

Additional file 3. Multiple sequence alignment of cotton aquaporins. Deduced amino acid sequences were aligned using the CLUSTALW 2.01 program. NPA motifs, bold black (italic in NPA denotes for non-conserved residues); ar/R filters (H2, H5, LE1, and LE2) are highlighted in yellow; Froger's 5 positions (P1 – P5) are also marked bold above alignment. Gene names with bold letters represent partial sequences.

PIP subfamily

PIP1_1	MEGKEEDVRLGANKFTE	RQPIGTAAQSQDDG	KDYTEPPAPFFEP	GELTSSWSFYRAGIAE	60	
PIP1_2	MEGKEEDVKLGANKFSE	RQPIGTSAQTD---	KDYKEPPAPFFEP	GELKSSWSFYRAGIAE	57	
PIP1_3	MEGKEEDVKLGANKFSE	RQPIGTSAQTD---	KDYKEPPAPLFE	GELKSSWSFYRAGIAE	57	
PIP1_4	MEGKEEDVKLGANKFSE	RQPIGTSAQTD---	KDYKEPPAPLFE	GELKSSWSFYRAGIAE	57	
PIP1_5	MEGKEEDVKLGANKFSE	RQPIGTSAQTD---	KDYKEPPAPFFEP	GELKSSWSFYRAGIAE	57	
PIP1_6	MEGQGEDVRLGANKYRE	RQPIGTAAQTQDT-	KDYKEPPAPLFE	PAELSSWSFYRAGIAE	59	
PIP1_7	MEGKEEDVRLGANKFSE	RQPIGTAAQSQDD-	KDYTEPPAPLFE	PSELTSSWSFYRAGIAE	59	
PIP1_8	MEGREEDVRLGANRFSE	RQPIGTAAQSQDEG	KDYTEPPAPFFEL	RELCSWSFYRAGIAE	60	
PIP1_9	MEDREEDVRLGANRFSE	RQPIGTAAQSQDEG	KDYTEPPAPFFEP	GELSSWSFYRAGIAE	60	
PIP1_10	-----					
PIP1_11	MEGKEEDVRLGANKFTE	RQPIGTAAQTQDDG	KDYSEPPAPFFEP	GELTSSWSFYRAGIAE	60	
PIP1_12	MEGKEEDVKLGANKFSE	RQPIGTSAQTD---	KDYKEPPAPLFE	GELKSSWSFYRAGIAE	57	
PIP1_13	MEGKEEDVKLGANKFSE	RQPIGTSAQTD---	KDYKEPPAPLFE	GELKSSWSFYRAGIAE	57	
PIP1_14	MEGKEEDVRLGANKFTE	RQPIGTAAQSQDDG	KDYTEPPAPFFEP	GELTSSWSFYRAGIAE	60	
PIP1_15	MEGKEEDVKLGANKFSE	RQPIGTSAQTD---	KDYKEPPAPLFE	GELKSSWSFYRAGIAE	57	
PIP2_1	---MAKDVEV-----	---GGEFQA---KDY	HDPPPAPLVD	AQELTQWSFYRAIAE	42	
PIP2_2	---MAKDIEV-----	---GGEFQA---KDY	HDPPPAPLVD	AQELAKWSFYRAVIAE	42	
PIP2_3	---MAKDVEV-----	---GGEFQA---KDY	HDPPPAPLVD	GEEELTKWSFYRAVIAE	42	
PIP2_4	---MSKEVSE-----	---EGQGR---KDY	VDDPPAPLID	MAELKSSWSFYRA---	37	
PIP2_5	---MSKEVSE-----	---EGMSR---KDY	VDDPPAPLID	VAEIKLWSFYRALIAE	41	
PIP2_6	---MSKEVSE-----	---EGVSR---KDY	VDDPPAPLID	VAEIKLWSFYRALIAE	41	
PIP2_7	---MSKEVSE-----	---EGMSR---KDY	VDDPPAPLID	VAEIKLWSFYRALIAE	41	
PIP2_8	---MENS	RDGKV-----QQLHG---KDY	VDDPPARLLD	MEELKTWSFYRALLAE	43	
PIP2_9	---MSKEVSE-----	---EGQGR---KDY	VDDPPAPLID	MAELKSSWSFYRALIAE	41	
PIP2_10	---MTKD	DIETTA-----EQGGGA	EFSA---KDY	QDPPAPLIDLEELTKWSLYRAAIAE	48	
PIP2_11	---MAKDIEV-----	---GGEFQA---KDY	HDPPPAPLVD	AQELAKWSFYRAVIAE	42	
PIP2_12	---MSKEVSE-----	---EGQGR---KDY	VDDPPAPLID	MAELKSSWSFYRALIAE	41	
PIP2_13	---MAKDVEV-----	---GGEFQA---KDY	HDPPPAPLVD	GEEELTKWSFYRAVIAE	42	
			H2			
PIP1_1	FVATFLFLYITILTVMGV	VKEKT-----KCPT	VGIQGI	AWAFGGMIFALVYCTAGIS	112	
PIP1_2	FVATFLFLYITVLTVMGV	SQSKT-----KCAT	VGIQGI	AWAFGGMIFALVYCTAGIS	109	
PIP1_3	FVATFLFLYITVLTVMGV	SQSKT-----KCTT	VGIQGI	AWAFGGMIFALVYCTAGIS	109	
PIP1_4	FVATFLFLYITVLTVMGV	SQSKT-----KCTT	VGIQGI	AWAFGGMIFALVYCTAGIS	109	
PIP1_5	FVATFLFLYITVLTVMGV	SQSKT-----KCAT	VGIQGI	AWAFGGMIFALVYCTAGIS	109	
PIP1_6	FVATFLFLYITVLTVMGV	AKSST-----KCST	VGIQGI	AWAFGGMIFALVYCTAGIS	111	
PIP1_7	FVATFLFLYISVLTVMGV	LKDKT-----KCTT	VGIQGI	AWAFGGMIFALVYCTAGIS	111	
PIP1_8	FMATFLFLYITILTVMGV	KENT-----KCRT	VGIQGI	AWAFGGMIFALVYCTAGIS	112	
PIP1_9	FMATFLFLYITILTVMGV	VKEKT-----KCPT	VGIQGI	AWAFGGMIFALVYCTAGIS	112	
PIP1_10	-----				MIFILVYCTAGIS	13
PIP1_11	FVATFLFLYITILTVMGV	VKEKT-----KCPT	VGIQGI	AWAFGGMIFALVYCTAGIS	112	
PIP1_12	FVATFLFLYITVLTVMGV	SQSKT-----KCTT	VGIQGI	AWAFGGMIFALVYCTAGIS	109	
PIP1_13	FVATFLFLYITVLTVMGV	SQSKT-----KCTT	VGIQGI	AWAFGGMIFALVYCTAGIS	109	
PIP1_14	FVATFLFLYITILTVMGV	VKEKT-----KCPT	VGIQGI	AWAFGGMIFALVYCTAGIS	112	
PIP1_15	FVATFLFLYITVLTVMGV	SQSKT-----KCTT	VGIQGI	AWAFGGMIFALVYCTAGIS	109	
PIP2_1	FIAALLFLYITVLT	VIGYKSQVDPDKG--GQDC	DGVGILGIAWAF	GGMIFILVYCTAGIS	100	
PIP2_2	FIAALLFLYITVLT	VIGYKTQTPAKG--GEDC	GGVILGIAWAF	GGMIFILVYCTAGIS	100	
PIP2_3	FIAALLFLYITVLT	VIGYKSQVDPDKG--SDEC	GGVILGIAWAF	GGMIFILVYCTAGIS	100	
PIP2_4	---LLFLY	VTVATVIGHKKQD-----ACD	GVLLGIAWAF	GGMIFILVYCTAGIS	85	
PIP2_5	FIAALLFLYVTIAT	VIGHKKQHD-----ACD	GVLLGIAWAF	GGMIFILVYCTAGIS	93	
PIP2_6	FIAALLFLYVTIAT	VIGHKKQHD-----ACD	GVLLGIAWAF	GGMIFILVYCTAGIS	93	
PIP2_7	FIAALLFLYVTIAT	VIGHKKQHD-----ACD	GVLLGIAWAF	GGMIFILVYCTAGIS	93	
PIP2_8	FVATLLFLYILVAT	VIGHKKQTG-----LCD	GVPLGIAWAF	GGMIFVLVYCTAGIS	95	
PIP2_9	FIAALLFLYVTVAT	VIGHKKQD-----ACD	GVLLGIAWAF	GGMIFILVYCTAGIS	93	
PIP2_10	FIAALLFLYVTVLT	VIGYKVQTPVKNTVDP	DCGGVILGIAWAF	GGMIFILVYCTAGIS	108	
PIP2_11	FIAALLFLYITVLT	VIGYKTQTDLAKG--GEDC	GGVILGIAWAF	GGMIFILVYCTAGIS	100	
PIP2_12	FIAALLFLYVTVAT	VIGHKKQD-----ACD	GVLLGIAWAF	GGMIFILVYCTAGIS	93	
PIP2_13	FIAALLFLYITVLT	VIGYKSQVDPDKG--SDEC	GGVILGIAWAF	GGMIFILVYCTAGIS	100	

