Dual molecular mechanisms govern escape at immunodominant HLA A2-restricted HIV epitope

David K. Cole¹, Anna Fuller¹, Garry M. Dolton¹, Ethalia Zerdouvi¹, Mateusz Legut¹, Kim Miles¹, Jennifer L. Blanchfield², Florian Madura², Christopher J. Holland¹, Anna M. Bulek¹, John S. Bridgeman¹, John J. Miles¹,³, Andrea J. Schauenburg¹, Konrad Beck¹, Brian D. Evavold², Pierre Rizkallah¹, Andrew K. Sewell¹

¹Cardiff University, United Kingdom, ²Emory University, United States, ³James Cook University Cairns, Australia

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Author contribution statement

DKC, AF, GMD, TZ, ML, KM, JLB, FM, CJH, AMB, JSB, JJM, AJAS, KB, BDE and PJR performed and/or directed experiments, analysed data and critiqued the manuscript. DKC and AKS, conceived, funded and directed the project and wrote the manuscript.

Keywords

T cell receptor, T cell, structure-function relationships, HIV-1, immune escape, Surface Plasmon Resonance, Crystallography, X-Ray, Protein Binding, biophysics (isothermal titration calorimetry)

Abstract

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Dual molecular mechanisms govern escape at immunodominant HLA A2-restricted HIV epitope

David K Cole†, Anna Fuller†, Garry Dolton†, Ethalia Zervoudi†, Mateusz Legut†, Kim Miles†, Jennifer L Blanchfield†, Florian Madura†, Christopher J. Holland†, Anna M. Bulek†, John S. Bridgeman†, John J. Miles†, Andrea J.A. Schauenburg†, Konrad Beck†, Brian D. Evavold†, Pierre J. Rizkallah† and Andrew K. Sewell†

1Cardiff University School of Medicine, University Hospital, Heath Park, Cardiff, CF14 4XN, United Kingdom.
2Department of Microbiology and Immunology, Emory University, 1510 Clifton Rd NE, Atlanta Georgia, 30322, USA.
3James Cook University, Cairns, QLD, Australia.
4Cardiff University School of Dentistry, University Hospital, Heath Park, Cardiff, CF14 4XY, United Kingdom.
5†These authors contributed equally to this study.

* Correspondence: Andrew Sewell sewellak@cardiff.ac.uk

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ABSTRACT

Serial accumulation of mutations to fixation in the SLYNTVATL (SL9) immunodominant, HIV p17 Gag-derived, HLA A2-restricted CTL epitope produce the SLFNTIAVL triple mutant ‘ultimate’ escape variant. These mutations in solvent-exposed residues are believed to interfere with TCR recognition, although confirmation has awaited structural verification. Here, we solved a TCR co-complex structure with SL9 and the triple escape mutant to determine the mechanism of immune escape in this eminent system. We show that, in contrast to prevailing hypotheses, the main TCR contact residue is 4N and the dominant mechanism of escape is not via lack of TCR engagement. Instead, mutation of solvent exposed residues in the peptide destabilize the peptide-HLA and reduce peptide density at the cell surface. These results highlight the extraordinary lengths that HIV employs to evade detection by high-affinity TCRs with a broad peptide-binding footprint and necessitate reevaluation of this exemplar model of HIV TCR escape.
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1. INTRODUCTION

CD8+ cytotoxic T lymphocytes (CTLs) form a critical component in immune control of HIV infection. However, the virus has adopted numerous strategies to evade detection by these important immune cells (1, 2). Notably, the high rate and poor fidelity of replication produces a viral quasispecies to allow rapid selection of sequence variants that evade CTLs. This immune escape mutation is often associated with loss of viral fitness (3). The effects of immune escape from some HLA class I alleles, particularly HLAs B27 and B57 (3, 4), can be significant and delay progression to AIDS. There has been considerable work on immune escape from HIV epitopes presented by the most frequent HLA worldwide, HLA A2 (5). The majority of these studies have focused on the immunodominant response through the p17 HIV Gag-derived epitope SL9 (amino acids 77–85, sequence SLYNTVATL) (6-23). Responses to SL9 are uncommon in acute infection but are dominant during the long, asymptomatic, chronic infection period where over 70% of HLA A2+ HIV infected individuals mount a strong response to this epitope (13, 18, 19). Immune escape from SL9-specific CTL during this period has been studied extensively and is known to follow well-described patterns (6, 7). The leucine residues at positions 2 and 9 in SL9, are located within an α helix (21) and are critical for trimerization of the P17 Gag protein (24). Mutations within these residues are believed to produce highly compromised virus (11, 24). These residues also act as the principal anchors for securing SL9 into the HLA A2 binding groove (22) and ensure that the virus does not use the archetypical escape strategy of mutating primary MHC anchors to block epitope presentation at the infected cell surface (25-27). Instead, in the face of SL9-specific CTL pressure, HIV has been observed to undergo preferred mutation at positions 3, 6 and 8 in the epitope (6, 7, 9). The dominant mutations seen at these positions (Y3F, V6I and T8V) correlate with a lower viral load suggesting that they result in a loss of viral fitness, a notion that is supported by the rapid reversion to the wildtype SL9 sequence in the absence of T-cell selection pressure (6, 7). The available evidence suggests that HIV balances the combined pressures of immune escape versus viral fitness at the SL9 epitope by successive fixation of mutations at positions 3, 6 and 8 in the subtype A, B and D SL9 SLYNTVATL consensus sequence over a >10-year period (6, 7). Indeed, McMichael and colleagues have described the triple mutant S[FL]NT[IA][AV]L sequence (3F6I8V; mutations in bold underlined text) as the ‘ultimate’ escape mutant in SL9 (6).
Here we use structure and protein biophysics to deconstruct how HIV escapes from the well-studied (9-11) SL9-specific 868 TCR. We add to the existing data by providing the first ever TCR-pMHC structures in this exemplar model of how HIV evades engagement by host TCRs. We find that the 868 TCR interacts with HLA A2-SLYNTVATL (A2-peptide from here on in) with the expected binding topography but exhibits an unusual degree of structural rearrangement upon interaction with A2-SLYNTVATL. The 868 TCR also contacts all five central residues in SL9 (position 3-8) and binds with an unprecedentedly high affinity for a natural TCR. Surprisingly, 4N is the major contact residue – not the 3Y, 6I or 8T that mutate to precipitate immune escape. This enabled the generation of a high-resolution structure of the 868 TCR in complex with the SLENJIAVL ultimate escape variant. These results challenge current thinking on the mechanism by which HIV escapes at SL9 and demonstrate the extraordinary tactics that the virus can employ to escape from CTL responses that can involve TCRs with a very broad footprint and a very high natural binding affinity.

2. MATERIALS AND METHODS

2.1 Construct design

The 868 TCR α and β chains, HLA A2 heavy chain and β2m chain were generated by PCR mutagenesis and cloning. All sequences were confirmed by automated DNA sequencing (Lark Technologies). TCR expression constructs were designed with a disulphide linked construct to produce the soluble domains (variable and constant) for both the α (residues 1-207) and β chains (residues 1 – 247) (44, 45). The HLA A2 heavy chain (residues 1-248) (α1, α2 and α3 domains), tagged, or not tagged with a biotinylation sequence, and β2m (residues 1 – 100) were also cloned and used to make the pMHCI complexes. The TCR α and β chains, the HLA A2 α chain and β2m sequences were inserted into separate pGMT7 expression plasmids under the control of the T7 promoter (46).

2.2 Protein expression, refolding and purification

Competent Rosetta DE3 E.coli cells were used to produce the TCR α and β chains, HLA A2 heavy chain and β2m in the form of inclusion bodies (IBs) using 0.5 mM IPTG to induce expression and protein were chemically refolded as described previously (47).
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Biotinylated pMHCI was prepared as previously described (48).

2.3 SPR experiments

SPR equilibrium binding analysis was performed using a BIACore T100™ equipped with a CM5 sensor chip as previously reported (48, 49). HLA DR1, generated as in (50), was used as a negative control on flow cell 1. SPR kinetic analyses were carried out to determine the $K_D$ values for the TCR, at 25°C. For all kinetic experiments, approximately 300 RUs of pMHCI was coupled to the CM5 sensor chip surface. The TCR was then injected at concentrations ranging from 10 times above and 10 times below the known $K_D$ of the interaction at 45 µl / min. The $K_D$ values were calculated assuming 1 : 1 Langmuir binding ($AB = B*AB_{MAX}/(K_D + B)$) and the data were analyzed using a global fit algorithm (BIAevaluation™ 3.1). The $k_{on}$, $k_{off}$ and $K_D$ values were calculated by global fitting of the data using BIAevaluation™ 3.1 software. For the thermodynamics experiments we used the $K_D$ determined by SPR at different temperatures with the standard thermodynamic equation $\Delta G = RT \ln K_D$ and the standard non-linear van’t Hoff equation ($\Delta G^\circ = \Delta H^\circ - T\Delta S^\circ + \Delta C_p^\circ(T - T_0) - T\Delta C_p^\circ \ln(T/T_0)$) with $T_0 = 298$ K. For stability experiments, single injections of 50 µM 868 TCR over the SL9 variants were performed after different incubation times at 37°C, and the RU values were recorded.

