_S: Ti_OMT_S: CMT1_PAPSO: 40MT1_PAPSO: 60MT1_PAPSO: 60MT1_COFJA:	I MIAGIVIIMADYVILMAS-ILDIVQH-ODESTATEIA-GRIFFVSSEHHAEFFEMAADSQLISKILDEVILT-GLA-SLUDGGGGTIAKIAMIVET-CUVTULEHVVALESENUTYAGUHEKIF- MWTYFILALDFIITEMW-LEWYQM-OFFETAM-GRIFFVSSEHHAFFEMAADSQLISKILGEVIL-GLA-SLUDVGGGTAMAIAAFH-CUVULEHVVALESENUTYAGUHEKIFVA LSYRFILALDFIITEMW-LEWYQM-OFFETAM-GRIFFVSSEHHAFFEMAADSQLISKILGEVIL-GLA-SLUDVGGGTAMAIAAFH-CUVULEHVVALGSGNURYAGUHEKIFVA LSYRFILALDFIITEMW-LEWYQM-OFFETAM-GRIFFVSSEHHAFFEMAADSQLISKILGEVIL-GLA-SLUDVGGGTAMAIAAFH-CUVULEHVVALGSGNURYAGUHEKIFVA LSYRFILALDFIITEMW-LEWYQM-OFFETAM-GRIFFVSSEHHAFFEMAADSQLISKILGEVIL-GLA-SLUDVGGGTAMAIAAFH-CUVULEHVVAGUSGNURYAGUHEKIFFIFA LSYRFILAUGFVITTEM-LEWYNG-OFFETAM-CHFETAWAGHENNVICTEGAGUAGUAUN-UNERGAUN-SLUVGGGTAMAIAAFH-CUVULEHVVAGUSGNURYAGUGGSNURYAGUGGSNURYAGUGGSG LSYRFIALMSDFVITTEM-LEWYNG-CYDEFAX-SHUFYGGTAMAFTGKUVULEHVVALFFFG
HTONT_CATRO: ONT3_HUMLU: Ti_ONT_4: RONT_VITVI: CSONT_VITVI: CSONT_MENET: SANT1_ORX37. ONT3_SORBI: Ti_ONT_9 BX7_MAIZE: TI_ONT_9 BX7_MAIZE: TI_ONT_6: UNT3_HAMLU: ONT1_CHARE: AONT1_PAPSO: 4ONT1_PAPSO: 4ONT2_PAPSO: 4ONT2_PAPSO:	<pre>NINGSTUTIADP/QLAWS-LEWYOR-0FSTATEIA-CHIPFY3SEMENFFTEAMABDQLISHLIGETHEGL-3LUDGGGGTIAAIANTPU-CUVULEHVVALESEWUTYAGUEFLIFABA WITFILALLOFITIENG</pre>
HTONT_CATRO: ONT3_HWMLU: Ti_ONT_4: RONT_VITVI: QSONT_VITVI: QSONT_MENPE: SANT1_ONX33: ONT3_GORBJ: Ti_ONT_3 SANT1_ONX34: ONT3_GORBJ: Ti_ONT_5: Ti_ONT_5: Ti_ONT_5: Ti_ONT_5: Ti_ONT_5: CONT1_PAPBO: 40NT1_PAPBO: 40NT1_PAPBO: MTONT_PAPBO: NTONT_PAPBO: NTONT_PAPBO: NTONT_PAPBO: NTONT_PAPBO:	INIAGIVIINADYVILKAS-LEDVQNE-O
HTONT_CATRO: ONT3_HUMLU: Ti_OMT_4: RONT_VITVI: QSONT_VITVI: QSONT_VITVI: QSONT_MENT3 SANT1_ORX37: ONT3_GORDI: Ti_OMT3_ BX7_MAIZE: TONT_PAPBO: ONT3_HAMIU: ONT3_CHRAE: TI_OMT_5: TI_OMT_6: HONT1_PAPBO: HONT1_PAPBO: HONT1_PAPBO: HONT1_PAPBO: HONT1_PAPBO: TONT6_HEDSA: TONT6_HEDSA:	I MIABUVILMADYVLIKABS-LEDVYUR
HTONT_CATRO: ONTHUNLU: Ti_ONT_4: RONT_VITVI: QSONT_MENPI: QSONT_MENPI: SANT1_ONY33: ONT_3 SANT1_ONY33: ONT_3 SANT1_ONY33: ONT_1 ONT_1 CHAL SANT2 ONT_1 CHAL SANT2 ONT_1 CHAL SANT2 ONT_1 CHAL SANT2 ONT_1 CHAL SANT2 ONT_1 CHAL SANT2 CHA	I NIAGUVILIAAPVQLAKES-LEUVQKE-DDESTATEIAM-CHIPFVSSEHKAEFFEMAADBQLISKILDGYHL-FGLA-SUDGGGGTIAAIANFH-CUVULUHVVAALESE-NVIFYAGUHEIAPTA- MYTFFLIALDFILTENKU-LEUVQK-DFFEVISE-GTIFUCABERLAFFENDAABBQLISKILGKYT-GGL-SUDVGGGGTAAIAAFH-CUVULUHVVAALESE-NVIFYAGUHEIAPTUVAA HYTFFLIALDFILTENKU-LEUVQK-DFFEVISE-GTIFUCABERLAFFENDAABBQLISVIEKKVY-GGL-SUDVGGGTAAAIAAFH-CUVULUHVVAALESENVIFYAGUHEIAFTU LYYSFLAALGFIITENKU-LEUVQK-DFFEVISE-GTIFUCABERLAYEINGABBQALVSUULKKVY-GGL-SUDVGGGTAAAIAAFH-CUVULUHVVAALESENVIFYAGUHEIAFTU LYYSFLAALGFIITENKU-LEUVQK-DFFEVISE-GTIFUCABERLAYEINGABBQALVSUULKKVY-GGL-SUDVGGGTAAAIAAFH-CUVULUKVVAGUSUUKKVY-GGL- SUDVGGGTAVAAAJAAFH-CUVULUKVVGGLAGE
HTONT_CATRO: ONT3_HUMLU: Ti_OMT_4: ROMT_VITVI: GGONT_MENPI: GFONT_MENPI: GFONT_MENPI: GFONT_GENPI GFONT_GENPI GFONT_GFONT_GFONT_GFONT GONT1_PAPBO: GONT1_PAPBO: GONT1_PAPBO: GONT1_PAPBO: GONT1_PAPBO: MINT_PAPBO: TONT1_PAPBO: TO	I MIABOVULTMADYVULTABE-LEDVYURE
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Figure S2: Amino acid sequence alignment of N10OMT with characterized and uncharacterized OMTs. asterisks indicate conserved residues for SAM binding. N10OMT is highlighted in red.



Figure S3: Phylogenetic trees of I10H (TOP) and N10OMT(Bottom) with characterized and uncharacterized proteins. CYP71D12 *C.roseus* tabersonine hydroxylase, T16H; HTOMT CATRO, *C.roseus* 16OMT. I10H and N10OMT are highlighted in red.



Figure S4: SDS-PAGE of recombinant OMTs produced in *Escherichia coli*. The left lane contains molecular weight protein markers and corresponding sizes are indicated to the left of the panel. All other lanes feature purified protein from *E. coli* strain soluBL21. Purification of polyhistidine-tagged recombinant proteins was achieved using a Nickel-affinity column and size exclusion chromatography. Visualization was achieved using Coomassie blue staining.