Table S3. Analysis of MHCI-derived peptides from MoDCs.

AS1 [A2, 3; B8, 41; C7, 17] [a]

						Unlabeled		72 h labeled (p = 4.75%) [e]				
Molecule	**Residues**	**Sequence** [b]	***m/z* (pred)** [c]	***m/z* (obs)**	***z***	**Abundance**	**RMSD (%)** [d]	**Abundance**	**RMSD (%)**	**n**	***k* (%/h)** [f]	***k* iso (%/h)**
A2	98-108	`MYGCDVGSDWR`	673.27	673.27	2	2.00E+07	0.41%	1.42E+07	0.40%	7	9.09 ± 1.15	9.62 ± 0.83
A2	132-144	`SWTAADMAAQTTK`	691.32	691.33	2	3.99E+07	0.68%	2.20E+07	0.35%	9	7.89 ± 2.07	
A2	316-341	`KGGSYSQAASSDSAQGSDVSLTACKV`	854.40	854.40	3	6.94E+06	0.29%	1.16E+07	0.17%	14	7.88 ± 2.08	
A iso	76-82	`VDLGTLR`	387.23	387.23	2	1.57E+08	0.61%	1.13E+08	1.55%	5	12.1 ± 0.85	
A iso	36-44	`FDSDAASQR`	498.72	498.72	2	4.81E+06	0.43%	1.33E+06	0.48%	9	10.9 ± 2.41	
B41	36-44	`FDSDATSPR`	498.23	498.23	2	2.09E+07	4.84%	6.05E+05	0.48%	10	10.6 ± 3.24	10.3 ± 0.86
B iso	49-62	`APWIEQEGPEYWDR`	888.41	888.40	2	6.19E+07	0.17%	4.88E+07	0.38%	15	12.8 ± 1.15	
B iso	220-239	`DGEDQTQDTELVETRPAGDR`	1116.50	1116.50	2	3.28E+06	0.37%	2.77E+06	0.76%	25	9.49 ± 1.61	
B iso	317-338	`GGSYSQAACSDSAQGSDVSLTA`	1059.95	1059.95	2	1.09E+07	0.46%	7.42E+06	0.27%	13	9.01 ± 1.24	

HD1 [A1, 2; B37, 49; Cw6, w7] [a]

						Unlabeled		72 h labeled (p = 4.93%) [e]				
Molecule	**Residues**	**Sequence** [b]	***m/z* (pred)** [c]	***m/z* (obs)**	***z***	**Abundance** [g]	**RMSD (%)** [d]	**Abundance**	**RMSD (%)**	**n**	***k* (%/h)** [f]	**k_{iso} (%/h)**
A1	49-65	`APWIEQEGPEYWDQETR`	1067.48	1067.48	2	*1.17E+07*		2.25E+07	1.28%	20	5.78 ± 2.62	5.75 ± 1.00
A2	98-108	`MYGCDVGSDWR`	673.27	673.27	2	*5.95E+06*		1.82E+07	0.97%	5	6.17 ± 1.04	
A iso	22-35	`FIAVGYVDDTQFVR`	815.42	815.41	2	*1.01E+08*		1.42E+08	0.14%	7	5.23 ± 0.81	
B iso	49-62	`APWIEQEGPEYWDR`	888.41	888.40	2	*9.29E+06*		3.27E+07	0.94%	13	7.23 ± 2.06	7.23 ± 2.06
C iso	132-145	`SWTAADTAAQITQR`	760.38	760.38	2	*2.25E+06*		5.44E+06	1.10%	9	6.90 ± 2.43	6.90 ± 2.43

HD2 [A2, 32; B35, 60 *(*40:01)* ; Cw4, w10 *(*03:04)*] [a]

