

SUPPLEMENTAL MATERIAL

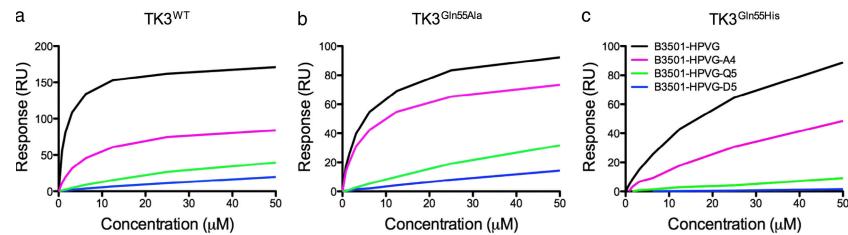
Gras et al., <http://www.jem.org/cgi/content/full/jem.20100603/DC1>

Figure S1. SPR analysis of the TK3^{WT}, TK3^{Gln55His}, and TK3^{Gln55Ala} TCRs with HLA-B*3501 bound to HPVG and its natural variants. (a–c) Binding curves for the TK3^{WT} (a), TK3^{Gln55Ala} (b), and TK3^{Gln55His} (c) TCRs are shown using graded concentrations of HLA-B*3501 bound to HPVG or variant peptides (only showing from 50 to 0 μM). The experiments were conducted in duplicate with very similar results.

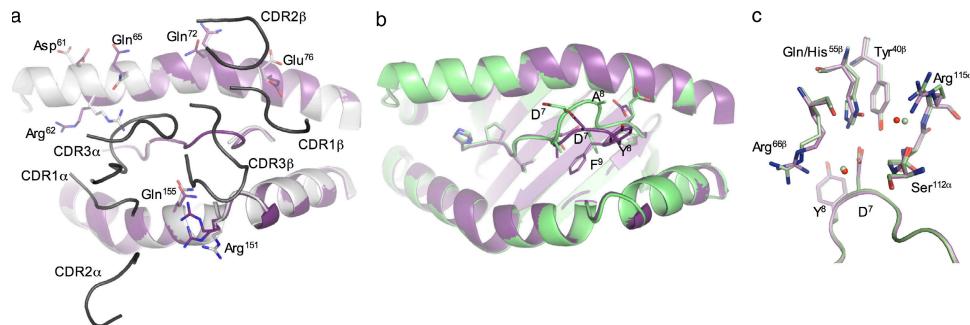


Figure S2. Conformational changes upon ligation. (a) Upon TK3^{WT} ligation onto HLA-B*3501, some of the HLA residues changed conformation to make specific interactions or to avoid steric clashes with the TCR (represented as a stick). HLA-B*3501 is in white for its unliganded state and in purple when bound to the TK3^{WT} TCR. The HPVG peptide is represented as a worm with the same colors, and the CDR loops of the TK3^{WT} TCRs are in gray. The central region of the HPVG peptide was unmodeled in the unliganded HLA-B*3501^{HPVG} complex, and fully modeled when in complex with the TCR. (b) The peptide conformation changes upon TK3^{WT} ligation are represented by superimposition of the HLA-B*3501^{HPVG} unliganded structure (green, with alanine in position 8 instead of tyrosine as it was agitated) with the HLA-B*3501^{HPVG} liganded structure (purple). (c) The superimposition of the TK3^{WT} and TK3^{Gln55His} structures, where the TK3^{WT} structure is in pink, the TK3^{Gln55His} structure is in pale green, and the spheres represent water molecules involved in the interaction with corresponding colors.

Table S1. Data collection and refinement statistics

	TK3 ^{WT} -HLA-B*3501 ^{HPVG}	TK3 ^{Gln55His} -HLA-B*3501 ^{HPVG}	TK3 ^{Gln55Ala} -HLA-B*3501 ^{HPVG}
Data collection statistics			
Temperature (K)	100	100	100
Space group	P1	P1	P1
Cell dimensions			
(a, b, c; Å)	44.86, 62.24, 92.56	44.76, 63.61, 88.14	44.9, 62.57, 98.14
(α, β, γ; °)	94.64, 103.92, 109.31	101.12, 97.59, 111.99	92.04, 102.29, 109.18
Resolution (Å)	100–2 (2.1–2)	100–2.1 (2.2–2.1)	100–2.7 (2.8–2.7)
Total number of observations	218,583 (26,804)	184,748 (22,372)	85,432 (8,216)
Number of unique observations	55,363 (6,870)	47,082 (5,655)	23,154 (2,248)
Multiplicity	3.9 (3.9)	3.9 (3.9)	3.7 (3.6)
Data completeness (%)	90.7 (82.6)	93.5 (86.4)	86 (79.5)
I/σ _I	11.65 (4.49)	12 (3.43)	13.32 (3.65)
R _{merge} (%) ^a	9.6 (45.4)	9.3 (41.7)	7.8 (35)
Refinement statistics			
<i>Nonhydrogen atoms</i>			
Protein	7,105	6,858	6,678
Water	297	201	62
Resolution (Å)	2	2.1	2.7
R _{factor} (%) ^b	22.5	22.89	24.02
R _{free} (%) ^b	28.6	27.64	32.69
<i>Rms deviations from ideality</i>			
Bond lengths (Å)	0.01	0.26	0.01
Bond angles (°)	1.25	1.04	0.84
<i>Ramachandran plot (%)</i>			
Most-favored region	89	88.5	80.1
Allowed region	9.2	9.7	16.2
Generously allowed region	1.7	0.8	1.9

