

## Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see [Authors & Referees](#) and the [Editorial Policy Checklist](#).

### 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 |
|-----|-----------|
- The exact sample size ( $n$ ) for each experimental group/condition, given as a discrete number and unit of measurement
  - A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
  - The statistical test(s) used AND whether they are one- or two-sided  
*Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
  - A description of all covariates tested
  - A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
  - 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)
  - For null hypothesis testing, the test statistic (e.g.  $F$ ,  $t$ ,  $r$ ) with confidence intervals, effect sizes, degrees of freedom and  $P$  value noted  
*Give  $P$  values as exact values whenever suitable.*
  - For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
  - For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
  - 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

BD FACSDiva Software 8.0.3, Biacore 8K Control Software 2.0.15.12933, GLOMAX 1.9.3, Octet Data Acquisition 9.0.0.26, UNICORN 7.0.0.953 and XDS Program Package (Jan 31,2020).

Data analysis

FlowJo 7.6.1, Biacore Insight Evaluation 1.0.5.11069, GraphPad Prism 6.01, CCP4 7.0.072, Coot 0.8.9, Phenix 1.10.1-2155, Pymol 2.3.3 and ForteBio Data Analysis 9.0.0.10.

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/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research [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 list of figures that have associated raw data
- A description of any restrictions on data availability

The accession number for the atomic coordinates and diffraction data reported in this study is PDB code 7C01. The sequences of CA1 and CB6 MAbs have been deposited in GenBank with the accession codes MT470194- MT470197.

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

Please select the one below that is

For a reference copy of the document with all sections, see [nature.com/documents/nr-reporting-summary-flat.pdf](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

## Life sciences study design

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

Sample size	No statistical methods were used to predetermine sample size. For the animal study, there are three groups investigated, including the control group without administration of MAbs (n=3), prophylactic group (n=3) and treatment group (n=3). The numbers of monkeys in each group meet the requirement for statistical analysis (at least 3 for each group), which is sufficient given the excellent technical reproducibility.
Data exclusions	No data were excluded.
Replication	The NHP experiments were not repeated in BSL-3 lab.
Randomization	We divided nine monkeys (three females and six males) into three groups, including the control group, the prophylactic group and the treatment group. Monkeys of the same sex were randomly divided into three groups.
Blinding	The investigators were not blinded to allocation during experiments and outcome assessment. Data collection and analysis were performed by different people, the sample classification were replaced by simple marks during data analysis.

## Behavioural & social sciences study design

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

Study description	Briefly describe the study type including whether data are quantitative, qualitative, or mixed-methods (e.g. qualitative cross-sectional, quantitative experimental, mixed-methods case study).
Research sample	State the research sample (e.g. Harvard university undergraduates, villagers in rural India) and provide relevant demographic information (e.g. age, sex) and indicate whether the sample is representative. Provide a rationale for the study sample chosen. For studies involving existing datasets, please describe the dataset and source.
Sampling strategy	Describe the sampling procedure (e.g. random, snowball, stratified, convenience). Describe the statistical methods that were used to predetermine sample size OR if no sample-size calculation was performed, describe how sample sizes were chosen and provide a rationale for why these sample sizes are sufficient. For qualitative data, please indicate whether data saturation was considered, and what criteria were used to decide that no further sampling was needed.
Data collection	Provide details about the data collection procedure, including the instruments or devices used to record the data (e.g. pen and paper, computer, eye tracker, video or audio equipment) whether anyone was present besides the participant(s) and the researcher, and whether the researcher was blind to experimental condition and/or the study hypothesis during data collection.
Timing	Indicate the start and stop dates of data collection. If there is a gap between collection periods, state the dates for each sample cohort.
Data exclusions	If no data were excluded from the analyses, state so OR if data were excluded, provide the exact number of exclusions and the rationale behind them, indicating whether exclusion criteria were pre-established.
Non-participation	State how many participants dropped out/declined participation and the reason(s) given OR provide response rate OR state that no participants dropped out/declined participation.
Randomization	If participants were not allocated into experimental groups, state so OR describe how participants were allocated to groups, and if allocation was not random, describe how covariates were controlled.