P1

PIP1_1 GGHINPAVTFGLFLARKLSLTRAIFYMVMQCLGAICGAGVVKGF~~FG~~KTQYGMLGGGANSV 172
 PIP1_2 GGHINPAVTFGLFLARKLSLTRAIFYMIMQCLGAICGAGVVKGF~~CG~~DNRYEMLGGGANVV 169
 PIP1_3 GGHINPAVTFGLLLARKLSLTRAIFYMIMQCLGAICGAGVVKGF~~FG~~GDSRYEMLGGGANVV 169
 PIP1_4 GGHINPAVTFGLLLARKLSLTRAIFYMIMQCLGAICGAGVVKGF~~FG~~GDSRYEMLGGGANVV 169
 PIP1_5 GGHINPAVTFGLFLARKLSLTRAIFYMIMQCLGAICGAGVVKGF~~CG~~DNRYEMLGGGANVV 169
 PIP1_6 GGHINPAVTFGLFLARKLSLIRAVFYMIMQCLGAICGA~~AVVKSFC~~-KTQYERLGGGANTV 170
 PIP1_7 GGHINPAVTFGLFLGRKLSLTRAIFYMVMQCLGAICGAGVVKGF~~FG~~MKTRYGALGGGANSV 171
 PIP1_8 GGHINPAVTFGLFLARKLSLIRAVFYMAMQCLGAICGAGVVKGF~~FG~~MKTRYGLLGGGANAV 172
 PIP1_9 GGHINPAVTFGLFLARKLSLTRAIFYMVMQCLGAICGAGVVKGF~~FG~~MKTRYGLLGGGANAV 172
PIP1_10 GGHINPAVTFGLFLGRKLSLTRAIFYMVMQCLGAICGAGVVKGF~~FG~~MKTRYGALGGGANSV 73
 PIP1_11 GGHINPAVTFGLFLARKLSLTRAIFYMVMQCLGAICGAGVVKGF~~FG~~MKKTQYGMLGGGANSV 172
PIP1_12 GGHINPAVTFGLLLARKLSLTRAIFYMIMQCLGAICGAGVVKGF~~FG~~GDSRYEMLGGGANVV 169
PIP1_13 GGHINPAVTFGLLLARKLSLTRAIFYMIMQCLGAICGAGVVKGF~~FG~~GDSRYEMLGGGANVV 169
 PIP1_14 GGHINPAVTFGLFLARKLSLTRAIFYMVMQCLGAICGAGVVKGF~~FG~~MKKTQYGMLGGGANSV 172
 PIP1_15 GGHINPAVTFGLLLARKLSLTRAIFYMIMQCLGAICGAGVVKGF~~FG~~GDSRYEMLGGGANVV 169
 PIP2_1 GGHINPAVTFGLFLARKVSLVRAILYMAAQCLGAICGCGLVKAFC-~~KS~~SYYNKYGGGANS 159
 PIP2_2 GGHINPAVTFGLFLARKVSLVRAIFYMGAQCLGAICGCGLVKAFC-~~NS~~SYYNQYGGGANS 159
 PIP2_3 GGHINPAVTFGLFLARKVSLVRAIFYMAAQCLGAICGCGLVKAFC-~~KS~~SYYNKYGGGANS 159
 PIP2_4 GGHINPAVTFGLFLARKVSLIRAVAYMVSQCLGAICGVGLVKAFC-~~KH~~PYNSLGGGANTV 144
 PIP2_5 GGHINPAVTFGLFLARKVSLIRAVAYMVAQCLGAICGVGLVKAFC-~~KS~~EYNSLGGGANTV 152
 PIP2_6 GGHINPAVTFGLFLARKVSLIRAVAYMVAQCLGAICGVGLVKAFC-~~KS~~EYNSLGGGVNTV 152
 PIP2_7 GGHINPAVTFGLFLARKVSLIRAVAYMVAQCLGAICGVGLVKAFC-~~KS~~EYNSLGGGANTV 152
 PIP2_8 GGHINPAVTLGLFLARKVSLFRAVAYMVAQCLGAICGAGLAKSLM-~~KH~~PYNRLGGGTNLV 154
 PIP2_9 GGHINPAVTFGLFLARKVSLIRAVAYMVSQCLGAICGVGLVKAFC-~~KH~~PYNSLGGGANTV 152
 PIP2_10 GGHINPAVTFGLFVGRKVSILIRALLYMVAQCLGAICGCGLVKAFC-~~KT~~YYSYGGGANEL 167
 PIP2_11 GGHINPAVTFGLFLARKVSLVRAIFYMGAQCLGAICGCGLVKAFC-~~NS~~SYYNQYGGGANS 159
 PIP2_12 GGHINPAVTFGLFLARKVSLIRAVAYMVSQCLGAICGVGLVKAFC-~~KH~~PYNSLGGGANTV 152
 PIP2_13 GGHINPAVTFGLFLARKVSLVRAIFYMTAQCLGAICGCGLVKAFC-~~KS~~SYYNKYGGGANS 159

