Cooperative binding of T cell receptor and CD4 to peptide-MHC enhances antigen sensitivity

Antigen recognition by the T cell receptor (TCR) of CD4+ T cells can be greatly enhanced by the coreceptor CD4. Yet, understanding of the molecular mechanism is hindered by the ultra-low affinity of CD4 binding to class-II peptide-major histocompatibility complexes (pMHC). Here we show, using two-dimensional (2D) mechanical-based assays, that the affinity of CD4–pMHC interaction is 3-4 logs lower than that of cognate TCR–pMHC interactions, and it is more susceptible to increased dissociation by forces (slip bond). In contrast, CD4 binds TCR-pre-bound pMHC at 3-6 logs higher affinity, forming TCR–pMHC–CD4 tri-molecular bonds that are prolonged by force (catch bond), and modulated by protein mobility on the cell membrane, indicating profound TCR-CD4 cooperativity. Consistent with a tri-crystal structure, using DNA origami as a molecular ruler to titrate spacing between TCR and CD4 we show that 7-nm proximity optimizes TCR–pMHC–CD4 tri-molecular bond formation with pMHC. Our results thus provide deep mechanistic insight into CD4 enhancement of TCR antigen recognition.

CD4+ T cells play vital and versatile roles in the adaptive immunity by differentiating into lineages of various functions upon activation by antigen. Antigen recognition is achieved by the T cell receptor (TCR) interacting with its cognate peptide bound to major histocompatibility complex (MHC, or pMHC when including the peptide) expressed on an antigen-presenting cell (APC) or target cell. TCR–pMHC binding triggers phosphorylation of CD3 immunoreceptor tyrosine-based activation motifs (ITAM), leading to a signaling cascade that results in T cell activation and effector function. Expressed on the surface of their respective T cell subsets, CD8 and CD4 coreceptors are thought to facilitate the initiation of the intracellular signaling cascade by stabilizing TCR–pMHC binding and delivering its associated Lck to TCR. However, unlike CD8, CD4’s extremely low affinity for MHC hinders our understanding of these proposed mechanisms that require CD4 binding to pMHC. Indeed, surface plasmon resonance (SPR) was unable to measure CD4–MHC interactions in three-dimensions (3D), except for one report of a ~200 μM $K_d$ that was not reproduced. Although affinity measurements were successfully attained using B
Here we analyze, combining our 2D kinetic assays and mathematical modeling, the bimolecular CD4–MHC interaction and TCR–CD4 cooperativity using both purified protein ectodomains and cell systems. We identify significant cooperative binding of CD4 to TCR-prebound pMHC, which has 3–6 logs higher affinity than binding to free pMHC. By presenting TCR and CD4 on different surfaces to modulate molecular diffusion or DNA origami to modulate molecular spacing, we show that the TCR–CD4 cooperativity requires molecular mobility to allow for their colocalization within a 7-nm proximity, consistent with that reported in TCR–pMHC–CD4 tri-crystal structure. Our results explain how CD4 could efficiently augment TCR antigen recognition via cooperative binding to TCR-prebound pMHC, thereby boosting TCR sensitivity. They also underline the importance of physical factors in regulating T cell antigen recognition, which may be imposed on molecular organization at the cell membrane via signaling-dependent and/or independent mechanisms.

**Results**

**CD4-MHC binding displays low 2D affinity**

We used our adhesion frequency assay (Fig. 1a), which analyzes cross-junctional interactions upon initial brief cell-cell encounters, to quantify the 2D binding between HLA-DR1 presenting a melanoma antigenic peptide derived from the glycolytic enzyme triosephosphate isomerase (TPH:HLA-DR1, referred hereafter as pMHC, unless specified) and its cognate E8 TCR, wild-type (WT) CD4, or a high-affinity mutant (MT) CD4 generated via directed evolution. Ectodomains of each binding pair were respectively coated on two opposing RBCs, which were brought into contact and then separated to detect adhesion by RBC elongation. Results were presented as adhesion frequency ($P_a$) of many repeated contact-separation cycles, which was ligand. $c$ Mean ± SEM (n = 3 cell pairs per data point) $P_a$ vs $t_c$ curves for pMHC interacting with MT CD4 at various coating densities as indicated by the number in legend. $d$ The normalized bond number $<n>/m r_l$ vs $t_c$ curve for pMHC interaction with E8 TCR (green), WT CD4 (purple), or MT CD4 (orange). Different symbols represent independent experiments using different molecular densities that are shown in Supplementary Table 1. $e$ Normalized bond number at steady-state calculated from $d$ was plotted vs receptor and ligand densities. Source data are provided as a Source Data file.

**Fig. 1** 2D kinetic analysis of TPI/HLA-DR1 interaction with E8 TCR or CD4. **a** Schematics of micropipette binding frequency assay (top) and molecular coating (bottom). A pMHC-coated RBC (left) was repeatedly brought into contact with an opposing RBC coated with E8 TCR, or WT/MT CD4 (right) and separated to detect bond formation across the contact interface. **b** Specificity is shown by the significantly higher (p-value indicated, by two-tailed Mann-Whitney test) of steady-state (contact time $t_c$ = 4 s) adhesion frequencies ($P_a$, mean ± SEM (n = 6, 6, 9, 3 cell pairs) of indicated points each determined from 50 cycles of contact) between pMHC-coated RBCs and RBCs coated with E8 TCR, WT CD4, or WT CD4, than that without ligand. $c$ Mean ± SEM (n = 3 cell pairs per data point) $P_a$ vs $t_c$ curves for pMHC interacting with MT CD4 at various coating densities as indicated by the number in legend. $d$ The normalized bond number $<n>/m r_l$ vs $t_c$ curve for pMHC interaction with E8 TCR (green), WT CD4 (purple), or MT CD4 (orange). Different symbols represent independent experiments using different molecular densities that are shown in Supplementary Table 1. $e$ Normalized bond number at steady-state calculated from $d$ was plotted vs receptor and ligand densities. Source data are provided as a Source Data file.
higher between RBCs functionalized with designated molecules at appropriate densities than between blank ones at the same contact time $t_c$ indicating specific interactions (Fig. 1b). $P_3$ increased initially and plateaued as the probability of bond formation was balanced by that of dissociation with prolonged $t_c$, resulting in a steady-state (Fig. 1c). We evaluated the effective 2D affinity ($A_iK_i$) and off-rate ($k_{-i}$) by fitting the $P_3$ vs $t_c$ curve (Fig. 1c) or the log-transformed and molecular density-normalized counterparts (Fig. 1d) to a published model \cite{3,39} (Table 1). The log transformation converts $P_3$ to the average number of bonds per contact, $<\eta> = \ln(1-P_3)$, which, after normalization by densities of the receptor ($m_a$) and ligand ($m_l$) collapses three curves measured at different $m_a$ vs $m_l$ at large $t_c$ values (indicated by different symbols in Fig. 1d) and approaches to $A_iK_i$ at large $t_c$. This model was well supported as the steady-state $<\eta>$ increased linearly with $m_a$ vs $m_l$.

