Supplementary table 1: peptides screened in the array

Peptide	Sequence	Rev binding – relative spot intensity (%) *	IN binding – relative spot intensity- (%) *
IN 66-80	THLEGKIILVAVHVA	-	-
IN 66-80 T66A	AHLEGKIILVAVHVA	-	-
IN 66-80 H67A	TALEGKIILVAVHVA	-	-
IN 66-80 L68A	THAEGKIILVAVHVA	-	-
IN 66-80 E69A	THLAGKIILVAVHVA	-	-
IN 66-80 G70A	THLEAKIILVAVHVA	-	-
IN 66-80 K71A	THLEGAIILVAVHVA	-	-
IN 66-80 I72A	THLEGKAILVAVHVA	-	-
IN 66-80 I73A	THLEGKIALVAVHVA	-	-
IN 66-80 L74A	THLEGKIIAVAVHVA	-	-
IN 66-80 V75A	THLEGKIILAAVHVA	-	-
IN 66-80 V77A	THLEGKIILVAAHVA	-	-
IN 66-80 H78A	THLEGKIILVAVAVA	-	-
IN 66-80 V79A	THLEGKIILVAVHAA	-	-
IN 66-79	THLEGKIILVAVHV	-	-
IN 66-78	THLEGKIILVAVH	-	-

Peptide	Sequence	Rev binding – relative spot intensity (%) *	IN binding – relative spot intensity- (%) *
IN 66-77	THLEGKIILVAV	-	-
IN 66-76	THLEGKIILVA	-	-
IN 66-75	THLEGKIILV	-	-
IN 66-74	THLEGKIIL	-	-
IN 66-73	THLEGKII	-	-
IN 67-80	HLEGKIILVAVHVA	-	-
IN 68-80	LEGKIILVAVHVA	-	-
IN 69-80	EGKIILVAVHVA	-	-
IN 70-80	GKIILVAVHVA	-	-
IN 71-80	KIILVAVHVA	-	-
IN 72-80	IILVAVHVA	-	-
IN 73-80	ILVAVHVA	-	-
IN 66-80 D-Thr66	(D-T)HLEGKIILVAVHVA	-	-
IN 66-80 D-His67	T(D-H)LEGKIILVAVHVA	-	-
IN 66-80 D-Leu68	TH(D-L)EGKIILVAVHVA	-	-
IN 66-80 D-Glu69	THL(D-E)GKIILVAVHVA	-	-
IN 66-80 D-Lys71	THLEG(D-K)IILVAVHVA	-	-

Peptide	Sequence	Rev binding – relative spot intensity (%) *	IN binding – relative spot intensity- (%) *
IN 66-80 D-Ile72	THLEGK(D-I)ILVAVHVA	-	-
IN 66-80 D-Ile73	THLEGKI(D-I)LVAVHVA	-	-
IN 66-80 D-Leu74	THLEGKII(D-L)VAVHVA	-	-
IN 66-80 D-Val75	THLEGKIIL(D-V)AVHVA	-	-
IN 66-80 D-Ala76	THLEGKIILV(D-A)VHVA	-	-
IN 66-80 D-Val77	THLEGKIILVA(D-V)HVA	-	-
IN 66-80 D-His78	THLEGKIILVAV(D-H)VA	-	-
IN 66-80 D-Val79	THLEGKIILVAVH(DV)A	-	-
IN 66-80 D-Ala80	THLEGKIILVAVHV(D-A)	-	-
IN 66-80 (N-Me)-Thr66	(N-Me)T-HLEGKIILVAVHVA	-	-
IN 66-80 (N-Me)-Leu68	TH-(N-Me)L-EGKIILVAVHVA	-	-
IN 66-80 (N-Me)-Glu69	THL-(N-Me)E-GKIILVAVHVA	-	-
IN 66-80 (N-Me)-Gly70	THLE-(N-Me)G-KIILVAVHVA	-	-
IN 66-80 (N-Me)-Lys71	THLEG-(N-Me)K-IILVAVHVA	-	-
IN 66-80 (N-Me)-Ile72	THLEGK-(N-Me)I-ILVAVHVA	-	-
IN 66-80 (N-Me)-Ile73	THLEGKI-(N-Me)I-LVAVHVA	-	-
IN 66-80 (N-Me)-Leu74	THLEGKII-(N-Me)L-VAVHVA	-	-

