

## Reporting Summary

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Please do not complete any field with "not applicable" or n/a. Refer to the help text for what text to use if an item is not relevant to your study. For [final submission](#): please carefully check your responses for accuracy; you will not be able to make changes later.

### Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed
<input type="checkbox"/>	<input checked="" type="checkbox"/> The exact sample size ( $n$ ) for each experimental group/condition, given as a discrete number and unit of measurement
<input type="checkbox"/>	<input checked="" type="checkbox"/> A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
<input type="checkbox"/>	<input checked="" type="checkbox"/> The statistical test(s) used AND whether they are one- or two-sided <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
<input checked="" type="checkbox"/>	<input type="checkbox"/> A description of all covariates tested
<input type="checkbox"/>	<input checked="" type="checkbox"/> A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
<input type="checkbox"/>	<input checked="" type="checkbox"/> A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
<input type="checkbox"/>	<input checked="" type="checkbox"/> For null hypothesis testing, the test statistic (e.g. $F$ , $t$ , $r$ ) with confidence intervals, effect sizes, degrees of freedom and $P$ value noted <i>Give <math>P</math> values as exact values whenever suitable.</i>
<input checked="" type="checkbox"/>	<input type="checkbox"/> For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
<input checked="" type="checkbox"/>	<input type="checkbox"/> For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
<input checked="" type="checkbox"/>	<input type="checkbox"/> Estimates of effect sizes (e.g. Cohen's $d$ , Pearson's $r$ ), indicating how they were calculated

*Our web collection on [statistics for biologists](#) contains articles on many of the points above.*

### Software and code

Policy information about [availability of computer code](#)

Data collection	Gel electrophoresis data was captured using the GE Typhoon FLA 9000. Flow cytometry for particle-analysis was performed using a BD LSR-Fortessa. Particle fluorescence was also assessed using a Molecular Devices SpectraMax M5. Flow cytometry for cell-analysis was performed using a Thermo Attune. Particle images were captured using a spinning disk confocal (CSU-22 and Nikon Ti). Nanoparticle sizes were measured using Zetasizer.
Data analysis	Gel electrophoresis and particle imaging data was analyzed using ImageJ and Excel. Microplate fluorescence data was analyzed using Excel. Flow cytometry data was analyzed using FlowJo version 10. Data was plotted using GraphPad Prism version 9.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [guidelines for submitting code & software](#) for further information.

## Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

Any raw data that supports the plots within this paper are available from the corresponding authors upon reasonable request.

## Human research participants

Policy information about [studies involving human research participants and Sex and Gender in Research](#).

### Reporting on sex and gender

*Use the terms sex (biological attribute) and gender (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design whether sex and/or gender was determined based on self-reporting or assigned and methods used. Provide in the source data disaggregated sex and gender data where this information has been collected, and consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected. Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.*

### Population characteristics

*Describe the covariate-relevant population characteristics of the human research participants (e.g. age, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."*

### Recruitment

*Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.*

### Ethics oversight

*Identify the organization(s) that approved the study protocol.*

Note that full information on the approval of the study protocol must also be provided in the manuscript.

## Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

Life sciences       Behavioural & social sciences       Ecological, evolutionary & environmental sciences

## Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

### Sample size

Sample size for polymer and antibody conjugation reactions were chosen to be representative of typical reactions. Sample size for particle analysis was chosen to capture typical batch-to-batch variability. Sample size for particle flow cytometry was chosen to capture typical batch-to-batch loading variability. Sample size for polyclonal T cell expansion and phenotyping was chosen to be representative to typical donor-to-donor variability.

### Data exclusions

No data was excluded in this study.

### Replication

Most data for polymer and antibody related conjugations or size analysis include at least three experimental replicates or technical replicates (specified in text).

### Randomization

No randomization was necessary for this study

### Blinding

No blinding was necessary for this study.

## Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

## Materials & experimental systems

- n/a  Involved in the study
- Antibodies
- Eukaryotic cell lines
- Palaeontology and archaeology
- Animals and other organisms
- Clinical data
- Dual use research of concern

## Methods

- n/a  Involved in the study
- ChIP-seq
- Flow cytometry
- MRI-based neuroimaging

## Antibodies

Antibodies used	<p>For T cell activation, the antibodies used were from BioXCell Anti-human CD3, Clone: OKT-3 (BioXCell, cat. no. BE0001-2, RRID: AB_1107632) and Anti-human CD28, Clone: 9.3 (BioXCell, cat. no. BE0248, RRID: AB_2687729).</p> <p>For flow cytometry, antibodies were obtained from either Biolegend, BD, or ThermoFisher as listed: Anti-human CD45RA-BV605 (Biolegend, cat. no. 304134), Anti-human CCR7-BV711 (BD, cat. no. 566602), Anti-human LAG-3 PerCP-eF710 (Invitrogen, cat. no. 46-2239-42), Anti-human PD-1 BV421 (BD, cat. no. 562516), Anti-human TIM-3-PE-CF594 (BD, cat. no. 565560), Anti-human CD27-PE (BD, cat. no. 557330)</p>
Validation	Antibodies in this study were validated by the companies from which they were purchased

## Flow Cytometry

### Plots

Confirm that:

- The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).
- The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).
- All plots are contour plots with outliers or pseudocolor plots.
- A numerical value for number of cells or percentage (with statistics) is provided.

### Methodology

Sample preparation	Human PBMCs were obtained from leukophoresed products followed by either CD4 or CD8 enrichment (StemCell). Cells were expanded, washed, and stained using viability dyes and antibodies. Cells were then fixed using a fixation/permeabilization kit.
Instrument	Thermo Attune
Software	FlowJo version 10
Cell population abundance	At least 20,000 events were captured for each sample
Gating strategy	Cells were gated on FSC-A/SSC-A followed by singlet gating using SSC-H/SSC-A. Dead-cells were excluded via live-dead stain. Live cells were then analyzed for either memory/differentiation phenotype (CD45RA/CCR7) or inhibitory receptors (LAG-3, PD-1, TIM-3).

- Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.