						Unlabeled		72 h labeled (p = 4.98%) [e]				
Molecule	**Residues**	**Sequence** [b]	***m/z* (pred)** [c]	***m/z* (obs)**	***z***	**Abundance** [g]	**RMSD (%)** [d]	**Abundance**	**RMSD (%)**	**n**	***k* (%/h)** [f]	**k_{iso} (%/h)**
A2	132-144	`SWTAADM[ox]AAQTTK`	699.32	699.33	2	*2.49E+06*		2.07E+06	0.92%	8	6.35 ± 1.11	6.37 ± 0.46
A32	49-65	`APWIEQEGPEYWDQETR`	1067.48	1067.48	2	*4.68E+06*		4.36E+06	0.58%	17	5.50 ± 0.84	
A32	112-131	`GYQQDAYDGKDYIALNEDLR`	783.03	783.04	3	*2.16E+07*		1.11E+07	0.45%	21	7.51 ± 0.11	
B35	98-108	`MYGCDLGPDGR`	620.76	620.76	2	*9.54E+06*		1.00E+07	0.41%	7	17.5 ± 1.12	(14.2 ± 2.52) (p = 0.039)
B60	132-145	`SWTAADTAAQISQR`	753.37	753.37	2	*1.89E+07*		5.10E+06	0.37%	11	11.1 ± 2.13	

HD3 [A2, 24; B27, 51; C14, 15] [a]

						Unlabeled		72 h labeled (p = 4.16%) [e]				
Molecule	**Residues**	**Sequence** [b]	***m/z* (pred)** [c]	***m/z* (obs)**	***z***	**Abundance** [g]	**RMSD (%)** [d]	**Abundance**	**RMSD (%)**	**n**	***k* (%/h)** [f]	**k_{iso} (%/h)**
A iso	158-169	`AYLEGTCVDGLR`	677.33	677.33	2	*7.75E+06*		5.60E+06	0.69%	8	5.89 ± 2.21	5.89 ± 2.21
B iso	49-62	`APWIEQEGPEYWDR`	888.41	888.40	2	*8.21E+06*		1.62E+07	0.28%	15	6.24 ± 1.69	6.24 ± 1.69

HD4 [A3, 24; B7, 27; Cw2, w7] [a]

						Unlabeled		72 h labeled (p = 5.08%) [e]				
Molecule	**Residues**	**Sequence** [b]	***m/z* (pred)** [c]	***m/z* (obs)**	***z***	**Abundance** [g]	**RMSD (%)** [d]	**Abundance**	**RMSD (%)**	**n**	***k* (%/h)** [f]	**k_{iso} (%/h)**
A3	316-341	`KGGSYTQAASSDSAQGSDVSLTACKV`	859.07	859.08	3	*1.10E+07*		2.53E+06	0.21%	10	8.47 ± 1.61	7.80 ± 0.65
A3	158-169	`AYLDGTCVEWLR`	741.86	741.86	2	*4.11E+07*		6.52E+06	0.48%	8	5.61 ± 0.86	
A3	132-144	`SWTAADMAAQITK`	697.34	697.34	2	*2.96E+07*		4.96E+06	0.32%	7	7.43 ± 1.49	
A3	132-144	`SWTAADM[ox]AAQITK`	705.34	705.34	2	*2.36E+07*		3.62E+06	0.74%	8	6.01 ± 1.85	
A3	115-131	`QDAYDGKDYIALNEDLR`	666.99	666.99	3	*6.15E+07*		1.02E+07	0.30%	17	7.19 ± 1.00	
A3	49-65	`APWIEQEGPEYWDQETR`	1067.48	1067.48	2	*1.30E+07*		3.45E+06	0.28%	17	6.35 ± 1.18	
A24	158-169	`AYLEGTCVDGLR`	677.33	677.33	2	*2.91E+07*		6.56E+06	0.19%	7	12.3 ± 2.27	
A iso	22-35	`FIAVGYVDDTQFVR`	815.42	815.42	2	*8.99E+07*		3.76E+07	0.60%	7	11.1 ± 2.30	
B7	112-131	`GHDQYAYDGKDYIALNEDLR`	786.03	786.03	3	3.42E+07		3.49E+06	0.49%	16	13.6 ± 2.82	12.3 ± 1.53