2.4 Isothermal Titration Calorimetry (ITC)

ITC experiments were performed using a Microcal VP-ITC (GE Healthcare) as previously described (29), with 30 µM pHLA-I in the calorimeter cell and 210 µM soluble 868 TCR in the syringe. Buffer conditions were 20 mM Hepes (pH 7.4) containing 150 mM NaCl and 20 injections of 2µl volume each were performed. Results were processed and integrated with the Origin 6.0™ software distributed with the instrument. ITC experiments were performed in duplicate.

2.5 Adhesion frequency assay

We used an adhesion frequency assay to measure the 2D affinity of TCR–pMHCI interactions at the cell membrane as previously described (51). Briefly, human T-cells transfected with the 868 TCR were mounted onto one micro-pipette and, on the other pipette, human red blood cells coated with pMHCI by biotin–streptavidin coupling served as both a surrogate APC and an adhesion sensor for detecting the TCR–pMHCI interaction. Site densities of TCR and pMHCI were measured by flow cytometry as previously described (52). All assays were performed using at least 5 cell pairs, and
calculated as an average of 100 cell-cell contacts.

2.6 Crystallization, diffraction data collection and model refinement

All protein crystals were grown at 18 °C by vapour diffusion via the sitting drop technique. 200 nL of 1:1 molar ratio TCR and pMHCI (10 mg/ml) in crystallization buffer (10 mM TRIS pH 8.1 and 0.1 mM NaCl) was added to 200 nL of reservoir solution. 868 crystals were grown in TOPS (53) in 0.1 M sodium cacodylate pH 6.5, 20% PEG 8000 and 0.2 M ammonium sulphate (53). 868-A2- SLYNTVAL crystals were grown in TOPS in 0.1 M sodium cacodylate pH 6.0, 15% PEG 4000 and 0.2 M ammonium sulphate (53). 868-A2-SLYNTIATL co-crystals were grown in TOPS in 0.1 M sodium cacodylate pH 6.0, 15% PEG 4000 and 0.2 M ammonium sulphate (53). 868-A2- SLFNTIAYL crystals were grown in TOPSi in 0.1 M sodium cacodylate pH 5.5, 15% PEG 4000 and 0.2 M ammonium sulphate (53). A2-SLYNTIATL crystals were grown in TOPS in 0.1 M sodium cacodylate pH 6.0, 25% PEG 4000 and 0.2 M ammonium sulphate (53). A2-SLFNTIAYL crystals were grown in TOPS in 0.1 M sodium cacodylate pH 6.0, 25% PEG 4000 and 0.2 M ammonium sulphate (53). All crystals were soaked in 30% ethylene glycol before cryo-cooling. All crystallization screens and optimization experiments were completed using an Art-Robbins Phoenix dispensing robot (Alpha Biotech Ltd, UK). Data were collected at 100 K at the Diamond Light Source (DLS), Oxfordshire. All datasets were collected at a wavelength of ~0.98Å using an ADSC Q315 CCD or PILATUS Pixel detectors. Reflection intensities were estimated with the XIA2 package (54) and the data were scaled, reduced and analyzed with SCALA and the CCP4 package (55). Structures were solved with molecular replacement using PHASER (56). Sequences were adjusted with COOT (57) and the models refined with REFMAC5. Graphical representations were prepared with PYMOL (58). The reflection data and final model coordinates were deposited with the PDB database (868, PDB: 5NMD; 868-A2-SLYNTVAL, PDB: 5NME; 868-A2-SLYNTIATL, PDB: 5NMF; 868-A2-SLFNTIAYL, PDB: 5NMG; A2-SLYNTIATL, PDB: 5NMH; A2-SLFNTIAYL, PDB: 5NMK).

2.7 Thermal stability CD analysis of HLA A2 complexes

Thermal stability of HLA A2/β2m/peptide complexes was determined by circular dichroism spectroscopy following the change of ellipticities Θ at 218 nm using an Aviv 215 instrument (Aviv Biomedical Inc., Lakewood, NJ). Proteins were dissolved in 137 mM NaCl, 3 mM KCl, 8 mM Na₂HPO₄, 1 mM KH₂PO₄, pH 7.4, at concentrations of ~3 µM as determined spectroscopically using
calculated extinction coefficients (59). Melting curves were recorded from 4 °C up to a maximum temperature when protein aggregation was observed using a heating rate of -0.5 °C/min. Melting curves were analysed assuming a two-state trimer-to-monomer transition from the native (N) to unfolded (U) conformation N₃ ↔ 3U with an equilibrium constant K = [U]³/[N]₃ = F/[3c² (1-F)]³
where F and c are the degree of folding and protein concentration, respectively. Data were fitted as described (60) using the non-linear least-squares routine of Origin V7.5 (OriginLab, Northampton, MA). Fitted parameters were the melting temperature Tm, van't Hoff's enthalpy ΔHᵥH at the transition midpoint, and the slope and intercept of the native baseline assumed as a linear function of the temperature. As protein complexes aggregated at various degrees of unfolding, the ellipticity of the unfolded state was set as a constant of -4,500 deg cm² dmol⁻¹ (61).

2.8 Generation of 868 TCR transgenic T-cells

868 TCR construct (codon-optimized for human expression) was cloned into the third-generation lentiviral expression vector pELNS (kindly provided by James R. Riley, University of Pennsylvania, PA, USA). pELNS vector was engineered to contain rat CD2 (rCD2) gene to be used as a marker of lentiviral transduction of target cells. 868 TCR-α and TCR-β, and rCD2 were separated by a pair of ‘self-cleaving’ 2A sequence (11). Lentiviral particles were prepared by calcium phosphate transfection of packaging plasmids (pRSV-Rev, pMDLg/pRRE, pMD2.G) together with 868-encoding pELNS into HEK293T cells. Supernatant was harvested 48- and 72h post transfection, and was subsequently concentrated by ultracentrifugation. Primary CD8+ T-cells were obtained from healthy donor blood bags (Welsh Blood Service) by density gradient centrifugation and positive selection using CD8 MicroBeads (Miltenyi Biotec, Bergisch Gladbach, Germany). Isolated T-cells were stimulated overnight with Gibco human T-activator CD3/CD28 Dynabeads (ThermoFisher Scientific, Waltham, MA) at 3:1 bead to T-cell ratio, and transduced with concentrated lentiviral stock in presence of 5 µg/ml polybrene (Santa Cruz Biotechnology, Santa Cruz, CA). After 72 h rCD2+ cells were enriched by magnetic bead selection to yield >95% purity. For tetramer staining experiments CD8+ T-cells were used without magnetic enrichment to leave a non-transduced internal control cell population. Similar methodology was used to transduce TCRβ chain negative Jurkat cells to allow the examination of tetramer binding in the absence of the CD8 glycoprotein.

2.9 Tissue culture

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T2 cells were maintained as suspension cells in R10 (RPMI 1640 media, 10% FBS, penicillin, streptomycin and L-Glutamine, all Life Technologies, Paisley, UK) and passaged weekly or when required. Post enrichment, primary CD8+ T-cells were routinely expanded with allogeneic feeder PBMCs and phytohaemagglutinin (PHA) in T-cell media as previously described (40). 868 TCR expression was checked prior to assay using anti-rCD2 antibody and SLYNTVATL tetramer, with the protein kinase inhibitor Dasatinib (62) (Axon Medchem, Reston, VA), and unconjugated anti-PE antibody (PE001, BioLegend, London, UK) used to enhance tetramer staining, as previously described (40, 63).

