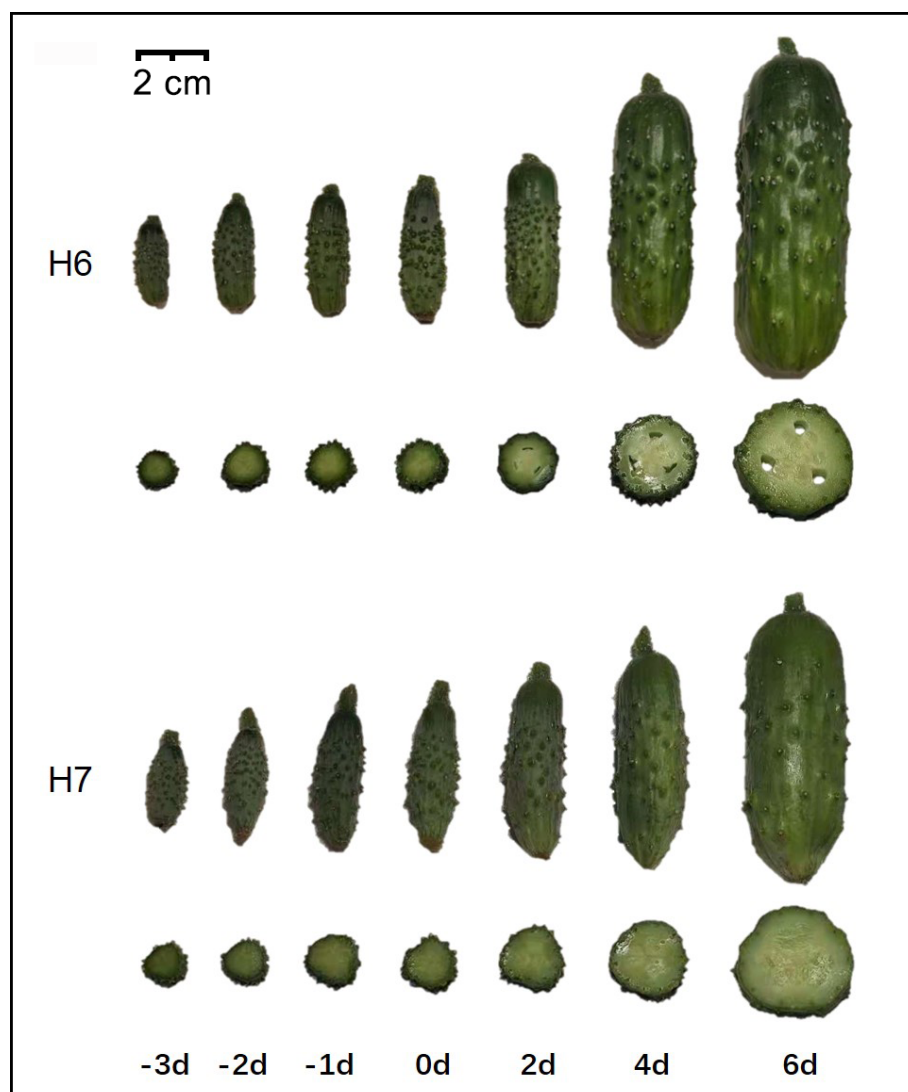
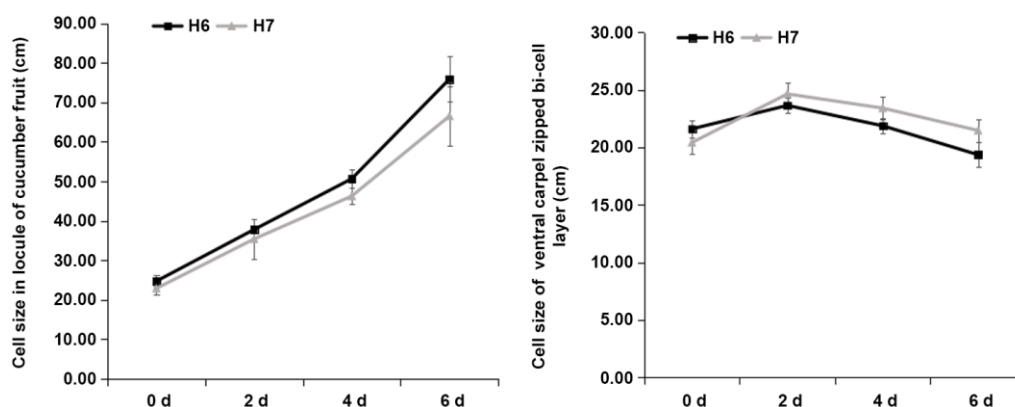


# The Formation of Fruit Hollow in Cucumber (*Cucumis sativus* L.) is Controlled by *CsALMT2*



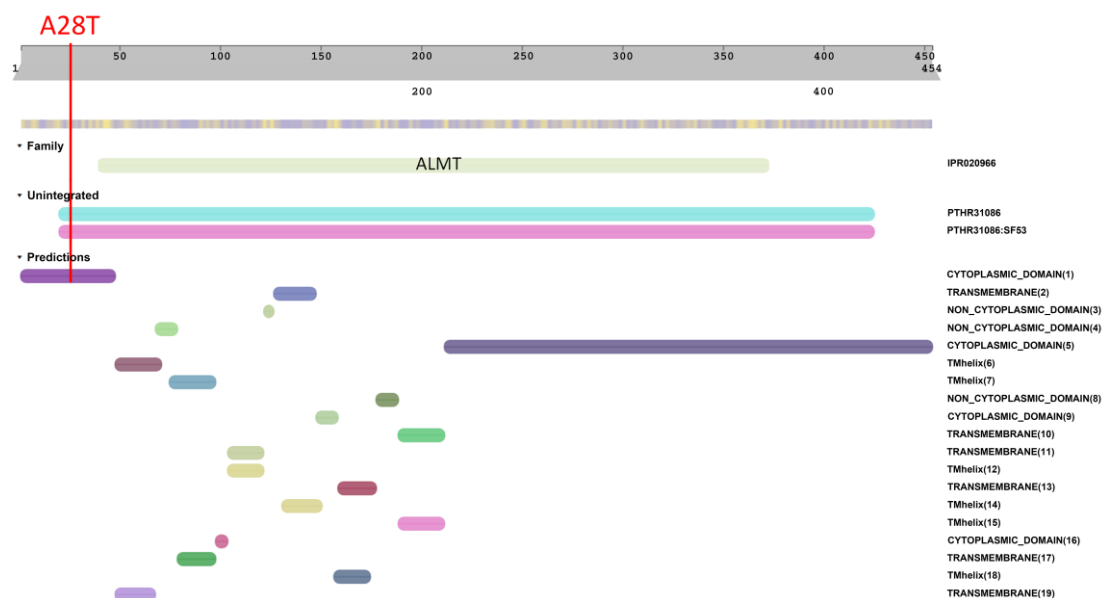
**Figure S1.** Hollow fruit trait of cucumber H6 and H7 from 3 days before flowering to 6 days after pollination. Scale bar = 1 cm.