B iso	49-62	`APWIEQEGPEYWDR`	888.41	888.40	2	*1.16E+08*		4.09E+07	0.40%	13	11.2 ± 1.53	12.3 ± 1.53

HD4 [A3, 24; B7, 27; Cw2, w7] [a] **(LPS-stimulated)**

						Unlabeled		**72 h labeled** (p = 5.02%) [e]				
Molecule	**Residues**	**Sequence** [b]	***m/z* (pred)** [c]	***m/z* (obs)**	***z***	**Abundance** [g]	**RMSD (%)** [d]	**Abundance**	**RMSD (%)**	**n**	***k* (%/h)** [f]	**k_{iso} (%/h)**
A3	316-341	`KGGSYTQAASSDSAQGSDVSLTACKV`	859.07	859.08	3	*1.08E+07*		6.07E+07	0.53%	10	4.41 ± 3.22	4.20 ± 0.99
A3	158-169	`AYLDGTCVEWLR`	741.86	741.86	2	*4.11E+07*		1.73E+08	0.58%	6	2.95 ± 3.53	
A3	132-144	`SWTAADM[ox]AAQITK`	705.34	705.34	2	*2.34E+07*		6.59E+07	0.74%	7	2.94 ± 4.67	
A3	115-131	`QDAYDGKDYIALNEDLR`	666.99	666.99	3	*5.75E+07*		1.89E+08	0.50%	15	4.55 ± 1.43	
A3	49-65	`APWIEQEGPEYWDQETR`	1067.48	1067.48	2	*1.79E+07*		1.31E+08	0.53%	16	3.91 ± 2.18	
A24	158-169	`AYLEGTCVDGLR`	677.33	677.33	2	*2.90E+07*		1.55E+08	0.30%	7	5.75 ± 7.69	
A24	316-341	`KGGSYSQAASSDSAQGSDVSLTACKV`	854.40	854.40	3	*4.25E+06*		4.93E+07	0.45%	11	6.02 ± 3.36	
A iso	22-35	`FIAVGYVDDTQFVR`	815.42	815.42	2	*8.90E+07*		6.20E+08	0.26%	6	4.45 ± 2.34	
B27	22-35	`FITVGYVDDTLFVR`	822.94	822.93	2	*7.40E+07*		6.21E+08	0.08%	5	4.95 ± 4.83	4.91 ± 2.06
B iso	49-62	`APWIEQEGPEYWDR`	888.41	888.40	2	*1.16E+08*		1.04E+09	0.13%	12	4.86 ± 1.58	

HD5 [A2, 11; B27, 60 *(*40:01)* ; Cw1, w10 *(*03:02)*] [a]