Peptide	Sequence	Rev binding – relative spot intensity (%) *	IN binding – relative spot intensity- (%) *
IN 66-80 (N-Me)-Val75	THLEGKIIL-(N-Me)V-AVHVA	-	-
IN 66-80 (N-Me)-Ala76	THLEGKIILV-(N-Me)A-VHVA	-	-
IN 66-80 (N-Me)-Val77	THLEGKIILVA-(N-Me)V-HVA	-	-
IN 66-80 (N-Me)-Val79	THLEGKIILVAVH-(N-Me)V-A	-	-
IN 66-80 (N-Me)-Ala80	THLEGKIILVAVHV-(N-Me)A	-	-
IN 118-128	GSNFTSTTVKA	100	100
IN 118-128 G118A	ASNFTSTTVKA	77	116
IN 118-128 S119A	GANFTSTTVKA	146	177
IN 118-128 N120A	GSAFTSTTVKA	151	198
IN 118-128 F121A	GSNATSTTVKA	31	133
IN 118-128 T122A	GSNFASTTVKA	120	228
IN 118-128 S123A	GSNFTATTVKA	182	135
IN 118-128 T124A	GSNFTSATVKA	107	231
IN 118-128 T125A	GSNFTSTAVKA	124	182
IN 118-128 V126A	GSNFTSTTAKA	64	129
IN 118-128 K127A	GSNFTSTTVAA	0	85

Peptide	Sequence	Rev binding – relative spot intensity (%) *	IN binding – relative spot intensity- (%) *
IN 118-127	GSNFTSTTVK	201	242
IN 118-126	GSNFTSTTV	0	27
IN 118-125	GSNFTSTT	0	19
IN 118-124	GSNFTST	0	34
IN 118-123	GSNFTS	0	0
IN 119-128	SNFTSTTVKA	177	207
IN 120-128	NFTSTTVKA	152	119
IN 121-128	FTSTTVKA	280	236
IN 122-128	TSTTVKA	111	135
IN 123-128	STTVKA	187	144
IN 118-128 D-Ser119	G(D-S)NFTSTTVKA	190	346
IN 118-128 D-Asn120	GS(D-N)FTSTTVKA	144	133
IN 118-128 D-Phe121	GSN(D-F)TSTTVKA	211	229
IN 118-128 D-Thr122	GSNF(D-T)STTVKA	52	58
IN 118-128 D-Ser123	GSNFT(D-S)TTVKA	124	92
IN 118-128 D-Thr124	GSNFTS(D-T)TVKA	176	150
IN 118-128 D-Thr125	GSNFTST(D-T)VKA	60	85

Peptide	Sequence	Rev binding – relative spot intensity (%) *	IN binding – relative spot intensity- (%) *
IN 118-128 D-Val126	GSNFTSTT(D-V)KA	107	97
IN 118-128 D-Lys127	GSNFTSTTV(D-K)A	53	109
IN 118-128 D-Ala128	GSNFTSTTVK(D-A)	137	136
IN 118-128 (N-Me)-Gly118	(N-Me)G-SNFTSTTVKA	294	181
IN 118-128 (N-Me)-Ser119	G-(N-Me)S-NFTSTTVKA	293	182
IN 118-128 (N-Me)-Phe121	GSN-(N-Me)F-TSTTVKA	177	195
IN 118-128 (N-Me)-Thr122	GSNF-(N-Me)T-STTVKA	200	165
IN 118-128 (N-Me)-Ser123	GSNFT-(N-Me)S-TTVKA	279	312
IN 118-128 (N-Me)-Thr124	GSNFTS-(N-Me)T-TVKA	197	249
IN 118-128 (N-Me)-Thr125	GSNFTST-(N-Me)T-VKA	168	265
IN 118-128 (N-Me)-Val126	GSNFTSTT-(N-Me)V-KA	215	273
IN 118-128 (N-Me)-Lys127	GSNFTSTTV-(N-Me)K-A	191	185
IN 118-128 (N-Me)-Ala128	GSNFTSTTVK-(N-Me)A	141	136
IN 174-188	TAVQMAVFIHNFKRK	100	100
IN 174-188 T174A	AAVQMAVFIHNFKRK	80	83
IN 174-188 V176A	TAAQMAVFIHNFKRK	106	115