2.10 T-cell activation assays

For peptide pulsing assays, T2 cells were incubated with peptide for 1h in 0.5 ml of AIM-V serum free media (ThermoFisher Scientific) in 5 ml FACS tubes at 37°C and 5% CO₂, followed by 4 washes with 4 ml of RPMI 1604 media. In assays using primary CD4+ T-cells as targets, these cells were purified from PBMC using magnetic microbead separation (Miltenyi Biotech). Peptides were synthesized to >95% purity, stored as 20 mM DMSO stocks at -80 °C and 1 mM RPMI dilutions made on the day of assay. DMSO controls were treated the same as peptide pulsed. Post pulsing, T2 or CD4+ T-cells were incubated in 4.5 ml of AIM-V media at 37°C and 5% CO₂ for 3-24h or used immediately (0 h), such that cells were ready at the same time. 868 TCR transduced and non-transduced T-cells (30,000) were rested overnight in R5 (as for R10 but with 5% fetal bovine serum) then co-incubated in 96U well plates with T2 or CD4+ T-cells (60,000) in the presence of GolgiStop and GolgiPlug according the manufacturers (BD Biosciences, Oxford, UK), and anti-CD107a PE Antibody (H483, BD Biosciences). Controls included T-cells alone and T-cells with unpulsed T2s (negative control) or PHA. After 3.5-5h of incubation cells were labelled with the violet LIVE/DEAD fixable dead cell stain Vivid, anti-CD8 APC (BW135/80; Miltenyi Biotech) and anti-CD19 pacific-blue (T2s) (BioLegend), rCD2 (CD4 assay) and anti-CD4 APC-Vio770 (M-T466, Miltenyi Biotech; CD4 assay) antibodies. Cells were then stained with anti-TNFα PE-Vio770 antibody (CA2, Miltenyi Biotech) using a Cytofix/Cytoperm kit (BD Biosciences) according to manufacturer's instructions. Flow cytometry was preformed on a FACSCount II (BD Biosciences) and data analysed with FlowJo software (TreeStar, Ashland, OR). For peptide alanine scans 868 TCR transduced T-cells were rested overnight in R5 then incubated with T2s (60,000) and peptides at specified concentrations for 18h in 96U well plates in 100 μl of R5. Supernatants (50 μl) were used...
for MIP-1β ELISA (R&D Systems, Minneapolis, Canada) and GraphPad Prism (GraphPad Software, Inc., La Jolla, CA) used to fit nonlinear regression curves and calculate EC$_{50}$ for each peptide.

2.11 T2 peptide HLA-A2 stability assays

For conventional peptide binding assays, T2s were pulsed for 22h with 10$^{-5}$ M peptide in 0.2 ml of AIM-V media (ThermoFisher Scientific) in 5ml FACS tubes at 37°C and 5% CO$_2$. Washed then stained with anti-HLA-A2 antibody (BB7.2 BioRad, Hercules, CA) for 10 minutes at RT, washed with PBS and fixed with 2% paraformaldehyde for 20 min on ice. Peptides were synthesised to >95% purity, stored as 20 mM DMSO stocks at -80 °C and 1 mM AIM-V dilutions made on the day of assay. DMSO controls were treated the same as peptide pulsed. For peptide on-rates, T2s were treated as before but for the durations specified in the results (1-3h) then stained and fixed. For peptide off-rates T2s were pulsed overnight, then a proportion of them stained immediately and fixed as above, with remaining cells being washed in an excess of media (2 times using 4 mls) and incubated in 4.5 ml of AIM-V for the specified times (h) at 37°C and 5% CO$_2$, to allow peptide to dissociate, then stained and fixed as before. Flow cytometry was performed on a FACSCanto II (BD Biosciences) and data analysed with FlowJo software (TreeStar).

2.12 Peptides used in this study

This study made use of the HIV SL9 peptide and variants thereof. The sequences and origin of these peptides, and other control peptides utilized, are listed in Table 1.

3. RESULTS

3.1 868 TCR binding to A2-SLYNTVATL involves extensive structural re-organisation

Previous studies have demonstrated that over 1.7% of CD8+ T-cells from HLA A2+ HIV infected patient 868, stained with A2-SLYNTVATL tetramer (10). 75% of these tetramer+ cells expressed a TRBV5-6+ TCR and an identical TRBV5-6 ß-chain was observed in 10/18 transcripts sequenced in this study (CDR3 sequence CASSLSAVQNNEQF) (10). This same ß-chain was later shown to be present in all A2-SLYNTVATL tetramer+ cells in a T-cell line grown from patient 868 in 1996 (9).

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TCR chain antibody staining showed that all of these A2-SLYNTVATL tetramer+ T-cells co-expressed a TRAV12-2 chain (11). Our previous study confirmed that CD8+ T-cells expressing this TCR were unable to control HIV virus in vitro (11). Nevertheless, we were able to use phage display to select an artificially enhanced version of the 868 TCR that could recognise the SLFTIAYL ultimate escape variant; thereby engineering foresight into an immune receptor (11). The detection of common SL9 escape mutants on the surface of HIV-infected HLA A2+ cells by CD8+ T-cells expressing engineered, but not wildtype, 868 TCR reinforced earlier studies suggesting that these mutants are presented by HLA A2 and that escape from the wildtype epitope is mediated by loss of TCR binding (so-called ‘TCR escape’) (6, 7, 11, 18). To understand how positions 3, 6 and 8 in SL9 impinge on TCR binding, we solved the structure of the wildtype 868 TCR in complex with A2-SLYNTVATL to 2.9Å resolution (Table 2). The 868 TCR bound to A2-SLYNTVATL with a conventional, centrally-located, diagonal orientation with the TCR α-chain positioned over the α2 helix of MHC class I and the TCR β-chain positioned over the α1 helix (Fig 1A). The TCR crossing angle of 51.6° lies within the normal range for human TCR-pMHC complexes (28), enabling positioning of the TCR CDR3 loops centrally over the peptide, and the CDR1 and CDR2 loops predominantly over the MHC helices (Fig 1B). To gain extra insight into the mechanism by which the 868 TCR adopted this binding mode, we also solved the structure of the unbound 868 TCR (Table 2). Comparison with the 868-A2-SLYNTVATL complex structure showed that extensive structural reorganisation of the CDR3 loops was required to avoid clashes with the solvent exposed residues in the SL9 peptide. This resulted in an induced fit, or conformational pre-equilibrium binding mode where the TCR exists in two conformations in the unbound state, with the CDR3α loop ‘moving’ 6.9Å and the CDR3β moving 3.2Å between the bound and unbound TCR structures (Fig 1C).

Closer examination of the interface between the TCR and the pMHC showed that the CDR3 loops almost exclusively made contacts with the peptide, forming a pincer around the solvent exposed 4N and 5T residues in the peptide (Fig 2A&B). The TCR-peptide interaction included 10 hydrogen bonds and 52 vdW contacts, mainly focused on 4N. The CDR1 and CDR2 loops primarily contacted the α helices of the MHC, including interactions with all three restriction triad residues (MHC residues 65R, 69A and 155Q) as well as strong interactions with MHC residues 72Q and 154E (Fig 2C&D). Although most of the TCR-pMHC interactions were focused on these two peptide residues and five MHC residues, the 868 TCR bound with a broad footprint, making additional bonds with all...
but two peptide residues (1S and 9L) and a further 14 MHC residues. In total, the 868 TCR made 20 hydrogen bonds, and 121 van der Waals (vdWs) contacts with A2-SLYNTVATL (Table 3), which is in the higher range compared to previously published viral TCR-pMHC complexes (29). In summary, the 868 TCR utilized an induced fit, or conformation selection, binding mode to form a pincer-like interaction around the central solvent-exposed portion of the peptide. Additional contacts with distal peptide residues enabled a relatively extensive and broad binding interface between the TCR and pMHC.

3.2 TCR structure with the ultimate SL9 escape variant

The 868-A2-SLYNTVATL complex structure demonstrated that the dominant contacts with the SL9 peptide were with the 4N residue rather than with the 3Y, 6V or 8T residues that result in immune escape when substituted to create the SLFNTIAL ultimate escape variant (6, 7). Alanine scan mutation across the SL9 peptide backbone showed an almost complete loss of recognition with the L2A and Y3A changes. Alanine substitution at positions 4, 5 and 6 had the next greatest effect whereas peptides substituted at positions 1, 8 and 9 exhibited recognition equivalent to the wild type peptide (Fig 2E). In order to gain insight as to how natural escape mutations impinge on TCR binding, we also solved the structure of the 868 TCR with the SLFNTIAL variant present in the patient at the time the blood sample was used to grow the 868 T-cell clone (9), and the SLFNTIAL ultimate escape variant (Table 2). Comparison of these structures with the 868 TCR in complex with the A2-SLYNTVATL index sequence showed that the 868 TCR engaged all the antigens in a similar conformation and crossing angle (Fig 3A&B). We were initially surprised at being able to solve the structure of the 868 TCR in complex with the SLFNTIAL peptide as this triple mutant is known to escape from CD8+ T-cells (6, 7). Indeed, this mutation is not well recognized by T-cells bearing the 868 TCR (9, 11). The failure of CD8+ T-cells to recognize the SLFNTIAL mutation has previously been attributed to reduced interactions with the TCR (6, 7, 18, 23). Earlier structural analyses of A2-SLYNTVATL and A2-SLFNTIAL have concluded that all three substitutions directly affected TCR recognition (6, 7). However, we observed only minor differences at the TCR-peptide interface with these two ligands. For example, the 868 TCR made 3 hydrogen bonds and 12 vdWs with peptide residues 3Y, 6V and 8T in the SLYNTVATL peptide compared to 2 hydrogen bonds and 15 vdWs contacts with 3F, 6I and 8V in the SLFNTIAL peptide (Fig 3C&E). The total number of contacts in each complex (868-A2-SLYNTVATL: 141, 868-A2-SLFNTIAL: 146) was also similar, demonstrating that the 868 TCR could tolerate mutations at residues 3, 6 and 8 in SL9 (Table 3).