### Table 1 | Kinetic parameters of the purified protein system and the measurement methods

| E8 TCR | CD4 | Mutant CD4 |
|--------|-----|------------|
| $A_{1,TCR}$ (µm$^2$) | Source $A_{1,CD4}$ (µm$^2$) | Source $A_{1,MTC4}$ (µm$^2$) |
| 7.70 ± 0.40 × 10$^{-4}$ | Fig. 1d | 4.35 ± 0.49 × 10$^{-3}$ | Fig. 1d |
| 3.01 ± 0.69 × 10$^{-1}$ | Fig. 5a | 7.74 ± 0.60 × 10$^{-7}$ | Fig. 5b |
| 8.31 ± 0.46 × 10$^{-1}$ | Fig. 2a,b | 4.57 ± 1.02 × 10$^{-3}$ | Fig. 3a, purple |
| 2.87 ± 0.49 × 10$^{-1}$ | Fig. 3a, green | 6.57 ± 0.64 × 10$^{-6}$ | Fig. 3d, purple |
| 3.39 ± 0.37 × 10$^{-4}$ | Fig. 3d, green | $k_{-1,CD4}$ (s$^{-1}$) | Source $A_{1,MTC4}$ (µm$^2$) |
| 1.42 ± 0.46 × 10$^{-4}$ | Fig. 3d, black | 0.37 ± 0.11 | Fig. 1d |
| 6.45 ± 0.58 × 10$^{-4}$ | Fig. 3h, green | 4.0 ± 0.03 | Fig. 2d |
| 5.30 ± 0.33 × 10$^{-4}$ | Fig. 3h, black | 0.84 ± 0.22 | Fig. 3a, purple |
| 6.09 ± 0.62 × 10$^{-4}$ | Fig. 3h, orange | 0.66 ± 0.08 | Fig. 3d, purple |
| 2.02 ± 0.18 × 10$^{-4}$ | Fig. 3h, blue | $A_{1,CD4}$ (µm$^2$ s$^{-1}$) | Source |
| 8.39 ± 1.07 × 10$^{-1}$ | Fig. S2c | 1.62 ± 0.35 × 10$^{-4}$ | Fig. 1d |
| 1.29 ± 0.52 × 10$^{-4}$ | Fig. 5a | $K_{+1,CD4}$ (µm$^2$) | Source |
| $k_{+1,TCR}$ (s$^{-1}$) | Source | 5.26 ± 0.72 × 10$^{-2}$ | Fig. 2a,b |
| 0.48 ± 0.07 | Fig. 1d | (8.33 ± 4.32 × 10$^{-7}$)$^9$ | Fig. 3b, black |
| 0.13 ± 0.05 | Fig. 2a,b | 2.69 ± 1.14 × 10$^{-1}$ | Fig. 3e, black |
| 11 ± 0.19 | Fig. 2d | (7.26 ± 1.52 × 10$^{-4}$)$^9$ | Fig. 3e, brown |
| 0.56 ± 0.12 | Fig. 3a, green | 2.99 ± 0.27 × 10$^{-1}$ | Fig. 3h, black |
| 0.34 ± 0.05 | Fig. 3d, green | 1.0 ± 42,000 × 10$^{-4}$ | Fig. 3h, orange |
| 1.60 ± 1.06 | Fig. 3d, black | 3.75 ± 0.97 × 10$^{-4}$ | Fig. 3h, blue |
| 0.41 ± 0.09 | Fig. 3h, green | 4.87 ± 1.07 × 10$^{-4}$ | Fig. S2c |
| 1.11 ± 0.11 | Fig. 3h, black | 5.0 ± 1.5 × 10$^{-2}$ | Fig. 5a |
| 0.99 ± 0.34 | Fig. 3h, orange | $k_{+2,CD4}$ (s$^{-1}$) | Source |
| (0.99 ± 0.34)$^8$ | Fig. 3h, blue | 1.99 ± 1.6 | Fig. 2a,b |
| $A_{1,TCR}$ (µm$^2$ s$^{-1}$) | Source | (0.12 ± 0.11)$^1$ | Fig. 3b, black |
| 3.66 ± 0.42 × 10$^{-4}$ | Fig. 1d | 0.13 ± 0.12 | Fig. 3e, black |
| 4.38 ± 0.48 × 10$^{-4}$ | Fig. 2a,b | (10 ± 17)$^1$ | Fig. 3e, brown |
| 2.66 ± 0.46 × 10$^{-3}$ | Fig. 3h, green | 4.2 ± 2.5 | Fig. 3h, black |
| 5.88 ± 0.69 × 10$^{-4}$ | Fig. 3h, black | 2.0 ± 3.8 | Fig. 3h, orange |
| 6.03 ± 2.2 × 10$^{-4}$ | Fig. 3h, orange | (2.0 ± 3.8)$^1$ | Fig. 3h, blue |
| 2.00 ± 0.71 × 10$^{-4}$ | Fig. 3h, blue | $k_{+2,CD4}$ (µm$^2$ s$^{-1}$) | Source |
| 0.11 ± 0.093 | Fig. 2a,b | 0.35 ± 0.35 | Fig. 3e, black |
| 7.2 ± 12$^1$ | Fig. 3e, brown | 1.28 ± 0.78 | Fig. 3h, black |
| 2.0 ± 84,000 × 10$^{-4}$ | Fig. 3h, orange | 0.75 ± 1.4 | Fig. 3h, blue |

$^9$Use the same value as Fig. 3h, orange.

$^8$Two-parameter fit values.

Methods:
- Figure 1d: Micropipette adhesion frequency assay with fitting to Eq. 8.
- Figure 2a,b: BFP adhesion frequency assay with fitting to Eqs. 1 and 2.
- Figure 2d: BFP thermal fluctuation assay with fitting to $ln(p)=-k_{-1}t$.
- Figure 3a,b,d,e: BFP adhesion frequency assay with the single-species data fitting to Eq. 8 and dual-species data fitting to Eqs. 1 and 2.
- Figure 3e, brown: BFP adhesion frequency assay with the black data fitting to Eqs. 1 and 2 using only two parameters ($K_{+1,CD4}$ and $k_{+2,CD4}$) after fixing $A_{1,TCR}$ and $k_{-1,TCR}$ at values obtained from fitting the green and purple data by Eq. 8.
- Figure 3h: Micropipette adhesion frequency assay with fitting to Eq. 8 (green curve) and Eqs. 1 and 2 (green and black curves, orange curve, and blue curve with $k_{+1,TCR}$ and $k_{+2,CD4}$ fixed at the values obtained from fitting the orange curve).
- Figure 5a: Micropipette adhesion frequency assay with fitting to Eq. 4 at steady-state.
- Figure S1a-c: Micropipette adhesion frequency assay with fitting to Eq. 7 at steady-state.
- Figure S2c: Micropipette adhesion frequency assay with fitting to Eq. 3 at steady-state.
TCR and CD4 cooperatively bind to pMHC

To explain how CD4–MHC binding could disproportionately recruit Lck to TCR, we tested the hypothesis that TCR and CD4 bind pMHC synergistically as observed for TCR and CD813,15,16. ES TCR and CD4 were co-functionalized on RBCs at different density ratios (mTCR/mCD4) while keeping their sum constant and tested against RBCs bearing pMHC with the same density (m_{\text{pMHC}}). We first analyzed the P_2 vs t_\text{c} curves so measured (Fig. 2a) using a dual-species concurrent and independent binding model3,29–31, opposite to our synergistic binding hypothesis. Without synergy, this model predicts that the average whole number of bonds <n>_W would be equal to the sum of its parts, i.e., the average numbers of TCR–pMHC bonds, <n>_TCR, plus the average numbers of CD4–MHC bonds, <n>_CD4. Given the low CD4 density, which was far from enough to make up its low affinity, the measured <n>_W should have yielded <n>_TCR as its only detectable component and normalizing it by m_{\text{TCR}} and m_{\text{pMHC}} should have collapsed the entire family of curves as did Fig. 1d. Contrary to this prediction based on the dual-species concurrent and independent binding model3,29–31, the <n>_W/m_{\text{TCR}} vs t_\text{c} curve upward shifted as m_{\text{CD4}} increased (Fig. 2b and Supplementary Fig. 2a), falsifying the independent binding assumption3,29. Instead of increasing linearly as in Supplementary Fig. 1, the steady-state <n>_W increased nonlinearly with increasing m_{\text{TCR}}m_{\text{pMHC}} (Supplementary Fig. 2b). Instead of being a constant as Fig. 1e, the TCR- and pMHC-density normalized whole bond number, <n>_W/m_{\text{pMHC}} increased linearly with increasing CD4 density m_{\text{CD4}} (Supplementary Fig. 2c). These results demonstrate that TCR and CD4 cooperatively bind to pMHC as we hypothesized, manifesting higher number of whole bonds than the sum of TCR–pMHC and CD4–pMHC bonds as parts.

From the difference between the whole and the sum of parts, we identified a new bond species — the emerging TCR–pMHC–CD4 trimolecular bonds whose average number is <n>_\text{tri} = <n>_W <n>_\text{TCR} <n>_\text{CD4}. We developed a kinetics model in which CD4 binding of free pMHC is ignored due to its negligible affinity compared to TCR binding, but CD4 is allowed to bind TCR-prebound pMHC with a higher affinity K_{\text{a,CD4}} = k_{\text{-CD4}}/k_{\text{+CD4}}. This model predicts (see Methods):

$$\frac{\langle n \rangle_W}{m_{\text{TCR}}m_{\text{pMHC}}} = A_K A_{\text{TCR}}m_{\text{CD4}} K_{\text{a,CD4}}$$

$$\left[1 + A_{\lambda_1}k_{\text{-TCR}} - k_{\text{-CD4}} + A_2k_{\text{-CD4}} \right]$$

$$\left[1 - A_1k_{\text{-TCR}}k_{\text{-CD4}} + k_{\text{+CD4}} \right]$$

$$= A_K A_{\text{TCR}}m_{\text{CD4}} K_{\text{a,CD4}}$$

$$\left[1 + A_{\lambda_1}k_{\text{-TCR}} - k_{\text{-CD4}} + A_2k_{\text{-CD4}} \right]$$

$$\left[1 - A_1k_{\text{-TCR}}k_{\text{-CD4}} + k_{\text{+CD4}} \right]$$

$$= A_K A_{\text{TCR}}m_{\text{CD4}} K_{\text{a,CD4}}$$

where \(\lambda_1\) and \(\lambda_2\) are positive functions of off-rate of TCR–pMHC bond (k_{\text{-TCR}}, on- and off-rate of CD4 binding to (k_{\text{+CD4}}) and dissociating from (k_{\text{-CD4}}) TCR-prebound pMHC, and CD4 density (m_{\text{CD4}}):

$$\lambda_1,2 = \frac{1}{2} \left[ k_{\text{-TCR}} + k_{\text{-CD4}} + m_{\text{CD4}}k_{\text{+CD4}} \right]$$

$$\left[ k_{\text{-TCR}} - k_{\text{-CD4}} + m_{\text{CD4}}k_{\text{+CD4}} \right]^{1/2}$$

The steady-state solution as t_\text{c} → is

$$\frac{\langle n \rangle_W}{m_{\text{TCR}}m_{\text{pMHC}}} = A_K A_{\text{TCR}} + m_{\text{CD4}} A_K A_{\text{TCR}} K_{\text{a,CD4}}$$

The second term on the right-hand side of Eq. 3 can be identified as the steady-state average number of trimolecular bonds <n>_\text{tri} per densities of TCR and pMHC. Both the original (Fig. 2a) and normalized (Fig. 2b) data were well fitted by Eq. 1 & 2. Fitting returned values of A_KA_{\text{TCR}} = 8.31 ± 0.46 × 10^{-2} μm^4 and k_{\text{-TCR}} = 0.53 ± 0.05 × s^{-1} for the TCR–pMHC interaction from the dual receptor species experiment in the presence of CD4, which agree well with the previous single receptor species experiment in the absence of CD4 (Table 4). Remarkably, the value of K_{\text{a,CD4}} is 0.0526 ± 0.0072 μm^2, >250 times higher than the previous value obtained using CD4-reconstituted supported lipid bilayers2 and >350,000 times higher than the CD4 affinity for free pMHC calculated by dividing the A_KA_{\text{CD4}} value determined from Fig. 1d by the -3 μm^2 contact area A_c estimated from the side-view microscopic image.

