

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 our [Editorial Policies](#) 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 |
|-------------------------------------|--|
| <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 type="checkbox"/> | <input checked="" 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 P 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

Cell Quest Pro v5.2 (BD)
CytExpert v2.3(Beckman Coulter)
FACS Diva (BD)
AxioVision (r4.8.2, Carl Zeiss MicroImaging)
VS-ASW (Olympus Corp)
Zen 2011 SP3 (Carl Zeiss) v8.1.11.484
MRI (Bruker Biospin MRI)
OneStep real-time PCR (Applied Biosystems) - v2.3
Magellan (Tecan) - v6.6
OlyVIA v2.9 (Olympus Soft Imaging Solutions)

Data analysis

CytExpert v5.2 (Beckman Coulter)
FIJI ImageJ version 1.53c (NIH)
Imaris (Bitplane) - v8.0.2 and v9.3.1
FlowJo (FlowJo LLC) - v.10
Prism (GraphPad Software, Inc) - v6-8
AngioTool v0.5 (NIH)
Excel (MicrosoftOffice 2010, v14.0.7208.5000)
OMERO v5.6 (Open Microscopy Environment)
QuPath v0.3.1
Scikit-learn v1 (BSD license)
Miseq marker gene pipeline v1.8
VSEARCH v2.12.06 a
UNOISE3 algorithm

BLASTn 2.7.1
 Rstudio version 1.3.1056 and R 4.0
 GMRP v0.1.3
 ampvis2 (version 2.6.4)
 ggplot2 (v3.3.2)

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 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

RNA-seq data sets will be deposited online in the Gene Expression Omnibus (GEO database) upon acceptance of the manuscript. Source data are provided with this paper.

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

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	Sample sizes were chosen on the basis of standard power calculations (with $\alpha = 0.05$ and power of 0.8) performed for similar experiments that were previously published. In general, statistical methods were not used to re-calculate or predetermine sample sizes.
Data exclusions	No samples were excluded by the analysis
Replication	Number of reproductions of each experimental finding is stated in each figure legend.
Randomization	Animals from different cages, but within the same experimental group, were selected to assure randomization. Age and sex matched mice were randomly allocated into experimental groups. Randomization was not relevant for human tissue studies, which were descriptive studies, and for in vitro experiments, in which each experimental group was treated under the same experimental conditions.
Blinding	Blinding was performed in the assessment of the EAE clinical score. Investigators were not blinded in other experimental setups since the data collection and the analysis were performed with quantitative instruments. Descriptive imaging data that did not compare groups cannot be blinded.

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.

Ecological, evolutionary & environmental sciences study design

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, hierarchical), nature and number of experimental units and replicates.
Research sample	Describe the research sample (e.g. a group of tagged <i>Passer domesticus</i> , all <i>Stenocereus thurberi</i> 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?	<input type="checkbox"/> Yes <input type="checkbox"/> 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 & 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	Involved in the study
<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 and archaeology
<input type="checkbox"/>	<input checked="" type="checkbox"/> Animals and other organisms
<input type="checkbox"/>	<input checked="" type="checkbox"/> Human research participants
<input type="checkbox"/>	<input checked="" type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern

Methods

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input type="checkbox"/>	<input checked="" type="checkbox"/> Flow cytometry
<input type="checkbox"/>	<input checked="" type="checkbox"/> MRI-based neuroimaging

Antibodies

Antibodies used

For surface staining the following mouse anti-rat mAbs were used: $\alpha\beta$ TCR-AF647 (clone R73, Biolegend), RT1B-FITC (clone OX-6, BD Biosciences), CD4-PE/Cy7 (clone W3/25; Biolegend), CD8 α -PE (clone OX-8; Biolegend), CD11b/c-PE and CD11b/c-AF647 (clone OX-42, Biolegend), CD25-PE (clone OX-39, Biolegend), CD45-AF647 and CD45-PerCP (clone OX-1; Biolegend), CD45RA-PE (clone OX-33; Biolegend), CD31-PE (clone TLD-3A12, Bio-Rad), CD134-AF647 (clone OX-40, Biolegend) and CD134-BV421 (clone OX-40, BD Biosciences OptiBuild). Mouse IgG1 κ (MOPC 31C, Sigma-Aldrich) served as isotype control. For non-conjugated anti-CD25 (clone OX39, BioRad) and anti-CD134 (clone OX40, BioRad) antibodies, APC-labelled anti-mouse IgG antibody (Jackson) was used as secondary antibody.

For intracellular cytokine staining, cells were stained with anti-IFN γ -AF647 (clone DB-1, Biolegend), and anti-IL17A-PE (clone TV11-18H10.1, Biolegend) antibodies.

