

L27N

<i>Dmvari</i>	-----MVRWSARSRRQARQDKVELLARNNKVNGEDDTS	DNAAF	RNSTD-----	LS	DH	DE	IF	LK	G	L	L	R	S	N	S	N	T	P	H	K	E	L	M	N	P	T	E	P	Q	P	V	L	F	L	F	A	H	L	N	N	K	P	89																																																								
<i>AmMAGUK</i>	MKNSKSLMDIEDICGCSKLP	S	I	P	R	K	E	L	P	H	R	S	T	S	V	S	L	P	L	A	H	D	E	V	T	R	C	V	M	E	K	C	L	V	T	V	P	A	A	F	M	H	V	R	D	N	L	E	E	L	G	K	V	A	D	D	T	D	L	L	F	L	K	G	L	L	D	S	P	V	V	T	S	L	V	K	V	Q	E	R	L	E	D	P	P	--	L	H	V	E	P	V	C	S	S	V	C	D	118
<i>XtNP_001017060</i>	-----	MQQ	V	L	D	N	L	T	D	L	P	--	T	S	T	G	A	E	E	I	I	I	F	L	K	G	L	M	E	D	P	I	V	R	S	L	A	K	A	H	E	R	L	E	D	T	K	L	E	A	V	S	E	N	N	V	E	L	L	N	D	62																																					
<i>MmMAGUK6</i>	-----	MQQ	V	L	E	N	L	T	E	L	P	--	S	S	T	G	A	E	E	I	D	I	I	F	L	K	G	I	M	E	N	P	I	V	K	S	L	A	K	A	H	E	R	L	E	D	S	K	L	E	A	V	S	D	N	N	L	E	L	V	N	E	62																																				
<i>MmMAGUK2</i>	-----	MPV	A	A	T	N	S	E	S	A	M	Q	V	L	D	N	L	G	S	L	P	--	N	A	T	G	A	A	E	L	D	I	F	L	R	G	I	M	E	S	P	I	V	R	S	L	A	K	A	H	E	R	L	E	D	T	K	L	E	A	V	R	D	N	N	L	E	L	V	Q	E	73																											
<i>XtNP_001096176</i>	-----	MPV	A	L	P	S	H	N	S	D	P	A	M	Q	R	V	L	H	G	L	S	D	L	P	----	A	S	S	D	L	D	L	I	F	L	Q	G	I	M	E	S	P	----	K	A	H	E	C	M	E	E	I	R	L	E	A	V	R	E	N	N	L	Q	L	V	Q	E	66																															
<i>DrLOC431770</i>	-----	MPV	A	S	A	S	S	D	S	A	M	Q	S	L	L	D	T	L	S	D	S	T	--	S	S	T	A	N	D	L	D	L	I	F	L	K	G	I	M	E	S	P	----	V	S	R	E	H	Y	E	E	P	K	L	E	A	V	R	D	N	N	L	V	Q	D	67																																	

L27C

Dmvari	I	C	D	D	I	R	K	F	S	P	S	R	R	L	E	S	R	E	L	A	K	L	L	A	Q	P	H	F	R	A	L	L	R	A	H	D	E	I	G	A	L	Y	E	Q	R	L	K	A	A	G	G	S	T	S	Q	L	E	I	A	S	Q	R	Q	T	G	G	Y	L	F	T	E	D	V	L	N	T	K	M	P	V	E	T	I	K	M	V	G	L	R	R	D	P	S	K	P	L	G	L	T	V	E	L	D	E	F	K	Q	L	V	V	A	R	I	L	A	G	G	V	I	209
AmMAGUK	I	V	D	E	V	C	H	A	L	R	S	S	R	D	E	N	A	R	E	L	V	R	L	L	R	N	S	H	L	K	A	L	L	E	T	H	D	A	V	E	R	K	E	A	P	P	S	K	-----	P	E	P	S	L	L	A	M	P	T	N	R	M	E	A	V	R	V	V	G	L	R	R	Q	P	D	E	P	L	G	L	T	V	Q	V	N	E	S	G	N	L	I	A	R	I	L	G	G	S	T	A	220																			
XtNP_001017060	I	I	K	D	I	S	P	L	E	H	E	D	--	N	V	Q	E	L	I	G	I	L	K	E	P	H	F	Q	S	L	L	E	A	H	D	V	V	A	S	K	C	Y	D	S	P	P	S	-----	P	E	V	N	S	L	G	N	H	Q	I	A	P	V	D	A	I	R	M	V	G	I	H	K	R	A	G	E	P	L	G	V	T	F	K	V	E	N	--	N	N	L	V	I	A	R	I	L	H	G	G	M	I	162																		
MmMAGUK6	I	L	E	D	I	T	P	L	I	S	V	D	--	N	V	A	E	L	V	G	I	L	K	E	P	H	F	Q	S	L	L	E	A	H	D	I	V	A	S	K	C	Y	D	S	P	P	S	-----	P	E	M	N	I	P	S	L	N	N	Q	L	P	V	D	A	I	R	I	L	G	I	H	K	K	A	G	E	P	L	G	V	T	F	R	V	E	N	--	N	D	L	V	I	A	R	I	L	H	G	G	M	I	162																		
MmMAGUK2	I	L	R	D	L	A	E	L	A	E	Q	S	--	T	A	A	E	L	A	R	I	L	K	E	P	H	F	Q	S	L	L	E	T	H	D	S	V	A	S	K	T	Y	E	T	P	P	S	-----	P	G	L	D	P	T	F	S	N	Q	P	V	P	D	A	V	R	M	V	G	I	R	K	T	A	G	E	H	L	G	V	T	F	R	V	E	G	--	G	E	L	V	I	A	R	I	L	H	G	G	M	V	173																			
XtNP_001096176	I	L	Q	D	M	A	G	V	R	D	P	S	G	--	V	A	A	E	L	Q	G	I	L	K	E	P	H	F	Q	S	L	L	Q	T	H	D	S	V	A	S	K	N	Y	E	T	P	P	S	-----	P	M	L	D	P	T	L	S	N	Q	P	V	P	D	A	V	R	M	V	G	I	R	K	S	A	G	E	H	L	G	V	T	F	R	V	E	G	--	G	E	L	V	I	A	R	I	L	H	G	G	M	V	166																		
DrLOC431770	I	L	R	D	E	N	T	L	S	P	D	S	P	--	A	A	H	E	L	I	C	I	L	K	E	P	H	F	Q	S	L	L	E	T	H	D	S	V	A	S	K	S	Y	E	T	P	P	S	-----	A	F	M	D	P	A	F	N	N	Q	P	V	P	D	A	V	R	M	V	G	I	R	K	V	S	G	E	H	L	G	V	T	F	R	V	E	G	--	G	E	L	V	I	A	R	I	L	H	G	G	M	I	169																		