						Unlabeled		**72 h labeled** (p = 4.78%) [e]				
Molecule	**Residues**	**Sequence** [b]	***m/z* (pred)** [c]	***m/z* (obs)**	***z***	**Abundance** [g]	**RMSD (%)** [d]	**Abundance**	**RMSD (%)**	**n**	***k* (%/h)** [f]	**k_{iso} (%/h)**
A2	49-65	`APWIEQEGPEYWDGETR`	688.31	688.31	3	*8.29E+06*		5.61E+06	0.43%	17	13.9 ± 1.68	9.51 ± 0.78
A2	244-256	`WAAVVVPSGQEQR`	713.88	713.88	2	*4.63E+07*		9.79E+06	0.53%	6	9.39 ± 1.85	
A2	132-144	`SWTAADMAAQTTK`	699.32	699.32	2	*4.61E+06*		2.45E+06	0.40%	7	7.01 ± 1.30	
A11	49-65	`APWIEQEGPEYWDQETR`	1067.48	1067.48	2	*1.12E+07*		2.88E+06	0.53%	16	6.92 ± 0.61	
A11	115-131	`QDAYDGKDYIALNEDLR`	666.99	666.98	3	*2.74E+07*		7.15E+06	0.36%	18	9.62 ± 2.30	
A iso	220-243	`DGEDQTQDTELVETRPAGDGTFQK`	879.74	879.74	3	*8.02E+07*		4.20E+07	0.21%	22	14.3 ± 2.59	
B40	132-145	`SWTAADTAAQISQR (3+)`	502.58	502.58	3	*2.61E+07*		4.77E+06	0.34%	10	10.3 ± 2.79	12.1 ± 1.51
B40	132-145	`SWTAADTAAQISQR (2+)`	753.37	753.37	2	*4.99E+07*		6.05E+06	0.26%	9	11.9 ± 2.90	
B iso	220-239	`DGEDQTQDTELVETRPAGDR`	744.67	744.67	3	*1.49E+08*		4.51E+07	0.32%	23	14.0 ± 1.99	
Cw1	112-131	`GYDQYAYDGKDYIALNEDLR`	794.70	794.73	3	*6.15E+07*		4.51E+06	0.55%	18	25.9 ± 7.26	23.7 ± 2.72
C iso	132-145	`SWTAADTAAQITQR`	760.38	760.38	2	*2.15E+07*		3.08E+06	0.59%	9	25.4 ± 4.98	
C iso	318-341	`GGSCSQAASSNSAQGSDESLIACK`	791.34	791.34	3	*4.87E+06*		7.93E+05	0.40%	14	15.6 ± 4.71	
C iso	257-273	`YTCHVQHEGLPEPLTLR (3+)`	684.01	684.01	3	*8.83E+06*		2.78E+06	0.84%	10	34.8 ± 5.85	
C iso	257-273	`YTCHVQHEGLPEPLTLR (4+)`	513.26	513.26	4	*4.50E+06*		6.47E+06	0.35%	9	20.7 ± 6.35	

HD6 [A1, 24; B8, 27; Cw2, Cw7] [a]

						Unlabeled		**72 h labeled** (p = 5.11%) [e]				
Molecule	**Residues**	**Sequence** [b]	***m/z* (pred)** [c]	***m/z* (obs)**	***z***	**Abundance** [g]	**RMSD (%)** [d]	**Abundance**	**RMSD (%)**	**n**	***k* (%/h)** [f]	**k_{iso} (%/h)**
A1	115-131	`QDAYDGKDYIALNEDLR`	666.99	666.99	3	*7.36E+07*		4.98E+07	0.34%	20	7.23 ± 0.29	10.7 ± 1.26
A24	36-44	`FDSDAASQR`	498.72	498.72	2	*5.96E+07*		1.32E+07	0.39%	10	10.9 ± 4.33	
A24	49-66	`APWIEQEGPEYWDEETGK`	1082.48	1082.479	2	*2.33E+07*		1.42E+07	0.55%	21	14.4 ± 2.97	
A24	316-341	`KGGSYSQAASSDSAQGSDVSLTACKV`	854.40	854.40	3	*8.91E+06*		3.60E+07	0.60%	17	8.14 ± 2.98	
A iso	22-35	`FIAVGYVDDTQFVR`	815.42	815.42	2	*1.91E+08*		1.94E+08	0.23%	9	13.6 ± 4.12	
A iso	220-243	`DGEDQTQDTELVETRPAGDGTFQK`	879.74	879.74	3	*2.08E+08*		2.49E+08	0.42%	26	12.6 ± 2.49	
B8	7-17	`YFDTAM[ox]SRPGR`	658.81	658.81	2	*9.63E+06*		4.20E+06	0.38%	12	9.79 ± 2.30	13.1 ± 1.26
B8	171-181	`YLENGKDTLER`	669.34	669.34	2	*4.81E+07*		6.29E+06	0.71%	9	20.2 ± 5.03	
B8	112-131	`GHNQYAYDGKDYIALNEDLR`	785.71	785.71	3	*3.67E+07*		3.92E+07	0.38%	16	10.7 ± 2.06	
B27	22-35	`FITVGYVDDTLFVR`	822.94	822.94	2	*1.72E+08*		1.22E+08	0.43%	8	18.3 ± 6.48	
B iso	49-62	`APWIEQEGPEYWDR`	592.61	592.61	3	*7.65E+06*		7.26E+06	0.88%	15	9.46 ± 1.70	
B iso	220-239	`DGEDQTQDTELVETRPAGDR`	744.67	744.68	3	*3.29E+08*		2.40E+08	0.23%	25	14.1 ± 2.98	

