

K155 (At)

	10	20	30	40	50	60	70	80	90	100	110	120	130	140	150																												
CtrNT1	MTQTA	EKPFGLRSL	WPK	IHMHE	ELKKV	LPMFLMF	FCISFN	YTLRDT	KDTLIVT	APGSGA	EAIPI	FKLWLV	VP	SAVV	FMLIYAK	LSNINLNKQAL	FAVLS	PVVVF	FALF	FPV																							
CtrNT2	MSSSEV	KFSKFRGYF	FP	IYRS	EFSKF	IPLFFLA	FFVGVN	YALLKTT	KDSLVLV	GSRAGA	EIVPI	FLKVVGI	VP	GAVI	VTMIYGM	SRYSRGT	VFISL	VGGF	LGF	FALF	FATV																						
PamNT1	MSQDA	KQDFGKWR	AFP	WHY	ELKKV	LPMFMM	FFISFN	YTLRDT	KDTLIVT	SAGA	EAIPI	FLKSVGI	VP	AAIL	FMIYAK	LSNTLSREN	EYVTL	LP	FIF	FFGL	FVFM																						
PamNT2	SQQA	SFGKLR	AFP	IHG	EYKKV	LPMLML	FLICFN	YTLRNV	KDAIVVT	AKASGA	EIVPI	FLKVVWL	LP	AVLFT	LIFTK	LSNRFSQEK	EVYI	VI	ST	FLL	FFGS	FSTYIF																					
PamNT3	MSQTP	TGSRE	SPWR	SNL	WHY	ELKKV	IPMLLI	FFISFD	YTLRDK	LSLIT	AKSSGA	EIVPI	FVKVWAM	FP	GAILMT	LFTWLS	NSR	LSRE	IV	EY	FLIT	SLF	SFY	FFIFT	FIL																		
PamNT4	MSKTN	NEFGK	VRSIL	WPK	IQA	E	WYAV	FLSFI	YFCV	LAAYV	IRPIR	DQMAVE	VP	ST	ELVP	---	---	---	---	---	---	---	---	---	---																		
PamNT5	MKNQ	NSV	SSTL	WPK	L	ILK	KL	SL	IL	LFQ	FLI	I	VY	HT	LK	D	K	D	T	IV	IT	AS	D	A	G	A	E	I	P														
SnegNT1	MSQ	SQ	NE	FGK	VRSIL	WPK	IHG	F	EL	KKL	VP	MVLL	FL	IL	FN	Y	T	LR	D	T	LV	IT	AP	G	G	A	E	I	P														
SnegNT2	MST	QT	DV	S	K	WR	SFL	WPK	IQR	E	IK	KF	LP	LL	LI	Y	AL	CL	NY	S	L	K	V	A	K	D	T	LV	IT	AP	G	G	A	E	I	P							
SnegNT3	MS	ST	E	Y	K	ST	WTQ	WPK	IRR	F	EL	KKV	LP	LL	LI	L	K	FL	V	S	M	Y	AT	L	K	T	LV	IT	AP	G	G	A	E	I	P								
SnegNT4	ML	R	K	K	F	A	S	L	K	S	E	L	LS	Y	S	A	V	E	R	L	I	V	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
RickNT1	MT	I	N	P	S	N	I	E	N	S	S	K	I	N	S	F	S	K	L	T	D	Y	I	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
RickNT2	MNT	P	K	---	ND	N	L	S	E	L	S	K	V	I	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
RickNT3	MDS	V	D	S	N	C	T	I	W	N	K	A	R	N	S	K	F	R	D	I	V	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
RickNT4	ML	P	P	K	---	I	F	F	E	K	V	K	E	I	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
CcarNT1	MEN	S	Q	---	K	S	F	T	A	E	L	R	R	V	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
LasNT1	MA	H	N	Q	---	K	I	L	S	V	L	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
LintNT1	MS	D	K	G	K	T	G	S	M	P	E	E	D	T	G	W	R	A	I	L	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
EcumNT2	MSE	I	G	S	V	P	V	N	E	N	R	P	L	L	T	E	D	E	V	E	A	Q	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
EcumNT3	MST	F	L	S	A	S	S	K	S	Y	L	R	T	E	E	E	E	E	V	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
EcumNT4	MNE	V	E	N	N	H	S	F	P	R	E	D	I	P	T	E	D	E	I	E	E	A	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
ThomNT1	MSE	N	R	E	I	D	A	T	D	R	R	D	K	T	F	O	K	E	K	L	R	P	H	V	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
ThomNT2	MK	R	I	H	M	A	K	P	G	T	F	D	S	F	S	I	K	K	Y	L	N	R	E	L	R	D	M	R	E	E	A	S	E	G	A	S	L	N	S	I	S		
ThomNT3	MN	V	R	D	S	E	A	N	N	P	L	S	A	E	E	I	E	Q	I	A	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
ThomNT4	MP	N	Q	N	D	L	A	H	E	I	R	T	L	T	E	N	E	V	E	Q	A	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		