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Thus, because our structural data were inconsistent with the hypothesis that SL\textsubscript{Y}NT\textsubscript{A}V\textsubscript{L} primarily affects TCR binding, and because sum contact numbers do not necessarily represent the accurate binding energy between two molecules, we undertook further structural and biophysical experimentation to determine the mechanism that results in poor T-cell recognition of SL\textsubscript{Y}NT\textsubscript{A}V\textsubscript{L}.

### 3.3 A2-SL\textsubscript{Y}NT\textsubscript{V}AT\textsubscript{L} does not alter conformation when bound to 868 TCR

Previous studies comparing SLYNTVATL and the SL\textsubscript{Y}NTVATL mutated peptide showed that they adopted different conformations within the HLA A2 binding groove (7, 22). The T-cell recognition and on-rate kinetics with the G10 SL9-specific TCR in this study were very similar with A2-SLYNTVATL and A2-SLF\textsubscript{N}TVATL, leading the authors to conclude that one conformation, common to both peptides, was recognised by TCRs (22) and suggesting that TCR interactions with either A2-SLYNTVATL or A2-SLF\textsubscript{N}TVATL required an induced fit in the pMHC. Thus, SL9 derived peptides may bind to MHC dynamically and undergo conformational changes during TCR docking. Conformational peptide changes would likely elicit an entropic penalty during TCR ligation, not revealed by differences in contacts, and could contribute to weaker binding. However, based on previously solved structures (A2-SLYNTVATL (22), A2-SL\textsubscript{Y}NTVATL (22) A2-SL\textsubscript{A}NTVATL (21), A2-SLYNT\textsubscript{I}ATL (21), A2-SLYLTVATL (21), A2-SLYNYVATL (21), A2-SLYNT\textsubscript{A}AL (21) and A2-SLF\textsubscript{N}TVATL (21)), some of which we replicated in this study, we show that A2-SLYNTVATL, A2-SLYNT\textsubscript{I}ATL and A2-SLF\textsubscript{N}TVATL all adopt a similar structure to every unbound SL9 peptide variant, apart from A2-SLF\textsubscript{N}TVATL (22), when ligated to the 868 TCR (Fig. 4). These data make it possible to be more definitive about the direction of travel of the previously suggested induced fit model (22) (i.e. the odd one out is A2-SLF\textsubscript{N}TVATL and this peptide presumably adopts the more conventional structure for A2-SLYNTVATL type ligands prior to, or at the time of, TCR binding). Furthermore, these data do not support the notion that HIV escape is mediated by dynamic differences in ligand engagement during TCR binding to SL9 variants.

### 3.4 The 868 TCR adopts a similar energetic strategy during binding to SL9 escape variants

We next explored the evidence for HIV escape being mediated by distinct TCR binding parameters. It has been previously shown that the G10 SL9-specific TCR binds with a similar affinity to both A2-SLYNTVATL ($K_D = 2.2 \mu M$) and A2-SLF\textsubscript{N}TVATL ($K_D = 5.2 \mu M$) by surface plasmon resonance (SPR) (22). Another study demonstrated that half maximal pMHC tetramer binding ($DR_{50}$) to the SL9-specific D3 TCR was near identical for A2-SLYNTVATL, A2-SLF\textsubscript{N}TVATL, A2-
SLYNTVAVL, A2-SLENTVAVL and A2-SLENTIAYV (21). Finally, we have previously shown
that the 868 TCR binds to a range of SL9 variants (11) (A2-SLYNTVATL, A2-SLYNTIATL, A2-
SLYNTIAYL, A2-SLYNTAVL, A2-SLENTIAYL, A2-SLENTVAVL and A2- A2-SLENTVATL,
A2-SLENTIAYL). Consequently, the available data shows that SL9-specific TCRs can engage SL9
variants within an affinity range that would be expected to easily activate T-cells. Here, we
reproduced SPR binding assays with the 868 TCR for the three ligands included in this study. These
data demonstrated that the 868 TCR bound to A2-SLYNTVATL with a K_D of 82 nM (Fig 5A)
confirming that this is, by far, the strongest binding natural TCR-peptide-MHC interaction ever
recorded (30, 31). Indeed, the affinity was even greater with the A2-SLYNTIATL variant (K_D =38
nM; Fig 5B) that dominated in the patient at the time the blood sample was taken that was used to
generate the 868 T-cell line (9, 10). 868 TCR interactions with A2-SLYNTVATL and the A2-
SLYNTIATL variant were characterized by a relatively slow off-rate (k_off = 1.6x10^{-2} – 7.3x10^{-3} s^{-1})
comparied to the majority of other natural TCR-pMHC interactions (average k_off ~2x10^{-1} s^{-1}) (30).
Although the strength of the 868-A2-SLENTIAYL interaction was 21-fold and 45-fold weaker than
for A2-SLYNTVATL or A2-SLYNTIATL respectively, due to a much faster off-rate (k_off = 2.1x10^{-1}
s^{-1}), the affinity (K_D of 1.77 µM; Fig 5C) was still in the range of the very best natural anti-pathogen
TCRs (31, 32). Thus, this weaker affinity alone was unlikely to explain the ability of the
SLFNTIAYL variant to evade T-cell detection. Indeed, we have described a functional HLA A2-
restricted TCR that binds its cognate pMHC with over 100-fold weaker affinity than the 868 TCR
and A2-SLENTIAYL (33, 34). To get a more complete picture of how the 868 TCR engages its
cognate ligands we also undertook thermodynamic analyses by SPR (Fig 5D-F, Table 4) and directly
by isothermal calorimetry (ITC, Fig 5G-I). The results of these independent techniques correlated
well and showed that 868 TCR engagement was driven by energetically favorable enthalpy and
entropy changes to all three ligands. Thus, for the 868 TCR, there was a net increase in the number of
electrostatic interactions and a transition from order-disorder during binding. Considering that the
868 TCR CDR3 loops underwent similarly large conformational changes during engagement to all
three SL9 variants studied here (shown for 868-A2-SLY interaction in Fig. 1C), a movement that
would probably be entropically unfavorable, the expulsion of ordered water molecules from the
interface, and/or order-disorder transitions in other parts of the molecules presumably contributed to
the net favorable entropic change of the interaction. The lower affinity of 868 TCR for A2-
SLFNTIAYL compared to A2-SLYNTVATL or A2-SLYNTIATL was associated with a much
reduced enthalpic component, but more favorable entropy. We used 2D binding analysis to confirm
our observations using SPR (Fig 5J&K). In accordance with our previous findings with other TCRs

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(34, 35), we observed an identical relationship between the strength of interaction between 868 and the three SL9-derived ligands by 2D analysis and SPR. 868-A2-SLYNTIATL was characterized by the strongest 2D effective affinity (1.6x10^{-5} μm^{-4}), followed by 868-A2-SLYNTVATL (1.0x10^{-5} μm^{-4}), with 868-A2-SLFNTIAVVL generating the weakest effective 2D affinity (5.9x10^{-4} μm^{-4}). To further confirm our observations from 2D and 3D binding experiments, we next examined the binding of pMHC tetramers to the 868 TCR at the T-cell surface. Staining of 868 TCR transduced CD8+ primary T-cells was similar for tetramers made with A2-SLYNTVATL, A2-SLYNTIATL and A2-SLFNTIAVVL (Fig 6A). The CD8 coreceptor is known to bind to a site on MHC class I distinct from the TCR docking platform and cooperates with the TCR to aid the engagement of pMHC tetramers (36) and the absence of CD8 binding is known to raise the TCR affinity threshold required for tetramer staining (37, 38). 868 TCR+ Jurkat T-cells, that do not express CD8, also stained equally well with A2-SLYNTVATL, A2-SLYNTIATL and A2-SLFNTIAVVL tetramers (Fig 6B). Given our observations that the TCR affinity threshold required for T-cell activation is considerably lower than that required for pMHC tetramer binding (37) and finding that these reagents can even fail to stain fully functional T-cells (39, 40), our results suggest that the SLFNTIAVVL ultimate escape variant would still be a very efficient T-cell agonist. Indeed, the 868 TCR transduced primary CD8+ T-cells exhibited similar reactivity to SLYNTVATL and SLFNTIAVVL peptides when using standard T-cell activation assay whereby T-cells, antigen-presenting cells and peptide are added directly to tissue culture wells and allowed to incubate (Fig 6C). We conclude that while there is a substantial reduction of TCR binding to the SLFNTIAVVL triple mutant sequence, this reduction cannot explain the observed immune escape per se as assumed by all previous studies in this system (6, 7, 11, 23).