**Figure S2.** Cell size in locule and ventral carpel zipped bi-cell layer of cucumber fruit.

Benincasa_hispida	MEMANDKSEGVLARWGEGLAKFSKLKAKVIELFRKTKKLAKDDPRRIVHSLKVGLAITL	60
Cucumis_melo	MEMSNEKSGGALARWSDGLKAKISKLKAKVIELFKKTKKLAKDDPRRIVHSLKVGLAITL	60
H7	MEMANEKSGGLLASWSEGLKAKISKIMAKVIELFKKTKKLAKDDPRRVHSLKVGLAITL	60
Cucumis_sativus_Gyl4	MEMANEKSGGLLASWSEGLKAKISKIMAKVIELFKKTKKLAKDDPRRVHSLKVGLAITL	60
Cucumis_sativus_PI183967	MEMANEKSGGLLASWSEGLKAKISKIMAKVIELFKKTKKLAKDDPRRVHSLKVGLAITL	60
Cucumis_sativus_9930	MEMANEKSGGLLASWSEGLKAKISKIMAKVIELFKKTKKLAKDDPRRVHSLKVGLAITL	60
H6	MEMANEKSGGLLASWSEGLKAKISKIMTKVIELFKKTKKLAKDDPRRVHSLKVGLAITL	60
	***:*:* * * * * .*:*:*:*: :*****:*****:*****:***	
Benincasa_hispida	VSLFYFPEPLYDGLGASAMWAILTVVVFEFSVGATLGRGLNRVLATFFAAALGFGAHFL	120
Cucumis_melo	VSLFYFPEPLYDGLGASAMWAILTVVVFEFSVGATFGRGLNRVLATFLAAALGFGVHFL	120
H7	VSLFYFPEPLYDGLGASAMWAILTVVVFEFSIGATLGRGLNRVLATFLAAALGFGAHFL	120
Cucumis_sativus_Gyl4	VSLFYFPEPLYDGLGASAMWAILTVVVFEFSIGATLGRGLNRVLATFLAAALGFGAHFL	120
Cucumis_sativus_PI183967	VSLFYFPEPLYDGLGASAMWAILTVVVFEFSIGATLGRGLNRVLATFLAAALGFGAHFL	120
Cucumis_sativus_9930	VSLFYFPEPLYDGLGASAMWAILTVVVFEFSIGATLGRGLNRVLATFLAAALGFGAHFL	120
H6	VSLFYFPEPLYDGLGASAMWAILTVVVFEFSIGATLGRGLNRVLATFLAAALGFGAHFL	120
	*****:***:*****:*****:***	
Benincasa_hispida	ADLAGDKAQIMLSLVFFL	140
Cucumis_melo	ADLAGDKAQIMLSLVFFL	140
H7	ADLAGDTAQIMLSLVFFL	140
Cucumis_sativus_Gyl4	ADLAGDTAQIMLSLVFFL	140
Cucumis_sativus_PI183967	ADLAGDTAQIMLSLVFFL	140
Cucumis_sativus_9930	ADLAGDTAQIMLSLVFFL	140
H6	ADLAGDTAQIMLSLVFFL	140
	***** *****	

**Figure S3.** Alignment of the multiple protein sequence of CsALMT2.



**Figure S4.** Domain analysis of CsALMT2.

**Table S1.** Investigation on hollow trait of cucumber varieties in different regions of China.

Classification	Variety number	Provinces	Hollow Character
North China type	ZhongNong38	Beijing	Non-hollow
	ZhongNong48	Beijing	Non-hollow
	ZhongNong106	Beijing	Non-hollow
	18C54	Beijing	Non-hollow
	18C56	Beijing	Non-hollow
	YD109	Jiangsu	Non-hollow
	YD110	Jiangsu	Non hollow
	JYXM	Beijing	Non-hollow
	JYXM2	Beijing	Non-hollow
	JYCQL2	Beijing	Non-hollow
	YueFeng	Guangdong	Non-hollow
	ChuanCui13	Sichuan	Non-hollow
South China type	HN1	Hunan	Hollow
	HN2	Hunan	Hollow
	HN3	Hunan	Hollow
	HN4	Hunan	Hollow
	LiFeng2	Guangdong	Hollow
	LiFeng3	Guangdong	Hollow
	ZaoQing8	Guangdong	Hollow
	15D036	Chongqing	Hollow
	15D044	Chongqing	Hollow
	15D088	Chongqing	Hollow
	15D095	Chongqing	Hollow
	YanBai	Chongqing	Hollow
	ChuanLv11	Sichuan	Non-hollow
	ChuanLv15	Sichuan	Hollow
	ChuanCai19-1	Sichuan	Non-hollow
	ChuanCai19-2	Sichuan	Hollow
	ChuanCai19-3	Sichuan	Hollow

**Table S2.** Percentage of average hollow area of P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub> and F<sub>2</sub> population plants.

Generation	Sample number	Percentage of average hollow area (%)	Range (%)	CV (%)
P <sub>1</sub>	19	8.17±2.35a	4.16~13.11	28.72
P <sub>2</sub>	20	0c	0.00~0.00	0
F <sub>1</sub>	20	4.54±2.21b	1.33~10.74	48.67
F <sub>2</sub>	345	4.95±3.92b	0.00~19.54	79.17

Note: Values followed by different letters (a-c) : Significantly different ( $p < 0.01$ ).

**Table S3.** Frequency distribution of hollow area percentage.

Generation	Hollow area percentage (%)											Sample number	Sample average (%)	Standard deviation (%)
	0.0	0.1–2.0	2.1–4.0	4.1–6.0	6.1–8.0	8.1–10.0	10.1–12.0	12.1–14.0	14.1–16.0	16.1–18.0	18.1–20.0			
P <sub>1</sub>	-	-	-	3	7	6	1	2	-	-	-	19	8.17	2.35
P <sub>2</sub>	20	-	-	-	-	-	-	-	-	-	-	20	0	0
F <sub>1</sub>	-	2	6	8	3	-	1	-	-	-	-	20	4.54	2.21
F <sub>2</sub>	7	91	65	60	49	36	15	13	6	1	2	345	4.95	3.92

**Table S4.** Raw sequencing data statistics.

Sequencing data ID	Number of raw reads	Number of raw bases	GC%	Bases Q30%
F <sub>2</sub> hollow	44,635,824 bp	6,695,373,600 bp	38.91%	91.79%
F <sub>2</sub> non-hollow	40,274,958 bp	6,041,243,700 bp	39.19%	91.86%
H6	36,593,864 bp	5,489,079,600 bp	39.59%	91.40%
H7	38,006,642 bp	5,700,996,300 bp	39.46%	90.29%