H5

PIP1_1 AHGYTKGDGLGAEIVGTFVLVYTVFSATDAKRSARD~~SHVP~~-ILAPLPIGFAVFLVELATI 231
 PIP1_2 NHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARD~~SHVP~~-ILAPLPIGFAVFLVELATI 228
 PIP1_3 NHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARD~~SHVP~~-ILAPLPIGFAVFLVELATI 228
 PIP1_4 NHGYTKGDGLGAEIVGTFILVYTVFSATDAKRNARD~~SHVP~~-ILAPLPIGFAVFFVELATI 228
 PIP1_5 NHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARD~~SHVP~~-ILAPLPIGFAVFLVELATI 228
 PIP1_6 SSGYSKSSGLGAEIVGTFVLVYTVFSATDAKRNARD~~SHVP~~-ILAPLPIGFAVFLVELATI 229
 PIP1_7 NHGYTKGDGLGAEIVGTFVLVYTVFSATDAKRSARD~~SHVP~~-ILAPLPIGFAVFLVELATI 230
 PIP1_8 NPGYTKGAGLGAEIVGTFVLVYTVFSATDAKRSARD~~SHVP~~-ILAPLPIGFAVFLVELATI 231
 PIP1_9 NPDYTNGAALGAEIIGTFVLVYTVFSATDAKRSARD~~SHVP~~-ILAPLPIGFAVFLVELATI 231
PIP1_10 NHGYTKGDGLGAEIVGTFVLVYTVFSATDAKRSARD~~SHVP~~-ILAPLPIGFAVFLVELATI 132
 PIP1_11 AHGYTKGDGLGAEIVGTFVLVYTVFSATDAKRSARD~~SHVP~~-ILAPLPIGFAVFLVELATI 231
PIP1_12 NHGYTKGDGLGAEIVGTFILVYTVFSATDAKRNARD~~SHVP~~-ILAPLPIGFAVFLVELATI 228
PIP1_13 NHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARD~~SHVP~~-ILAPLPIGFAVFLVELATI 228
 PIP1_14 AHGYTKGDGLGAEIVGTFVLVYTVFSATDAKRSARD~~SHVP~~-ILAPLPIGFAVFLVELATI 231
 PIP1_15 NHGYTKGDGLGAEIVGTFILVYTVFSATDAKRNARD~~SHVP~~-ILAPLPIGFAVFLVELATI 228
 PIP2_1 ADGYSTGTGLAAEIIIGTFVLVYTVFSATDPKRNARD~~SHVP~~-VLAPLPIGFAVFMVELATI 218
 PIP2_2 AEGYSTGTGLAAEIIIGTFVLVYTVFSATDPKRNARD~~SHIPVVLAPLP~~IGFAVFMVELATI 219
 PIP2_3 ADGYSTGTGFAAEIIIGTFVLVYTVFSATDPKRNARD~~SHIP~~-VLAPLPIGFAVFMVELATI 218
 PIP2_4 ASGYNKGTALGAEIIGTFVLVYTVFSATDPKRSARD~~SHVP~~-VLAPLPIGFAVFMVELATI 203
 PIP2_5 ATGYNKGTALGAEIIGTFVLVYTVFSATDPKRSARD~~SHVP~~-VLAPLPIGFAVFMVELATI 211
 PIP2_6 ATGYNKGTALGAEIIGTFVLVYTVFSATDPKRSARD~~SHVP~~-VLAPLPIGFAVFMVELATI 211
 PIP2_7 ATGYNKGTALGAEIIGTFVLVYTVFSATDPKRSARD~~SHVP~~-VLAPLPIGFAVFMVELATI 211
 PIP2_8 DSGYSKGTALGAEIIGTFVLVYTVFSATDPKRSARD~~SHVP~~-VLAPLPIGFAVFMVELATI 213
 PIP2_9 ASGYNNGTALGAEIIGTFVLVYTVFSATDPKRSARD~~SHVP~~-VLAPLPIGFAVFMVELATI 211
 PIP2_10 QDGFNKGTGLGAEIIGTFVLVYTVFSATDPKRSARD~~SHVP~~-VLAPLPIGFAVFMVELATI 226
 PIP2_11 AEGYSTGTGLAAEIIIGTFVLVYTVFSATDPKRNARD~~SHIPVVLAPLP~~IGFAVFMVELATI 219
 PIP2_12 ASGYNNGTALGAEIIGTFVLVYTVFSATDPKRSARD~~SHVP~~-VLAPLPIGFAVFMVELATI 211
 PIP2_13 ADGYSTGTGLAAEIIIGTFVLVYTVFSATDPKRNARD~~SHIP~~-VLAPLPIGFAVFMVELATI 218

