Table S 1. Predicted peptides and their binding to FLA-E*01801 evaluated by *in vitro* refolding

Name	Derived protein	Position	sequence	IC50 (nM)	Stability with FLA I[b]
RMA9	gag protein (FIV)	39-48	RMANVSTGR	4715.8	++
KMV9	gag protein (FIV)	151-159	KMVSIFMEK	3874.3	++
DTV9	VP2 protein (FCV)	9-17	DTVTNTIGK	40839.1	--
FTA9	gag protein (FIV)	228-237	FTAAEIMGI	24185.1	--
TVN9	gag protein (FIV)	138-147	TVNGAPQYV	30832.6	--
AVM9	gag protein (FIV)	434-443	AVMPSAPPM	830.2	--
YSY9	VP2 protein (FCV)	80-88	YSYTNQNFY	2589.1	--
YVP9	VP1 protein (FPV)	560-568	YVPNNIGAM	6919.5	--
YTI9	VP1 protein (FPV)	397-405	YTIENSVPV	4226.2	--
ARM9	gag protein (FIV)	252-260	AMANVSTGR	308.4	--
KQR9	pop protein (FIV)	1031-1039	KQRGRIGGM	221.4	--
NTP9	pop protein (FIV)	213-221	NTPVFAIKK	40321.9	++
NAG9	env protein (FIV)	79-87	NAGKFRRAR	20714.8	+-
RMA9-P1A	mutant RMA9	/	AMANVSTGR	/	++
RMA9-P2A	mutant RMA9	/	RAANVSTGR	/	++
RMA9-P4A	mutant RMA9	/	RMAAVSTGR	/	++
RMA9-P5A	mutant RMA9	/	RMAVASTGR	/	++
RMA9-P6A	mutant RMA9	/	RMANVATGR	/	+-
RMA9-P7A	mutant RMA9	/	RMANVSAGR	/	++
RMA9-P8A	mutant RMA9	/	RMANVSTGR	/	++
RMA9-P9A	mutant RMA9	/	RMANVSTAR	/	+-
RMA9-P2T	mutant RMA9	/	RTANVSTGR	/	++
RMA9-P6F	mutant RMA9	/	RMANVFTGR	/	++
DTV9-P2M	mutant DTV9	/	DMVTNTIGK	/	--
DTV9-P6F	mutant DTV9	/	DTVTNFIGK	/	--
DTV9-P2MP6F	mutant DTV9	/	DMVTNFIGK	/	--
KMV9-P2T	mutant KMV	/	KTVSIFMEK	/	++

RMA9-P1D	mutant RMA9	/	DMANVSTGR	/	--
RMA9-P1I	mutant RMA9	/	IMANVSTGR	/	++
RMA9-P1T	mutant RMA9	/	TMANVSTGR	/	++
RMA9-P1Y	mutant RMA9	/	YMANVSTGR	/	++
RMA9-P1W	mutant RMA9	/	WMANVSTGR	/	++
RMA9-P1Q	mutant RMA9	/	QMANVSTGR	/	++
DTV9-P1A	mutant DTV9	/	ATVTNTIGK	/	++
DTV9-P1K	mutant DTV9	/	KANVSTGR	/	++

[a] % Random is a base value for estimating the binding affinities of peptides with the NetMHCpan 2.8 server (http://www.cbs.dtu.dk/services/NetMHCpan/): Low ID50 (nM) = good binders.

[b] ++, peptide binds strongly and can tolerate anion-exchange chromatography; +-, peptide binds FLA I but cannot tolerate anion-exchange chromatography. --, indicates no refolded product