**Table S5.** Comparison data statistics.

Sequencing data ID	Genome length	Number of bases compared	Coverage	Average depth
F <sub>2</sub> hollow	196,481,733 bp	190,317,945 bp	97.00%	17.68
F <sub>2</sub> non-hollow	196,481,733 bp	190,672,050 bp	97.00%	23.14
H6	196,481,733 bp	190,568,736 bp	97.00%	21.46
H7	196,481,733 bp	190,435,487 bp	97.00%	19.12

**Table S6.** Plant cis-acting regulatory elements prediction of *CsALMT2*.

Promoter element	Sequence	Function	Organism
ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness	<i>Arabidopsis thaliana</i>
ACE	CTAACGTATT	cis-acting element involved in light responsiveness	<i>Petroselinum crispum</i>
ARE	AAACCA	cis-acting regulatory element essential for the anaerobic induction	<i>Zea mays</i>
AT-rich sequence	TAAAATACT	element for maximal elicitor-mediated activation (2copies)	<i>Pisum sativum</i>
G-box	TACGTG	cis-acting regulatory element involved in light responsiveness	<i>Arabidopsis thaliana</i>
GCN4-motif	TGAGTCA	cis-regulatory element involved in endosperm expression	<i>Oryza sativa</i>
MBS	CAACTG	MYB binding site involved in drought-inducibility	<i>Arabidopsis thaliana</i>
P-box	CCTTTTG	gibberellin-responsive element	<i>Oryza sativa</i>
TC-rich repeats	GTTTTCTTAC	cis-acting element involved in defense and stress responsiveness	<i>Nicotiana tabacum</i>
TCA-element	CCATCTTTTT	cis-acting element involved in salicylic acid responsiveness	<i>Nicotiana tabacum</i>
TGA-element	AACGAC	auxin-responsive element	<i>Brassica oleracea</i>

**Table S7.** KASP primer information.

<b>Cucumber-SNP ID</b>	<b>Primer name</b>	<b>Primer sequence</b>
CHM1_19454233	Primer_AlleleX	GAAGGTGACCAAGTTCATGCTATACCTCGTTCAGTTCTTCTGTGTG
	Primer_AlleleY	GAAGGTCGGAGTCAACGGATTTAATACCTCGTTCAGTTCTTCTGTGTA
	Primer_Common	GAAGAGCAGATAAACATAACCCCTTCAAAA
CHM1_19830655	Primer_AlleleX	GAAGGTGACCAAGTTCATGCTCTGCGTTACAGGAAGACTGTCAG
	Primer_AlleleY	GAAGGTCGGAGTCAACGGATTACTGCGTTACAGGAAGACTGTCAA
	Primer_Common	CGGAGGGGATGGAAATGATAGAGTT
CHM1_20065780	Primer_AlleleX	GAAGGTGACCAAGTTCATGCTCATCGCTATCAGTGGCCAAGATAAT
	Primer_AlleleY	GAAGGTCGGAGTCAACGGATTATCGCTATCAGTGGCCAAGATAAC
	Primer_Common	GTTAGATAATCATTTTGCTTAACCTACAAGGTTT
CHM1_21642977	Primer_AlleleX	GAAGGTGACCAAGTTCATGCTAGGAATGCCAGCTAAAATCATTCTTGA
	Primer_AlleleY	GAAGGTCGGAGTCAACGGATTGGAATGCCAGCTAAAATCATTCTTGC
	Primer_Common	TAACAATGGTGAAATGGATGACTTTCTAGTT
CHM1_21892895	Primer_AlleleX	GAAGGTGACCAAGTTCATGCTCTTGTACATTTTCAATCATTGGGATTGC
	Primer_AlleleY	GAAGGTCGGAGTCAACGGATTCTTGTACATTTTCAATCATTGGGATTGT
	Primer_Common	CATCGCCGGTGGTGACTTGACTT
CHM1_25854734	Primer_AlleleX	GAAGGTGACCAAGTTCATGCTGGAAGTACCAATGCAAGTATTCCCT
	Primer_AlleleY	GAAGGTCGGAGTCAACGGATTGAAGTACCAATGCAAGTATTCCCC
	Primer_Common	CTCCTAGCCCTAGTGATCCTAATCTT
CHM1_28330443	Primer_AlleleX	GAAGGTGACCAAGTTCATGCTCTATGTACTGATGAAGGAGTATGAGAAT
	Primer_AlleleY	GAAGGTCGGAGTCAACGGATTTATGTACTGATGAAGGAGTATGAGAAG
	Primer_Common	GCAAGAACTGTAGTCTCAATGAAGCAA

	Primer_AlleleX	GAAGGTGACCAAGTTCATGCTCTACCCAAAGCTCCGATTCCGA
CHM1_28340789	Primer_AlleleY	GAAGGTCGGAGTCAACGGATTACCCAAAGCTCCGATTCCGG
	Primer_Common	TACCGTTTCCTTCGGCCGCCTT
	Primer_AlleleX	GAAGGTGACCAAGTTCATGCTCTAATCTTTTCTAAAGGGATCTAGTTTGTTT
CHM1_28663072	Primer_AlleleY	GAAGGTCGGAGTCAACGGATTCTAATCTTTTCTAAAGGGATCTAGTTTGTTA
	Primer_Common	GTCAAACATGAGTTGGAAACCTCTTGATA
	Primer_AlleleX	GAAGGTGACCAAGTTCATGCTCTACATCTAATCCTTATTCTTGAGCAGAA
CHM1_28681211	Primer_AlleleY	GAAGGTCGGAGTCAACGGATTACATCTAATCCTTATTCTTGAGCAGAG
	Primer_Common	CATCACATTGTTGACATGAATCCAACCTGTA
	Primer_AlleleX	GAAGGTGACCAAGTTCATGCTTTCTTTTCAATAAGCGACATTATTTCTCGA
Chr1_21902047	Primer_AlleleY	GAAGGTCGGAGTCAACGGATTTTCTTTTCAATAAGCGACATTATTTCTCGT
	Primer_Common	ATATGGAAAATTGAGAGGTAGAAAATGGAAATAA
	Primer_AlleleX	GAAGGTGACCAAGTTCATGCTCCTTAAACAGTCTCTCTAGCCACTA
Chr1_22288154	Primer_AlleleY	GAAGGTCGGAGTCAACGGATTCCTTAAACAGTCTCTCTAGCCACTT
	Primer_Common	CACCCTTTCAAGAGAAAAAGGGCCTTT
	Primer_AlleleX	GAAGGTGACCAAGTTCATGCTTGGGATTAAGATTAGGATTAGTTTACTTTTG
Chr1_23662100	Primer_AlleleY	GAAGGTCGGAGTCAACGGATTATTGGGATTAAGATTAGGATTAGTTTACTTTTA
	Primer_Common	CTACTACAGTTAATTTTTTAATAAGAGAAACTGAA
	Primer_AlleleX	GAAGGTGACCAAGTTCATGCTAAACATACATGAACGTTTCAAACGTCAC
Chr1_24702649	Primer_AlleleY	GAAGGTCGGAGTCAACGGATTATAAACATACATGAACGTTTCAAACGTCAT
	Primer_Common	AACTAAATTATTGTTTAAAGTTGCGACTTGAAATT
	Primer_AlleleX	GAAGGTGACCAAGTTCATGCTGAGCTAAGGTGGGACGACAAAAC
Chr1_24906295	Primer_AlleleY	GAAGGTCGGAGTCAACGGATTGAGCTAAGGTGGGACGACAAAAT
	Primer_Common	TTTGGCCGCCGTCACAAGCTAAAAT