To visualize the emergence of TCR–pMHC–CD4 trimolecular bonds, we transformed the data according to Eq. 3: subtracting the black data set (m_{\text{CD4}} = 0) from the colored data sets (m_{\text{CD4}} > 0) and normalizing them by their corresponding CD4 density. This nearly collapses the three colored data sets into the average number of trimolecular bonds per unit densities of TCR, pMHC, and CD4. This data set shows (Fig. 2e) that the interactions between pMHC probes and CD4 are much stronger than TCR and pMHC interaction, in contrast, behaving as a catch-slip bond where the lifetime increased, reached a peak, and decreased in a biphasic fashion as force increased3,29. The force-clamp assay found the CD4–pMHC–CD4 trimolecular bond shows a much greater catch than TCR–pMHC bimolecular bond.

To examine whether the trimolecular bond can better sustain mechanical force, we used the biomembrane force probe (BFP) thermal fluctuation2 and force-clamp3,29,30 assays to measure respective force-free and force-dependent lifetimes of single bonds between glass beads bearing pMHC and targets presenting ecodomains of ES TCR, CD4, or both mixed at a 1:1 concentration ratio. The thermal fluctuation assay yielded fairly linear survival probability vs bond lifetime semi-log plots for dissociation of single-receptor species (TCR or CD4) and dual-receptor species (TCR and CD4) from TPE:HLA-DR1, which were much longer lived than the negative control 9V:HLA-A2 (Fig. 2d), confirming binding specificity of TCR and/or CD4.

The force-clamp assay found the CD4–MHC bond lifetimes to decrease with increasing force, displaying a slip-only bond behavior30,37,38 (Fig. 2e). The TCR–pMHC interaction, in contrast, behaved as a catch-slip bond where the lifetime increased, reached a peak, and decreased in a biphasic fashion as force increased3,29. Remarkably, the interactions between pMHC probes and targets co-presenting TCR and CD4 exhibited a much more pronounced catch-slip bond (Fig. 2e). Since lifetimes were measured at frequent binding (<20%) to ensure >89% single-bond probability, the “whole” lifetime ensemble included subpopulations of single TCR–pMHC, CD4–MHC, and TCR–pMHC–CD4 bond lifetimes, where the whole lifetime represented a weighted sum of all three contributions. Average lifetimes of whole bonds were much longer than the weighted sum of two parts—the average lifetimes of TCR–pMHC and CD4–MHC bonds—regardless of how their relative weights were adjusted (Fig. 2e), as it cannot be longer than the longer component lifetime of the two. This demonstrates the existence of a more “catchy” and longer-lived trimolecular bond species.
We used a single-state, single-pathway dissociation model for the slip-only bonds of CD4–MHC interaction and two two-state, two-pathway dissociation models for the catch-slip bonds of the respective TCR–pMHC and TCR–pMHC–CD4 interactions (Supplementary Fig. 3a) to globally fit the measured lifetime vs force scattergrams (Supplementary Fig. 3b). The models fit the mean ± SE bond lifetime vs force data well (Fig. 2e) and predict the probability and fraction of strong state of TCR–pMHC and TCR–pMHC–CD4 bonds (Supplementary Fig. 3e–h) as well as the average bond lifetime vs force curves of the strong state, weak state, and their sum (Fig. 2f), which reveals how the TCR–pMHC–CD4 bond is activated to a strong state by force to form a cooperative catch bond.

**TCR-CD4 cooperativity on cells**

We performed two sets of experiments to confirm that the TCR-CD4 cooperativity observed using purified ectodomain proteins was operative when these proteins were expressed on cells. First, we analyzed binding of beads coated with E8 TCR, CD4, or both to THP-1 cells

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**Fig. 2|** Ectodomains of TCR and CD4 bind cooperatively to pMHC. a $P_A$ vs $t_c$ data (points, presented as Mean ± SEM) and their model fits (curves) of pMHC-coated RBCs ($38 \mu m^2$) binding to RBCs coated with TCR alone, or a mixture of TCR and CD4 at densities ($\#$ of molecules/$\mu m^2$) indicated by the numbers in legend. b Normalized whole bond number $<\tau_{TCR-pMHC}>_{CD4}$ vs $t_c$ data (points, presented as Mean ± SEM) and their respective model fits (curves) for interactions in a. Arrow indicates decreasing density of TCR and increasing density of CD4. c Normalized trimolecular bond number $<\tau_{TCR-pMHC-CD4}>_{CD4}$ vs $t_c$ data (points, presented as Mean ± SEM) and their respective model fits (curves) calculated from b by subtracting the black data from colored data followed by further normalization by $n_{CD4}$. d Survival probabilities plotted as ln(# of events with lifetime greater than t) vs bond lifetime for pMHC-coated beads interacting with beads coated with TCR, CD4, or a 1:1 mixture of TCR and CD4 measured by BFP thermal fluctuation at zero force. Each data set (points) was fitted by a straight line with the negative slope representing off-rate for TCR ($k_{off, TCR}$, $n = 71$) or CD4 ($k_{off, CD4}$, $n = 92$), or apparent off-rate for the mixed TCR and CD4 ($n = 97$). As a negative control, class-I MHC 9 V:HLA-A2 was used instead of TPHL-A to measure non-specific binding ($n = 42$). e Mean ± SEM bond lifetime vs force data (points), measured by BFP force clamp experiment using beads bearing TPHL-DRI interacting with E8 TCR ($n = 230$), CD4 ($n = 335$), or a 1:1 mixture of E8 TCR and CD4 ($n = 424$) coated on beads, are compared with theoretical curves (mean ± SE) predicted using the model and best-fit parameters in Supplementary Fig. 3. f Model predicted trimolecular bond lifetime vs force plots for strong (red) and weak (blue) states as well as their sum (black). Data in a–c were from two independent experiments for each curve. Their model fits (mean ± SE) were calculated using Eqs. 1 and 2 based on the best-fit parameters listed in Table 1. Source data are provided as a Source Data file.
 pulsed with TPI peptide after stimulation with IFN-γ to upregulate HLA-DRI expression\(^2\). Analyses of adhesion frequency \(P_c\) (Fig. 3a) and of the corresponding normalized bond number \(<n>/w_{m_{Receptor}}\times m_{pMHC}\) (Fig. 3b) mediated by the TCR–pMHC (green) and CD4–MHC (purple) bimolecular interactions yielded \(A_K_{\text{TCR}} = 2.87 ± 0.49 \times 10^{-4} \mu m^2\) and \(A_K_{\text{CD4}} = 4.57 ± 1.02 \times 10^{-4} \mu m^2\). The former value is a comparable to, and the latter values is a log higher, than the corresponding values of TCR and CD4, respectively, for the purified MHC.

When tested against beads coated with both TCR and CD4, the \(P_c\) (Fig. 3a, black) and the corresponding normalized whole bond number \(<n>/w_{m_{TCR}}\times m_{pMHC}\) (Fig. 3b, black) were much higher than the predicted mediated by the sum of TCR–pMHC and CD4–MHC interactions calculated using their measured kinetic rates and molecular densities (Fig. 3a, dashed curves), demonstrating that purified TCR and CD4 cooperatively bind cellular pMHC. Interestingly, fitting the dual species data to Eq. 1 & 2 while holding the TCR–pMHC and CD4–MHC kinetic rates the same values as in their bimolecular interactions yielded a good fit of the data with \(K_{\text{TCR}} = 8.33 ± 4.32 \times 10^{-4} \mu m^2\), which is 0.16 times of that obtained using purified pMHC (Fig. 2a, b). Assuming a contact area of 1 \(\mu m^2\), the affinity of CD4 binding to TCR-engaged pMHC is \(1.823 \times\) that of free pMHC. This fold increase is smaller than that obtained using purified pMHC and is likely due to the fact that in this case TCR and CD4 are immobilized on BFP beads instead of being freely diffusible on the RBC membrane.

To further confirm TCR-CD4 cooperativity for cellular pMHC, we measured bond lifetime vs force curves, finding that THP-1 expressed TPIHLA-DRI formed a slip-only bond, weak catch-slip bond, and strong catch-slip bond with beads coated with CD4 only, E8 TCR only, and both E8 TCR and CD4, respectively, similar to their purified protein counterparts (Fig. 3e). In addition, Jurkat cells expressing a higher level of TCR than CD4 formed a more pronounced catch bond than those express similar levels of TCR and CD4 (Fig. 3f), suggesting a higher degree of cooperativity.