The other way by which peptides can escape from host CTL surveillance is by mutating MHC anchors to reduce binding and presentation at the infected cell surface. However, previous studies have shown that the SLFNTIAVVL peptide binds to HLA A2 with 50-400% of the affinity the index SL9 sequence depending on the study (Table 5). Such minor relative differences were not thought to be able to explain how the triple mutant peptide escapes from CTL (6, 7, 9, 18). Our own studies with a modified version of the 868 TCR that recognizes the escape variants well, showed that this TCR could recognize CD4+ T-cells infected with primary HIV isolates carrying known escape variants (11). Thus, these variants must be presented at the cell surface in the context of HLA A2. Importantly, these variants were not recognized by T-cells expressing the wildtype 868 TCR thus verifying that these viruses are indeed escape mutants (11). Consequently, the established literature

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indicates that the common variant peptides in this system bind sufficiently well to HLA A2 to be presented (6, 7, 9, 18) and sufficiently well to the 868 and D3 TCRs to be recognized by T-cells expressing these SL9-specific receptors. These apparently incongruous findings prompted us to next re-examine peptide binding in the SL9 system.

3.5 CTL escape by the ultimate SL9 escape variant mediated by a fast peptide off-rate

Detailed analysis of the thermal melting of A2-SLYNTVATL, A2-SLYNTIALTL and A2-SLENTIALVL by circular dichroism showed the melting temperature (T\textsubscript{m}) of the wild-type peptide was higher than that of the triple mutant (57 °C compared to 49 °C; Fig 7A&B) suggesting that the triple mutant is less stable. These data are in accordance with two previous studies showing that SLENTIALVL binds to HLA A2 with ~50% reduced affinity compared to SL9 (9, 18) but at odds with two studies indicating that SLENTIALVL is the better ligand (6, 7). Peptide binding to HLA A2 has not previously been thought to result in the immune escape observed with this epitope, which instead has been attributed to a lack of recognition by SL9-specific TCRs (6, 7, 11, 23). Stabilization of HLA A2 at the T2 cell surface in the continuous presence of 100 µM peptide (steady state binding; Fig 7C) showed that the SLENTIALVL peptide stabilized HLA A2 with 89% of that seen with the wildtype SL9 peptide after 3 h. This relatively minor difference increased in an overnight assay where stabilization with SLENTIALVL was ~65% of that seen with the wildtype peptide. Our previous examinations of HLA A2 peptide stability by SPR have shown that good agonists produce pMHC with a half-life of >6 h in a cell free system (41). Similar experiments, performed by examining the relative binding of 868 TCR to A2-peptide by SPR over a time course at 37 °C, showed that both A2-SLYNTVATL and A2-SLYNTIALTL had a half-life of >7 h. In contrast, the half-life of A2-SLENTIALVL on the same chip was <2 h (Fig 8A). We thus reasoned that the stabilization of peptide-HLA measured in a short-term binding assay like those previously used in this system (9, 18) would be determined more by peptide on-rate than the peptide off-rate or dwell time. To further test this possibility, we examined the ‘on rate’ of peptide in T2 cell stabilization assays. Relative stabilization was similar for the SLYNTVATL, SLENTIALVL and the GILGFVFTL influenza matrix-derived peptide that is often used as a positive control for HLA A2 binding (Fig 8B, left panel). We also examined the stability of these A2-peptide complexes at the cell surface by monitoring the amount of HLA A2 on T2 cells incubated with each peptide prior to washing and further culture. The vast majority of HLA A2 stabilized with GILGFVFTL or SLYNTVATL peptide was still present at the cell surface 3 h after the peptide was removed from the assay by cell washing.

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In stark contrast, most of the HLA A2 stabilized by the SLFNTIAYL peptide had decayed in half this time (Fig 8B, right panel). Collectively, these binding data explain how previous studies, using short-term binding assays in the continuous presence of peptide, have shown minor differences in the binding of SL9 and SLFNTIAYL escape variant (Table 5). They also suggest that the dominant mechanism by which the SLFNTIAYL mutant allows immune escape is due to this peptide producing a much shorter-lived peptide-HLA complex. This reduced half-life of antigen at the infected cell surface would be expected to considerably reduce the antigen density on infected cells and thereby facilitate immune escape. To test this notion, we next examined how long peptide pulsed cells could remain as T-cell targets for CD8+ T-cells transduced with the wildtype 868 TCR. These revealing experiments allowed examination of the combined effects of differences in TCR binding and HLA stability in a relevant biological context. Cells pulsed with the SLYNTVATL remained effective targets for 868 TCR-expressing CD8+ T-cells after 24 h of culture (Fig 8C; Supp Fig 1). In contrast, targets pulsed with the SLFNTVATL, SLYNTIAL or SLYTAVAYL variant peptides showed reduced levels of recognition after 24 h. The SLFNTIAYL triple mutant sequence produced the largest effect and was recognized well if experiments were performed immediately but recognition dropped to less than 20% of that seen for the SLYNTVATL peptide at t0 after targets were cultured for 24 h prior to the T-cell recognition assay. Similar data were observed when primary CD4+ T-cells, which form the major reservoir for HIV virus in vivo, were used as targets (Fig 8D). Relative to SLYNTVATL, the SLFNTIAYL pulsed cells made better target at t0 (125%) but their ability to activate the 868 TCR cells diminished to 18% when allowed to culture for 24 h prior to assay (Fig 8D; Supp Fig 2). These results suggest that the major mechanism by which SLFNTIAYL escapes from CTL is through loss of peptide-HLA stability, although reduced TCR interaction with this mutant is also likely to play a secondary role.

4. DISCUSSION

Recognition and escape from the HLA A2-restricted HIV epitope SL9 has been examined in well over 50 studies to date but major questions are still outstanding in this system as there has been no TCR-A2-SL9 co-complex structure. Here we solved the structure of the free 868 TCR, a TCR first described almost 20 years ago (10), and the structure of this TCR in complex with A2-SLYNTVATL. Comparison of the free and ligated TCR structures suggested an 'induced fit' mechanism that involved major structural reorganization of the antigen binding face of the TCR. The CDR3 loops made the biggest movement (almost 7Å for CDR3α and >3Å for CDR3β) to avoid...
steric clashes with the central portion of the peptide, whilst the CDR1 and CDR2 loops interacted mainly with MHC via a more ‘lock-and-key’ interaction.

It has been known for over a decade that the SLYNTVATL and SLFNTVATL bind to HLA A2 with very different conformations, but engage the G10 TCR with near identical on-rates, leading the authors to conclude that one conformation, common to both peptides, was recognized by TCRs (22). Since A2-SLYNTVATL does not change upon TCR binding, we can now be confident that the conformation adopted by this, and many other SL9 variants (21), dominates during TCR recognition. Thus, the evidence suggests that A2-SLFNTVATL undergoes an induced fit upon TCR binding (22) although conclusive proof will await a TCR-A2-SLFNTVATL structure. We further solved the co-complex structure of the 868 TCR with the A2-SLYNTIAL (the variant that predominated in patient 868 in 1996 when the patient blood sample from which this T-cell clone was grown was taken), and the structure of the 868 TCR in complex with the A2-SLFNTIAL, the ultimate escape variant in this system. Resolution of the latter structure came as a surprise as residues that mutate in positions 3, 6 and 8 to produce this mutant are known to be solvent exposed and had been assumed to act as prominent TCR contacts (6, 7, 21-23). In contrast to this prevailing hypothesis we found that the asparagine at position 4 was the dominant contact residue. Indeed, there were more contacts with this residue than with the position 3 tyrosine, position 6 valine and position 8 threonine combined. An alanine mutation scan across the peptide backbone showed that while positions 4 and 5 in SLYNTVATL were important for recognition, the most severe non-MHC anchor change was Y3A. In accordance, the position 3Y sub-library also gave the strongest response of the 180 sub-libraries during a 9-mer positional scanning combinatorial library (PS-CPL) screen of T-cells transduced with the 868 TCR (42). The importance of the tyrosine residue at position 3 is consistent with our previous observation that large bulky amino acids at this position in HLA A2-bound peptides can form a bridge with more C-terminal residues (usually position 5) (43). Replacing residue 3 with a smaller alanine side chain can abolish this important intra-peptide stabilization and have knock-on effects at peptide residue 4 that abrogate TCR binding. Thus, our findings here point towards a common mechanism of peptide presentation by HLA A2 in which peptide residue 3 can be essential for maintaining antigenic identity.