Chr1_25118463	Primer_AlleleX	GAAGGTGACCAAGTTCATGCTGCGTTTAGGGTTTTGGTTCTGTTTTG
	Primer_AlleleY	GAAGGTCGGAGTCAACGGATTGCGTTTAGGGTTTTGGTTCTGTTTTC
	Primer_Common	TGCAATTCCAAGAATCTTCAGTCAGCTT
Chr1_25185078	Primer_AlleleX	GAAGGTGACCAAGTTCATGCTCTATCTTTCCTCCCATTTCCTTCTTT
	Primer_AlleleY	GAAGGTCGGAGTCAACGGATTATCTTTCCTCCCATTTCCTTCTTG
	Primer_Common	GGGAGAACCTGAGTTGAGATTGAATATAT
Chr1_25203154	Primer_AlleleX	GAAGGTGACCAAGTTCATGCTATCAACCAACAACATCAGCCTCAAC
	Primer_AlleleY	GAAGGTCGGAGTCAACGGATTGATCAACCAACAACATCAGCCTCAAT
	Primer_Common	GTTTTGGTCTTTACTTCTTATGATTGTAGTAAATT
Chr1_25430140	Primer_AlleleX	GAAGGTGACCAAGTTCATGCTGTCTAAATCGCCAAAATTGAACACTTAAAT
	Primer_AlleleY	GAAGGTCGGAGTCAACGGATTTCTAAATCGCCAAAATTGAACACTTAAAC
	Primer_Common	CCCACTTCTAATTTGAGTATAAGAAGTAAAATTT
Chr1_25510362	Primer_AlleleX	GAAGGTGACCAAGTTCATGCTCAACCAACTGACTTCAGTTTGGTCA
	Primer_AlleleY	GAAGGTCGGAGTCAACGGATTAACCAACTGACTTCAGTTTGGTCG
	Primer_Common	TTAGGGGTGAGCATGATAGGTTGAAAAA

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**Table S8.** Amino acid sequence for construction phylogenetic tree of ALMT2.

Name	Amino Acid Sequence
CsALMT2	MEMANEKSGGLASWSEGLKAKISKIMAKVIELFKKTKKLAKDDPRRVVHSLKVGLAITLVSLFYFFEPLYDGLGASAMWAI LTVVVVFESIGATLGRGLNRVLATFLAAALGFGAHFLADLAGDTAQPIMLSLSVFFLAAITTFVRFFPRIKARYDYGFLIFILT FCLVSVSGYREDEILKVAYRRALTILIGTFIAILICILICPVWAGDDLHSLVSNNIEQLANFFQGFVEYSNEWKEDEGIVEGFKS VLTSRQTEESLVNFARWEPGHGTFKFRHPWKQYRKIGSLTRQCAYRLESLNTYLLAESQTPLHIRDQLKESCSKMSTESGKAL KDLASSIRTMTPRLPNPHIEKSKAAAKDLKAALKIRPCNSSIDLEIVPMATVASLLIDSISCIEKIAESVGELASLANFKRFEV EKSASLKFQQEQQQKLATPAIVSGHCHVVTID
CmALMT2	MEMSNEKSGGALARWSDGLKAKISKLKAKVIELFKKTKKLAKDDPRRIVHSLKVGLAITLVSLFYFFEPLYDGLGASAMWAI LTVVVVFESVSGATFGRGLNRVLATFLAAALGFGVHFLADLAGDKAQPIMLSLSVFFLAAITTFVRFFPRIKARYDYGFLIFILT FCLVSVSGYREDEILKVAYRRALTILIGTFIAILICILICPVWAGDDLHSLVSNNIEQLANFFQGFVEYSNEWKEDERIVEGFKS VLSSRQTEESLVNFARWEPHGHGTFKFRHPWKQYSRIGSLTRQCAYRLESLNTYLLAESQTPLHIRDQLKESCTKMSTESGKAL KDLASSIRTMTPRLPNPHIEKSKAAAKDLKAALKIRPCNSSIDLEIVPMATVASLLIDSISCIEKIAESVGELASLANFKCLEV GKSASLKFQQEQQQKLATPAIVSGHCHVVTVD
BhALMT2	MEMANDKSEGVLARWGEGLEAKFSKCLKAKVIELFRKTKKLAKDDPRRIVHSLKVGLALTLVSLFYFFEPLYDGLGASAMWA ILTVVVVFESVSGATLGRGLNRVLATFFAAALGFGAHFLADLAGDKAQPIMLSLSVFFLATITTFVRFFPRLKARYDYGFLIFIL TFCLVSVSGYREDEILNVAYRRALTILIGTFIAILICICICPVWAGDDLHSLVSNNIELLANFLEGFGGQYSNEWKENEVVEECK SVLTSRQTEESLVNFARWEPGHGTFKFRHPWKQYRKIGSLTRQCAYRLESLNTYLVTECQTPLHIRDQLKESCSKMSIESKAL KVLASAIRTMTRPTFPNPHIERSKAVAKDLKAALKIRPCDSGMDLLEIVPMATVASLLIDSISCIEKIAESVGELASLANFKCVE VGKSASMKLEQHQEQLPTPAIVNGHCHVVTID
McALMT2	MEMADHKSEGVSSARWAEGLRAKSSRLTVKVGELARKTKKLAKDDPRRIAHSLKVALAITLVSLFYFFEPLYDGFASAMW AILTVVVVFESVSGATLGRGLNRVLATFSAAALGFGAHFLADLAADKGEPILAFFVFLAATTTFVRFFPRIKARYDYGFLIFI LTFCLVSVSGYRDDEILQVAYTRALTILIGTFIAILICIFICPVWAGEDLHSLVSNNVELLGNFLQGFGARYSDEWKGDQVEGC KSVLTSRQTEESLVNFARWEPGHGSFKFRHPWKQYRKIGSLTRQCAYRLESLNGYLTETQIPLHIRDQLKDSCSKMSIESGKA LKDLASAIRTMTRPTFPNPHVEKSKAAAKNLKVALKIGPCNDGIDLLEIVPAATVASLLIDSISCIEKIAESVGELASMAQFKK CVEAGKLAGLELEQDQQQNLPTPAIVNGHCHVV