As an additional confirmation, we analyzed CD4'CD4 and CD4'CD8 single-positive T cells\(^6\) from 3L2 TCR transgenic mice, which recognizes a hemoglobin (Hb) epitope presented by mouse class-II pMHC Hb\(I-E^\alpha\) (Hb\(I-E^\alpha\)). Our previous adhesion frequency experiment was unable to detect mouse CD4-Hb\(I-E^\alpha\) binding, indicating an \(A_K_{\text{CD4}} < 7.0 \times 10^{-4} \mu m^2\) (the detection limit), no less than a log lower than the human CD4–HLA-DRI effective 2D affinity, and observed a TCR–pMHC catch-slip bond between BFP probes bearing Hb\(I-E^\alpha\) and CD4 CS\(6^\alpha\) 3L2 T cells by force-clamp BFP experiment\(^6\). Interestingly, when using CD4'CS\(6^\alpha\) T cells we observed a much more pronounced catch-slip bonds, which was suppressed by anti-CD4 (GK1.5) blocking to the level of using CD4-CD8\(^+\) T cells (Fig. 3g). These data confirm that the prolonged lifetimes were CD4-dependent and further support the formation of more durable and force-resistant TCR–pMHC–CD4 tricolomic bonds by TCR-CD4 cooperation.

**TCR-CD4 cooperativity requires molecular mobility**

The faster kinetics of the cellular TCR-CD4 cooperative binding to pMHC (Fig. 3e) may suggest enhanced CD4 recruitment to TCR–pMHC, a process that requires both molecular mobility and proxility. To test whether cooperativity depends on molecular diffusion, we used four different pairings of surfaces to present proteins: (1) pMHC on RBCs interacting with TCR only on RBCs; (2) pMHC on RBCs interacting with TCR and CD4 on RBCs; (3) pMHC on RBCs interacting with TCR and CD4 on beads; and (4) pMHC on beads interacting with TCR and CD4 on RBCs. The idea is to allow lateral diffusion of TCR and CD4 on the RBC membrane but prevent them from doing so on the bead surface. The data were presented as average number of whole bonds per unit densities of TCR and pMHC as in Fig. 2 b. When interacting proteins on both sides were coated on RBCs (2nd pairing), pMHC interaction with TCR-CD4 dual-receptor species (Fig. 3h, black) generated a much higher \(<n>/w_{m_{TCR}}\times m_{pMHC}\) curve than did TCR single-receptor species (Fig. 3h, green), indicating cooperative binding as in Fig. 2 b.
sharp contrast, when pMHC was coated on RBCs and TCR and CD4 were co-functionalized on beads (3rd pairing), the binding curve was substantially downward shifted to the level indistinguishable to the curve generated by coating TCR-only on RBCs binding to RBCs bearing pMHC (1st pairing, Fig. 3h, orange). This indicates that the cooperativity between TCR and CD4 vanished when they were immobilized at low densities on glass bead surface. When pMHC was coated on beads and the TCR/CD4 mixture was coated on RBCs (4th pairing), the binding curve was upward shifted to a level higher than that resulted from coating proteins from both sides on RBCs, as predicted by the lower CD4 density (Fig. 3h, blue).

Using Eq. 1 & 2 to globally fit the green and black data (Fig. 3h) returns $A_0$, $k_{a,TCR}$ and $k_{a,CD4}$ values comparable to, and $K^*_a$, $k_1$, $k_{-1}$, $k_2$, $k_{-2}$ values even larger than, those obtained by fitting Fig. 2b.
Optimal TCR-CD4 cooperativity is achieved at 7 nm spacing

We hypothesized that the mobility effect might stem from the requirement for sparsely distributed TCR and CD4 to diffuse into close proximity for them to physically reach the same pMHC. To test this hypothesis, we designed a DNA nanostructure—a 250-nm 10-helix bundle (10HB) DNA origami nanorod, which can be used as a molecular ruler for precise control of the arrangement and relative locations of proteins. 10HB nanorods functionalized with TCR and CD4 were captured on a magnetic bead to form a surrogate T cell (Fig. 4a) to test against a pMHC bearing RBC in the 2D kinetic assay (Fig. 4b). Many poly-A DNA strands protrude from one side of 10HB to bind poly-T strands on the bead surface, while TCR and CD4 are anchored by “capture” DNA strands on the other side of 10HB (Fig. 4c). The position of the capture DNA strands was changed to adjust the TCR-CD4 intermolecular spacing, which was designed to be 6, 13, 20, and 100 nm for this study (Fig. 4d). To bind the proteins to their complementary capture DNA strands on 10HB, CD4 was covalently linked to biotinylated DNA strand on the 10HB (Fig. 4c). Successful assembly of 10HB nanorods was confirmed via native agarose gel electrophoresis (SDS PAGE) (Fig. 4e). C-terminally biotinylated E8 TCR was bound to a streptavidin (SA), which was in turn bound to a biotinylated DNA strand on the 10HB (Fig. 4c). Successful assembly of 10HB nanorods was confirmed via native agarose gel electrophoresis (Fig. 4f). A slight decrease in mobility was observed after the addition of a single-stranded extensions (poly-T strands and capture strands), compared to naked 10HB nanorods. The nanorods were extracted from the gel bands, purified, and used for attachment of TCR and CD4. Subsequent transmission electron microscopy imaging on negatively stained samples clearly showed the binding of TCR and CD4 and their 13-nm and 20-nm designed intermolecular spacings (Fig. 4g). We should note that the designed spacing are nominal, as the actual spacing can be affected by the length of DNA handles, the size of streptavidin, and the flexibility of the linkage.

To examine how TCR-CD4 spacing impacted their synergistic binding to pMHC, we measured adhesion frequencies between RBCs bearing pMHC and origami beads coated with E8 TCR, CD4, or both with defined spacing. CD4-alone origami adhered negligibly as did protein/handle negative or origami negative controls, whereas the same density of TCR-alone origami yielded ~20% of P_s at steady-state (t_e = 4 s), consistent with its >3 logs higher affinity (Supplementary Fig. 4). Multiplexing TCR and CD4 on the origami 100 and 20 nm apart generated indistinguishable adhesions comparable to the TCR-alone group. Strikingly, further decreasing the spacing to 13 and 6 nm profoundly increased P_s (Supplementary Fig. 4) and its density-normalized log transformation (Fig. 5a), indicating strong cooperativity as in Figs. 2b and 3h.

We extended Eq. 3 by assuming that increasing separation between TCR and CD4 would decrease the trimolecular bond formation exponentially, obtaining a phenomenological model that fits the data well:

\[
\frac{m_{TCR}m_{pMHC}}{m_{CD4}} = A_{K_{a,TCR}} [1 + m_{CD4} \exp(-X/X_0)^{l_0}] \tag{4}
\]

where \(A_{K_{a,TCR}} = (L_29 \pm 0.52 \times 10^{-3} \mu m^2)\) was obtained from the TCR-alone measurement. Its smaller than other values in Table 1 may be explained by presenting TCR on different surfaces (RBCs vs origami-coated beads). Fitting returned an apparent separation \(X_0 = 7.0 \pm 1.7 \text{ nm}\) required for optimal cooperativity, decay length scale \(l = 1.7 \pm 2.1 \text{ nm}\), and CD4 affinity for TCR pre-engaged pMHC \(K_{a,CD4} = 0.050 \pm 0.015 \mu m^2\). The \(X_0\) value agrees well with the 7-nm gap between the membrane anchors of TCR and CD4 found in their ternary structure complexed with pMHC, and values <7 nm lead to worse fits. The \(l\) value describes how fast the ability of CD4 to bind TCR engaged pMHC would decay exponentially as \(X\) increases beyond \(X_0\), underscoring the requirement for spatial proximity. The \(K_{a,CD4}\) value is statistically indistinguishable from the value estimated from Fig. 2b using Eqs. 1 & 2 (Table 1).

To obtain independent support for the existence of trimolecular bonds, we analyzed single-bond stiffness to distinguish bimolecular vs trimolecular interactions (Fig. 5b, c). When TCR and CD4 were spaced 20 or 100 nm apart, the histograms of molecular stiffness exhibited a single peak well fitted by a Gaussian distribution, yielding a mean stiffness of 0.32 pN/μm for both samples (Fig. 5c). Spacing the molecules 13 nm apart gave rise to a double-peak histogram (Fig. 5c). The first peak has nearly the same mean stiffness of 0.31 pN/μm but the second peak represents a subpopulation (38% of total) of nearly doubling the stiffness (0.58 pN/μm), indicating the presence of trimolecular bonds. The 6-nm spacing further populates the second peak (5%) but maintains the mean stiffness values for the two peaks (Fig. 5c). Interestingly, these fractions are consistent with the corresponding fractions with low and high average numbers of whole bonds (>\(n_w\)) normalized by the TCR and pMHC densities (\(m_{TCR}\) and \(m_{pMHC}\)) measured at 13 and 6 nm using the 2D assay (Fig. 5a). Overall, the data indicate that a threshold distance is required for TCR and CD4 to form trimolecular bonds with pMHC.