E245 (At)

	160	170	180	190	200	210	220	230	240	250	260	270	280	290	300	310	
CtrNT1	YPCRH	IHLH	PTAF	ADTLQ	SILP	SGFM	GF	---	---	---	---	---	---	---	---	---	
CtrNT2	YPI	GDA	LH	L	N	K	L	A	A	K	L	Q	S	I	L	P	P
PamNT1	YPAR	E	V	L	M	P	H	A	S	A	E	A	L	K	A	Y	L
PamNT2	YPL	R	D	V	L	H	P	H	O	L	C	D	Y	L	E	T	I
PamNT3	YPI	R	D	I	H	P	H	A	T	A	D	Y	L	E	T	I	L
PamNT4	FLN	K	N	L	L	S	P	---	---	---	---	---	---	---	---	---	
PamNT5	YPR	F	R	K	F	F	Y	L	E	N	V	A	D	Y	L	H	
SnegNT1	YPAR	D	Y	L	H	P	N	A	L	C	D	T	L	Q	N	T	
SnegNT2	YPL	R	D	F	L	H	P	H	D	T	A	D	K	L	Q	A	
SnegNT3	YPM	G	I	L	T	P	S	D	S	A	N	L	L	T	A	K	
SnegNT4	GK	I	P	---	---	---	---	---	---	---	---	---	---	---	---		
RickNT1	YPN	I	H	I	F	H	V	P	D	N	L	A	D	W	M		
RickNT2	FPN	H	E	M	L	H	F	S	P	A	T	V	Q	N	L		
RickNT3	YYP	P	D	L	V	H	P	D	E	T	I	E	S	W	S		
RickNT4	FPY	R	D	F	H	P	D	P	E	L	I	K	H	I	T		
RickNT5	YPN	Q	I	Y	H	P	N	D	E	M	I	N	K	L	I		
CcarNT1	YYP	P	F	F	H	P	N	H	Q	T	I	E	G	L	Y		
LasNT1	YYP	R	D	F	L	H	P	S	P	E	I	R	A	L	A		
LintNT1	YPL	T	E	Y	H	M	S	Y	E	T	I	S	H	L	Q		
EcumNT2	YPL	F	A	E	K	I	Q	P	G	L	Y	F	S	R	D		
EcumNT3	W	L	K	G	I	Q	K	D	F	Y	S	R	D	I	F		
EcumNT4	W	P	Y	C	K	R	L	O	P	D	F	F	S	R	D		
ThomNT1	I	Y	F	K	R	L	D	N	E	F	L	V	A	D	I		
ThomNT2	L	P	L	R	E	I	E	P	S	K	F	I	T	I	D		
ThomNT3	L	P	L	Q	D	T	I	E	S	S	N	F	I	N	A		
ThomNT4	L	H	E	V	A	S	E	V	G	T	M	L	S	L			



E 385 (At)

Multiple sequence alignment of E 385 (At) protein across various species including CtrNTT1, PamNTT1, and ThomNTT1. The alignment shows conserved regions with a green highlight at the E 385 site. Residue numbers 320-460 are indicated above the alignment.

K527 (At)

Multiple sequence alignment of K527 (At) protein across various species including CtrNTT1, PamNTT1, and ThomNTT1. The alignment shows conserved regions with a green highlight at the K527 site. Residue numbers 470-620 are indicated above the alignment.

ThomNTT1
CtrNTT1
RickNTT3