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CcALMT2	ESIKALLGKMRTKVTEFPGKIKKLGQDDPRRIVHSLKVGLAITLVSLFYFDPLYVGFSSAMWAVLTVVVVFEFSVGATLGK GLNRGLATFLAGSLGFGAHLATLPGEKFQIPILLGFFVFLATTVSFIRFFPRMKARYDYGLVIFILTFCLISVSGYRDEEVLELA HKRVSTILIGGFTALFVCIFICPVWAGDDLHNLAANNIEKLANFLEEFGEYFKESKDRESNKAQLQGYKSVLNSKQNEESLV NFARWEPRHGRFRFRHPWKQYQKIGSLTRHCAYRVEALNGYLSNDVKASLETRGKIKEACMKLSCESGKALKELASALRT MTQPPSQCPHIAKSKNAANSLKSLLKTGLCKDIDLQEIVAVATVASLLLDVLSCTERISESVHEIASLARFKSLEDDKVADGAK INQKGQVNNKPCSNSIEQPNHHVITID
XsALMT2	VADQKEAGMIFRGWGWLKAFFPGKIISKVVEFARKTKKLGQDDPRRIIHSLKVGLAITLVSMFYFFEPLYDGFVGSAMWAVLT VVVVFEFSVGATLSKGFNRGLATFLAGTLGFGAHLAILSGEKAEPILLGLFVFLAAMMTFVRFFPRMKAKYDYGVLVFLT FCLISVSGYRDDEVLEMAHKRVSTILLGGFAALLVCIVICPVWAGNDLHNLVANNIEQLASFLEGFGPEYFNTSEDVESNNTL LEGYKSVLHSHKQTEESLANFARWEPCHGQFRFGHPWKHYLKIGSLTRKCAYRIEALHGYNLTKNQTSQEIRSKIQDESIKVSS ESVKALKELAMAIETMITPSAATLHITKSIAAKNLKMLNADLCKETDLLEVIPAFTMASLLVDVVSCEKIAESVHELASL AKFKSVKPEVAARKPSLQKMQSYSSVNVVSQSHHVITVE
CoALMT2	ESIKALVGKMRTKVTEFPGKIKKLGQDDPRRIVHSLKVGLAITLVSLFYFDPLYVGFSSAMWAVLTVVVVFEFSVGATLGK GLNRGLATFLAGSLGFGAHLATLPGEKFQIPILLGFFVFLATTVSFIRFFPRMKARYDYGLVIFILTFCLISVSGYRDEEVLELA HKRVSTILIGGFTALFVCIFICPVWAGDDLHNLAANNIEKLANFLEEFGEYFKESGDRESNKAQLQGYKSVLNSKQNEESLV NFARWEPRHGRFRFRHPWKQYQKIGSLTRHCAYRVEALNGYLSNDVKASVETRKGKIKEACMKLSSESGLKALNELALAVRT MTQPPSECPHIAKSKNAANSLKSLLKTGLCKDIDLQEIVAVATVASLLLDVLSCTEKISESVHELASLARFKGVEDDQVADGE KKLNQKGEVNNKSCSNSIEQPNHHVITID
PdALMT2	QNNGGCFSRGCGWIKSLPERSKAKIVECARKIKKLGQDDPRRVNHSVKVGLAITLVSLFYFFEPLYDGFSDSAMWAVMTVV VVFEFSVGATLGRGLNRGLATFLAGALGFGAHLATLSGEKGEPMLLGLFVFLATTVTFTVRFFPRMKARYDYGLLIFILTFCL LISVSGYRDDEVLDMAHKRVSTILIGGLTAVLVCICICPVWAGDDLHNLAATNIEKLGIFLEHFGVEFFRKPGESESINKASLQ GYKSVLNSKNMEESLVNFARWEPGHGQFKFRHPWKHYLKFGSLTRQCAIRVEALNGYLSNDIKTPPEIQGMIQDSCTKMSS ELGKALKELALAIKRMTTPSSASSHLVKSNAAKNLKFLYSDLCSGINLLEVPAFTVTSLLEVISCTEKIAEAIHELASLAQ FENVEQERPKLPEQGEMQQGANMDVHHHVITID
CiALMT2	VSGWGRLKALPGRGLTKIVEAAMKIKKLGQDDPRRIIHSLKVGLAITLVSLIYYVESLYEGFGGSAMWAILTVIVVLEFSVGAT LGRGLNRGLATFIAGALGFGAHLASRSGDKVEPMLLGLFVFLIAGLVTFTIRFFPQMKARYDYGLLIFMLTFCLVVISGYRDED LLDVAHRRVSTILIGSFTSVFVCICICPVWAGDDLHNLVASNIENLGSFLQGFGIEYFKISGEFGESKTAVMQRYKTVLNSKQSE SLANFARWEPGHGQFRFSHPWKQYLKIGSLTRQCAIRIDALNGYLNSEIRTPPEFLSKIQATCTMMSMESGKALTELASVIKT