Discussion

A previous study using FRAP to analyze the mobility of TCR-CD3 or CD4 at the interface with pMHC observed reduced mobility of CD4 in

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**Fig. 3 | Cellular TCR and CD4 bind cooperatively to pMHC.** a. P_s vs t_e data (Mean ± SEM of 3-6 cells per data point) and their model fits (curves) of TPR-pulsed IFN-γ treated TPH-1 cells binding to beads presenting TCR, CD4, or both at densities (μm^-2) indicated in the legends. b. Normalized whole bond number \( <n_w>/m_{pMHC}\) vs \( t_e\) data, points, presented as Mean ± SEM) and their respective model fits (curves) for interactions in a. c. Mean ± SEM bond lifetime vs force data of TPR-pulsed IFN-γ treated TPH-1 cells interacting with beads presenting E8 TCR (n = 201), CD4 (n = 200), or E8 TCR and CD4 of similar density (n = 225). d. P_s vs \( t_e\) data (Mean ± SEM of 3-7 cells per point) and their model fits (curves) of pMHC-coated beads binding to Jurkat cells expressing TCR, CD4, or both at densities (μm^-2) indicated by the legends. e. Normalized whole bond number \( <n_w>/m_{pMHC}\) vs \( t_e\) data, points, presented as Mean ± SEM) and their respective model fits (curves) for interactions in d. Predications were made after normalizing the densities in different curves. TCR + CD4 curve was fitted with (brown) or without (black) keeping the same TCR affinity and off-rate as in the bimolecular interaction.

f. Mean ± SEM bond lifetime vs force data of BFP beads bearing TPRHLA-DRI interacting with Jurkat cells expressing E8 TCR (n = 598), CD4 (n = 283), E8 TCR and CD4 of similar density (n = 279) or more TCR than CD4 (n = 288) expressed on Jurkat cells. g. Mean ± SEM bond lifetime vs force data of BFP beads bearing HbI-E8 interacting with 3.12 CD8+CD4 + T cells (n = 298), CD8+CD4 + T cells (n = 711), or CD8+CD4 + T cells with CD4 blocking antibody clone GKL5 (n = 240). h. Comparison among normalized bond numbers for pMHC interaction with TCR or mixed TCR and CD4 coated in four ways at densities (# of molecules/μm^2) indicated by the number in legend. Data (points) are presented as mean ± SEM of two independent experiments for each curve. Their model fits (mean ± SE curves) are calculated using Eqs. 1 and 2 based on the best-fit parameters listed in Table 1. Source data are provided as a Source Data file.
the presence of TCR–pMHC interaction and reduced TCR-CD3 mobility in the presence of CD4–MHC interaction, suggesting the binding of cellular TCR and CD4 to the same pMHC. Using two ultrasensitive mechanical assays to measure adhesion frequencies and single-bond lifetimes of three related 2D interaction systems – purified TCRβ and CD4 ectodomains vs purified pMHC ectodomain, purified TCRβ and CD4 ectodomains vs cellular pMHC, and cellular TCR-CD3 and CD4 vs purified pMHC ectodomain – and presenting the soluble proteins on the surface of RBCs, glass beads, and DNA origami, we showed in detail how and why this occurs despite the extremely low CD4–MHC affinity. By demonstrating that CD4 binds TCR-prebound pMHC with 3–6 logs higher affinity than it binds free pMHC, our results explain how CD4 could efficiently augment TCR antigen recognition via stabilizing TCR–pMHC bonds and recruiting Lck to TCR-CD3. This also answered a perplexing question of why anti-CD4 results explain how CD4 could not even bind pMHC. While CD4 alone cannot even bind pMHC, our findings are the molecular basis of the enhanced affinity of CD4 for TCR-prebound pMHC. The present work has ruled out the possibility that the TCR-CD4 cooperativity requires TCR-pMHC binding to induce inside-out signaling of CD4 to upregulate its affinity for pMHC, since soluble TCRβ and CD4 proteins coated on RBC, glass bead, and DNA-origami surfaces are capable of cooperative binding to purified and cellular pMHC. Another possibility is that TCR binding to pMHC induces conformational changes in the CD4 binding site of MHC that increase affinity for CD4. However, crystallographic studies of numerous TCR and pMHC molecules in free and bound form provide no evidence of TCR-induced structural changes at the site on the MHC class II β2 domain where CD4 binds. This would argue against an allosteric mechanism to explain increased CD4 affinity for TCR-prebound MHC. It is also possible that the relevant changes may be in protein dynamics, a parameter that cannot be addressed via the static snapshots provided by X-ray crystallography. Indeed, several NMR studies have found that pMHC binding to TCR induces long-range allosteric changes in TCR dynamics that could be relayed to CD3, even in the absence of obvious structural changes in the TCR.\(^\text{(13–15)}\) The reverse situation (i.e. long-range allosteric changes in pMHC dynamics upon TCR binding) has not been examined by NMR, but probably should be given our results here.

The proposed structural mechanisms are supported by our modeling analysis, which was used to fit the bond lifetime data measured by the BFP experiments (Fig. 2d–f, Supplementary Fig. 3). To show this, we first compared the abilities of three models to simultaneously fit the three specific interaction data measured by thermal fluctuation (Fig. 2d). The first model is depicted in Supplementary Fig. 3a except that the activation to and dissociation from the strong state (TCR-pMHC) is neglected because force was zero. Also, the weak (TCR–pMHC–CD4) and strong (TCR–pMHC–CD4) trimolecular bonds are assumed to be in equilibrium and the two states dissociate concurrently to free molecules TCR + pMHC + CD4 in a single step (hence called concurrent model). The second model is a single-pathway, two-step, sequential dissociation model (sequential model I). It differs from the concurrent model in that the TCR–pMHC–CD4 trimolecular bond has only a single state that dissociates sequentially from right to left in Eq. 9 (Methods), first the pMHC–CD4 arm reversibly to generate TCR–pMHC complex + CD4, and then the TCR–pMHC bimolecular bond to free molecules TCR + pMHC + CD4. The third model is also a single-pathway, two-step, sequential dissociation model (sequential model II). It is similar to the sequential model I except that the order of sequential dissociation of the TCR–pMHC–CD4 trimolecular bond is reversed, which occurs first at the TCR–pMHC arm reversibly to generate pMHC–CD4 complex + TCR, and then at the pMHC–CD4 bimolecular bond to generate free molecules TCR + pMHC + CD4. Using the Akaike Information Criterion (AIC) to choose between two non-nested models, we found that the concurrent model is more likely to be valid.
correct than sequential model I by >58,000 times and even much more times than sequential model II. This conclusion still holds even when we analyzed data measured by force-clamp assay (Supplementary Fig. 3b) to evaluate their force-dependent kinetic parameters (Supplementary Fig. 3c, d). The concurrent model suggests a strong functional coupling between the spatially separate TCR binding site and the CD4 binding site on the pMHC, supporting our allosteric hypothesis. Future studies are required to test this hypothesis. Moreover, to confirm that association and dissociation happen preferentially via pathway I instead of pathway II, we considered a more general two-pathway, two-step model that combines both sequential models I and II, and globally fit the adhesion frequency data from Fig. 2a, b. We compared it to the sequential model I by AIC, and found little difference statistically, suggesting that both association and dissociation along the second pathway (i.e., sequential model II) dominates over the first pathway (i.e., sequential model I) over an activation threshold (p = 0.01 for pathway I and II, respectively, of the two-pathway, two-step model).

This work builds upon our previous findings of TCR-CD8 cooperativity for class I pMHC binding6,13 and adds to our previously proposed mechanistic model16. In live-cell systems, cooperativity relies on the recruitment of coreceptor to phosphorylated CD3 via a Lck “bridge”, where both the adaptor function and kinase function of Lck are required14,15,36,37, as seen with co-immunoprecipitation studies that identify similar molecular assembly connecting CD4 or CD8 to triggered TCR-CD336,41. Here we show that using purified TCR and CD4 lacking cytoplasmic domains and CD3, the synergistic cooperation could still occur if both molecules are allowed to diffuse on the RBCs or packed closed enough on the bead surface, suggesting that modulation of ectodomain cooperation could be decoupled from intracellular regulation. This is also consistent with the observation that CD4 lacking the ability of binding Lck is still required for TCR-mediated IL-2 production38. On the other hand, our data of cellular TCR and CD4 cooperating with a faster kinetics than their purified ectodomain counterparts regardless of being tested against purified pMHC or cellular pMHC suggest that there may be cellular regulation(s) to expedite TCR-CD4 cooperativity. Modulation of ectodomain by physical factors such as mobility and colocalization are intuitive, but require 2D analyses to decipher. Indeed, by limiting mobility using different surface and controlling TCR-CD4 proximity using DNA origami, we found a 7-nm apparent spacing for TCR-CD4 cooperativity, such that increasing the spacing resulted in an exponential decay in the capacity to form TCR-pMHC-CD4 trimolecular bonds. Such physical regulatory mechanisms revealed by the in vitro system further advance our understanding of how interactions between membrane receptors and ligands critically depend on their cell surface organization. Methodologically, our DNA origami-based 2D kinetic assays hold great potential to dissect the spatial requirement of the cooperation of single- or multi-receptor–ligand species by ectodomain binding and/or intracellular crosstalk.

**Methods**

All experiments in this study were conducted with the compliance to the Institutional Review Board of Georgia Institute of Technology.