	LE1	LE2	P2	P3	P4	P5								
PIP1_1	PITGIGINPA	RS	SLGAA	IIFN	KDKG	WDDHW	IFWVGPF	GAA	LAALYH	VV	VIRA	IPFK	SK--	289
PIP1_2	PITGIGINPA	RS	SLGAA	I IY	NDHAW	DDHW	FEWVGPF	GAA	LAAYH	QI	IRA	IPFK	TRD-	287
PIP1_3	PITGIGINPA	RS	SLGAA	I IY	NDHAW	DDHW	FEWVGPF	GAA	LAAYH	QI	IRA	IPFK	TRA-	287
PIP1_4	PITGIGINPA	RS	SLGAA	I IY	NDHAW	DDHW	FEWVGPF	GAA	LAAYH	QI	IR	GIPFK	TRA-	287
PIP1_5	PITGIGINPA	RS	SLGAA	I IY	NDHAW	DDHW	FEWVG	WTLH	WTCTCCS	-----	LPP	DN	P--	278
PIP1_6	PVTGIGINPA	RS	SLGAA	I IY	NDQAW	DDHW	FEWVGPF	GAA	LAALYH	QI	VIRA	IPFK	SK--	287
PIP1_7	PITGIGINPA	RS	SLGAA	IIFN	KDKG	WGGH	WIFWVGPF	GAA	LAALYH	VV	VIRA	IPFK	SK--	288
PIP1_8	PVTGIGINPA	RS	SLGAA	IIFN	KDKG	WDDH-	-----	-----	-----	-----	-----	-----	-----	259
PIP1_9	PVTGIGINPA	RS	SLGAA	IIFH	KQGGLG	-----	-----	-----	-----	-----	-----	-----	-----	257
PIP1_10	PITGIGINPA	RS	SLGAA	IIFN	KDKG	WDDHW	IFW	LGPFI	G-----	-----	-----	-----	-----	177
PIP1_11	PITGIGINPA	RS	SLGAA	IIFN	KDKG	WDDHW	IFWVGPF	GAA	LAALYH	VV	VIRA	IPFK	SK--	289
PIP1_12	PITGIGINPA	RS	SLGAA	I IY	NDHAW	DDHW	FEWVG	PLHWT	-----	-----	-----	-----	-----	267
PIP1_13	PITGIGINPA	RS	SLGAA	I IY	NDHAW	DDHW	IFW	LGPFI	G-----	-----	-----	-----	-----	266
PIP1_14	PITGIGINPA	RS	SLGAA	IIFN	KDKG	WDDHW	IFWVGPF	GAA	LAALYH	VV	VIRA	IPFK	SK--	289
PIP1_15	PITGIGINPA	RS	SLGAA	I IY	NDHAW	DDHW	FEWVGPF	GAA	LAAYH	QI	IRA	IPFK	TRA-	287
PIP2_1	PITGIGINPA	RS	FGAA	VMFN	QDKPW	DDHW	FEWVGPF	GAA	IAAYH	QY	IL	RAGAA	KALGS	278
PIP2_2	PITGIGINPA	RS	SLGAA	VIFN	QDKIW	DDHW	FEWVGPF	GAA	IAAYH	QY	FIL	RASGA	KALGS	279
PIP2_3	PITGIGINPA	RS	FGAA	V IY	NQDKP	DDHW	MEWVGPF	GAA	IAAYH	QY	FIL	RAAAV	KALGS	278
PIP2_4	PITGIGINPA	RS	FGAA	V IY	NNDKAW	DEHW	FEWVGPF	V	GALAAAYH	QY	IL	RATAI	KALGS	263
PIP2_5	PITGIGINPA	RS	FGAA	V IY	NNDKAW	DDQW	IFWVG	PMV	GALAAAYH	QY	IL	KAAAI	KALGS	271
PIP2_6	PITGIGINPA	RS	FGAA	V IY	NNDKAW	DDQW	IFWVG	PMV	GALAAAYH	QY	IL	RAAAI	KALGS	271
PIP2_7	PITGIGINPA	RS	FGAA	V IY	NNDKAW	DDQW	IFWVG	PMV	GALAAAYH	QY	I	P-----	-----	261
PIP2_8	PITGIGINPA	RS	SLGAA	V IY	NNEKAW	DDQW	IFWVGPF	GAA	IAAAAYH	QY	IL	RATAI	KALKS	273
PIP2_9	PITGIGINPA	RS	FGAA	V IY	NNDKAW	DDHW	FEWVGPF	V	GALAAAYH	QY	IL	RAAAI	KALGS	271
PIP2_10	PITGIGINPA	RS	FGAA	V IY	NQEK	-----	-----	-----	SLAMING	---	YSGL	DP	SLGA	266
PIP2_11	PITGIGINPA	RS	SLGAA	VIFN	QDKIW	DDHW	FEWVGPF	GAA	IAAYH	QY	FIL	RASGA	KALGS	279
PIP2_12	PITGIGINPA	RS	FGAA	V IY	NNDKAW	DDHW	FEWVGPF	V	GALAAAYH	QY	IL	RAAAI	KALGS	271
PIP2_13	PITGIGINPA	RS	FGAA	V IY	NQDKP	DDHW	FEWVGPF	GAA	IAAYH	QY	FIL	RAAAV	KALGS	278

PIP2_1	FRSSSAM	285
PIP2_2	FRSSFAM	286
PIP2_3	FRSSSAM	285
PIP2_4	FRSNPTN	270
PIP2_5	FRSNPSN	278
PIP2_6	FRSNPSN	278
PIP2_8	FRSSPTN	280
PIP2_9	FRSNPTN	278
PIP2_10	FVAAF--	271
PIP2_11	FRSSFAM	286
PIP2_12	FRSNPHN	278
PIP2_13	FRSSSAM	285