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	<p>MTPPSSAKPHIAKSENAAKGLKSLQAGLCKDIDLLEVLPAATVASLLVDVVSSTEKITESINELATLARYESIEHIIIVDEKEAA ESLHLQPIAPCSNTSGEHHVITID</p>
ArALMT2	<p>SHAEAGPFTRAHWLKAPEKLWSKFVSVATKAKKLGQDDPRRIVHSLKVGLAITLVSLFYFFELYDGLGVSAMWAVLTV VVVFEFSVGATLGRGVNRGLATLLAGALGFGAHLASFSGNICEPILLGLFVFLAAVVTYIRFFPRMKARYDYGLLIFILTFCL ISVSGYRDDEVLDMAQKRLSTILIGGATALFVCVFICPVWAGDDLHNLAANMEKLGSFLEGFGNEYFKTPSQGQSMEDKEI LQGYRSVLNSKTTEESLANFAKWEPRHGRFRYRHPWQQYLRLIGSLTRQCAIRIEALNGYLSSELKASQEIRAKIEDPCKKMSK DCSCALKELAQAVKTMTPKPSAANCHIANSKIAAKSLKSMKLTGLWQDLDLLEIVPAATVASLLIDIVSSTEEIAESVNELASL ANFRSVDNTEVAKGESKLSCSSSIKGPHHIITI</p>
ZjALMT2	<p>SGGRLGFRVKALFEKLKNWVVEIAMKTKKLGEDDPRRIVHSLKVGLAVSLVSLFYNFDFVYDGFSSAMWAVLTVVVVFE FSVGATLGRGLNRGLATFLAGALGFGAHLANLSGDKVQPILLTLFVFLAACVTFIRFFPRMKARYDYGLLIFILTFMISVS GYRDEEILEMAHKRVSTILIGGLTALSVCILICPVWAGDDLHNSVANNIEKLGNFLEGFGNVYFKKSEDGESNKAFLQGYKS VLNLKQSEESQVNFARWEPRHGRFGRHPWKHYLTVTGLTRQCAIRIDALNGYIQSEIQAPLEIGSEMEEACMKMSSES GKALKELAAATMRTMTLPCSGGGAAPHIAKSRLAAKSLKSLKLTGLMLEDNSTDLLNLVPAATVASLLVDVVCCTEKIDKAIE ELASLAKFKSSEPTMEDHKPKLNRQMAFLQQRSTSFGPHHVVTI</p>
MnALMT2	<p>LKNLAENVRAKVSQVANNVKKLGKDDPRRIHSLKVGVSLVSLVSIFFYYYQPLYDNFGVSAMWAVMTVVVVFEYTVGATLGK GLNRGLATLLAGALGVGAHHLASLSGDIGEPILLGFFVFLQAATSTFIRFFPKVKARYDYGLLIFILTFSLISVSGFRDDEILEMA HKRLSTILIGGSACVVISILVCPVWAGEDLHNLIALNLEKLGNFLEGFGDEYFNNTAMNEESKDDKAYLQGYKSVLNSKSSEE SLANFARWEPGHGRFKFRHPWKQYLKVGTGLTRQCAIRIEALHGRSLADKIQTSPEIREQIQEACMKVSSSESGKALKELATSV KKMTKPSSANPHLASSKVAAKSLRSLKSGSWDNIDLLEVIPSVTVASILLDVVNCTEKIAESVNELASLAHFK</p>
HsALMT2	<p>KIRRKVAEFPEKIKKVAQDDPRRVVHSFKFGLAITLVSLFYFFDPLYVGFNSAMWAILTVVVVFEFSVGATLVKGLNRGLATF LAGALGFGVHHLATLPGDIVRPILLGIFVFILATTVSFIRFFPRMKARYDYGLLIFILTFCLISVSGYRDEEVLQMAHKRVSTILIG ALAALLVCIFICPVWAGDDLHNLAANNLENLATFLQGFGDEYFTKSSEMESNKASLQGYKSILNSKQVEESWVNSARWEPR HGRFKFRHPWKQYLMVASLTRQCAIRVEALNGCLSDVQASPETCGKFQETCTEISSESGKAMKELASAIKTMSAPSSHRA HIAKAKDATEKLNLSLLKTRLCEDIDVVEILAVATVASLLHDVLACTEKISESVHELATLAHFKNEKDGGKQELDKQKQVQKTS NSIDLNHVITVE</p>
GhALMT2	<p>GGSSNSWLALVDSIVKIRSKVAEFPGMKMKVAEDDPRRIVHSFKVGLAITLVSLFYFFDHLYVGFSSAMWAVLTVIVVIEFSV GATLGKGLNRGLATFLAGTLGFGAHLANLPGRELQPILLGIFVFILAATVSFIRFFPRMKVRYDYGLLIFMLTFCLISVSGYR</p>

	DEEVLEMAHKRVSTILIGGFTAIFVCIFICPVWAGEDLHNLAANNLEKLASFLEGFGDEYFRKSSEPESNKASLQAYKSILNSK QSEESLVNFARWEPHPGPFRRHPWKQYLKIGSLTRQCAYRIEALNGCLNSDVQASPETCRNFREAFIKASSETGKAVKGLAS AMRTMTLPTGDCPQTAKSKNAADNLKSLRLTGLCEGIDIVEILEVATVASLLLDILACTEKISESIHELASLAHFKRLEPDEKD GNPDLKQKQVWQSSNSIASNHHHHIITIE
MiALMT2	EKAGFCAGAWLLLKGLPEKLKHKVAELASKAIKLGKDDPRRVVHSLKVGLALNVVSLLYLRPLYNDFGVSATWAIMTVVF VFEYSVGATLGKGLNRGFATFIGGALSVGAHQIACLSGEKAEPIMLGLFVFLQAAASTFLRFFPKIKARYDYALLIFILTFSMIS VSGFRDDEIIDLARRRLTILIGGFVCVVICILICPVWAGQDLHNLIATNIDKLGNFLEGFGNEYFNKEGETEDDKSFLQQYKSV LTSKSTEESTNSAKWEPGHGQFQFRHPWNLYLKIGTLTRQCAYRIDALNGYLNAEIQTSEMRYKIEEVYREMSLESGLKALK ELALAIKTMSQPSAATKTHIENSKSAKSLNSLFSNIWGD TDLQA AVPVA AVASLLIDVVACTEKIAQSVYELASMANFKSI EVTLSPEKSQIRQQDNAKSLAKVDDCPYVCVTVN
SpALMT2	KIFANIVGIAKQFKKNAKDDPRRVHSLKVGLSLTLVSLFYFQPLYNGFGVSTMWAIMTVVVVFEFSVGATLGKGLNRGMA TLLAGALGVGAHYLASASGKVVEPILLGLFVFLQAFALTFIRFFPQVKARYDYGMLIFILTFCLVSISGFRVDEIVDLAHKRISTI LMGASVCVIVSIFVCPVWAGEDLHKLVAKNMEKIGNFLEGFGDEIFKSSEDITESKVAKPSLIEYKSVLNSKNTEETLANFAK WEPGHGQFKYRHPWKQYLKIGGLIRQCACRIDALNGYINSEIKAPEEIKEMIKETSMKMSIECGKALKELSKSMRKMNLPIS ADEHVTNAKNSAKKLNSLLKSRINNWEEMNLLQVIPLTTIASILRDIVTCVEEIGQGVNELASLANFK
SlALMT2	KIFANIVGIAKQFKKNAKDDPRRVHSLKVGLSLTLVSLFYFQPLYNGFGVSTMWAIMTVVVVFEFSVGATLGKGLNRGMA TLLAGALGVGAHYLASASGKVVEPILLGLFVFLQAFALTFIRFFPQVKARYDYGMLIFILTFCLVSISGFRVDEIVDMAHKRIST ILMGASVCIIVSIFVCPVWAGEDLHKLVAKNMEKIGNFLEGFGDEIFKSSEDITESKVAKPSLIEYKSVLNSKNTEETLANFAK WEPGHGQFKYRHPWKQYLKIGGLIRQCACRIDALNGYINSEIKAPEEIKEMIKETSMRMSIECGKALKELSKSMRKMNLPIS ADEHVTNAKNSAKKLNSLLKSRINNWEEMNLLQVIPLTTIASILRDIVTCVEEIGQGVNELASLANFK
CaALMT2	TNGLLWFKSLYEKLFAKIIGIAKQFKKIGKDDPRRVHSLKVGVALTTLVSLFYFQPLYNGFGVSTMWAIMTVVVVFEFSVGAT LGKGLNRGMATLLAGALGVGAHYLASASGKVVEPILLALFVFLQAFATTIRFFPQVKARYDYGMLIFILTFCLVSISGFRVDE IVDMAHKRLSTILIGASVCVVISIFVCPVWAGEDLHKLVAKNMEKLGKFLEGFGDEIFKSAEVEESKDAKKSLEIYKSVLNSKN AEETLANFARWEPGHGQFKYRHPWRQYLKIGGLIRQCACRIDALNGYINSEIKAPEEIKEKIKETSKEMSIECGKALKELSNS VRKMNLPISADEHITNAKKSANLNSLLKSGINNWEEMNLLQVIPLATIASILTIVICVDEIGQGVNELATLAHFKK
AtALMT2	MEKVREIVREGRRVGKEDPRRVVHAFKVGGLALALVSSFYYYQPLYDNFGVNMWAVMTVVVVFEFSVGATLGKGLNRAVA TLVAGGLGIGAHHLASLSGPTVEPILLAIFVFVLAALSTFVRFFPRVKARYDYGVILIFILTFALISVSGFREDEILDLAHKRLSTVI