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

Study description	Briefly describe the study. For quantitative data include treatment factors and interactions, design structure (e.g. factorial, nested,
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# Ecological, evolutionary & environmental sciences study design

*(hierarchical), nature and number of experimental units and replicates.*

**Research sample** *Describe the research sample (e.g. a group of tagged *Passer domesticus*, all *Stenocereus thurberi* within Organ Pipe Cactus National Monument), and provide a rationale for the sample choice. When relevant, describe the organism taxa, source, sex, age range and any manipulations. State what population the sample is meant to represent when applicable. For studies involving existing datasets, describe the data and its source.*

**Sampling strategy** *Note the sampling procedure. Describe the statistical methods that were used to predetermine sample size OR if no sample-size calculation was performed, describe how sample sizes were chosen and provide a rationale for why these sample sizes are sufficient.*

**Data collection** *Describe the data collection procedure, including who recorded the data and how.*

**Timing and spatial scale** *Indicate the start and stop dates of data collection, noting the frequency and periodicity of sampling and providing a rationale for these choices. If there is a gap between collection periods, state the dates for each sample cohort. Specify the spatial scale from which the data are taken*

**Data exclusions** *If no data were excluded from the analyses, state so OR if data were excluded, describe the exclusions and the rationale behind them, indicating whether exclusion criteria were pre-established.*

**Reproducibility** *Describe the measures taken to verify the reproducibility of experimental findings. For each experiment, note whether any attempts to repeat the experiment failed OR state that all attempts to repeat the experiment were successful.*

**Randomization** *Describe how samples/organisms/participants were allocated into groups. If allocation was not random, describe how covariates were controlled. If this is not relevant to your study, explain why.*

**Blinding** *Describe the extent of blinding used during data acquisition and analysis. If blinding was not possible, describe why OR explain why blinding was not relevant to your study.*

Did the study involve field work?  Yes  No

## Field work, collection and transport

**Field conditions** *Describe the study conditions for field work, providing relevant parameters (e.g. temperature, rainfall).*

**Location** *State the location of the sampling or experiment, providing relevant parameters (e.g. latitude and longitude, elevation, water depth).*

**Access and import/export** *Describe the efforts you have made to access habitats and to collect and import/export your samples in a responsible manner and in compliance with local, national and international laws, noting any permits that were obtained (give the name of the issuing authority, the date of issue, and any identifying information).*

**Disturbance** *Describe any disturbance caused by the study and how it was minimized.*

## 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	Involvement
<input type="checkbox"/>	<input checked="" type="checkbox"/> Antibodies
<input type="checkbox"/>	<input checked="" type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology
<input type="checkbox"/>	<input checked="" type="checkbox"/> Animals and other organisms
<input type="checkbox"/>	<input checked="" type="checkbox"/> Human research participants
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data

### Methods

n/a	Involvement
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input type="checkbox"/>	<input checked="" type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

## Antibodies

**Antibodies used** *anti-His/PE: Miltenyi Biotec, Cat No: 130-120-718, Clone No. GG11-8F3.5.1, Lot No. 5200110309, Dilution: 1:10; anti-hCD3/PE-Cy<sup>™</sup>5: BD Pharmingen<sup>™</sup>, Cat No: 555334, Clone No. UCHT1, Lot No. 7037531, Dilution: 1:20; anti-hCD16/PE-Cy<sup>™</sup>5: BD Pharmingen<sup>™</sup>, Cat No: 555408, Clone No. 3G8, Lot No. 7045714, Dilution: 1:20;*

anti-hCD19/APC-Cy™7: BD Pharmingen™, Cat No: 557791, Clone No. SJ25C1, Lot No. 7118676, Dilution: 1:20;  
 anti-hCD27/Pacific Blue™: BioLegend, Cat No: 302821, Clone No. O323, Lot No. B223941, Dilution: 1:50;  
 anti-hCD38/APC: BD Pharmingen™, Cat No: 555462, Clone No. HIT2, Lot No. 7125887, Dilution: 1:20;  
 anti-CD235a/PE-Cy™5: BD Pharmingen™, Cat No: 559944, Clone No. GA-R2, Lot No. 7012580, Dilution: 1:20;  
 anti-hlgG/FITC: BD Pharmingen™, Cat No: 555786, Clone No. G18-145, Lot No. 6363638, Dilution: 1:20;  
 anti-hlgG/APC: BioLegend, Cat No: 409306, Clone No. HP6017, Lot No. B265810, Dilution: 1:100.  
 Anti-mIgG/APC: BD Pharmingen™, Cat No: 550874, Clone No. X56, Lot No. 7128657, Dilution: 1:100.