For intranuclear FoxP3 staining, cells were stained with an anti-rat/human/mouse FoxP3-PE antibody (clone 150D, Biolegend).

For mouse experiments, the following antibodies were used: CD11b-PeCy7 (clone M1/70, Biolegend), CD3e-APC (clone 145-2C11, Biolegend), CD4-BV785 (clone RM4-5, Biolegend), CD8-BV650 (clone 53-6.7, Biolegend), CD44-FITC (clone IM7, Biolegend), CD45-BV420 (clone 30-F11, Biolegend), Ly6G-BV650 (clone 1A8, Biolegend), Ly6C-APC-Cy7 (clone HK1.4, Biolegend).

For immunohistochemical stainings the samples were incubated free-floatingly with the following antibodies: mouse anti-rat-RT1B-MHC class II antigen (clone OX-6, Serotec), rabbit anti-Iba-1 (Wako), mouse anti-rat-CD68 (clone ED1, BioRad), mouse anti-rat CD68 (clone ED1, Serotec), mouse anti-rat-CD43 (clone W3/13, BioRad), rabbit anti-Lyve1 (Origene) and chicken anti-GFP antibody (ab13970 Abcam). Goat anti-mouse or goat anti-rabbit IgG Abs labelled with Alexa Fluor 488, Alexa Fluor 555 or Alexa Fluor 647 were used as secondary antibodies. For the GFP staining, Alexa Fluor 488 labelled goat anti-chicken was used as secondary antibody. All antibodies were used at a 1:100 dilution.

Validation

All antibodies used in this study were from commercial vendors and were validated for the specific application (immunohistochemistry, flow cytometry/cell sorting) by the manufacturers. The validation is reported on their websites.

Eukaryotic cell lines

Policy information about [cell lines](#)

Cell line source(s)

GP+E86 ecotropic retroviral packaging cell line (ATCC).
 Lewis rat CD4 effector T cell lines specific for myelin basic protein (Establishment protocol reported in METHODS).
 Lewis rat CD4 effector T cell lines specific for beta-synuclein ((Establishment protocol reported in METHODS)).
 Lewis rat CD4 effector T cell lines specific for ovalbumin ((Establishment protocol reported in METHODS)).

Authentication

No authentication was performed for GP+E86 and derivative cell lines.
 For T cell lines, authentication reported in METHODS.

Mycoplasma contamination

All used cell lines were tested negative for mycoplasma contamination.

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

No commonly misidentified cell lines were used in the study

Animals and other organisms

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

Laboratory animals

Lewis rats on a LEW/Crl background and C57BL/6J mice (wt, RFP, 2D2 and Nur77-GFP) were bred at the animal facility of the University Medical Centre Göttingen (Germany). T cell receptor transgenic Lewis rat strain (ubiquitous expression of GFP-TCRa-TCRb transgene; unknown integration site) specific for beta-synuclein antigen and MBP were previously generated in our lab (Lodygin et al Nature 2019) and maintained at the animal facility of University Medical Centre Göttingen. Breeder pairs Prox-1-eGFP transgenic rats on a Sprague-Dawley background (Eunson Jung, Scientific Reports volume 7, Article number: 5577 (2017) were kindly provided by Young-Kwon Hong (University of Southern California, Los Angeles, California, USA). Rats between 6 and 8 weeks of age and mice between 10 and 15 weeks of age were used for experiments. Both sexes were used in rat and mouse experiments as no difference in experimental outcome was observed.

Wild animals

The study did not involve wild animals

Field-collected samples The study did not involve samples collected from the field

Ethics oversight All animal experiments were performed according to the local animal welfare regulations.

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 Described in Table 1

Recruitment Human samples were obtained from the archives of the Institute of Neuropathology at the University medical Centre Göttingen. Brain tissue of MS patients was collected in the frame of a prospective brain donor programme.

Ethics oversight The study was approved by the ethical committee of the University medical Centre Göttingen.

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 ClinicalTrials.gov 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.

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

To isolate the brain dura, the skull cap was removed by performing two lateral incisions starting from the foramen magnum, proceeding rostrally until the nasal bone. The nasal bone was severed and the skullcap detached. The brain with attached leptomeninges was then scooped out. For entire brain dura preparation (indicated in the legend as brDura), the brain dura of the hemispheres, sagittal and transversal sinuses and basicranium was detached from the skull, taking care to first remove any visible remnants of optical nerves, epiphysis and hypophysis. When required, the dura of the cranial vault was separated into hemispheric dura and sinuses under a dissection microscope (Leica). The areas of the dura analyzed are stated in the figure labels. Specifically, the term "brDura" is used to indicate the entire dura (including hemispheres and peri-sinus areas), whereas the terms "brDura (hemispheres)" and "brDura (sinuses)" refer to the analysis of the specific dural areas. To remove the leptomeninges, the cerebellum was discarded and the brain hemispheres were cut in half. The leptomeninges were separated from the brain parenchyma under a dissection microscope by identifying the proximal middle cerebral artery on the ventral surface of the hemisphere. From there, the leptomeninges were grabbed with fine forceps and carefully detached from the brain hemisphere.

