

	Peptide	Sequence	N-terminus	MW	M/3
Figure 1	MPER ₍₆₆₂₋₆₈₃₎	ELDKWASLWVNFNITNWLWYIK	Biotin-PEG2-	3,467	1,157
	MPER ₍₆₆₂₋₆₈₃₎	ELDKWASLWVNFNITNWLWYIK	FITC-βAla-	3,385	1,129
	SAH-MPER ₍₆₆₂₋₆₈₃₎ (A)	XLDKXASLWVNFNITNWLWYIK	FITC-βAla-	3,320	1,108
	SAH-MPER ₍₆₆₂₋₆₈₃₎ (B)	EXDKWXSLLWVNFNITNWLWYIK	FITC-βAla-	3,451	1,151
	SAH-MPER ₍₆₆₂₋₆₈₃₎ (C)	ELXKWAXLWVNFNITNWLWYIK	FITC-βAla-	3,433	1,145
	SAH-MPER ₍₆₆₂₋₆₈₃₎ (D)	ELDKWASXWVNFNITNWLWYIK	FITC-βAla-	3,394	1,132
	SAH-MPER ₍₆₆₂₋₆₈₃₎ (E)	ELDKXASLXWVNFNITNWLWYIK	FITC-βAla-	3,263	1,089
	SAH-MPER ₍₆₆₂₋₆₈₃₎ (F)	ELDKWASLWVNFNITNWLWYIK	FITC-βAla-	3,450	1,151
	SAH-MPER ₍₆₆₂₋₆₈₃₎ (G)	ELDKWASLWVNFNITNWLWYIK	FITC-βAla-	3,335	1,113
	SAH-MPER ₍₆₆₂₋₆₈₃₎ (H)	ELDKWASLWVNFNITNWLWYIK	FITC-βAla-	3,409	1,137
	SAH-MPER ₍₆₆₂₋₆₈₃₎ (I)	ELDKWASLWVNFNITNWLWYIK	FITC-βAla-	3,348	1,117
	SAH-MPER ₍₆₆₂₋₆₈₃₎ (J)	ELDKWASLWVNFNITNWLWYIK	FITC-βAla-	3,358	1,120
	SAH-MPER ₍₆₆₂₋₆₈₃₎ (K)	ELDKWASLWVNFNITNWLWYIK	FITC-βAla-	3,336	1,113
	SAH-MPER ₍₆₆₂₋₆₈₃₎ (L)	ELDKWASLWVNFNITNWLWYIK	FITC-βAla-	3,394	1,132
	SAH-MPER ₍₆₆₂₋₆₈₃₎ (M)	ELDKWASLWVNFNITNWLWYIK	FITC-βAla-	3,407	1,137
	SAH-MPER ₍₆₆₂₋₆₈₃₎ (N)	ELDKWASLWVNFNITNWLWYIK	FITC-βAla-	3,336	1,113
	SAH-MPER ₍₆₆₂₋₆₈₃₎ (O)	ELDKWASLWVNFNITNWLWYIK	FITC-βAla-	3,421	1,141
	SAH-MPER ₍₆₆₂₋₆₈₃₎ (P)	ELDKWASLWVNFNITNWLWYIK	FITC-βAla-	3,335	1,113
	SAH-MPER ₍₆₆₂₋₆₈₃₎ (Q)	ELDKWASLWVNFNITNWLWYIK	FITC-βAla-	3,286	1,096
SAH-MPER ₍₆₆₂₋₆₈₃₎ (R)	ELDKWASLWVNFNITNWLWYIK	FITC-βAla-	3,409	1,137	
SAH-MPER ₍₆₆₂₋₆₈₃₎ (S)	ELDKWASLWVNFNITNWLWYIK	FITC-βAla-	3,321	1,108	
Figure 2	MPER _(671-683KKK)	NWFNITNWLWYIKKKK	Ac-	2,222	742
	SAH-MPER _(671-683KKK) (Q)	NWFNITNWLWYIKKKK	Ac-	2,123	709
	SAH-MPER _(671-683KKK) (q)	NWFNITNWLWYIKKKK	Ac-	2,095	699
Figure 3	SAH-MPER _(671-683KKK) (q)	NWFNITNWLWYIKKKK	Ac-	2,095	699
Figure 5	SAH-MPER _(671-683KKK) (q)pSer	NWFNITNWLWYIKKKK	Ac-	2,291	765
Figure 6	SAH-MPER ₍₆₆₂₋₆₈₃₎ (q)	ELDKWASLWVNFNITNWLWYIK	FITC-βAla-	3,258	1,087
	SAH-MPER ₍₆₆₂₋₆₈₃₎ (A,q)	XLDKXASLWVNFNITNWLWYIK	FITC-βAla-	3,194	1,066
	SAH-MPER ₍₆₆₂₋₆₈₃₎ (B,q)	EXDKWXSLLWVNFNITNWLWYIK	FITC-βAla-	3,325	1,109
	SAH-MPER ₍₆₆₂₋₆₈₃₎ (C,q)	ELXKWAXLWVNFNITNWLWYIK	FITC-βAla-	3,307	1,103