## Validation

We follow the manufactures's instruction to use the above listed antibodies to stain human PBMCs. All antibodies work well.  
 anti-His/PE: (Miltenyi Biotec; Mouse; specific for His tag; applicable for Flow cytometry/Cell sorting [FC/FACS])  
<https://www.citeab.com/antibodies/7058497-130-120-718-anti-his-pe?des=d6e817455032c7cc>

anti-hCD3/PE-Cy™5: (BD Pharmingen™; Mouse BALB/c IgG1, κ; specific for Human [QC Testing] CD3; applicable for flow cytometry [Routinely Tested]; 20 μL/test)  
<https://www.bdbiosciences.com/us/applications/research/t-cell-immunology/th-1-cells/surface-markers/human/pe-cy5-mouse-anti-human-cd3-ucht1-also-known-as-ucht-1-ucht-1/p/555334>

anti-hCD16/PE-Cy™5: (BD Pharmingen™; Mouse BALB/c x DBA/2, also known as CD2F1 or CDF1 IgG1, κ; specific for Human [QC Testing], Rhesus, Cynomolgus, Baboon [Tested in Development] CD16; applicable for Flow cytometry [Routinely Tested]; 20 μL/test).  
<https://www.bdbiosciences.com/us/applications/research/stem-cell-research/cancer-research/human/pe-cy5-mouse-anti-human-cd16-3g8/p/555408>

anti-hCD19/APC-Cy™7: (BD Pharmingen™, Mouse BALB/c IgG1, κ; specific for Human [QC Testing] CD19; applicable for flow cytometry [Routinely Tested], 5 μL/test)  
<https://www.bdbiosciences.com/us/applications/research/clinical-research/oncology-research/blood-cell-disorders/surface-markers/human/apc-cy7-mouse-anti-human-cd19-sj25c1-also-known-as-sj25-c1/p/557791>

anti-hCD27/Pacific Blue™: (BioLegend, Mouse IgG1, κ; specific for Human, African Green, Baboon, Cynomolgus, Rhesus, Squirrel Monkey CD27; applicable for flow cytometry [Quality tested], 5 μL/test)  
<https://www.biolegend.com/en-us/products/pacific-blue-anti-human-cd27-antibody-6442>

anti-hCD38/APC: (BD Pharmingen™, Mouse BALB/c IgG1, κ; specific for Human [QC Testing] CD19; applicable for flow cytometry [Routinely Tested], 20 μL/test)  
<https://www.bdbiosciences.com/us/applications/research/t-cell-immunology/regulatory-t-cells/surface-markers/human/apc-mouse-anti-human-cd38-hit2/p/555462>

anti-CD235a/PE-Cy™5: (BD Pharmingen™, Mouse IgG2b, κ; specific for Human [QC Testing] CD19; applicable for flow cytometry [Routinely Tested])  
<https://www.bdbiosciences.com/us/reagents/research/antibodies-buffers/immunology-reagents/anti-human-antibodies/cell-surface-antigens/pe-cy5-mouse-anti-human-cd235a-ga-r2-hir2/p/559944>

## Eukaryotic cell lines

Policy information about [cell lines](#)

Cell line source(s)

HEK293T cells: ATCC, CRL-3216;  
 Huh7 cells: Institute of Basic Medical Sciences CAMS, 3111C0001CCC000679;  
 Calu-3 cells: ATCC, HTB-55;  
 Vero E6 cells: ATCC, CRL-1586.

Authentication

The cell lines were not authenticated since they were purchased commercially and are not commonly misidentified.

Mycoplasma contamination

The cells were not tested for mycoplasma contamination.

Commonly misidentified lines  
 (See [ICLAC](#) register)

The cell lines used in this study do not appear on the ICLAC register.

## Palaeontology

Specimen provenance

*Provide provenance information for specimens and describe permits that were obtained for the work (including the name of the issuing authority, the date of issue, and any identifying information).*

Specimen deposition

*Indicate where the specimens have been deposited to permit free access by other researchers.*

Dating methods

*If new dates are provided, describe how they were obtained (e.g. collection, storage, sample pretreatment and measurement), where they were obtained (i.e. lab name), the calibration program and the protocol for quality assurance OR state that no new dates are provided.*

Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.