HD7 [A24, 30; B13, 27; Cw2, w6] [a]

						Unlabeled		**72 h labeled** (p = 4.76%) [e]				

Molecule	Residues	Sequence [b]	*m/z* (pred) [c]	*m/z* (obs)	*z*	Abundance [g]	RMSD (%) [d]	Abundance	RMSD (%)	n	*k* (%/h) [f]	k_{iso} (%/h)
A iso	36-44	FDSDAASQR	498.72	498.73	2	*6.29E+07*		2.62E+06	0.59%	8	12.4 ± 3.02	14.4 ± 1.93
A iso	220-243	DGEDQTQDTELVETRPAGDGTFQK	879.74	879.75	3	*5.00E+07*		1.70E+08	0.46%	23	16.4 ± 2.86	
B13	22-35	FITVGYVDDTQFVR	830.42	830.43	2	*7.61E+07*		1.28E+08	0.24%	7	11.9 ± 1.22	11.5 ± 1.32
B27	22-35	FITVGYVDDTLFVR	822.94	822.95	2	*5.64E+07*		6.79E+07	0.36%	7	12.4 ± 0.60	
B iso	49-62	APWIEQEGPEYWDR	888.41	888.42	2	*9.30E+07*		2.66E+07	0.29%	13	13.3 ± 3.55	
B iso	220-239	DGEDQTQDTELVETRPAGDR	1116.50	1116.52	2	*2.92E+07*		9.29E+06	0.57%	22	7.99 ± 2.69	

HD8 [A2, A2, B15, B35, C10 *(*0302)* , C4] [a]

						Unlabeled		**72 h labeled** (p = 4.96%) [e]				
Molecule	**Residues**	**Sequence** [b]	***m/z* (pred)** [c]	***m/z* (obs)**	***z***	**Abundance**	**RMSD (%)** [d]	**Abundance**	**RMSD (%)**	**n**	***k* (%/h)** [f]	**k_{iso} (%/h)**
A2	317-340	GGSYSQAASSDSAQGSDVSLTACK	1167.51	1167.52	2	2.46E+06	1.61%	4.37E+06	0.28%	14	9.00 ± 6.29	11.0 ± 1.80
A2	220-243	DGEDQTQDTELVETRPAGDGTFQK	879.74	879.74	3	1.40E+08	0.06%	1.16E+09	0.63%	21	12.7 ± 2.82	
B15	152-157	EAEQWR	409.69	409.70	2	1.27E+07	1.82%	2.88E+08	0.50%	7	11.7 ± 4.02	14.3 ± 1.46
B iso	49-62	APWIEQEGPEYWDR	888.41	888.41	2	1.98E+08	0.17%	3.25E+09	0.56%	12	14.3 ± 2.14	
B iso	317-338	GGSYSQAASSDSAQGSDVSLTA	1023.45	1023.46	2	4.59E+07	4.20%	5.75E+08	0.55%	13	18.2 ± 1.30	
B iso	220-239	DGEDQTQDTELVETRPAGDR	744.67	744.68	3	2.51E+08	0.16%	6.03E+09	0.83%	19	14.2 ± 2.61	
C10	18-35	GEPHFIAVGYVDDTQFVR	684.01	684.01	3	1.40E+07	1.39%	1.62E+08	0.14%	13	14.9 ± 5.31	15.9 ± 2.52
C iso	122-131	DYIALNEDLR	611.31	611.31	2	4.31E+06	2.11%	3.06E+07	0.31%	12	15.6 ± 5.43	
Ciso	132-145	SWTAADTAAQITQR	760.38	760.38	2	1.44E+07	0.31%	1.72E+08	0.17%	13	15.2 ± 1.56	
Ciso	256-273	YTCHVQHEGLPEPLTLR	684.01	684.01	3	5.19E+06	1.41%	8.48E+07	0.40%	12	18.8 ± 12.3	