We next undertook a detailed biophysical and thermodynamic study of 868 TCR binding to A2-SLYNTVATL, A2-SLYNTIAL and A2-SLFNTIAL. The 868 TCR exhibited, by far, the strongest affinity of a peptide-HLA ligand for a natural TCR (31) and bound to A2-SLYNTVATL.

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and A2-SLYNTIATL ligands with $K_D$ of 82 nM and 38 nM respectively, or over 10X stronger binding than the next highest TCR-pMHC interaction measured by BIAcore (31). The median affinity for human anti-viral TCR-pMHC interactions is $K_D \sim 5$ µM (31). 868 TCR binding was characterized by a relatively slow off-rate from the A2-SLYNTVATL and A2-SLYNTIATL ligands. The other SL9-TCR that has been examined by SPR, G10, had an off-rate 3.75 times faster than 868, and a 4.5 times slower on rate, resulting in a weaker affinity of $K_D$ of 2.2 µM for A2-SLYNTVATL compared to 868 (22). While binding of the 868 TCR was much reduced for A2-SLFNTIAVL compared to the other ligands, it still had a very respectable affinity ($K_D=1.77$ µM) that falls at the higher end of the spectrum for TCR agonists (31).

The mode of 868 TCR engagement and its affinity with the A2-SLFNTIAVL ultimate escape variant in this system did not lend full support to the prevailing belief that loss of recognition of SL9 occurs mainly via interfering with TCR binding. The fact that CD8+ T-cells transduced with the 868 TCR could recognize SLYNTIATL pulsed target cells well and stained with A2-SLFNTIAVL tetramers was also a surprise, but in accordance with an earlier study that showed that A2-SLFNTIAVL bound to the D3 TCR as well as A2-SLYNTVATL in tetrameric form and that the SLYNTIATL concentration required for half maximal lysis was a highly respectable $4 \times 10^{-10}$ M (21). In further accordance with positions 3, 6 and 8 not dominating A2-SL9-specific TCR binding, the position 4 asparagine sub-library was by far the most potent of the 180 sub-mixtures for activating T-cell clone 003 known to express a different SL9-specific TCR (42). These combined data do not support the notion that the SLYNTIATL escapes from CTL via lack of TCR binding, prompting us to take a closer look at the MHC binding of ligands in this system. Data from three different studies using three different methodologies show that SLYNTIATL binds to HLA A2 with 50-400% of the affinity of SLYNTVATL. Our previous SPR experiments have shown that good agonists produce pMHC with a half-life of >6 h in a cell free system (41). Indeed, our data here show that both A2-SLYNTVATL and A2-SLYNTIATL had half-lives of over 7 h on an SPR chip maintained at 37 °C compared to <2 h for A2-SLFNTIAVL. We reasoned that the peptide binding assays that have been performed previously in this system, including by ourselves (9), would be most influenced by peptide on-rate but that the biology would be most linked to peptide off-rate at the target cell surface. HLA A2+ target cells pulsed with SLYNTVATL peptide remained effective targets for SL9-specific CD8+ T-cells after 24 h of culture as has been observed with a different HIV Gag-derived epitope (27). The SLYNTVATL, SLYNTIATL and SLYNTIAVL peptides (which bind to the 868 TCR with
dissociation constants of 2.9 µM, <100 nM and ~300 nM respectively (31)) were seen well when targets presenting these ligands were used immediately for T-cell assays but exhibited only 67%, 60% and 35% recognition of that observed with SLYNTVATL peptide when targets were cultured for 24 h prior to the T-cell assay. The biggest effect was observed with the SLFNTIALV where >80% of the activity was lost after 24 h of culture. These results were supported by other experiments looking the stability of the A2-SLFNTIALV complex in comparison to other ligands.

Collectively, our results suggest that the instability of the A2-SLFNTIALV molecule is likely to provide the major mechanism of escape from SL9-specific CTL. The accumulation of mutations at positions 3, 6 and 8 to fixation over a 10-year period (6, 7) demonstrates the extraordinary lengths that HIV will go to in order to avoid detection by these key antiviral cells. Our study further highlights that the results of short-term, steady state peptide binding assays can be misleading and suggests that future studies should employ more relevant biological readouts.

5. CONFLICT OF INTEREST

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

6. AUTHOR CONTRIBUTIONS

DKC, AF, GMD, TZ, ML, KM, JLB, FM, CJH, AMB, JSB, JJM, AJAS, KB, BDE and PJR performed and/or directed experiments, analysed data and critiqued the manuscript. DKC and AKS, conceived, funded and directed the project and wrote the manuscript.

7. FUNDING

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9. REFERENCES


Escape from immunodominant HLA A2-restricted HIV epitope


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10. FIGURE LEGENDS

Figure 1. Structural analysis of the 868-A2-SL9 binding mode. A. The overall binding mode of the 868 TCR (red and magenta cartoon) interacting with HLA A2 (grey cartoon) and the SLYNTVATL peptide (red sticks and surface). B. Surface representation of the A2-SLYNTVATL complex looking down at the peptide. Positions of the 868 TCR CDR loops (1α - red, 2α - green, 3α - blue, 1β - yellow, 2β - cyan, 3β - orange) and the crossing angle of the TCR with the MHC groove is shown. C. The positions of the 868 TCR CDR3 loops differ considerably between the ligated (red cartoon) and unligated (grey cartoon) structures.

Figure 2. The 868 TCR focuses on residues 4N and 5T in the peptide. Hydrogen bonds show as red dotted lines, van der Waal’s contacts shown as black dotted lines in panels A-D. A. The 868 TCR (CDR3α in blue, CDR1α red and CDR3β orange sticks) binding to the solvent exposed peptide residues 4N and 5T in the peptide (red sticks). B. The 868 TCR (CDR3α in blue, CDR1α red sticks and surface) forms a tight pocket around peptide residue 4N (red sticks) during binding. C&D. The restriction triad residues 72Q, 69A and 155Q (grey sticks) play a central role in 868 TCR-MHC mediated interactions (TCR CDR3α residues shown in blue, CDR2β in cyan and CDR1α in green sticks). E. 868 TCR transduced CD8+ T-cells from two HLA A2+ donors were co-incubated with T2 cells and alanine substituted peptides of SLYNTVATL (alanine already at position 7) overnight and supernatants used for MIP-1β ELISA. Nonlinear regression curves and pEC50 for each peptide are displayed.

Figure 3. The 868 TCR uses a virtually identical conformation when interacting with the common escape mutants SLYNTIATL and SLFNTIAVL. A. Identical overall binding mode of 868 TCR interacting with A2-SLYNTVATL (red), A2-SLYNTIATL (orange) and A2-SLFNTIAYL (green). HLA A2 in grey cartoon. B. Surface representation of the A2-SLYNTVATL complex looking down at the peptide. Positions of the 868 TCR CDR loops in the A2-SLYNTVATL (red), A2-SLYNTIATL (orange) and A2-SLFNTIAYL (green) complexes. Crossing angle of the TCR is indicated. C. Contacts between the 868 TCR and residues 3Y, 6V and 8T in the SLYNTVATL peptide that constitute the positions that a commonly mutated by HIV. D. Contacts between the 868 TCR and residues 3Y, 6I and 8V in the SLYNTIATL peptide. Although slightly different, the total number of contacts between the 868 TCR and A2-SLYNTIATL is similar to the 868-A2-SLYNTVATL complex. E. Contacts between the 868 TCR and residues 3F, 6I and 8V in the A2-
Escape from immunodominant HLA A2-restricted HIV epitope

838 SLENTIAYL triple escape mutant peptide. Again, the total number of contacts between the 868 TCR and A2-SLENTIAYL is similar to the complex with the wildtype index peptide. Hydrogen bonds show as red dotted lines, van der Waal’s contacts shown as black dotted lines in panels C-E.

Figure 4. 868 TCR binding alters the peptide conformation of the A2-SLYNTVATL escape mutants. Structural comparison of the A2-SLYNTVATL escape variants unligated and in complex with the 868 TCR. A&B. A2-SLYNTVATL in complex with the 868 TCR (red sticks) vs unligated A2-SLYNTVATL (cyan sticks). Small changes in the positions of the side chains that occur during TCR binding are circled. C&D. A2-SLYNTIATL (orange sticks) in complex with the 868 TCR vs unligated A2-SLYNTIATL (yellow sticks). Small changes in the positions of the side chains that occur during TCR binding are circled. E&F. A2-SLENTIAYL (green sticks) in complex with the 868 TCR vs unligated A2-SLENTIAYL (purple sticks). Small changes in the positions of the side chains that occur during TCR binding are circled.