## Animals and other organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

Laboratory animals	Nine Rhesus macaques (6-8 years old).
Wild animals	The study did not involve wild animals.
Field-collected samples	The study did not involve samples collected from the field.
Ethics oversight	Chinese Academy of Sciences

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

## Human research participants

Policy information about [studies involving human research participants](#)

Population characteristics	We used the blood from one convalescent COVID-19 patient (female, 33 years old) in China.
Recruitment	The patient agreed to provide the biospecimen for detection, further diagnostic and scientific research when hospitalization.
Ethics oversight	Chinese Academy of Sciences

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

## Clinical data

Policy information about [clinical studies](#)

All manuscripts should comply with the ICMJE [guidelines for publication of clinical research](#) and a completed [CONSORT checklist](#) must be included with all submissions.

Clinical trial registration	Provide the trial registration number from <a href="#">ClinicalTrials.gov</a> or an equivalent agency.
Study protocol	Note where the full trial protocol can be accessed OR if not available, explain why.
Data collection	Describe the settings and locales of data collection, noting the time periods of recruitment and data collection.
Outcomes	Describe how you pre-defined primary and secondary outcome measures and how you assessed these measures.

## ChIP-seq

### Data deposition

- Confirm that both raw and final processed data have been deposited in a public database such as [GEO](#).
- Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

Data access links <i>May remain private before publication.</i>	For "Initial submission" or "Revised version" documents, provide reviewer access links. For your "Final submission" document, provide a link to the deposited data.
Files in database submission	Provide a list of all files available in the database submission.
Genome browser session (e.g. <a href="#">UCSC</a> )	Provide a link to an anonymized genome browser session for "Initial submission" and "Revised version" documents only, to enable peer review. Write "no longer applicable" for "Final submission" documents.

### Methodology

Replicates	Describe the experimental replicates, specifying number, type and replicate agreement.
Sequencing depth	Describe the sequencing depth for each experiment, providing the total number of reads, uniquely mapped reads, length of reads and whether they were paired- or single-end.
Antibodies	Describe the antibodies used for the ChIP-seq experiments; as applicable, provide supplier name, catalog number, clone name, and lot number.
Peak calling parameters	Specify the command line program and parameters used for read mapping and peak calling, including the ChIP, control and index files used.
Data quality	Describe the methods used to ensure data quality in full detail, including how many peaks are at FDR 5% and above 5-fold enrichment.

Software

Describe the software used to collect and analyze the ChIP-seq data. For custom code that has been deposited into a community repository, provide accession details.

## 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
- Instrument
- Software
- Cell population abundance
- Gating strategy
- Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.

## Magnetic resonance imaging

### Experimental design

- Design type
- Design specifications
- Behavioral performance measures

### Acquisition

- Imaging type(s)
- Field strength
- Sequence & imaging parameters
- Area of acquisition
- Diffusion MRI  Used  Not used

### Preprocessing

- Preprocessing software
- Normalization
- Normalization template
- Noise and artifact removal

Volume censoring

*Define your software and/or method and criteria for volume censoring, and state the extent of such censoring.***Statistical modeling & inference**

Model type and settings

*Specify type (mass univariate, multivariate, RSA, predictive, etc.) and describe essential details of the model at the first and second levels (e.g. fixed, random or mixed effects; drift or auto-correlation).*

Effect(s) tested

*Define precise effect in terms of the task or stimulus conditions instead of psychological concepts and indicate whether ANOVA or factorial designs were used.*Specify type of analysis:  Whole brain  ROI-based  BothStatistic type for inference  
(See [Eklund et al. 2016](#))*Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.*

Correction

*Describe the type of correction and how it is obtained for multiple comparisons (e.g. FWE, FDR, permutation or Monte Carlo).***Models & analysis**

n/a

Involved in the study

 Functional and/or effective connectivity Graph analysis Multivariate modeling or predictive analysis

Functional and/or effective connectivity

*Report the measures of dependence used and the model details (e.g. Pearson correlation, partial correlation, mutual information).*

Graph analysis

*Report the dependent variable and connectivity measure, specifying weighted graph or binarized graph, subject- or group-level, and the global and/or node summaries used (e.g. clustering coefficient, efficiency, etc.).*

Multivariate modeling and predictive analysis

*Specify independent variables, features extraction and dimension reduction, model, training and evaluation metrics.*