SUPPLEMENTAL MATERIAL

Archbold et al., http://www.jem.org/cgi/content/full/jem.20082136/DC1

Table S1. Data collection and refinement statistics

	HLA-B*4402^{EENL}	HLA-B*4403^{EENL}	HLA-B*4405^{EENL}	DM1 TCR	DM1–HLA-B*4405^{EENL}
Data collection					
Space group	$P2_12_12_1$	$P2_12_12_1$	$P2_12_12_1$	$P2_1$	$P\ 6_5\ 2\ 2$
Cell dimensions					
a, b, c (Å)	50.7, 81.95, 109.77	50.41, 81.79, 109.1	50.78, 82.35, 110.14	41.74, 70.73, 154.41	121.95, 121.95, 695.91
α, β, γ (°)	90, 90, 90	90, 90, 90	90, 90, 90	90, 94.67, 90	90, 90, 120
Resolution (Å)	1.7	1.6	2.1	2.75	3.5
R_{pim} or R_{merge}	6 (31.9)	2.9 (18.5)	3 (18)	6.3 (15.4)	6.4 (10.9)
$I/\sigma I$	19.2 (3.4)	6.3 (2.2)	27.4 (4.9)	11.8 (4.4)	4.8 (2.8)
Completeness (%)	94.8 (95.8)	97.9 (87.5)	96 (95)	96.3 (100)	98.8 (99.3)
Multiplicity	3.9	6.6	3.6	3.9	7.1
Refinement					
Resolution (Å)	1.7	1.6	2.1	2.75	3.5
No. reflections	51,015	60,310	27,685	23,540	40,244
R_{work}/R_{free}	20.8/25.1	18.3/21	19.3/25.2	20.1/26.3	28.5/32.9
No. atoms					
Protein	3,447	3,353	3,258	7,098	20,171
Ligand/ion	48	28	12	0	0
Water	480	401	223	159	0
B-factors					
Protein	19.52	19.26	28.92	43.5	71.7
Ligand/ion	47.13	41.7	65.07	–	–
Water	33.23	34.19	34.2	35.44	–
r.m.s. deviations					
Bond lengths (Å)	0.008	0.006	0.011	0.011	0.008
Bond angles (°)	1.206	1.12	1.435	1.49	1.346

Values in parentheses are for highest resolution shell.

Table S2. Sequence conservation between the CDR loops in DM1 and LC13

	DM1	LC13
CDR1α	TISGNEY	TISGTDY
CDR2α	GLKN	GLTSN
CDR3α	IVWGGYQKVT	ILPLAGGTSYGKLT
CDR1β	SEHNR	SGHVSL
CDR2β	FQNEAQ	FQNEAQ
CDR3β	ASRYRDDSYNEQF	ASSLGQAYEQY

Table S3. TCR α chain homology of EENL-specific receptors

Donor[a]	TRAV[b]	CDR3												TRAJ[b]	Frequency[c]
DM	26	C	I	V	W	G	G	Y	Q	K	V	T	F	13*02	12/12
		tgt	atc	gtc	tgg	ggg	ggt	tac	cag	aaa	gtt	acc	ttt		
EM	5	C	A	E	W	R	G	Y	Q	K	V	T	F	13*01	6/7
		tgt	gca	gag	tgg	cgg	ggt	tac	cag	aaa	gtt	acc	ttt		
PM	5	C	A	E	W	R	G	Y	Q	K	V	T	F	13*02	7/7
		tgt	gca	gag	tgg	agg	ggt	tac	cag	aaa	gtt	acc	ttt		
EM	5	C	A	E	W	K	G	Y	Q	K	V	T	F	13*02	1/7
		tgt	gca	gag	tgg	aag	ggt	tac	cag	aaa	gtt	acc	ttt		

Germline-encoded nucleotides are highlighted in gray.

[a]The first two letters designate the donor origin of the TCR transcript.

[b]The designations TRAV and TRAJ follow the IMGT TCR gene nomenclature (Lefranc, M.-P., V. Giudicelli, Q. Kaas, E. Duprat, J. Jabado-Michaloud, D. Scaviner, C. Ginestoux, O. Clement, D. Chaume, and G. Lefranc. 2005. IMGT, the international ImMunoGeneTics information system. *Nucleic Acids Res.* 33:D593–D597).

[c]Frequency of TRAV TCR transcript in the sequence bacterial clones.