TIP subfamily

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TIP1_1      ---MPIRNIAVGRPEEATHPDALKAALAEFISTLIFVFAGSGSGMAFNKLTDNGATTPPAG 57
TIP1_10    -----GSGMAFNKLTDDDGSSTPPAG 19
TIP1_11    -----GSGMAFNKLTDNGSSTPPAG 19
TIP1_12    -----GSGMAFNKLTDDDGSSTPPAG 19
TIP1_13    -----GSGMAFNKLTDNGSSTPPAG 19
TIP1_14     ---MPIRNIAVGRPEEATHPDALKAALAEFISTLIFVFAGSGSGMAFNKLTDGGATTPPAG 57
TIP1_2      ---MPISRIAVGSPAEAGQADALKAALAEFISVLIFVFAGSGSGMAFNKLTDDDGSSTPPAG 57
TIP1_3      ---MPIRNIAVGRPEEATHPDALKAALAEFISTLIFVFAGSGSGMAFNKLTDNGATTPPAG 57
TIP1_4      ---MPIRNIAVGRPEEATQPDALKAALAEFISTLIFVFAGSGSGMAFNKLTDNGATTPPAG 60
TIP1_5      ---MPIRNIAVGRPEEATHPDALKAALAEFISTLIFVFAGSGSGMAFNKLTDGGATTPPAG 57
TIP1_6     ---GTSRNIAVGRPEEATQPDALKAALAEFISTLIFVFAGSGSGMAFNKLTDNGATTPPAG 57
TIP1_7      ---MPISRIAVGSPAEAGQADALKAALAEFISVLIFVFAGSGSGMAFNKLTDDDGSSTPPAG 57
TIP1_8      ---MPIRNIPVGRPEEATHPDALKAALAEFISTLIFVFAGSGSGMAFNKLTDNGATTPPAG 57
TIP1_9     -----GSGMAFNKLTDDDGSSTPPAG 19
TIP2_1      -----MAGIAFRGFDDSFSLGTVKAYLAEFISTLVFVFAGVGSAIAYNKLTTDAALDPDG 55
TIP2_2     -----SARGRGFDDSFSLGTVKAYLAEFISTLVFVFAGVGSAIAYNKLTTDAALDPDG 52
TIP2_3      -----MAGIAFRGFDDSFSLGTVKAYLAEFISTLVFVFAGVGSAIAYNKLTTDAALDPDG 55
TIP2_4     -----
TIP2_5     -----
TIP2_6      -----MVKIAFGSIGDSFSVGSLKAYLAEFIATLLFVFAGVGSAIAYNKLTSDAALDPPG 55
TIP2_7      -----MVKIAFGSIGDSFSVGSLKAYLAEFIATLLFVFAGVGSAIAYNKLTSDAALDPPG 55
TIP4_1      -----MPKIALGTSQEAAQPDCIKALVVEFITTFLFVFGVGAAMAAD---ESGANALVG 52
TIP4_2      -----MPKIALGTSQEAAQPDCIKALVVEFITTFLFVFGVGAAMAAD---ESGANALVG 52

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H2

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TIP1_1      LVAAALAHGFLFVAVSVGANISGGHVNPAVTFGAFVGGNITLLRGILYWIAQLLGSTVA 117
TIP1_10    LVAAALAHALALFVAVSIGANISGGHVNPAVTFGAFVGGHITLVRSILYWIAQLLGSVVA 79
TIP1_11    LVAASVAHAFALFVAVSVGANISGGHVNPAVTFGAFVGGHITLFRSILYWIAQLLGSVVA 79
TIP1_12    LVAAALAHALALFVAVSVGANISGGHVNPAVTFGAFVGGHITLVRSILYWIAQLLGSVVA 79
TIP1_13    LVAAALAHALALFVAVSIGANISGGHVNPAVTFGAFVGGHITLVRSILYWIAQLLGSVVA 79
TIP1_14     LVAASLAHGFALFVAVSVGANISGGHVNPAVTFGAFVGGNITLLRGILYWIAQLLGSTVA 117
TIP1_2      LVAAALAHALALFVAVSIGANISGGHVNPAVTFGAFVGGHITLVRSILYWIAQLLGSVVA 117
TIP1_3      LVAAALAHGFLFVAVSVGANISGGHVNPAVTFGAFVGGNITLLRGILYWIAQLLGSTVA 117
TIP1_4      LVAASIAHGLGLFVAVSVGANISGGHVNPAVTFGAFVGGNISLLRGILYWIAQLLGSTVA 120
TIP1_5      LVAASLAHGFALFVAVSVGANISGGHVNPAVTFGAFVGGNITLLRGILYWIAQLLGSTVA 117
TIP1_6     LVAASIAHGLGLFVAVSVGANISGGHVNPAVTFGAFVGGNISLLRGILYWIAQLLGSTVA 117
TIP1_7      LVAAALAHALALFVAVSVGANISGGHVNPAVTFGAFVGGHITLVRSILYWIAQLLGSVVA 117
TIP1_8      LVAAALAHGFLFVAVSVGANISGGHVNPAVTFGAFVGGNITLLRGILYWIAQLLGSTVA 117
TIP1_9     LVAASLAHAFALFVAVSIGANISGGHVNPAVTFGAFVGGHITLVRSILYWIAQLLGSVVA 79
TIP2_1      LVAIAVCHGFALFVAVAIGANISGGHVNPAVTFGLALGGQITILTGIFYWIAQLLGSIVA 115
TIP2_2     LVAIAVCHGFALFVAVAIGANISGGHVNPAVTFGLALGGQITILTGIFYWIAQLLGSIVA 112
TIP2_3      LVAIAVCHGFALFVAVAIGANISGGHVNPAVTFGLALGGQITILTGIFYWIAQLLGSIVA 115
TIP2_4     -----NISGGHVNPAVTFGLALGGQITILTGIFYWIAQLLGSIVA 40
TIP2_5     -----NISGGHVNPAVTFGLALGGQITILTGIFYWIAQLLGSIVA 40
TIP2_6      LVAIAVAHAFALFVGVAIAANISGGHVNPAVTFLAIGGNITILTGIFYWVAQCLGSIVA 115
TIP2_7      LVAIAVAHAFALFVGVAIAANISGGHVNPAVTFLAIGGNITILTGIFYWVAQCLGSIVA 115
TIP4_1      LFAVAVAHALVVGVMISAG-HISGGHLNPAVTLGLLFGGHITVVRAILYWIDQLLASSAA 111
TIP4_2      LFAVAVAHALVVGVMISAG-HISGGHLNPAVTLGLLFGGHITVVRAILYWIDQLLASSAA 111

