S1 Table. Analysis of MHCI-derived tryptic peptides from KG-1 cells.

					Experiment 1 (p = 4.2%) [a]						Experiment 2 (p = 4.9%) [a, d]					
					Unlabeled		Fully labeled				Unlabeled		Labeled			
Molecule	Sequence [b]	Residues [c]	Calculated *m/z*	Observed *m/z*	*z*	Abundance	RMSD	Abundance	RMSD	n [e]	FSR (%/h, mean ± SEM) [f]	Abundance	RMSD	Abundance	RMSD	n [e]	FSR (%/h, mean ± SEM) [f]
HLA-A30	FDSDAASQR	36-44	498.72	498.72	2	2.79E+07	0.18%	5.30E+07	0.07%	13	5.59 ± 0.56	1.39E+08	0.25%	7.87E+07	0.35%	13	6.22 ± 0.41
	GYEQHAYDGK	112-121	584.26	584.26	2	7.11E+06	1.80%	5.95E+06	0.47%	12	6.21 ± 0.64	8.92E+06	0.47%	8.00E+06	0.52%	11	7.08 ± 0.57
	RAEQLR	152-157	386.73	386.73	2	2.93E+07	0.92%	6.88E+07	0.57%	7	5.29 ± 0.45	1.41E+08	0.46%	7.09E+07	0.42%	7	5.67 ± 0.46
	SWATAADM[ox]AAQITQR	132-145	783.38	783.38	2	2.23E+07	0.92%	3.98E+07	0.16%	16	5.84 ± 0.74	2.25E+07	0.14%	5.23E+07	0.31%	18	4.50 ± 0.22
	APWIEQERPEYWDQETR	49-65	745.02	745.02	2	5.71E+07	0.52%	1.30E+08	0.37%	25	7.71 ± 0.58	2.06E+08	2.19%	1.71E+08	0.27%	30	6.69 ± 0.32
	KGGSYTQAASSDSAQGSDVSLTACK	316-340	826.05	826.05	3							1.62E+07	0.53%	3.52E+07	0.24%	26	6.01 ± 0.49
HLA-B iso	DGEDQTQDTELVETRPAGDR	220-239	744.68	744.68	2	3.37E+08	0.36%	3.70E+08	0.23%	32	8.19 ± 0.33	2.06E+08	0.34%	1.68E+08	0.22%	32	6.68 ± 0.32
	DYIALNEDLSSWTAADTAAQITQR	122-145	885.10	885.10	3	1.96E+07	0.30%	7.67E+07	0.20%	31	6.43 ± 0.37	3.95E+06	0.20%	2.64E+07	0.25%	33	5.21 ± 0.32
	GGSYSQAASSDSAQGSDVSLTA	317-338	1023.45	1023.45	2	3.30E+07	0.15%	5.75E+07	0.35%	26	6.58 ± 0.66	1.60E+07	0.47%	1.02E+07	0.40%	27	5.96 ± 0.44
HLA-B78	GHNQYAYDGK	112-121	576.76	576.76	2	1.94E+07	0.18%	1.85E+07	0.62%	8	5.89 ± 0.57	1.74E+07	0.31%	1.40E+07	0.39%	10	6.28 ± 0.77
HLA-B53	(none found)																
HLA-C iso	GGSCSQAASSNSAQGSDESLIACK	318-341	1186.52	1186.52	2	1.88E+06	0.95%	4.18E+06	0.25%	29	7.05 ± 1.12	7.88E+06	0.22%	8.56E+06	0.14%	31	9.09 ± 1.09
HLA-C4	EPWVEQEGPEYWDR	49-62	910.40	910.40	2							5.20E+06	1.21%	2.39E+07	0.87%	21	11.1 ± 0.67
	GYNQFAYDGK	112-121	581.76	581.76	2							3.50E+06	0.67%	7.57E+06	0.03%	9	10.3 ± 1.20
HLA-C16	GYDQSAYDGK	112-121	552.24	552.24	2	2.83E+06	0.49%	7.90E+06	0.62%	12	10.2 ± 1.28						
	APWVEQEGPEYWDR	49-62	881.40	881.40	2							1.61E+07	0.34%	7.15E+07	0.38%	23	10.8 ± 1.00
	Cell growth rate										1.90 ± 0.01						2.55 ± 0.07

Notes:

[a] $^{2}H_2O$ enrichment in media (average of samples), used as precursor pool enrichment (p) in MIDA models.

[b] Peptides were selected for allele- or isotype specificity, as described in text, and filtered to meet analytical criteria as described in Methods. Single-letter code ("ox" is M oxidation). The four N-terminal amino acids were used to identify the peptides in Fig. 3. Note that different peptides met analytical requirements in the two experiments (blanks = not detected or not suitable for analysis), yet fractional synthesis rates remained similar.

[c] Numbering from 1 = N terminus of mature polypeptide as specified in the IMGT/HLA database.

[d] Results from Experiment 2 are shown in Fig. 3.

[e] Number of labeling sites used in MIDA models. RMSD values are for deviations between modeled and observed mass isotopomer distributions.

[f] Fractional synthesis rate (per cent new protein per hour) calculated from curve fits for individual peptides. Peptides from the same allele or isotype yielded statistically indistinguishable values from one another ($p > 0.05$, F test), so pooled data were used in Fig. 3.