**Proteins**

Biotinylated CD4 and biotinylated ϒβ E8 TCR were prepared as previously described27. Briefly, a 17-amino acid tag (TPI, GGGLNDI-FEAQKIEWHE) was added to the C-terminus of CD4 ectodomain and to the C-terminus of the E8 TCR ectodomain. CD4 was expressed in E. coli30. The purified
proteins were biotinylated using biotin protein ligase (Avidite); excess biotin and ligase were removed with a Superdex 200 column (GE Healthcare). The control MHC-I (HLA-A2) presenting the melanoma antigen peptide NY-ESO-157-65 (9V, SLLMWITQV) was produced by the NIH Tetramer Facility at Emory University.

Biotinylated TPI, HLA-DRI was made by the NIH Tetramer Core facility (Atlanta, GA) with peptide (GELGTLNAAKVPAD) purchased from GenScript. Divalent streptavidin was generously gifted by Dr. Baoyu Liu (University of Utah).

**Cells**

Human RBCs were isolated from blood of healthy donors according to a protocol approved by the Institutional Review Board of Georgia Institute of Technology with informed consent from the donor. For adhesion frequency assay, RBCs were purified by Histopaque-1077, washed with ice-cold PBS, and resuspended in EAS-45 buffer (2 mM Adenine, 110 mM D-glucose, 55 mM D-Mannitol, 50 mM Sodium Chloride, 20 mM Sodium Phosphate, and 10 mM L-glutamine). Equal aliquots of RBCs were then mixed with various concentrations of EZ-Link Sulfo-NHS-LC-Biotin (Thermo Scientific) at a pH of 7.2 for 30 min at room temperature, yielding different densities of biotin sites on RBC surfaces. Biotinylated RBCs were washed with EAS-45 buffer and stored at 4 °C. For 2D flow experiments, fresh isolated human RBCs were biotinylated with biotin-PEG3500-NHS (Jenkem Technology) and then incubated with nystatin in N2 buffer (265.2 mM KCl, 38.8 mM NaCl, 0.94 mM KH2PO4, 4.74 mM Na2HPO4, and 27 mM sucrose; pH 7.2 at 388 mOsm) for 30 min on ice. Nystatin-treated biotinylated RBCs were washed twice with N2 buffer and stored at 4 °C for 2D experiments.

HEK 293 T cells were purchased from ATCC (Manassas, VA) and cultured in DME supplemented with 10% FBS, 100 U/mL penicillin, 100 µg/mL streptomycin, 2 mM L-glutamine, 588 mOsm) for 30 min on ice. Nystatin-treated biotinylated RBCs were brought into contact of de-adhesive event and material between the two cells.

**Site density measurements**

Site densities of TCR, CD4, and pMHC on RBCs, Jurkat cells, THP-1 cells, glass beads, or origami beads were measured by flow cytometry using PE-conjugated antibodies from BD Biosciences (San Jose, CA): anti-human TCR-β1 (clone JOV1.1, 1:20), anti-human CD4 (clone OKT4, 1:20), and anti-human HLA-DR (clone L243, 1:5). Isotype control antibodies were PE mouse IgG2a κ (clone G155-178, 1:20) for TCR and HLA-DR, and PE mouse IgG2b κ (Clone 27-35, 1:20) for CD4. RBCs or beads were incubated with corresponding antibodies in 1X PBS + 2% BSA for 30 min at 25 °C and washed three times before being analyzed using the BD Accuri or Fortessa Flow Cytometer. Data were collected with FACSDiva v9 and analyzed with Flowjo v10. An example of gating strategy is shown in Supplementary Figure 5. Site density was calculated based on antibody-conjugated PE fluorescence relative to the QuantiBRITE PE standard beads (BD Biosciences). For micropipette experiments, RBCs bearing protein of interest (TCR, CD4, or MHC) were prepared for flow cytometry using three separate samples: one saturating the RBC surface, one of the experimental conditions, and one isotype control. Brightness across all antibodies was normalized against the CD4 staining which was brighter than the TCR staining.

**Micropipette Adhesion Frequency Assay**

The theoretical framework and detailed experimental procedures of this assay have been described previously.[19,20,42] This assay leverages the ultra-soft RBC membrane to detect interactions with single-bond sensitivity. Briefly, RBCs with controlled biotin sites were first incubated with 200 µg/mL divalent streptavidin and washed, followed by subsequent coating with biotinylated pMHC, TCR, CD4, or a mixture of TCR and CD4. After washing, RBCs coated with receptor-ligand pairs were injected into an imaging chamber containing non-CO2 dependent L15 media supplemented with HEPES and 2% BSA. During experiment, two RBCs were aspirated by micropipette and repeatedly brought into contact of defined distance by a program-controlled piezo. Adhesion between two RBCs were detected by the deflection of RBC membrane during the separation after each contact with T indicating an adhesive event and ‘O’ indicating no adhesion. Each pair of RBCs were tested for 50 cycles of the same contact duration to yield the adhesion frequency (Pc), which is as the average score from the 50 cycles. The same process was repeated for multiple pairs of RBC of each contact duration (fc), yielding a Pd vs fc curve that is fitted to a published model.[19,20] (see below)

Non-specific controls were conducted for all sets of species coatings. To do so, RBCs coated with divalent streptavidin anchored irrelevant protein (OT1 TCR) were brought into contact with RBCs coated with proteins of interest. An adhesion frequency curve would be obtained for nonspecific adhesion. Then, for each contact time, the distribution of nonspecific adhesion frequency was removed from the measured distribution of adhesion frequency[19,20].

In some experiments, one or both sides of the RBCs were replaced by glass beads coated with pMHC (see below) or THP-1 cells expressing pMHC, or glass beads or origami beads coated with TCR, CD4, or both (see below), or expressed on Jurkat cells expressing TCR, CD4, or both. Data collection with precise pizeo movement control was used by Labview 2016&2019 and Excel 2016.

**Biomembrane Force Probe Assay**

The principle and experimental procedures for BFP assays have been described previously.[27] To coat proteins on beads, borosilicate glass beads were mercapto-propyl silanated and covalently functionalized to monovalent streptavidin-maleimide in phosphate buffer saline (pH 6.8) by overnight incubation at 25 °C. Streptavidinylated beads were then incubated with sub-saturating concentrations of biotinylated pMHC, TCR, CD4, or 1:1 mixture of TCR and CD4 for 2 h in HBSS + 2% BSA at 4 °C. For CD4 blocking, T cells were treated with antiCD4 (GK1.5, 1:10) for 30 min and analyzed with the presence of antiCD4 in the chamber. During the experiment, a protein-coated bead (tracking bead) was attached to the apex of a micropipette-aspirated RBC that serves as a spring with pre-adjusted spring constant of 0.1-0.3 pN/nm. For force clamp assay, the tracking bead was repeatedly contacted by a pizeo-driven target bead coated with (or target cell expressing) the corresponding binding partner(s). The displacement of tracking bead was monitored with a high-speed camera at 1000 fps and was translated into force by applying the pre-defined spring constant. During separation, bond formation between tracking bead and target bead/ cell pulled the tracking bead away from its baseline, manifesting positive force loading on the molecular bond. Bond lifetime was defined as the duration from the start of clamp at the preset force level to bond rupture. Several hundred bond lifetime events were collected
and pooled for various clamp forces using multiple bead-bead or bead-cell pairs. The stiffnesses of molecular bonds were modeled as Hookean spring constants which is determined by the difference between the displacements of the bead tracking system (F) and the displacements of the piezoelectric actuator-capacitance sensor feedback system (Δx). Two straight lines were fitted to the piecewise data: One was fitted to the compressive force regime where the bead was slowly ramping away from cell impingement (force <0), where the slope represents the spring constant of the cell membrane (compression). The other was fitted to the tensile force regime where the bead would ramp away from the cell beyond the point of initial contact (force >0), where the slope represents the resultant spring constant of cell membrane (extension) and molecular bond connected in series. By assuming the spring constant of cell membrane is identical during compression as during extension, the spring constant of molecular bond was extracted by applying Hooke’s law for springs in series. An ensemble of molecular spring constant was collected as histograms using similar force bins and fitted to single or double Gaussian distributions.

For thermal fluctuation assays, a target bead was driven by piezo to the proximity (-10 nm) of the probe bead, allowing bond formation between the two during intermittent contacts caused by thermal fluctuation, which would decrease the fluctuation of probe bead position. By analyzing the standard deviation (SD) of the tracking bead position, bond formation and rupture were identified by the decrease of SD below a cutoff of 3 nm and the subsequent resumption SD to baseline level. The cutoff baseline was determined as the lowest SD value of the probe bead before contact (i.e., SD of bead without bonds).

For adhesion frequency assays using BFP beads, the same process of RBC-based adhesion frequency assay was performed except that a target cell was repeatedly brought into contact with a pMHC-coated bead, held for a defined duration, and then separated. Adhesion was defined as the deflection of bead away from its equilibrium position.