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	P1	
TIP1_1	CLLLKFATGDLAVPAFGLSSGVGSNALVFEIVMTFGLVYTVYATAVDPKKGSLGTIAPL	177
TIP1_10	CLLLKFSTGGLTTSAFALSSGVGAWNAVVFIEIVMTFGLVYTVYATAVDPKKGNIGIIAPI	139
TIP1_11	CLLLKFSTGGLTTSAFALSSGVGAWNAVVFIEIVMTFGLVYTVYATAIDPKKGDLGVIAPL	139
TIP1_12	CLLLKFSTGGMTTSAFSLSSGVGAWNAVVFIEIVMTFGLVYTVYATAVDPKKGNIGIIAPI	139
TIP1_13	CLLLKFSTGGMTTSAFSLSSGVGAWNAVVFIEIVMTFGLVYTVYATAVDPKKGNIGIIAPI	139
TIP1_14	CLLLKFATSGLGVPAPFGLSSGVGALNAFVFEIVMTFGLVYTVYATAVDPKRGNLGVIAPL	177
TIP1_2	CFLMKFSTGGMTTSAFSLSSGVGAWNAVVFIEIVMTFGLVYTVYATAVDPKKGNIGIIAPI	177
TIP1_3	CLLLKFATGDLAVPAFGLSSGVGSNALVFEIVMTFGLVYTVYATAVDPKKGSLGTIAPL	177
TIP1_4	CLLLKFATSDMTVPAFGLSSGVGVNAVVFIEIVMTFGLVYTVYATAIDPKKGDLGVIAPL	180
TIP1_5	CLLLKFATSGLGVPAPFGLSSGVGALNAFVFEIVMTFGLVYTVYATAVDPKRGNLGVIAPL	177
TIP1_6	CLLLKFATSDMTVPAFGLSSGVGVNAVVFIEIVMTFGLVYTVYATAIDPKKGDLGVIAPL	177
TIP1_7	CLLLKFSTGGMTTSAFSLSSGVGAWNAVVFIEIVMTFGLVYTVYATAVDPKKGNIGIIAPI	177
TIP1_8	CLLLKFATGDLAVPAFGLSSGVGSNALVFEIVMTFGLVYTVYATAVDPKKGSLGTIAPL	177
TIP1_9	CFLLMFSTGGMTTSAFSLSSGVGAWNAVVFIEIVMTFGLVYTVYATAVDPKKGNIGIIAPI	139
TIP2_1	CFLKAVTGGLTVPIHGLGAGVGAIQGVVMEIIITFALVYTVYATAADPKKGSLGTIAPL	175
TIP2_2	CFLKAVTGGLTVPIHGLGAGVGAIQGVVMEIIITFALVYTVYATAADPKKGSLGTIAPL	172
TIP2_3	CFLKAVTGGLTVPIHGLGAGVGAIQGVVMEIIITFALVYTVYATAADPKKGSLGTIAPL	175
TIP2_4	CFLKAVTGGLTVPIHGLGAGVGAIQGVVMEIIITFALVYTVYATAADPKKGSLGTIAPL	100
TIP2_5	CFLKAVTGGLTVPIHGLGAGVGAIQGVVMEIIITFALVYTVYATAADPKKGSLGTIAPL	100
TIP2_6	CLLLQFVTNGLSVPTHTGVSAGMSAVGGVMEIVITFALVYTVYATAADPKKGSLGIAPL	175
TIP2_7	CLLLQFVTNGLSVPTHTSVASGMNAVGGVMEIVITFALVYTVYATAADPKKGSLGIAPL	175
TIP4_1	CILLKYLTGGLNTPVHTLASGMGFLQGVIWEIILTALLFTVYATIVDPKKGSIDGLGPM	171
TIP4_2	CILLKYLTGGLNTPVHTLASGMGFLQGVIWEIILTALLFTVYATIVDPKKGSIDGLGPM	171

	H5	LE1	LE2	P2	P3	P4	P5	
TIP1_1	AIGFIVGANI	L	L	L	L	L	L	237
TIP1_10	AIGFIVGANI	L	L	L	L	L	L	179
TIP1_11	AIGFIVGANI	L	L	L	L	L	L	179
TIP1_12	AIGFIVGANI	L	L	L	L	L	L	179
TIP1_13	AIGFIVGANI	L	L	L	L	L	L	179
TIP1_14	AIGLIVGANI	L	L	L	L	L	L	237
TIP1_2	AIGFIVGANI	L	L	L	L	L	L	237
TIP1_3	AIGFIVGANI	L	L	L	L	L	L	237
TIP1_4	AIGFIVGANI	L	L	L	L	L	L	240
TIP1_5	AIGLIVGANI	L	L	L	L	L	L	237
TIP1_6	AIGFIVGANI	L	L	L	L	L	L	237
TIP1_7	AIGFIVGANI	L	L	L	L	L	L	237
TIP1_8	AIGFIVGANI	L	L	L	L	L	L	237
TIP1_9	AIGFIVGANI	L	L	L	L	L	L	179
TIP2_1	AIGFIVGANI	L	L	L	L	L	L	235
TIP2_2	AIGFIVGANI	L	L	L	L	L	L	232
TIP2_3	AIGFIVGANI	L	L	L	L	L	L	235
TIP2_4	AIGFIVGANI	L	L	L	L	L	L	146
TIP2_5	AIGFIVGANI	L	L	L	L	L	L	146
TIP2_6	AIGFIVGANI	L	L	L	L	L	L	235
TIP2_7	AIGFIVGANI	L	L	L	L	L	L	235
TIP4_1	LTGFVVGANI	L	L	L	L	L	L	231
TIP4_2	LTGFVVGANI	L	L	L	L	L	L	231

TIP1_1	FIS-NTHEQLPTTDY-----	251
TIP1_14	FIN-QTHEQLPHH-----	249
TIP1_2	FIAPSTYEEVPSADF-----	252
TIP1_3	FIS-NTHEQLPTTDY-----	251
TIP1_4	FIN-QSHEQLPPTDY-----	251
TIP1_5	FIN-QTHEQLPNY-----	249
TIP1_6	FIN-QSHEQLPPTDYWKQFNFIMKNGFFPFPFSGGKVFLVEAFSFLGV	284
TIP1_7	FIAPSTYEELPSADF-----	252
TIP1_8	FIS-NTHEQLPTTDY-----	251
TIP2_1	FMNS-DHAPLSNDF-----	248
TIP2_2	FMNS-DHAPLVNDF-----	245
TIP2_3	FMNS-DHAPLSNDF-----	248
TIP2_6	FIGSYSAAPASEDYA-----	250
TIP2_7	FIGSYSAAPASEDYA-----	250
TIP4_1	FIVR-THVLLPQNEAF-----	246
TIP4_2	FIVR-THVLLPQNEAF-----	246