Figure 5. Binding affinity and thermodynamic analysis of the 868 TCR binding to A2-SLYNTVATL, A2-SLYNTIATL and A2-SLENTIAYL. A-C. Binding and kinetic analysis of the 868 TCR interaction with A. A2-SLYNTVATL, B. A2-SLYNTIATL and C. A2-SLENTIAYL. Experiments were performed independently using a BIAcore T100 equipped with a CM5 sensor chip and repeated in triplicate on different days using different protein preparations. Representative data are shown. D-F. Thermodynamic analysis of 868 TCR with the aforementioned ligands. SPR as above. Thermodynamic parameters were calculated according to the Gibbs-Helmholtz equation (\(\Delta G^\circ = \Delta H - T\Delta S^\circ\)). The binding free energies, \(\Delta G^\circ\) (\(\Delta G^\circ = RT\ln K_d\)), were plotted against temperature (K) using non-linear regression to fit the three-parameters Van’t Hoff equation, (\(RT\ln K_d = \Delta H^\circ - T\Delta S^\circ + \Delta C_p^\circ(T-T_0) - T\Delta C_p^\circ\ln(T/T_0)\) with \(T_0=298\) K). G-I. Thermodynamic analysis of the 868 TCR-pMHC interaction was also performed using isothermal titration calorimetry 200 instrument to directly measure \(\Delta H\). These analyses show consistent values to those generated by SPR. Overall, the 868 TCR uses a generally similar binding mechanism and thermodynamic signature to interact with all three ligands. J. Effective 2D binding frequency, using at least 5 cell pairs, and calculated as an average of 100 cell-cell contacts. K. Effective 2D affinity (A\(_K_a\)) calculated using adhesion frequency assays.

Figure 6. 868 TCR-expressing T-cells bind escape mutant tetramers efficiently without the need for CD8. A. Primary CD8\(^+\) T-cells were co-transduced with the 868 TCR and rat (r)CD2 prior to staining with 0.5 \(\mu\)g (with respect to MHC) of irrelevant (A2-ALWGPDPAAA), A2-SLYNTVATL.

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Escape from immunodominant HLA A2-restricted HIV epitope

A2-SLYNTIATL and A2-SLFNTIAYVL, PE conjugated peptide-MHC tetramers. Cells are gated on rCD2^+CD8^- cells. Histograms show staining with indicated PE-conjugated tetramer with the MFI of this population displayed. B. As for A, but 868 TCR and rat (r) CD2 were transduced into TCRβ chain negative Jurkat cells. MFI of tetramer staining is shown for cells in the rCD2^+ tet^+ gate. C. 868 TCR transduced were incubated with T2 cells and either SLYNTVATL or SLFNTIAYVL peptide at the concentrations shown for 5 h followed by the detection of CD107a and TNFα by flow cytometry.

Figure 7. Stability of A2-SLYNTVATL, A2-SLYNTIATL and A2-SLFNTIAYVL. A. CD thermal denaturation curves recorded at 218nm are shown for selected samples as indicated. Dots represent measured values fitted assuming a 2-state trimer-to-monomer transition (solid lines) as described in Materials and Methods. B. Bar graphs of the thermal stability with respect to melting temperature (upper) and van't Hoff's enthalpy of unfolding (lower panel). Error bars in A & B represent S.D. resulting from the multivariable curve fitting of data from one experiment with each peptide. C. T2s were incubated for 3h or 22h with 10^5 M of each peptide (Influenza (Flu) Matrix, GILGFVFTL, HIV Gag wild-type SLYNTVATL and Gag triple mutant SLFNTIAYVL) or DMSO control were stained for HLA-A2 and fixed. The dashed line is set at the mean fluorescence intensity (MFI) of the negative control peptide (EBV HPVGEADYFEY that binds HLA B*3501).

Figure 8 Instability at the cell surface mediates viral escape by the triple mutant epitope, A2-SLFNTIAYVL. A. Relative binding of 868 TCR to A2-peptide complexes by SPR over time. The SPR chip was maintained at 25°C. Functional half-life was determined by injecting the 868 TCR at a fixed concentration of 100 μM over 720 mins and recording the drop in total RUs over 8 different time points. A faster drop in RUs (converted into a T_1/2) was interpreted to indicate greater peptide instability, detected by loss of binding by and antigen specific 868 TCR. B. Left panel shows relative HLA-A2 expression following incubation (0 h, 3 h and 22 h) of T2s with indicated peptide. Results are normalized to the maximum MFI seen for each peptide. The right panel shows T2 cells incubated with peptide for 22h prior to being washed and cultured in an excess of AIM-V media for the indicated times prior to staining and fixing. Data displayed as HLA-A2 expression relative to the maximum seen at 22h. C. T2 cells were pulsed for 1 h with the peptides shown, washed extensively and then cultured in an excess of media for 3 h (black bar) or 24 h (open bar) before being co-incubated for 5 h with T-cells from two donors transduced with the 868 TCR. CD107α and TNFα were used to establish percentage reactivity by flow cytometry. Values were normalized relative to peptide washed extensively then.
Escape from immunodominant HLA A2-restricted HIV epitope

WT SLYNTVATL peptide. Standard error of the mean is shown for two different donor T-cells. Untransduced CD8+ T-cells did not respond to peptide (data not shown). Raw data for C is shown in Supplementary Fig 1. D. As C but using primary HLA-A2- and HLA-A2+ CD4+ T-cells as targets and culturing in excess media for either 0 h or 24 h prior to assay. Raw data for D is shown in Supplementary Fig 2.
### Table 1. Peptides used in this study

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<th>Peptide Sequence</th>
<th>Abbreviation</th>
<th>HLA-restriction</th>
<th>Parent Protein</th>
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<td>HLA A*0201</td>
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<td>HIV p17 Gag</td>
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<td>3F8I8V</td>
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</table>
Table 2

Data collection and refinement statistics for unligated 868 TCR and complex structures

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<td>Space group</td>
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<td>P 21 21 2</td>
<td>P 21 21 2</td>
<td>P 21 21 2</td>
<td>P 1 21 1</td>
<td>P 1 21 1</td>
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<tr>
<td><strong>Cell dimensions</strong></td>
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<td>a, b, c (Å)</td>
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<td>211.1, 85.1, 113.2</td>
<td>207.6, 84.7, 112.1</td>
<td>209.36, 85.1, 113.15</td>
<td>56.1, 80.1, 57.6</td>
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<td>90, 90, 90</td>
<td>90, 90, 90</td>
<td>90, 90, 90</td>
<td>90, 90, 90</td>
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<td>34.0-2.9</td>
<td>99.5-2.8</td>
<td>31.7-1.6</td>
<td>48.4-1.7</td>
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<td>Beam Line</td>
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<td>103</td>
<td>103</td>
<td>104-1</td>
<td>103</td>
<td>124</td>
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<tr>
<td>Beam time code</td>
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<td>4532-1</td>
<td>6232-1</td>
<td>6232-10</td>
<td>4532-1</td>
<td>3262-9</td>
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<td>Rmerge (%)</td>
<td>5.0 (72.3)</td>
<td>12.5 (95.9)</td>
<td>15.1 (84.0)</td>
<td>11.7 (86.7)</td>
<td>6.6 (73.3)</td>
<td>7.4 (130.3)</td>
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<tr>
<td>Completeness (%)</td>
<td>98.6 (99.6)</td>
<td>99.1 (99.8)</td>
<td>100 (100)</td>
<td>99.9 (100)</td>
<td>99.4 (97.7)</td>
<td>98.9 (99.8)</td>
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<tr>
<td>Redundancy</td>
<td>3.5 (3.8)</td>
<td>7.5 (7.1)</td>
<td>7.9 (8.2)</td>
<td>7.4 (7.6)</td>
<td>4.1 (4.0)</td>
<td>3.6 (3.7)</td>
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<td>No. reflections</td>
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<td>44,013</td>
<td>45,223</td>
<td>55,560</td>
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<td>53,691</td>
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<td></td>
<td>(4,492)</td>
<td>(3,213)</td>
<td>(3,284)</td>
<td>(3,895)</td>
<td>(4,752)</td>
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<td><strong>Refinement</strong></td>
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<tr>
<td>No Rmerge, reflections</td>
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<td>2,223</td>
<td>2,717</td>
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<td>Rwk / Rfree</td>
<td>18.9/22.3</td>
<td>19.4/28.9</td>
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<td>19.2/27.0</td>
<td>14.4/19.4</td>
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<td><strong>R.m.s. deviations</strong></td>
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<td>Bond lengths (Å)</td>
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<td>0.015</td>
<td>0.012</td>
<td>0.017</td>
<td>0.025</td>
<td>0.017</td>
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<tr>
<td>Bond Angles (°)</td>
<td>1.970</td>
<td>1.665</td>
<td>1.483</td>
<td>1.954</td>
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<td>Mean B value (Å²)</td>
<td>57.0</td>
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<td>31.2</td>
<td>16.8</td>
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<td>Wilson B-fac (Å²)</td>
<td>40.7</td>
<td>72.2</td>
<td>60.3</td>
<td>58.9</td>
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<tr>
<td>ML estimated coordinate error</td>
<td>0.144</td>
<td>0.387</td>
<td>0.365</td>
<td>0.300</td>
<td>0.049</td>
<td>0.070</td>
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</table>

* One crystal was used for solving each structure.