Values in parentheses are for the highest-resolution shell.

^aR_{merge} = $\sum |I_{hkl} - \langle I_{hkl} \rangle| / \sum I_{hkl}$.

^bR_{factor} = $\sum_{hkl} |F_o| - |F_c| | / \sum_{hkl} |F_o|$ for all data except ~5% that were used for R_{free} calculation.

Table S2. TCR-MHC contacts in the three TCR-pMHC complexes

	TCR residue	TK3 ^{WT}	TK3 ^{Gln55His}	TK3 ^{Gln55Ala}	Bond type
CDR1 α	Ser ²⁸	Arg ⁶² , Leu ¹⁶³	Arg ⁶² , Leu ¹⁶³	Arg ⁶² , Leu ¹⁶³	vdw
CDR1 α	Gly ²⁹	/	/	Leu ¹⁶³	vdw
CDR1 α	Arg ³¹	Gln ¹⁵⁵	Gln ¹⁵⁵	Gln ¹⁵⁵	vdw
CDR1 α	Arg ^{31-0e1}	Gln ^{155-NH1}	Gln ^{155-NH1}	Gln ^{155-NH1}	H bond
CDR2 α	Tyr ⁵⁷	Arg ¹⁵¹	Arg ¹⁵¹	Arg ¹⁵¹	vdw
CDR2 α	Tyr ^{57-OH}	/	/	Arg ^{151-NH1}	H bond
CDR3 α	Leu ¹⁰⁹	Tyr ¹⁵⁹ , Gln ¹⁵⁵ , Leu ¹⁶³	Leu ¹⁶³	Ala ¹⁵⁸ , Gln ¹⁵⁵ , Leu ¹⁶³	vdw
CDR3 α	Gly ¹¹⁰	Ile ⁶⁶	Ile ⁶⁶	Arg ⁶² , Ile ⁶⁶	vdw
CDR3 α	Ser ¹¹²	Gln ⁶⁵ , Ile ⁶⁶ , Thr ⁶⁹	Gln ⁶⁵ , Ile ⁶⁶ , Thr ⁶⁹	Ile ⁶⁶ , Thr ⁶⁹	vdw
CDR2 β	Tyr ⁵⁷	Glu ⁷⁶	Glu ⁷⁶	Glu ⁷⁶	vdw
CDR2 β	Glu ⁶⁰	Gln ⁷²	Gln ⁷²	Gln ⁷²	vdw
CDR2 β	Glu ^{60-0e1-0e2}	Gln ^{72-water mediated}	Gln ^{72-Ne2}	Gln ^{72-0e1}	H bond
CDR2 β	Glu ⁶¹	/	Gln ⁷²	/	vdw
CDR2 β	Glu ⁶¹⁻⁰	Gln ^{72-0e1}	Gln ^{72-0e1}	/	H bond
FW β	Arg ⁶⁶	Thr ⁶⁹ , Gln ⁷² , Thr ⁷³	Gln ⁷² , Thr ⁷³	Gln ⁷²	vdw
FW β	Arg ^{66-NH1}	Gln ^{72-0e1}	/	/	H bond
FW β	Arg ^{66-NH2}	Glu ^{76-0e1}	Glu ^{76-0e1}	/	Salt bridge
CDR3 β	Arg ¹⁰⁹	Ala ¹⁴⁹ , Ala ¹⁵⁰	Ala ¹⁴⁹ , Ala ¹⁵⁰	Ala ¹⁴⁹ , Ala ¹⁵⁰	vdw
CDR3 β	Ser ¹¹⁰	Ala ¹⁴⁹ , Arg ¹⁵¹	Ala ¹⁴⁹ , Arg ¹⁵¹	Arg ¹⁵¹	vdw
CDR3 β	Ser ¹¹⁰⁻⁰	Arg ^{151-NH2-Ne2}	Arg ^{151-NH1}	Arg ^{151-NH1}	H bond
CDR3 β	Ser ^{110-N}	Ala ¹⁴⁹⁻⁰	/	/	H bond
CDR3 β	Gly ¹¹¹	Arg ¹⁵¹	/	/	vdw