	MGGVSCVLISIFVCPVWAGQDLHSLLASNFDTLSHFLQEFGEYFEATEDGDIKEVEKRRRNLERYSVLNSKSNEEALANF AKWEPRHGQFRFRHPWRQYLAVGALLRQSAYRIDALNSNINSDMQIPMDIKKKIEEPLRRMSSESCKSMKEVSISLKNMTIS SSFDIHVVNSQSACKTLSTLLKSGILNDVEPLQMISLMTTVSLLIDIVNLTEKISESVHELASAA
AtALMT7	MEKVREIVREGRRVAKEDPRRVVHSFKVGLVLALVSSFYFYQPLYDSFGVNAMWAVMTVVVVFEFSVGATLGKGLNRVAAT LFAGGLGIGAHHLASMSGPTGEPILLAVFVFVQAALSTFVRFFPRVKARYDYSLIFILTFALISVSGFREEQVVKLTHKRISTVII GGLSCVIISIFVCPVWAGQDLHSLIASNFEKLSFFLLGNSFHYVSSDLNSITLLRKIKSWRLADFGDKYCEVVENDGAKEVDKR KKDFDNYKSVLNSKSNEESLANFAKWEPPGHGQFRFRHPWKQYLAVGELIRQCAYRIHALNSYLNADNQVSVDIKKKLGEP LRRMSLESCKAMKEMSISLKKMTKPSSSDLHVQNAKSACKSLTNLLNSGILKEVEPELVSLLTAISLLIDIINLTEKILESHEL ATAAKFK
AtALMT8	AQEKKAGFFQRLQDFPSKLKDDVTKRVKNVQKFAKDDPRRIHSMKVGVALTLVSLLYYVRPLYISFGVTGMWAILTVVVVF EFTVGGTSLKGLNRGFATLIAGALGVGAVHLARFFGHQGEPIVLGILVFSLGAAATFSRFFPRIKQRYDYGALIFILTFSFVAISG YRTDEILIMAYQRLSTILIGGTICILVSIFICPVWAGEDLHKMIANNINKLAKYLEGFEGEYFQPEKISKETSSCVREYKSILTSKST EDSLANLARWEPGHGRFRLRHPWKKYKIAGLVRQCAVHLEILNGYVLSNDKAPQEFESKIQEPITTMREVGEALKAIKS IKTMRNDSACVNAHIDNSKKAIKNLKIALKSSYPETYKDLLEIIPGVTMASILIEVVNCVEKIYEAVEEFSGLAHFKETLDSKLS AEIGQHQLLHRGCVKPVLDGDNEKEDNSSCHVL
AtALMT1	MEKVREIVREGIRVGNEPRRIIHAFKVGLALVLVSSFYFYQPFPGFTDYFGINAMWAVMTVVVVFEFSVGATLGKGLNRGV ATLVAGGLGIGAHQLARLSGATVEPILLVMLVVFVQAALSTFVRFFPWVTKFDYGILIFILTFALISLSGFRDEEIMDLAESRLST VVIGGVSCILISIFVCPVWAGQDLHSLLASNFDTLSHFLQDFGEYFEAREKGDYKVVEKRRKNLERYKSVLDSKSDDEALAN YAEWEPHGHGQFRFRHPWKQYVAVGALLRQCAYRIDALNSYINSDFQIPVDIKKKLETPLRRMSSESGNSMKEMSISLKQMIK SSSDIHVSNSQAACKSLSTLLKSGILNDVEPLQMISLMTTVSMLIDIVNLTEKISESVHELASAAARFKNKMRPTVLYEKSDSGS IGRAMPIDSHEDHHVTV
TaALMT1	RKVGGAAAREPRRVAHSLKVGLALALVSVVYFVTPLFNGLGVSAIWAVLTVVVVMEYTVGATLSKGLNRLATLVAGCIAV GAHQLAELAERCGDQGEPIVLTVLVFFVASAATFLRFIPEIKAKYDYGVTIFILTFGLVAVSSYRVEELIQLAHQRFYTIAGVFI CLCTTVFLFPVWAGEDVHKLASGNLDKLAQFIEGMEFNCFGENSVANNFGGKDSPQMHKSVLNSKATEDSLCTFAKWEPR HGQFRFRHPWSQYQKLGTLCRQCASSMEALASYVITTSKTQCPAAANPELSCKVRKTCGEMSLHSSKVLRDLAMATRTMT VPSPVNITMATAVKAAESLRSELAENTALLQVMHVAVTATLLADLVDRVKEIAECVDVLARLAHFKNPEDTKN
AtALMT10	WLKDLVMKVIMERVAKFMRKAWRIGADDPKVVHCLKVGLALSLSIFYMRPLYDGVGGNAMWAIMTVVVVFESNVG