Figures in brackets refer to the highest resolution bin.

This is a provisional file, not the final typeset article.
### Table 3.

**Summary of co-complex structures of 868-A2-SLYNTVATL, 868-A2-SLYNTIATL and 868-A2-SLFNTIAYL**

<table>
<thead>
<tr>
<th></th>
<th>868-A2-SLYNTVATL</th>
<th>868-A2-SLYNTIATL</th>
<th>868-A2-SLFNTIAYL</th>
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</thead>
<tbody>
<tr>
<td>H-bonds (≤3.4Å)</td>
<td>20</td>
<td>20</td>
<td>18</td>
</tr>
<tr>
<td>vdWs (≤4Å)</td>
<td>121</td>
<td>118</td>
<td>128</td>
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<tr>
<td>Total contacts</td>
<td>141</td>
<td>138</td>
<td>146</td>
</tr>
<tr>
<td>CDR1/CDR2/CDR3 contacts (≤4Å):</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>α chain</td>
<td>13/33/41</td>
<td>9/23/46</td>
<td>8/22/47</td>
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<tr>
<td>β chain</td>
<td>0/17/37</td>
<td>0/27/43</td>
<td>0/24/45</td>
</tr>
<tr>
<td>Peptide contacts</td>
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<td>56</td>
<td>63</td>
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<tr>
<td>MHC contacts</td>
<td>79</td>
<td>82</td>
<td>83</td>
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<tr>
<td>Crossing Angle</td>
<td>51.6°</td>
<td>50.3°</td>
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<tr>
<td>Buried surface area (Å²)</td>
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<td>2469</td>
<td>2698</td>
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<tr>
<td>Surface complementarity:</td>
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<tr>
<td>TCR-MHC</td>
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<td>0.51</td>
<td>0.55</td>
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<tr>
<td>TCR-peptide</td>
<td>0.72</td>
<td>0.70</td>
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<td>TCR-pMHC</td>
<td>0.56</td>
<td>0.55</td>
<td>0.59</td>
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</table>

HB = hydrogen bond, SB = salt bridge, WB = water bridge, vdWs = van der Waals interactions

*A 3.4Å cut-off was used for HBs, SBs and WBs, and a 4Å cut-off was used for vdWs*
Escape from immunodominant HLA A2-restricted HIV epitope

Affinity and kinetic measurements of 868-A2-SLYNTVATL, 868-A2-SLYNTIATL and 868-A2-SLYNTIAVL at different temperatures

<table>
<thead>
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<th>MHC-Peptide</th>
<th>Temp (°C)</th>
<th>$K_{on} (M^{-1} S^{-1})$</th>
<th>$K_{off} (S^{-1})$</th>
<th>$K_D^{kin}$ (µM)</th>
<th>$K_D^{equ}$ (µM)</th>
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<tbody>
<tr>
<td>A2-SLYNTVATL</td>
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<td>1.1x10^4</td>
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<td>0.23</td>
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<tr>
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<td>8</td>
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<td>0.11</td>
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<tr>
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<td></td>
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<tr>
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<tr>
<td>A2-SLYNTIATL</td>
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<td>0.13</td>
<td>0.16</td>
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<td>0.049</td>
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<tr>
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<td>6.4x10^3</td>
<td>3.2x10^2</td>
<td>0.05</td>
<td>0.11</td>
</tr>
<tr>
<td>A2-SLYNTIAVL</td>
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<td>7.7x10^2</td>
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<td>2.2</td>
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<tr>
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<td>1.0x10^4</td>
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<td>2.3</td>
</tr>
</tbody>
</table>

This is a provisional file, not the final typeset article
**Escape from immunodominant HLA A2-restricted HIV epitope**

**Table 5.**

Relative binding of SLYNTVAL and SLENTIAYL to HLA A2

<table>
<thead>
<tr>
<th>METHOD</th>
<th>METHOD</th>
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</thead>
<tbody>
<tr>
<td>S35 methionine pulse chase</td>
<td>Direct competition with radio-labelled ligand</td>
</tr>
<tr>
<td>100% (K_D = 50 nM)</td>
<td>100% (K_D = 100 nM)</td>
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</tbody>
</table>

**Table 5.**

Relative binding of SLYNTVAL and SLENTIAYL to HLA A2

<table>
<thead>
<tr>
<th>METHOD</th>
<th>METHOD</th>
</tr>
</thead>
<tbody>
<tr>
<td>HLA A2 ELISA</td>
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</tbody>
</table>
2.12 T-cell activation assays

For peptide pulsing assays, T2 cells were incubated with peptide for 2h in 0.5 ml of AIM-V media followed by 4 washes with 4 ml of RPMI 1604 media. Post pulsing, T2 cells were incubated in 4.5 ml of AIM-V media at 37°C and 5% CO₂ for 24h or used immediately (0 h), such that cells were ready at the same time. 868 TCR transduced and non-transduced T-cells (30,000) were rested overnight in R5 (as for R10 but with 5% FBS) then co-incubated in 96U well plates with T2s (60,000) in the presence of GolgiStop and GolgiPlug according the manufacturers (BD Biosciences, Oxford, UK), and anti-CD107a PE Antibody (H483, BD Biosciences). Controls included T-cells alone and T-cells with unpulsed T2s (negative control) or PHA. After 5h of incubation cells were labelled with the violet LIVE/DEAD fixable dead cell stain Vivid, anti-CD8 APC (BW135/80; Miltenyi Biotec) and anti-CD19 pacific-blue (BioLegend) antibodies. Cells were then stained with anti-TNFα PE-Vio770 antibody (CA2, Miltenyi Biotec) using a Cytofix/Cytoperm kit (BD Biosciences) according to manufacturer’s instructions. Flow cytometry was performed on a FACSCanto II (BD Biosciences) and data analysed with FlowJo software (TreeStar, Ashland, OR). For peptide alanine scans 868 TCR transduced T-cells were rested overnight in R5 then incubated with T2s (60,000) and peptides at specified concentrations for 18h in 96U well plates in 100 μl of R5. Supernatants (50 μl) were used for MIP-1β ELISA (R&D Systems, Minneapolis, Canada) and GraphPad Prism (GraphPad Software, Inc., La Jolla, CA) used to fit nonlinear regression curves and calculate EC₅₀ for each peptide.
Figure 1 (1 column)
Figure 2 (1 column)
Figure 3 (1 column)
Figure 4 (1 columns)
Figure 5

(A) 868-A2-SLYNTVATL
- $K_D = 0.082 \mu M$
- $k_{on} = 1.5 \times 10^6 \text{ M}^{-1}\text{s}^{-1}$
- $k_{off} = 1.6 \times 10^2 \text{ s}^{-1}$

(B) 868-A2-SLYNTIAL
- $K_D = 0.038 \mu M$
- $k_{on} = 1.4 \times 10^6 \text{ M}^{-1}\text{s}^{-1}$
- $k_{off} = 7.3 \times 10^3 \text{ s}^{-1}$

(C) 868-A2-SLFNTIAML
- $K_D = 1.77 \mu M$
- $k_{on} = 1.4 \times 10^6 \text{ M}^{-1}\text{s}^{-1}$
- $k_{off} = 2.1 \times 10^2 \text{ s}^{-1}$

(D) $\Delta H^0 = -7.2$
- $T\Delta S^0 = 2.5$

(E) $\Delta H^0 = -7.1$
- $T\Delta S^0 = 3.1$

(F) $\Delta H^0 = -2.5$
- $T\Delta S^0 = 5.4$

(G) $K_D = 0.029 \mu M$
- $\Delta H = -8.7 \text{ kcal/mol}$
- $T\Delta S = 1.5 \text{ kcal/mol}$

(H) $K_D = 0.12 \mu M$
- $\Delta H = -9.4 \text{ kcal/mol}$
- $T\Delta S = 0.04 \text{ kcal/mol}$

(I) $K_D = 6.7 \mu M$
- $\Delta H = -3 \text{ kcal/mol}$
- $T\Delta S = 5.3 \text{ kcal/mol}$

(J) Effective Binding Frequency

(K) 2D Effective Affinity (um$^{-1}$)
Figure 7.
In review.