PDZ

Dmvari	DKQSM LHVGDVILEVNVFPVRT-PDE LQVEVSRAKENLTLKIGPNVDEEIKSGRYTVSGGQVKQNGIASLETGKKLT	CYMRALFTYNPSEDSLPCRDIGLPFKSGDILLQIINVKDPNWW	328
AmMAGUK	ARQGLLR TGEVILEVNGKEVHN-PEELQEA IHEAKENLSLKLAPGIEKNTYFP-----	LQCYMRALFDYDPSEDTLLPCR EIGLPFKQGDVLQIVDQADPNWW	317
XtNP_001017060	DRQGLLVGTDIKEIENGHEVGNPKELQLLELLKSISSGVTLLKILPSYKDVTSPQ-----	QVYVKCHFDPNPSDNLIPCKEAGLKFSKGEILHIVNREDPNWW	259
MmMAGUK6	DRQGLLVHVDIIKEVNGHEVGNPKELQELLKNISGSVTLLKILPSYRDTITPQ-----	QVFKCHFDPNPFNDNLIPCKEAGLKFSKGEILQIVNREDPNWW	259
MmMAGUK2	AQQGLLVHVDIIKEVNGQPVGSDPRALQELLRSAGSVTLKILPSYQEPHLPR-----	QVFKCHFDPYDPARDSLSPCKEAGLRFNAGDLLQIVNQDDANWW	270
XtNP_001096176	DQQGLLVHGDVIREVNGREVGSDPQALQEM LREASGSVVLKILPSYQEQHPLR-----	QVFKCHFSDYDPSSDSLIPCKEAGLPFKAGDILLQIVNQEDPNWW	263
DrLOC431770	DQQGLLVHVDIIKEVNGKEVGSDPKVLQNMLKSSGSVTLKILPSYQEPHTPR-----	QAFVKCHFDPYDPSHDNLIPCKEAGLKFSGSDILLQIFNQEDPNWW	266

SH3

Dmvari	QAKNITAESD-KIGLIPSQELEERRKAFVAPEADYVH-KIGICGTRISKRRKRTMYRSVANCEFDKAELLLYEEVTRMPPFRRKTLVLIGVSGVGRRTLKNRLINSVDVKFGAVIPHTSR	446
AmMAGUK	QARRVEGEGGLPGPLIPSLLEERRKAFVPEADYVH-KISICGTKISKKKKKMYQSKSNGEFDASAELLYEEVARMPPFRKTLALVIGARGVGRRTLKNRLINSDPEKFGTIVPPTS	436
XtNP_001017060	QAS--HVKEGGSAGLIPSLQLEEKRAKFVRRDWDG---SQGFCGTISKKKKKMYLTTRNAEFDREHIIQIYEEVARMPPFRKTLVLIGAQGVGRSLKNRLIVLNPQTQFGTIVPPTS	374
MmMAGUK6	QAS--HVKEGGSAGLIPSQFLEEKRKAFVRRDWN---SGPFCGTISNKKKKMMYLTTRNAEFDREHIIQIYEEVAKMPPFQKRTLVLIGAQGVGRSLKNRIFVLNPARFGTIVPPTS	374
MmMAGUK2	QAC--HVE-GGSAGLIPSQLLEEKRAKFVKRDLELTPTSGTLCGSLSGKKKKMMYLTTKNAEFDREHELLIYEEVARMPPFRKTLVLIGAQGVGRSLKNKLILWDPDRYGTIVPPTS	387
XtNP_001096176	QAC--LVK-GGTAGLIPSQLLEEKRAKFVRKDEFTPNSSALCSIGGKKKKRMYVTTKNAEFDREHELLIYEEVARMPPFRKTLILIGAQGVGRSLKNKLLTSPSRYGTTIPYTS	380
DrlOC431770	QAC--HLE-GGSAGLIPSQLLEEKRAKFVKRDLBLASTG-PLCAGIGGKKKKMMYLTTKNAEFDREHELLIYEEVAKVPPFRKTLVLIGAQGVGRSLKNKLILVSDPHRYGTTIPYTS	382