**Kinetic models**

**Single-step model for bimolecular interaction.** The bimolecular interactions of either TCR or CD4 with pMHC are modeled as a single-step reversible reaction:

\[
R + L \rightleftharpoons B
\]

(5)

where \(R\), \(L\), and \(B\) denote, respectively, receptor, ligand, and bond; \(k_+\) and \(k_-\) denote, respectively, on- and off-rates. Their ratio is the binding affinity, \(K_a = k_+ / k_-\). Our published probabilistic kinetic model for the above reaction states that the probability of adhesion (\(P_a\)) depends on the contact time (\(t_c\)) and area (\(A_c\)) as well as the densities of receptors (\(m\)) and ligands (\(n\))^19,20.

\[
P_a = 1 - \exp\left\{-m_m A_c K_a [1 - \exp(-k_- t_c)]\right\}
\]

(6)

On the right-hand side, the term inside the braces after the minus sign is the average number of bonds per contact \(<nt>\).

\[
<n> = m_m A_c K_a [1 - \exp(-k_- t_c)]
\]

(7)

After normalizing \(<nt>\) by \(m_m\), the right-hand side should be independent of the molecular densities and approaches \(A_c K_a\), the effective 2D affinity, as \(t_c\) becomes large.

\[
\frac{n}{m_m} = A_c K_a [1 - \exp(-k_- t_c)] \rightarrow A_c K_a \quad \text{as} \ t_c \gg 1/k_-
\]

(8)

It follows from Eq. 8 that \(<nt>\) is proportional to \(m_m\) if measured at large contact time.

We use TCR or CD4 in the subscript to identify the interaction with which the kinetic parameters are associated, e.g., \(k_{+\text{TCR}}, k_{-\text{TCR}}, K_{\text{TCR}}\) are kinetic rates and binding affinity for the TCR–pMHC interaction, which are different from \(k_{+\text{CD4}}, k_{-\text{CD4}}, K_{\text{CD4}}\), which are corresponding parameters for the CD4–MHC interaction. Also, \(n_{\text{TCR}}, m_{\text{CD4}}\), and \(m_{\text{pMHC}}\) are used to designate the densities of TCR, CD4, and pMHC.

**Two-step model for trimolecular interaction.** We propose a two-step model for the formation of trimolecular bonds. Since the affinity and on-rate for the CD4–pMHC interaction are so much smaller than those of the TCR–pMHC interaction, it seems reasonable to assume that TCR interacts with pMHC at the same kinetic rates as bimolecular interaction in the first step as if CD4 does not interact with free pMHC. However, CD4 is able to interact with TCR-stabilized pMHC with a much higher affinity, thereby forming trimolecular bonds in the second step.

Two-step model for trimolecular interaction. We propose a two-step model for the formation of trimolecular bonds. Since the affinity and on-rate for the CD4–pMHC interaction are so much smaller than those of the TCR–pMHC interaction, it seems reasonable to assume that TCR interacts with pMHC at the same kinetic rates as bimolecular interaction in the first step as if CD4 does not interact with free pMHC. However, CD4 is able to interact with TCR-stabilized pMHC with a much higher affinity, thereby forming trimolecular bonds in the second step.

\[
f_{\text{TCR} + \text{pMHC} + \text{CD4}} = f_{\text{TCR} + \text{pMHC}} + f_{\text{TCR} + \text{CD4}}
\]
The corresponding initial condition of \( g \), obtained by substituting Eq. 15 into Eq. 11, is

\[ g_{00}(x,y;0) = 1. \] (16)

Solving \( x \) and \( y \) in terms of \( \mu x_{2} \) from Eq. 14, substituting them into Eq. 16, and comparing the resulting equation to Eq. 13 evaluated at \( t = 0 \) allows us to solve for a particular solution for \( f \)

\[ J_{00}(u_{1},u_{2}) = \exp[m_{\text{TCR}}m_{\text{pMHC}}A_{\text{KTCR}}(\lambda_{1} - k_{-\text{CD4}})u_{1} + (\lambda_{2} - k_{-\text{CD4}})u_{2} - (1 + m_{\text{CD4}}K_{\text{A},\text{CD4}})(u_{1} + u_{2})]. \] (17)

Substituting Eq. 17 into Eq. 13, we have

\[ g_{00}(x,y;\tau) = \exp \left( m_{\text{TCR}}m_{\text{pMHC}}A_{\text{KTCR}} \left[ k_{-\text{TCR}}e^{-\lambda_{1}t} - e^{-\lambda_{2}t} \right] - \left( 1 + m_{\text{CD4}}K_{\text{A},\text{CD4}} \right) \left[ k_{-\text{TCR}}e^{-\lambda_{1}t} - e^{-\lambda_{2}t} \right] \right) \times \frac{\left( \lambda_{2} - k_{-\text{TCR}}e^{-\lambda_{1}t} - (\lambda_{1} - k_{-\text{TCR}}e^{-\lambda_{2}t}) \right) x}{\lambda_{1} - \lambda_{2}}. \] (18)

Expanding the right-hand side of Eq. 18 into Taylor series of \( x \) and \( y \), and comparing the coefficients of the \( x^{3}y^{2} \) terms to those of the right-hand side of Eq. 11, we found

\[ P_{m,n}(\tau) = \left[ \frac{m^{m}}{m!} \exp(-m) \right] \left[ \frac{n^{n}}{n!} \exp(-n) \right] \] (19a)

where

\[ (m) = (n)_{\text{TCR}} = m_{\text{TCR}}m_{\text{pMHC}}A_{\text{KTCR}} \left[ \lambda_{1} - \lambda_{2} \right] \] (19b)

\[ (n) = (n)_{\text{TCR}}m_{\text{pMHC}}A_{\text{KTCR}}m_{\text{CD4}}K_{\text{A},\text{CD4}} \left[ \lambda_{1} - \lambda_{2} \right] \] (19c)

are the average numbers of TCR–pMHC bonds and TCR–pMHC–CD4 bonds. Thus, the solution is of the form of the product of two Poisson distributions. Except for the expressions for \( \langle m \rangle \) and \( \langle n \rangle \), this is the same as the bond distribution of the dual species concurrent independent binding model described previously.21-23

The adhesion probability is the probability of having at least one bond of either type, or one minus the probability of having no bond, which can be found from Eq. 19:

\[ P_{2}(\tau) = 1 - \exp \left\{ - m_{\text{TCR}}m_{\text{pMHC}}A_{\text{KTCR}} \left( 1 + m_{\text{CD4}}K_{\text{A},\text{CD4}} \right) k_{-\text{TCR}}e^{-\lambda_{1}t} - e^{-\lambda_{2}t} \right\} \times \left( \lambda_{2} - k_{-\text{TCR}}e^{-\lambda_{1}t} - (\lambda_{1} - k_{-\text{TCR}}e^{-\lambda_{2}t}) \right) \] (20)

Taking a log transformation, we obtain the average number of whole bonds \( \langle m \rangle_{W} = -\ln(1 - P_{2}) \). Normalizing \( \langle m \rangle_{W} \) by the densities of TCR and pMHC, we obtain Eq. 1. Setting \( k_{-\text{CD4}} = k_{-\text{CD4}} = 0 \) reduces Eq. 2 to \( \lambda_{1} = \lambda_{1} \) and \( \lambda_{2} = 0 \), which also reduces Eqs. 20 and 1 to Eqs. 6 and 8, respectively, as expected.

### DNA Origami preparation

Origami were created at 20 nM using p8064 scaffold, 5× staple excess, and 25× biotin strand for TCR capture. Following agarose gel electrophoresis in 1% agarose at 60 V for 90 min on ice bath, origami were purified with Freeze ‘n’ Squeeze spin columns. The four samples with different protein separation distances were indistinguishable based on gel mobility. However, a control sample with only handles for surrogate cell attachment ran with slightly increased mobility, while a complete blank 10 HB sample with no handle extensions ran markedly faster through the gel. To confirm proper assembly of protein onto the DNA origami, purified samples were incubated with excesses of CD4–DNA and wild type streptavidin at 4 °C overnight. After another agarose gel purification, a 10-fold molar excess of biotinylated TCR was added and allowed to incubate at 4 °C for 3 h. Excess protein was removed using 100 kD MWCO spin filters, then the samples were deposited on 400 mesh carbon formvar grids and stained with 1% uranyl formate solution for 30 s. During TEM imaging, the identity of blinded samples could be reliably divined by observing relative CD4, SA–TCR location.

An amine-modified DNA strand was conjugated to lysine residues in CD4. CD4 was reacted with 50-fold excess succinimidyl-6-hydrazino-nicotinamide (S-HyNic) (Solulink) for 4 h, and terminal amine DNA was reacted with 20-fold excess succinimidyl-4-formylbenzene (S-4FB) (Solulink) for 4 h. Amicon Ultra spin filters (Millipore) were used to remove excess linker and buffer exchange into citrate buffer (50 mM sodium citrate, 150 mM NaCl, pH 6). Functionalized DNA was combined with CD4 at a 3:1 ratio, and reacted overnight. CD4-DNA conjugates were purified on a Superdex 200 Increase 10/300 GL column using an AKTA Pure FPLC (GE Healthcare). Conjugation was verified with SDS/PAGE and Coomassie blue staining.

In order to examine the effect of geometric docking on the simultaneous interaction of two molecules with a third, origami structures differentially spacing TCR and CD4 were coated on beads to represent a simplified T cell surface. Beads were respectively coated with several different origami structures: those with handles for TCR and CD4 which were differentially spaced apart at 6, 13, 20, and 100 nm; those lacking protein handles; and origami lacking connecting strands to the beads. The purified samples were loaded onto surrogate T cells—3 μm diameter magnetic Dynabeads. For each sample, 15 μL of beads were washed 3× with PBS then added to 1 μg (~30 μL) of purified DNA origami. A large excess of CD4–DNA and streptavidin were added, and the samples were left to incubate on a rotating shaker at 4 °C overnight. The magnetically pelleted beads were washed with PBS supplemented with calcium and magnesium, and 2% BSA five times. Biotinylated (at the C-terminus of the α-chain) E8 TCR was added to the beads and incubated for 30 min. To this solution, blocking DNA strand (25 da) was added and the reaction incubated at 4 °C for an additional 1 h.

