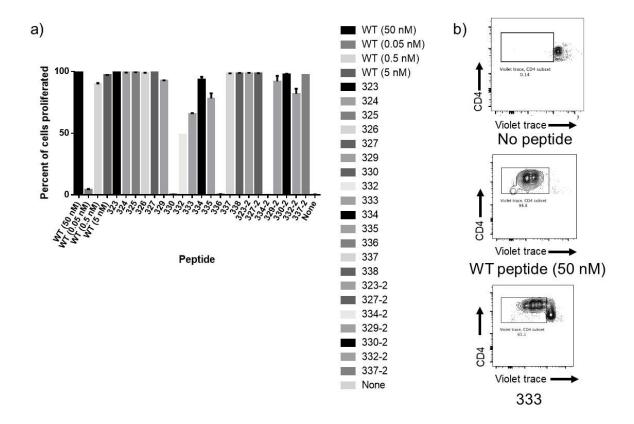
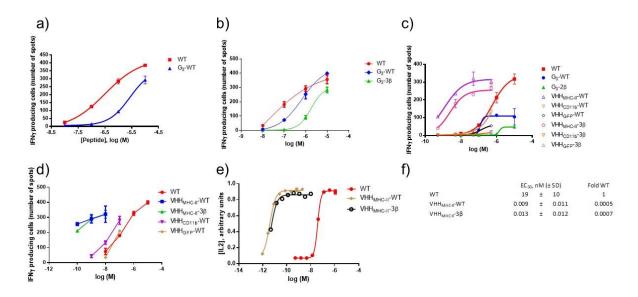
Peptide name Peptide mass calculated [M+H] Peptide mass observed Purity (%)				OT-II (I-A ^b), IFNy response DO11.10 (I-A ^d), IL2 response					response	
WT	1773.9	1773.7	>95	10 μM peptide, ELISpot			10 µM	10 μM peptide, ELISA		
323	1787.9	1787.9	>95		Average	SD		Mean	SD	
323-2	1787.9	1788.2	>9 5	WT	362	45	WT	1.23	0.082	
324	1787.9	1788.1	>95	323	351	35	323	1.12	0.064	
325	1787.9	1788.3	88	323-2	357	72	323-2	1.22	0.004	
326	1787.9	1788.5	92	324	295	107	324	1.26	0.077	
326-2	1787.9	1787.6	>95	325	368	51	325	1.31	0.043	
327	1787.9	1789.3	>95	326	383	42	326	1.23	0.217	
327-2	1787.9	1788.2	>95	326-2	ND		326-2	ND		
329	1787.9	1788.7	>95	327	381	80	327	1.18	0.066	
329-2	1787.9	1788.1	>95	327-2	343	105	327-2	0.77	0.073	
330	1787.9	1788.6	>95	329	106	41	329	0.29	0.070	
330-2	1787.9	1787.9	>95	329-2	93	14	329-2	0.28	0.048	
332	1787.9	1788.2	92	330	ND		330	ND		
332-2	1787.9	1787.8	>95	330-2	177	29	330-2	0.17	0.000	
333	1787.9	1788.2	>95	332	22	10	332	1.16	0.064	
334	1787.9	1788.2	>95	332-2	198	64	332-2	0.20	0.006	
334-2	1787.9	1787.6	77	333	7	1	333	0.13	0.014	
335	1787.9	1788.3	>95	334	11	12	334	0.19	0.009	
336	1787.9	1788.2	>95	334-2	13	6	334-2	0.15	0.006	
337	1787.9	1788.1	>95	335	53	16	335	0.50	0.037	
337-2	1787.9	1787.9	>95	336	8	7	336	0.92	0.060	
338	1787.9	1788	>95	337	339	56	337	1.18	0.012	
G_3 -WT	1944	1943.2	>95	337-2	320	33	337-2	0.97	0.050	
2β	1799.9	1800.1	93	338	399	80	338	1.19	0.046	
G_3 -3 β	1986	1985.2	87				Background	0.14	0.003	
				+++ is < 250 spots ++ is 100 <x<250 spots<br="">+ is 50<x<100 spots<="" td=""><td>+++ is < 0.9</td><td></td><td></td></x<100></x<250>			+++ is < 0.9			
							++ is 0.3 <x<0.9< td=""></x<0.9<>			
							+ is 0.2 <x<0.3< td=""></x<0.3<>			
	- is <50 spots					- is <0.2				

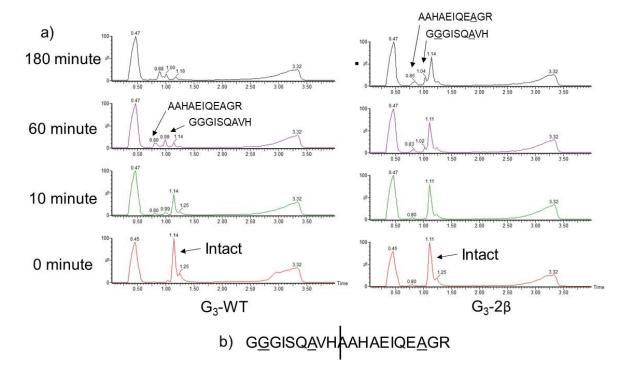
Supporting Figure 1: Tabulation of peptide analytical data (left) and T cell stimulation data (right). (Left) Observed peptide masses were recorded using mass spectrometry as described in the methods section. Peptide purities were quantified using C18 analytical HPLC. (Right) Averages represent the mean values from 4 independent experiments. SD indicates standard deviation. OT-II data represent the number of spots recorded in ELISpot assays. DO11.10 data represent the absorption recorded in an ELISA to measure media levels of IL2.



Supporting Figure 2: OT-II T cell proliferation induced by peptides. (a) Summary of OT-II proliferation in the presence of peptides at a dose indicated (50 nM, unless otherwise indicated). Proliferation was measured by flow cytometry as described in the methods section. Error bars represent standard deviation from replicate 2 or 3 experiments. (b) Representative flow cytometry plots measuring dye dilution of OT-II T cells in response to the peptide listed below the plot.



Supporting Figure 3. Effective stimulation of T cells by VHH_{MHC-II}-peptide conjugates. (**a-d**) Dose-response curves for stimulation of IFN γ release by peptides or VHH-peptide conjugates. Note that each of these panels have data from independent experiments. OT-II splenocytes were stimulated overnight and IFN γ production was measured using ELISpot as described in the methods section. (**e**) Representative dose-response curve for stimulation of IL2 release from DO11.10 cells. Data points are mean \pm SD and curves result from the fitting of four parameter dose-response model. (**f**) Tabulation of dose-response values for peptides and active VHH-peptide conjugates. Data are from \geq 2 independent experiments. Data in this table for WT are identical to those presented in Figure 3.



Supporting Figure 4: Characterization of peptide degradation by cathepsin S. (a) LC/MS spectra total ion chromatographs of peptides at indicated durations of incubation with protease. The peaks corresponding to the intact peptide and the fragments observed, as determined by mass spectra, are indicated in specific panels. Positions of β -residue incorporation are underlined. Retention times of peaks (m) are listed above the corresponding peaks. (b) Position of site of cleavage for each of the peptides tested. The bond cleavage by cathepsin S is indicated by the vertical line. Sites of β -residue incorporation in G₃-3 β are underlined.