	SAH-MPER ₍₆₆₂₋₆₈₃₎ (D,q)	ELDKWASXWVNFNITNWLWYIK	FITC-βAla-	3,268	1,090
	SAH-MPER ₍₆₆₂₋₆₈₃₎ (E,q)	ELDKXASLXWVNFNITNWLWYIK	FITC-βAla-	3,136	1,046
	MPER _(662-683KKK)	ELDKWASLWVNFNITNWLWYIKKKK	Ac-	3,351	1,118
	SAH-MPER _(662-683KKK) (q)	ELDKWASLWVNFNITNWLWYIKKKK	Ac-	3,224	1,076
	SAH-MPER _(662-683KKK) (A,q)	XLDKXASLWVNFNITNWLWYIKKKK	Ac-	3,159	1,054
	SAH-MPER _(662-683KKK) (B,q)	EXDKWXSLLWVNFNITNWLWYIKKKK	Ac-	3,290	1,098
	SAH-MPER _(662-683KKK) (C,q)	ELXKWAXLWVNFNITNWLWYIKKKK	Ac-	3,272	1,092
	SAH-MPER _(662-683KKK) (D,q)	ELDKWASXWVNFNITNWLWYIKKKK	Ac-	3,233	1,079
	SAH-MPER _(662-683KKK) (E,q)	ELDKXASLXWVNFNITNWLWYIKKKK	Ac-	3,102	1,035
	Figure 7	MPER _(RRR656-683RRR)	RRRNEQELLEDKWASLWVNFNITNWLWYIRRRR	Biotin-PEG2-	5,161
MPER ₍₆₆₂₋₆₈₃₎		ELDKWASLWVNFNITNWLWYIK	FITC-βAla-	3,385	1,129
SAH-MPER ₍₆₆₂₋₆₈₃₎ (q)		ELDKWASLWVNFNITNWLWYIK	FITC-βAla-	3,258	1,087
SAH-MPER ₍₆₆₂₋₆₈₃₎ (A,q)		XLDKXASLWVNFNITNWLWYIK	FITC-βAla-	3,194	1,066
SAH-MPER ₍₆₆₂₋₆₈₃₎ (B,q)		EXDKWXSLLWVNFNITNWLWYIK	FITC-βAla-	3,325	1,109
SAH-MPER ₍₆₆₂₋₆₈₃₎ (C,q)		ELXKWAXLWVNFNITNWLWYIK	FITC-βAla-	3,307	1,103
SAH-MPER ₍₆₆₂₋₆₈₃₎ (D,q)		ELDKWASXWVNFNITNWLWYIK	FITC-βAla-	3,268	1,090
SAH-MPER ₍₆₆₂₋₆₈₃₎ (E,q)		ELDKXASLXWVNFNITNWLWYIK	FITC-βAla-	3,136	1,046
SAH-MPER _(662-683KKK) (B,q)		EXDKWXSLLWVNFNITNWLWYIKKKK	Ac-	3,290	1,054
SAH-MPER _(671-683KKK) (q)		NWFNITNWLWYIKKKK	Ac-	2,095	699
Supp		MPER _(662-683KKK)	NWFNITNWLWYIKKKK	Ac-	2,222
	SAH-MPER _(662-683KKK) (q)	NWFNITNWLWYIKKKK	Ac-	2,095	699
	SAH-MPER _(662-683KKK) (q)pSer(*683)	NWFNITNWLWYIKKKK	Ac-	2,291	765
	SAH-MPER _(662-683KKK) (q)pSer(*685)	NWFNITNWLWYIKKKK	Ac-	2,291	765
	SAH-MPER _(662-683KKK) (q)	ELDKWASLWVNFNITNWLWYIKKKK	Ac-	3,224	1,076
	SAH-MPER _(662-683KKK) (D,q)	ELDKWASXWVNFNITNWLWYIKKKK	Ac-	3,233	1,079
SAH-MPER _(662-683KKK) (B,q)	EXDKWXSLLWVNFNITNWLWYIKKKK	Ac-	3,290	1,054	

Supplementary Table 1. MPER Peptide Compositions

gp41 Residue Range		RMSD* (Å)	
		C α	All Atoms ⁺
668	683	2.4	3.3
669	683	1.6	2.7
670	683	0.6	1.8
671	683	0.6	1.0
672	683	0.5	1.0

* Comparison of atoms in native and stapled peptide chains P.