	<p>ATFCKCVNRVVATILAGSLGIAVHWVATQSGKAEVFIGCSVFLFAFAATYSRFVPSFKARFDYGAMIFILTFSLVSVGGYRVD  KLVELAQQRVSTIAIGTSICIIITVFFCPIWAGSQLHRLIERNLEKLADSLDGCVAEYFKENEVSTNRNEDENTNMKLQGFKCV  LNSKGTTEEAMPLIRFSGFSFSQANLARWEPAHGSFNFRHPWKLYVKIGAAMRRCAYCLENLSICINYETEAPDQVKNHFGE  ACMKLSSASSKILRELADMMKNTRKSSKMDFLVFDMNSAVQELQETLKNVPINETNKPEEVPSEEENKVDSEERTTSMLEHEV  LPVATLVSLLIENAAARIQTAVEAVDELANLADFEQDSKKKTGDNNTKQ</p>
AtALMT14	<p>DRVHERSMGMEEEGSTKNMKTQVLELPTKIKKILKNIWKVGKDDPRRVKHALKVGVSLLTLVSLLYLMEPLFKGIGNSAIWA  VMTVVVVLEFSAGATLCKGLNRGLGTLIAGSLAFFIEFVANDSGKIFRAIFIGA AVFIIGALITYLRFIPYIKKNYDYGMLIFLLTF  NLITVSSYRVDTVIKIAHERFYTIAMGVGICLLMSLLVFPWISGEDLHKSTVAKLQGLSYSIEACVNEYFEEEEKDEETSDLSED  TIYNGYKTVLDSKSADEALAMYASWEPRHTRHCHRFPPWKHYVKVGSVLRQFGYTVVALHGCLKTEIQTTPRPLRGLFKDPC  VRLAGEICKVLSELAASIRN</p>
AtALMT12	<p>MEEGLSKTKWMVLEPSEKIKKIPKRLWNVGKEDPRRVHIALKVGSLTLVSLLYLMEPLFKGIGSNAIWAVMTVVVVLEFSA  GATLCKGLNRGLGTLIAGSLAFFIEFVANDSGKVLRAIFIGTAVFIIGAAATYIRFIPYIKKNYDYGVVIFLLTFNLITVSSYRVDS  VINIAHDRFYTIAVGCICLMSLLVFPWISGEDLHKTTVGKLQGLSRSEACVDEYFEEKEKEKTDSDKDRIYEGYQAVLDSKS  TDETLALYANWEPRHTLRCHRFPCQQYVKVGAVLRQFGYTVVALHGCLQTEIQTTPRSVRALFKDPCVRLAGEVCKALTELA  DSI</p>
AtALMT13	<p>KGLNLPKKMKKILRNLWNVGKEDPRRVHIALKVGVALTLVSLLYLMEPFFEGVGKNALWAVMTVVVVLEFSAGATLRKGL  NRGLGTLIAGSLAFFIEWVAIHSGKILGGIFIGTSVFTIGSMITYMRFIPYIKKNYDYGMLVFLTFNLITVSSYRVDTVIKIAHER  LYTIGMGIGICLMSLLFFPIWISGDDLHKSTITKLQGLSRCIEACVSEYFEEKLKDNETSDSESDDDEDLIYNGYNTVLDSKSADE  ALAMYAKWEPRHTRRCNKFPSQQYIKVGSVLRKFGYTVVALHGCLQTEIQTTPRSIRVLFKDPCVRLAGEICKVLSELSESIQN</p>
AtALMT9	<p>LSEKISGVYDDAKDVARKAWEMGVSDPRKIVFSAKIGLALTIVALLIFYQEPNPDLRSYSVWAILTVVVVFEFTIGATLSKGFN  RALGTLASAGGLALGMAELSTLFGDWEEIFCTLSIFCIGFLATFMKLYPSMKAYEYGFRVFLTYCYILISGFRTGQFIEVAISRFL  IALGAGVSLGVNMFYPIWAGEDLHNLVKNFMNVATSLEGCVNGYLRCLEYERIPSKILTYQASEDPVYKGYRSVESTSQE  ESLMSFAIWEPPHGPYKSNYPWKNYVKLSGALKHCAFTVMALHGCILSEIQAPEERRQVFRQELQRVGVEGAKLLRELGE  KVKKM</p>
AtALMT3	<p>KITGVVKKLKDVLVTAWEMGTADPRKMIFS AKMGLALTLSILIFFKIPGLELSGHYLWAILTVVVIFEFISIGATFSKGCNRLG  TASAGGLALGMSWISEMTGNWADVFNAA SIFVVAFFATYAKLYPTMKPYEYGFRVFLTYCYVIVSGYKTGEFME TAVSRFL  IALGASVGLIVNTCIYPIWAGEDLHNLVAKNFVNVATSLEGCVNGYLECVAYDTIPSRILVYEAVAEDPVYSGYRS AVQSTSQE</p>

	DTLMSFASWEPPHGPYKSFYRPWALYVKVGGALRHCAIMVMALHGCILSEIQAAEDRRREFRNELQRVGIEGAKVLR YIGES LKKM
AtALMT6	ELGHSDRRRIFFAVKMGMALALCSVVIFLKEPLHDASKYSVWGILTVVVVFEYSVGATLVKGFNRAIGTVSAGGLALGIARLS VLSRDFEQTHIITCIFLAGFIASYSKLHPAMKPYEYAFRVLLTFCIVLVSGNNTGDDFFSTAYYRFLFIVVGATTCLVVNIFIFIWA GEDLHKLVANNFKSVANSLEGCVNGYLQCVEYERVP SKILTYQTSDDPLYSGYRSAIQSTNQEESLLDFAIWEPPHGPYRTFN HPWK NYVKLSGAVRHCAFTVMAIHGCILSEIQAAPEKRQAFRHELQRVGN EGAKVLR LIGEKVEKM
AtALMT4	SDGITASWKALYDIGAKLYEMGRSDRRKVYFSVKMGMALALCSFVIYLKEPLRDASKYAVWAILTVVVVFEYSIGATLVKGFN RAIGTLSAGGLALGIARLSVSAGEFEELIIISIFIAGFSASYLKLYPAMKSYEYAFRVLLTYCIVLVSGNNSRDFFSTAYYRFL LIL VGAGICLGVNIFILPIWAGEDLHKL VVKNFKSVANSLEGCVNGYLQCVEYERIPSKILTYQASDDPLYSGYRSVVQSTS QEDSL LDFAVWEPPHGPYKTFHHPWANYVKLSGAVRHCAFMVMAMHGCILSEIQAAPEKRQAFRQELQRVGN EGAKVLR LFG EK VEKM
AtALMT5	KLYALGHSDRRKLYFSIKMGIALALCSFVIFLKEPLQDASKFAVWAILTVVLIFEYYVGATLVKGFNRALGTMLAGGLALGVA QLSVLAGEFEEV IIVICIFLAGFGASYLKLYASMKPYEYAFRVFKLTYCIVLVSGNNSRD FLSTAYYRILLIGLGATICLLVNVFLFP IWAGEDLHKLVAKNFKNVANSLEGCVNGYLQCVEYERIPSKILTYQASDDPLYSGYRS AVQSTS QEDSLLDFAIWEPPHGPYK TFNHPWK NYVKLSGAVRHCAFTVMAMHGCILSEIQASPEKRHVFSNELRRVGN EGAKVLR LFG EK VEKM
AtALMT11	LSKTKWMVLEPSEKIKKIPKRLWSVGKEDPRRVIHAFKVGHSLTLVSLLYFMENLFGKIGSN AIWAVMTV VAVLLEF