NIP subfamily

NIP1_1 -----MAEISGCNGNHEVVVLNVNGETHPPPPSSAPK 33
NIP1_2 -----
NIP1_3 -----
NIP2_1 -----MATTDVSPMDQNPTPPK 17
NIP5_1 -----MQMLSGDCPNVGS PHT 16
NIP5_2 -----
NIP6_1 MENEDVPSAPSTPVTPTGTPGAPLFGGFKGDHRGGFNKKSLKSKCFSVEDSMEEGR LPP 60
NIP6_2 -----PATPTGTPGAPLFGGFKGDHRNGFNKKSLKSKCFSVEDSMEEGR LPP 48
NIP6_3 -----RVTPGTPGAPLFGGFKGDHRGGFNKKSLKSKCFSVEDSMEEGR LPP 48
NIP6_4 -----PATPTGTPGAPLFGGFKGDHRGGFNKKSLKSKCFSVEDSMEEGR LPP 48
NIP6_5 -----PATPTGTPGAPLFGGFKGDHRGGFNKKSLKSKCFSVEDSMEEGR LPP 48
NIP6_6 -----PVTPGTPGAPLFGGFKGDHRGGFNKKSLKSKCFSVEDSMEEGR LPP 48

H2

NIP1_1 RKDSDLGFSVPFIQKLMAEVLGTYFLIFAGCAAVVNVNNEKVVSLPG--ISMVWGLAVM 91
NIP1_2 -----AEAMGTYFLIFAGCAAVVNVNNEKVVSLPG--ISIVWGLAVM 41
NIP1_3 -----AEVMGTYFLIFAGCAAVVNVNNEKVVSLPG--ISIVWGLAVM 41
NIP2_1 QPSFQQHCPPDFPRKVF AETIATYCRVFVTCGSAATSSVDEHKISR LG--ASVAGGLIVT 75
NIP5_1 CFTDFPAPDVSLTRKLGAEFVGTFFILIFAATAGPIVNQKYSGAETLLG--NATCAGLAVM 74
NIP5_2 -----FVGTFFILIFAATAGPIVNQKYSGAETLLG--NAAQAGLAVM 39
NIP6_1 VSCSLPPPPVSLTRKVGAEFIGTFILIFAGTATAIVNQKTQGSETLIG--LAASTGLAVM 118
NIP6_2 VSCSLPPPPVSLTRKVGAEFIGTFILIFAGTATAIVNQKTQGSETLIG--LAASTGLAVM 106
NIP6_3 VSCSLPPPPVSLTRKVGAEFIGTFILIFAGTATAIVNQKTQRSETLIGLALAASTGLAVM 108
NIP6_4 VSCSLPPPPVSLTRKVGAEFIGTFILIFAGTATAIVNQKTQRSETLIGLALAASTGLAVM 108
NIP6_5 VSCSLPPPPVSLTRKVGAEFIGTFILIFAGTATAIVNQKTQGSETLIG--LAASTGLAVM 106
NIP6_6 VSCSLPPPPVSLTRKVGAEFIGTFILIFAGTATAIVNQKTQGSETLIG--LAASTGLAVM 106

P1

NIP1_1 VLVYSLGHISGAHFNPAVTIAFATCKRFPLKQVPAYVLAQVIGSTLAAGTLRL LFSGPHD 151
NIP1_2 VLVYSLGHISGAHFNPAVTIAFATCKRFPLKQVPAYVLAQVIGSTLAAGTLRL LFSGPHD 101
NIP1_3 VLVYSLGHISGAHFNPAVTIAFATCKRFPLKQVPAYVLAQVIGSTLAAGTLRL LFSGPHD 101
NIP2_1 VMIYAVGHVSGAHMNP AVTLAFAAVRHFPWKQVPFYGAAQLTG AISASFTLRVLLH-PIK 134
NIP5_1 I I I L S T G H I S G A H L N P S L T I A F A A C R H F P W T Q V P A Y I A A Q V S A S I C A S F A L K G V F H - P F M 133
NIP5_2 I I I L S T G H I S G A H L N P S L T I A F A A C R H F P W T Q V P A Y I A A Q V S A S M C A S F A L K G V F H - P F M 98
NIP6_1 I V I L S T G H I S G A H L N P A V T I A F A A L K H F P R K H V P V Y I G A Q V M A S L C A A F G L K G V F H - P M M 177
NIP6_2 I V I L S T G H I S G A H L N P A V T I A F A A L K H F P R K H V P V Y I G A Q V M A S L C A A F G L K G V F H - P M M 165
NIP6_3 I V I L S T G H I S G A H L N P T V T I A F A A L K H F P R K H ----- 140
NIP6_4 I V I L S T G H I S G A H L N P T V T I A F A A L K H F P R K H ----- 140
NIP6_5 I V I L S T G H I S G A H L N P A V T I A F A A L K H F P R K H V P V Y I G A Q V M A S L C A A F G L K G V F H - P M M 165
NIP6_6 I V I L S T G H I S G A H L N P A V T I A F A A L K H F P R K H V P V Y I G A Q V M A S L C A A F G L K G V F H - P M M 165

H5

NIP1_1 VFAGTSPQGS DLQAFGI E F I I T F Y L M F I I S G V A T D N R A I G E L A G L A I G A T V L I N V M F A G P 211
NIP1_2 VFAGTSPQGS DLQAFG V E F I I T F Y L M F I I S G V A T D N R A I G E L A G L A I G A T V L I N V M F A G P 161
NIP1_3 VFAGTSPQGS DLQAFG V E F I I T F Y L M F I I S G V A T D N R A I G E L A G L A I G A T V L I N V M F A G P 161
NIP2_1 HVGTTSPSGS DLQAL I M E I V V T F S M M F I T S A V A T D T K A I G E L A G I A V G S A V C I T S I L A G P 194
NIP5_1 SGGVTVP SVSHGQAF A L E F L I T F N L L F V V T A V A T D T R A V G E L A G I A V G A T V M L N I L V A G P 193
NIP5_2 SGGVTVP SVSHGQAF A L K F L I T F N L L L V D T A V A T D T R A V R E L A G I A V G A T V M L N I L V A G P 158
NIP6_1 GGGVTVP SGGFGQAF A L E F I I S F N L M F V V T A V A T D T R A V G E L A G I A V G A T V M L N I L I A G P 237
NIP6_2 GGGVTVP SGGFGQAF A L E F I I S F N L M F V V T A V A T D T R A V G E L A G I A V G A T V M L N I L I A G P 225
NIP6_5 GGGVTVP SGGFGQAF A L E F M I S F N L M F V V T A V A T D T R A ----- 203
NIP6_6 GGGVTVP SGGFGQAF A L E F I I S F N L M F V V T A V A T D T R A V G E L A G I V V G A T V M L N I L I A G P 225