Peptide	Sequence	Rev binding – relative spot intensity (%) [*]	IN binding – relative spot intensity- (%) [*]
IN 174-188 Q177A	TAVAMAVFIHNFKRK	79	83
IN 174-188 M178A	TAVQAAVFIHNFKRK	172	113
IN 174-188 V180A	TAVQMAAFIHNFKRK	222	123
IN 174-188 F181A	TAVQMAVAIHNFKRK	216	104
IN 174-188 I182A	TAVQMAVFAHNFKRK	254	156
IN 174-188 H183A	TAVQMAVFIANFKRK	121	122
IN 174-188 N184A	TAVQMAVFIHAFKRK	105	33
IN 174-188 F185A	TAVQMAVFIHNAKRK	193	134
IN 174-188 K186A	TAVQMAVFIHNFARK	176	91
IN 174-188 R187A	TAVQMAVFIHNFKAK	234	127
IN 174-188 K188A	TAVQMAVFIHNFKRA	209	109
IN 174-187	TAVQMAVFIHNFKR	114	87
IN 174-186	TAVQMAVFIHNFK	127	120
IN 174-185	TAVQMAVFIHNF	0	0
IN 174-184	TAVQMAVFIHN	0	0
IN 174-183	TAVQMAVFIH	0	0
IN 174-182	TAVQMAVFI	0	0

Peptide	Sequence	Rev binding – relative spot intensity (%) *	IN binding – relative spot intensity- (%) *
IN 174-181	TAVQMAVF	0	0
IN 175-188	AVQMAVFIHNFKRK	141	99
IN 176-188	VQMAVFIHNFKRK	104	133
IN 177-188	QMAVFIHNFKRK	135	122
IN 178-188	MAVFIHNFKRK	88	106
IN 179-188	AVFIHNFKRK	111	120
IN 180-188	VFIHNFKRK	86	132
IN 181-188	FIHNFKRK	69	133
IN 174-188 D-Thr174	(D-T)AVQMAVFIHNFKRK	141	73
IN 174-188 D-Ala175	T(D-A)VQMAVFIHNFKRK	209	105
IN 174-188 D-Val176	TA(D-V)QMAVFIHNFKRK	226	115
IN 174-188 D-Gln177	TAV(D-Q)MAVFIHNFKRK	173	154
IN 174-188 D-Met178	TAVQ(D-M)AVFIHNFKRK	196	127
IN 174-188 D-Ala179	TAVQM(D-A)VFIHNFKRK	194	142
IN 174-188 D-Val180	TAVQMA(D-V)FIHNFKRK	152	108
IN 174-188 D-Phe181	TAVQMAV(D-F)IHNFKRK	231	120
IN 174-188 D-Ile182	TAVQMAVF(D-I)HNFKRK	108	99

Peptide	Sequence	Rev binding – relative spot intensity (%) *	IN binding – relative spot intensity- (%) *
IN 174-188 D-His183	TAVQMAVFI(D-H)NFKRK	105	105
IN 174-188 D-Asn184	TAVQMAVFIH(D-N)FKRK	92	116
IN 174-188 D-Phe185	TAVQMAVFIHN(D-F)KRK	156	112
IN 174-188 D-Lys186	TAVQMAVFIHNF(D-K)RK	120	110
IN 174-188 D-Arg187	TAVQMAVFIHNFK(D-R)K	169	93
IN 174-188 D-Lys188	TAVQMAVFIHNFKR(D-K)	110	86
IN 174-188 (N-Me)-Thr174	(N-Me)T-AVQMAVFIHNFKRK	93	84
IN 174-188 (N-Me)-Ala175	T-(N-Me)A-VQMAVFIHNFKRK	86	75
IN 174-188 (N-Me)-Val176	TA-(N-Me)V-QMAVFIHNFKRK	110	118
IN 174-188 (N-Me)-Met178	TAVQ-(N-Me)M-AVFIHNFKRK	134	103
IN 174-188 (N-Me)-Ala179	TAVQM-(N-Me)A-VFIHNFKRK	66	99
IN 174-188 (N-Me)-Val180	TAVQMA-(N-Me)V-FIHNFKRK	55	67
IN 174-188 (N-Me)-Phe181	TAVQMAV-(N-Me)F-IHNFKRK	152	141
IN 174-188 (N-Me)-Ile182	TAVQMAVF-(N-Me)I-HNFKRK	107	123
IN 174-188 (N-Me)-Phe185	TAVQMAVFIHN-(N-Me)F-KRK	50	122
IN 174-188 (N-Me)-Lys186	TAVQMAVFIHNF-(N-Me)K-RK	70	130
IN 174-188 (N-Me)-Arg187	TAVQMAVFIHNFK-(N-Me)R-K	75	123

Peptide	Sequence	Rev binding – relative spot intensity (%) *	IN binding – relative spot intensity- (%) *
IN 174-188 (N-Me)-Lys188	TAVQMAVFIHNFKR-(N-Me)K	201	117

* The intensity of the spots was estimated using ImageJ. For each spot, the intensity was averaged over the spot, and the background signal was subtracted from this signal. For each peptide, the relative signal compared to the non modified peptide is presented. No estimates were made for IN 66-80 due to the low intensity of the signals, and any spot for which the intensity was below the background was assigned an intensity of 0.