⁺ Excluding atoms unique to S5 and R3.

Supplementary Table 2. C α and all atom RMSDs comparing SAH-MPER_(662-683KKK)(B,q) and MPER_(RRR656-683RRR) peptides for residue ranges between 668-683.

A

		10E8-SAH-MPER _(662-683KKK) (B,q)			MPER _(RRR656-683RRR)		
Chain	Residue	ASA [‡] (Å ²)	BSA [§] (Å ²)	% BSA ^{§§}	ASA [‡] (Å ²)	BSA [§] (Å ²)	% BSA ^{§§}
gp41	P:SER668	127	1		83	34	
	P:LEU 669	145			131	39	
	P:TRP670	233	36		137	10	
	P:ASN671	73	31		73	32	
	P:TRP672	178	129		179	139	
	P:PHE673	163	85		148	93	
	P:ASP674	85			67		
	P:ILE 675	74			46		
	P:THR676	54	53		49	49	
	P:ASN677	123	11		99	19	
	P:R3 (678)				144		
	P:LEU 679	127	56		108	50	
	P:TRP680	169	88		131	66	
	P:S5 (681)				103		
	P:ILE 682	160	11		119	15	
	P:LYS 683	155	74		183	108	
	10E8 Heavy Chain	H:ASN 31				86	17
	H:TRP 33	30	26		33	31	
	H:ARG 50	26	11		14	5	
	H:THR 52	3	3		5	5	
	H:PRO 52B	65	1		70	30	
	H:GLY 52C	73	53		74	60	
	H:GLU 53	80	55		79	58	
	H:SER 56	52	6		53	7	
	H:ASP 58	68	3		72	7	
	H:LYS 97	115	43		111	40	
	H:TYR 98	121	4		118	4	
	H:TYR 99	111	78		111	82	
	H:PHE 100A	151	78		155	87	
	H:TRP 100B	225	45		225	29	
	H:SER 100C	94	1		93	6	
	H:GLY 100D	23	11		26	17	
	H:TYR 100E	170	33		179	26	
	H:PRO 100F	82	56		88	64	
	H:PRO 100G	140	69		133	65	
	H:GLY 100H	91	1				
	H:GLU 100I	65	3		98	1	
	H:GLU 100J	151	78		57	6	

*All interactions were performed with PISA (http://www.ebi.ac.uk/msd-srv/prot_int/cgi-bin/piserver).

‡ASA, Accessible Surface Area, Å².

§BSA, Buried Surface Area, Å².

§§Bars represent buried area percentage (100 x BSA/ASA), one bar per 10%.

Data shown are for Chain H, L, and P of the 10E8-SAH-MPER (B,q) structure and chains B, D, and F of the MPER_(RRR656-683RRR) structure.

B

		10E8-SAH-MPER _(662-683KKK) (B,q)			MPER _(RRR656-683RRR)		
Chain	Residue	ASA [‡] (Å ²)	BSA [§] (Å ²)	% BSA ^{§§}	ASA [‡] (Å ²)	BSA [§] (Å ²)	% BSA ^{§§}
gp41	P:TRP672	178	6		179	12	
	P:PHE673	163	52		148	52	
10E8 Light Chain	L:ARG 91	87	10		84	16	
	L:ARG 95B	224	46		226	55	

*All interactions were performed with PISA (http://www.ebi.ac.uk/msd-srv/prot_int/cgi-bin/piserver).

‡ASA, Accessible Surface Area, Å².

§BSA, Buried Surface Area, Å². Bars represent buried area percentage, one bar per 10%.

§§Bars represent buried area percentage (100 x BSA/ASA), one bar per 10%.

Data shown are for Chain H, L, and P of the 10E8-SAH-MPER_(662-683KKK) (B,q) structure and chains A, B, and C of the MPER_(RRR656-683RRR) structure.

Supplementary Table 3. Comparison of buried surface areas at the interface between SAH-MPER_(662-683KKK)(B,q) and MPER_(RRR656-683RRR) peptides and (A) 10E8 heavy chain and (B) 10E8 light chain.