HD8 [A2, A2, B15, B35, C10 *(*0302)* , C4] [a] **(LPS stimulated)**

						Unlabeled		**72 h labeled** (p = 4.65%) [e]				
Molecule	**Residues**	**Sequence** [b]	***m/z* (pred)** [c]	***m/z* (obs)**	***z***	**Abundance**	**RMSD (%)** [d]	**Abundance**	**RMSD (%)**	**n**	***k* (%/h)** [f]	**k_{iso} (%/h)**
A2	49-65	APWIEQEGPEYWDGETR	1031.96	1031.97	2	1.92E+08	0.67%	6.55E+07	0.81%	9	6.87 ± 0.65	(5.18 ± 0.88)
A2	220-243	DGEDQTQDTELVETRPAGDGTFQK	879.74	879.74	3	8.20E+08	0.11%	5.61E+07	0.50%	28	3.58 ± 0.60	(p = 0.031)
B15	152-157	EAEQWR	409.69	409.70	2	1.62E+08	0.75%	6.77E+06	0.39%	8	4.15 ± 0.69	4.49 ± 0.90
B35	98-108	MYGCDLGPDGR	620.76	620.76	2	5.16E+07	2.11%	1.01E+07	0.86%	6	4.54 ± 4.43	
B iso	49-62	APWIEQEGPEYWDR	888.41	888.41	2	1.58E+09	0.08%	1.43E+08	0.41%	15	4.65 ± 0.83	
B iso	220-239	DGEDQTQDTELVETRPAGDR	744.67	744.68	3	2.05E+09	0.18%	1.13E+08	0.78%	24	4.64 ± 0.75	
C10	18-35	GEPHFIAVGYVDDTQFVR	684.01	684.01	3	9.59E+07	1.54%	9.69E+06	1.00%	12	8.54 ± 1.09	9.06 ± 0.72
C iso	122-131	DYIALNEDLR	611.31	611.31	2	5.40E+07	1.05%	4.33E+06	0.88%	13	10.1 ± 1.65	
Ciso	132-145	SWTAADTAAQITQR	760.38	760.38	2	1.13E+08	0.48%	9.41E+06	0.16%	15	8.58 ± 1.48	

Notes:

[a] HLA types: given as serotypes (numerically equivalent to 2-digit genotypes except where noted in parentheses, in *italics).*
By default, the 4-digit subtypes most prevalent in Caucasians were used for alignments (usually *xx:01). B27 was assumed to be B*27:05.

[b] All peptides used for kinetic analysis are shown (single-letter code). Residue numbering is based on the mature protein sequence, with signal sequence cleavage as per the IMGT/HLA database.

[c] m/z: mass to charge ratio, predicted from monoisotopic elemental masses or observed in Orbitrap mass spectra as indicated. Abundances were summed over all mass isotopomers used in the analysis.

[d] RMSD, root mean square deviation of observed mass isotopomer distributions, as compared with MIDA models.

[e] "p" represents measured 2H2O enrichment in media. "n", number of labeling sites that yields best fit to MIDA models at this enrichment.

[f] "*k*" represents fractional synthesis rates (% per hour, mean ± SE) based on single-exponential curve fit to data. "k_{iso}" represents pooled data for isotypes shown in Figs 5-8.
Where k_{iso} values are shown in parentheses, the *k* values for individual peptides were significantly different (p value shown, F test).

[g] Abundances in *Italics* / RMSD blank: some unlabeled sample data acquired at 30,000 resolution, resulting in bias (R.B. et al., unpublished data).
Where abundances are in plain font reported and RMSD values are given, mass spectra were acquired at 7,500 resolution.
For consistency, fractional synthesis rates for all MoDC samples were calculated using the unlabeled MIDA model for baseline subtraction.
(Where available, baseline subtraction using unlabeled data acquired at 7,500 resolution yielded similar results.)