	LE1	LE2	P2	P3	P4	P5					
NIP1_1	ITGAS MNP ARS	LG	PAIVSNHYKGIWIY	LM	SP	TL	EA	VS	GAWVYNMVR	YTDKPLREITKSAS	271
NIP1_2	ITGAS MNP A										170
NIP1_3	ITGAS MNP ARS	LG									174
NIP2_1	ISGG S MNPARS	IG	PAIASGEYKGIWVY	VVG	PVT	GT	LM	GAWSYNLIR	MRDKPHHAIS	PHSS	254
NIP5_1	SSGG S MNPV	RTL	GPAVAAGNYRALWIY	LI	APT	LG	AVIGSATYTLV	KLREDEVD	APRQ	VRS	253
NIP5_2	SSGG S MNPV	RTL	GPAVAAGNYRALWIY	LI	APT	LG	AVIGSATYTLV	KLREDEVD	APRQ	VRS	218
NIP6_1	ITGAS MNP V	RTL	GPAIAANNYKAIWVY	FT	APIL	GS	PCGC	RTYT			280
NIP6_2	ITGAS MNP V	RTL	GPAIAANNYKAIWVY	FT	APIL	GA	LCGAGTYT	AVKLPEED	GEKP	STVRS	285
NIP6_6	ITGAS MNP V										234

NIP1_1	FPQSSRNSG	280
NIP2_1	SFKLR----	259
NIP5_1	FRR-----	256
NIP5_2	FRR-----	221
NIP6_2	FRR-----	288

SIP subfamily

H2

SIP1_1	MKGPIKIAIADMVISFMWVFCSSAFGLLTYLIATAAGVQTVRWASIVIITVVFFVFLSIF	60
SIP1_2	MR-PIKIAFGDMLITFMWVFCSSMFGLFTSWIATAIGVQAISWAPIVIITFIIIFVFVFIF	59
SIP1_3	-MGVIKSAMADALLTSMWVFSMPFLKILTFEIAAFLGLRPFPLAAFFITTLIVSLMMFIF	59
SIP1_4	-MGIITIAIGDALLTSMWVFSMPLLKIFTSKIVGFLGAQTLPLATLMVSTVIVSILVMIF	59
SIP1_5	-MGVITTAADALLTSMWVFSMPFLKILTFEIAAFLGLRPFPLAAFFITTLIVSLMMFIF	59
SIP1_6	-MGIITTAADALLTSIWVFSMPFLRILTLEIAAFLGLRPFPLAAFFITTLIVSLMMFIF	59
SIP1_7	-MGVIKTAIGDALLTSMWVFSMPLLKIFTSKIVGFLGAQTLPLATLMVSTVIVSILVMIF	59

P1

SIP1_1	NIIGGFLGGASFDPAAATTAFFYAAGSGAD-TLISMALRFPAQAAGAVGGALAIMEATPEQY	119
SIP1_2	NIIGGFLGGASFNPNTGTASFYAAGVGDD-SLISMGLRFPAQAAGAVGGALAITEVMPPEQY	118
SIP1_3	TIIGNALGGATFNPTASVAFYAAGLRKDSALSMAVRFPFQAVGGVVGVTVLGVLPREY	119
SIP1_4	SLTGNVFGGASFNPAASTFHVAGLRKNDLSILSMAVRFPQAAGGVAGVKAALGLIPAEY	119
SIP1_5	TIIGNALGGATFNPTASVAFYAAGLRKDSALSMAVRFPFQAVGGVVGVTVLGVLPREY	119
SIP1_6	TIVGNALGGATFNPTASVAFYAAGLRKDSALSMAVRFPFQAAGGVGVNAVLGVLPREY	119
SIP1_7	SFIGNVFGGASFNPAASTFHVAGLRKNDLSILSMAVRFPQAAGGVAGVKAALGLIPAEY	119

H5

SIP1_1	KHMIGGPSVKVDTHTGAFAGVLTFAITFIVLLIMLRGPQSEIFKTWFLSIVIVALVTFG	179
SIP1_2	KHMIVAPSLKVDTHTGAIAGVLTFFVITLAVLFIIKGPKSEIFKTWLLAIATVAIVLSG	178
SIP1_3	KETIKGPSLKVDIQTGFLAEGLLTFGLCLALLVILIRGPNNPLLKLLLMAISTVGFVGRG	179
SIP1_4	SNLTGPSLKVDLHTGAVAEGLFTFGRSLALLLIMFMGPKNGWVKQWLVS LATAILVLTG	179
SIP1_5	KETIKGPSLKVDIQTGFLAEGLLTFGLCLALLVILIRGPNNPLLKLLLMAISTVGFVGRG	179
SIP1_6	KETIKGPSLKVDMQTGILAEGLFTFGLCPALLVILVRGPNNPLLKLLLMAISTVGFVGRG	179
SIP1_7	SNLTGPSLKVDLHTGAVAEGLFTFGRSLALLLIMFMGPKNGWVKQWLVS LATAILVLTG	179

LE1LE2P2P3P4P5

SIP1_1	SAYTGPSMNPAFAFGWAYVHNQHDTWDHFYIYWICPFIGATLAGWVFRQFFSLP-PVK-V	237
SIP1_2	TAYTGPSMNPAFAFGWAYVNNWHNTWDQFYVYWICPFIGAILAAWVFRLFFPPSPVKKA	238
SIP1_3	ANYTGPSMNPAFAFGWAYVNSWHNSWEHYVYWWMGPLIGATLAAWVFRFLFSPSSSIKEK	239
SIP1_4	SRETGAPMNPAFAFGWAYVNNRHNSWELYYVYWIGALFGATLGAWVFRFMVSLPLPPPTK	239
SIP1_5	ANYTGPSMNPAFAFGWAYV-----	198
SIP1_6	ANYTGPSMNPAFAFGWAYV-----	198
SIP1_7	SRETGAPMNPAFAFGWAYV-----	198

SIP1_1	KKT-----	240
SIP1_2	KKTRKPKRA	247
SIP1_3	KA-----	241
SIP1_4	QKKA-----	243