Table S3. TCR contacts with the HPVGEADYFEY peptide in the three TCR–pMHC complexes

	TCR residue	TK3 ^{WT}	TK3 ^{Gln55His}	TK3 ^{Gln55Ala}	Bond type
CDR1 α	Arg ³¹	Gly ⁴ , Ala ⁶	Gly ⁴ , Ala ⁶	Gly ⁴ , Ala ⁶	vdw
CDR1 α	Arg ^{31-NH1-NH2}	Gly ⁴⁻⁰	Gly ⁴⁻⁰	Gly ⁴⁻⁰	H bond
CDR3 α	Leu ¹⁰⁹	Val ³ , Gly ⁴	Val ³ , Gly ⁴	Val ³ , Gly ⁴	vdw
CDR3 α	Leu ¹⁰⁹⁻⁰	Gly ^{4-N}	Gly ^{4-N}	Gly ^{4-N}	H bond
CDR3 α	Thr ¹¹¹	Gly ⁴	/	/	vdw
CDR3 α	Ser ¹¹²	Glu ⁵	Glu ⁵	Glu ⁵	vdw
CDR3 α	Gly ¹¹³	Glu ⁵ , Ala ⁶ , Asp ⁷	Glu ⁵ , Ala ⁶ , Asp ⁷	Glu ⁵ , Ala ⁶ , Asp ⁷	vdw
CDR3 α	Gly ^{113-N}	Glu ⁵⁻⁰	Glu ⁵⁻⁰	Glu ⁵⁻⁰	HB
CDR3 α	Ser ¹¹⁴	Ala ⁶ , Asp ⁷	Ala ⁶ , Asp ⁷	Asp ⁷	vdw
CDR3 α	Ser ^{114-0γ}	Asp ^{7-N}	Asp ^{7-N}	/	H bond
CDR1 β	Asp ²⁹	Tyr ⁸	Tyr ⁸	Tyr ⁸	vdw
CDR1 β	Leu ³⁰	Tyr ⁸	Tyr ⁸	Tyr ⁸	vdw
CDR1 β	Leu ^{30-N}	Tyr ^{8-OH}	Tyr ^{8-OH}	Tyr ^{8-OH}	H bond
CDR1 β	Ser ³¹	Asp ⁷ , Tyr ⁸	Asp ⁷	Asp ⁷ , Tyr ⁸	vdw
FW β	Tyr ⁴⁰	Asp ⁷	Asp ⁷	Asp ⁷	vdw
FW β	Tyr ^{40-OH}	Asp ^{7-0δ1-0δ2}	Asp ^{7-0δ1-0δ2}	Asp ^{7-0δ1-0δ2}	H bond
FW β	Gln ⁵⁵ /His ⁵⁵ /Ala ⁵⁵	Asp ⁷	Asp ⁷	/	vdw
FW β	Gln ^{55-Nε2} /His ^{55-Nε2}	Asp ^{7-0δ1-0δ2}	Asp ^{7-0δ1-0δ2}	/	H bond
CDR2 β	Tyr ⁵⁷	Tyr ⁸ , Glu ¹⁰	Tyr ⁸ , Glu ¹⁰	Tyr ⁸ , Glu ¹⁰	vdw
CDR2 β	Tyr ^{57-OH}	Glu ^{10-0ε2}	Glu ^{10-0ε1}	Glu ^{10-0ε1}	H bond
FW β	Arg ^{66-NH1}	Asp ^{7-0δ1}	Asp ^{7-water mediated}	Asp ^{7-water mediated}	Salt bridge
FW β	Arg ^{66-NH1-NH2}	Glu ^{10-0ε2-0ε1}	Glu ^{10-0ε2-0ε1}	Glu ^{10-0ε1}	Salt bridge
CDR3 β	Ser ¹⁰⁷	Asp ⁷ , Tyr ⁸	Asp ⁷ , Tyr ⁸	Asp ⁷ , Tyr ⁸	vdw
CDR3 β	Ser ^{107-0γ}	Asp ^{7-0δ2}	Asp ^{7-0δ2}	Asp ^{7-0δ2}	H bond
CDR3 β	Ser ¹⁰⁷⁻⁰	Tyr ^{8-OH}	Tyr ^{8-OH}	Tyr ^{8-OH}	H bond
CDR3 β	Ala ¹⁰⁸	Tyr ⁸	Tyr ⁸	Tyr ⁸	vdw
CDR3 β	Arg ¹⁰⁹	Tyr ⁸	Tyr ⁸	Tyr ⁸	vdw