### Fitting models to data

Linear fittings of data in Fig. 2d, Fig. 5b, Supplementary Fig. 1, and Supplementary Fig. 2c were implemented in Prism using linear regression to estimate the slope and y-intercept of the trend. Non-linear fittings of bimolecular kinetic equations to data in Fig. 1c,d were implemented in Prism using Non-linear regression to estimate the corresponding kinetic parameters. Gaussian fitting of data in Fig. 5c was implemented in Prism using non-linear regression to estimate the Gaussian distribution and frequency of each distribution. For all fitted parameters, fitting error was presented as Standard Error (SE) assuming symmetrical confidence intervals.

The model predicted curves in Fig. 2a–c and Supplementary Fig. 2a were obtained by globally fitting all data to Eqs. 1 & 2, which were also fit to data in Fig. 3a, b, d, e, h. For the Fig. 3h case, the green and black data were globally fit, the orange data was fit on its own, and the blue data was fit after constraining the off-rates obtained from the orange data fit to avoid overfitting. Best-fit Pa ± SE (curves) in Fig. 3a was calculated from best-fit \( \text{~} \rangle \pm \) SE in Fig. 3b. \( p = 0.0563, 0.0159, 0.0631, 0.1200, 0.0502, \) and 0.0405 for comparing measured Pa of...
whole interactions to predicted sum at tc = 0.5, 1, 2, 4, 8, and 16 s calculated from one-tailed t-test independently for each contact time. In Fig. 3b, predictions were made after normalizing the densities in different curves. TCR + CD4 curve was fitted while keeping the same TCR affinity and off-rate as in the bimolecular interaction, \( p = 0.0552, 0.0162, 0.0624, 0.1179, 0.0523, \) and 0.0473 for comparing measured whole bonds to predicted sum at tc = 0.5, 1, 2, 4, 8, and 16 s calculated from one-tailed t-test independently for each contact time. Best-fit \( Pa \pm SE \) in Fig. 3d was calculated from best-fit \( <-r> \pm SE \) in Fig. 3e, \( p = 0.0016, 0.0004, 0.0013, 0.0005, 0.0004, \) and 0.0066 for comparing measured \( Pa \) of whole interactions to predicted sum at tc = 0.5, 1, 2, 4, 8, and 16 s calculated from one-tailed t-test independently for each contact time. In Fig. 3e, \( p = 0.0022, 0.0006, 0.0019, 0.0001, 0.0011, \) and 0.0140 for comparing measured whole bonds to predicted sum at tc = 0.5, 1, 2, 4, 8, and 16 s calculated from one-tailed t-test independently for each contact time, \( p = 0.0044, 0.0013, 0.0066, 0.0029, 0.3089, \) and 0.5179 for comparing measured whole bonds to its fitted curve (brown) at tc = 0.5, 1, 2, 4, 8, and 16 s calculated from one-tailed t-test independently for each contact time.

The separation distance-dependent adhesion frequency of the DNA origami assay (Fig. 5a) was fit to Eq. 4. For Figs. 2a–c, 3a, b, d, e, h, a two-step optimization procedure was employed to minimize the mean squared error (MSE) of the fits with respect to the data, which explored a large parameter space by Differential Evolution to obtain an approximate solution, followed by L-BFGS to hone in the minimum. The parameters Standard Errors (SE) were calculated from the covariance matrix obtained by inverting the Hessian matrix of the loss function at the minimum found.

The SEs were then propagated through the model to display error bands of the fits as mean ± SE. The data in Fig. 5a were also fit by the aforementioned two-step optimization procedure but the parameters SE were obtained via bootstrapping, with 1000 bootstrap samples.

The force-dependent lifetimes of pMHC bonds with TCR alone or co-presented TCR and CD4 behaved as catch-slip bonds, while pMHC bonds with CD4 alone behaved as a slip bond. Although at zero force the two catch-slip bonds had mono-exponentially decaying survival probabilities (Fig. 2d), a second population appeared at forces >0, displaying biexponentially decaying survival probabilities, suggesting the presence of two bound species, even for the bimolecular TCR–pMHC. Therefore, while the CD4–pMHC bonds were modelled to dissociate along a single pathway, both TCR–pMHC and TCR–pMHC–CD4 bonds were modelled to dissociate along two pathways – a fast dissociating pathway from a weak state or a slow dissociating pathway from a strong state (indicated by *) allowed to exchange from each other as depicted in Supplementary Fig. 3a (left and right panels) similarly to previous catch bond models\(^4,14\). The force dependence of all kinetic rates follows Bell’s equation\(^6\):

\[
k_{ij}(f) = k_0 \exp \left( \frac{f - x_i}{k_B T} \right)
\]

where \( f \) is force, the superscript 0 denotes the zero-force kinetic rate constant, the subscript i denotes rates of dissociation along fast (-f) or slow (-s) pathways and of activation (a) or deactivation (d) transition between the weak and strong states, the subscript j denotes different bonds (TCR–pMHC or TCR–pMHC–CD4), \( x_i \) denotes distance to the transition state, or width of the energy well that traps the system in the bound state, \( k_B \) is Boltzmann constant, and \( T \) is absolute temperature. The weak state dissociates more rapidly than the strong state, so \( k_{ii} > k_{ij} \). The two-states, two-path catch-slip model can be expressed in terms of ordinary differential equations that govern the probability of having bonds \( P \) at a given time \( t \):

\[
\begin{align*}
\frac{dp_{i}}{dt} &= -k_{-i}P_i - k_{-s}P_{i,j} + k_{-s}P_{j,i} \\
\frac{dp_{j}}{dt} &= -k_{-s}P_{i,j} + k_{-s}P_{j,i} - k_{-s}P_{j} + k_{-s}P_{j,i}
\end{align*}
\]

where the subscript j, as above, stands for TCR–pMHC or TCR–pMHC–CD4 bonds in the weak (without *) or strong (with *) state, and all rates \( k \) vary as a function of force as given by Eq. 21. This two-state catch bond model could recapitulate the average bond lifetime as well as the biexponentially distributed bond survival probabilities of both TCR–pMHC and TCR–pMHC–CD4 interactions. All kinetic parameters were determined by globally fitting the models to the force-lifetime distributions as a whole via maximum likelihood estimation (MLE). The initial proportions of the two states at \( t = 0 \) were determined from the ratios of the kinetic rates assuming equilibrium. A two-step optimization procedure was employed to minimize the MLE, which explored a large parameter space by Differential Evolution to obtain an approximate solution, followed by L-BFGS to hone in the minimum. This returns the best-fit parameters summarized in Supplementary Fig. 3d. The force dependence of the kinetic rates is graphically depicted in Supplementary Fig. 3c. Using Eqs. 21 & 22 with the best-fit parameters we calculated the probability of the strong state and its fraction as functions of time and force for both TCR–pMHC and TCR–pMHC–CD4 interactions (Supplementary Fig. 3e–f). The same equations and best-fit parameters predict the mean ± SE of lifetime vs force of the TCR–pMHC, pMHC–CD4 and TCR–pMHC–CD4 bonds that agree well with the mean ± SEM data of these interactions (Fig. 2e). Also predicted are the average lifetime vs force of weak state, strong state, and their sum of the trimolecular bond that shows the force enhancement of cooperativity (Fig. 2f). It is important to note that although the two-state, two-path model fits the data as a catch-slip bond, this does not need to always be the case. In fact, the two-state, two-path model could in theory also yield slip bond or slip-catch-slip bond behavior given specific sets of parameters. Nevertheless, the catch-slip behavior naturally arises from maximizing the likelihood of the TCR–pMHC and TCR–pMHC–CD4 force-lifetime distributions, in good agreement with the average lifetimes of each bin obtained independently from the fitting. This further adds confidence both in the existence of the two catch-bonds as well as the reliability of the model. The standard error for each parameter was obtained by inverting the Hessian matrix of the negative log-likelihood at the MLE to obtain the approximate covariance matrix whose diagonal entries correspond to the variance of the fitted parameters. All kinetic modeling and associated statistics were programatically implemented in Matlab 2020a, Julia 1.6, and Python 3.7.

**Reporting summary**

Further information on research design is available in the Nature Portfolio Reporting Summary linked to this article.

**Data availability**

Data supporting the findings of this study are presented in the article and supplementary materials and are available from the corresponding authors upon reasonable request. Source data are provided with this paper.

**Code availability**

The code used to fit the data presented in this study is available at https://github.com/vaglino/TCR-MHC-CD4_kinetic_modeling under MIT license.
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Author contributions
M.N.R., V.P., C.Z., and Y.K. conceived and designed the study; C.Z. and Y.K. directed the study; M.N.R., V.P., K.L., H.-K.C., J.H., F.G., and P.A. performed experiments; C.Z. and S.T. developed mathematical models; S.T. analyzed data using mathematical model; R.A.M. provided critical reagents; M.N.R., V.P., K.L., Y.K., and C.Z. wrote the paper with contributions from other authors.

Competing interests
The authors declare no competing interests.

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