Spinal cord dura and leptomeninges were separated from the spinal cord parenchyma under a dissection microscope. The spinal nerve roots were removed from the spinal cord dura with a pair of fine tweezers. The spinal cord dura was peeled away from the rest of the spinal cord. Upon removal of the spinal cord dura, spinal cord leptomeninges were readily identifiable as tightly apposed to the parenchyma and by the presence of the anterior and posterior median spinal veins. To avoid contamination of the dura by the lumbosacral roots, the sacral part of the spinal cord was discarded. Meninges were collected in Eppendorf vials containing 1ml EH. To calculate the weight, each vial was weighted before and after addition of the meninges.

Brain and spinal cord parenchyma were passed through a cell strainer (40-µm2) and myelin debris were removed by a Percoll-density gradient (30min at 700xg and 4 °C). The pellet was washed once in PBS and resuspended in a definite volume of EH medium.

Dura and leptomeninges were first minced into small pieces, collected in 5 ml EH and centrifuged at 1200 rpm for 5min. The supernatant was removed and tissue fragments were suspended in either 500 µl of 0,15% collagenase type II from Clostridium histolyticum (Sigma) plus 60 U ml⁻¹ of DNase1 (Roche) in EH or, for endothelial cell isolation and antigen

presentation assay, in 0.41 U ml⁻¹ of Liberase TM (Roche) and 60 U ml⁻¹ of DNase1 in EH. Of note, in preliminary experiment collagenase type II was tested against collagenase type D24 and it was equivalently effective. The suspension was kept at 37° for 30-40min and resuspended every 5min. Afterwards, the cell suspensions were diluted in EH + EDTA 2mM and filtered through a 40-µm² cell strainer. Myelin debris were removed by a Percoll-density gradient (30min at 700xg and 4 °C), the pellet was washed once in PBS and resuspended in a definite volume of EH medium.

Inguinal (ingLNs), mediastinal (medLN), paraaortal (paLN), superficial cervical (scLN) and deep cervical lymph nodes (dcLNs) were isolated by following anatomical reference points, mashed through a cell strainer (40-µm²) and centrifuged at 290xg for 6min at 4 °C. The cell pellet was then dissolved in a defined amount of EH medium.

The spleen was removed by an incision in the abdominal wall and resection of the splenic hilum. The organ was mashed through a cell strainer (40-µm²) and centrifuged at 290xg for 6min at 4 °C. The cell pellet was incubated for 5min in 5 ml of ACK buffer on ice in order to lyse erythrocytes. After dilution of the lysate with 45 ml of ice-cold PBS, the sample was pelleted by centrifugation and suspended in 5 ml EH medium.

To isolate lymphocytes from blood, a density gradient separation was performed with Lymphocyte Separation Medium 1077 (PromoCell) underlay. Blood was then centrifuged for 30min at 840xg at 20°. The obtained interphase was collected and washed once with ice-cold PBS. The cell pellet was incubated for 2min in 1 ml of ACK buffer on ice in order to lyse erythrocytes. After dilution of the lysate with 49 ml of ice-cold PBS, the sample was pelleted by centrifugation and suspended in 5 ml EH medium.

For surface staining the cell were antibody labeled with a mix of primary antibodies described in the list above for 30 minutes at 4°, washed by PBS and FACS-analyzed.

For intracellular detection of IFN-gamma and IL17, ex vivo isolated cells were left unstimulated or stimulated in vitro with 1 µg/mL PMA (Phorbol 12-myristate 13-acetate, Sigma-Aldrich) and 5 µM Ionomycin calcium salt (Sigma-Aldrich) for 30 minutes. Brefeldin A (5 µg/mL) was added to block cytokine secretion. Cell were cultured for further 2 h and surface stained with anti-rat αβTCR-AlexaFluor647 (Clone R73, Biolegend), anti-rat CD4-PE/Cy7 (Clone W3/25, Biolegend) and anti-CD8α-PerCP (Clone OX-8, Biolegend) for 30 minutes at 4°C. The cells were fixed with 2 % PFA, permeabilized with BD Perm/Wash buffer (BD Biosciences) and stained with rat anti-mouse anti-IL17-BV42 (clone TC11-8H4, Biolegend) and mouse anti-rat IFNγ-PE (Clone DB1, Biolegend) for 45 minutes at 4°C. For intracellular staining for FoxP3 detection, ex vivo isolated cells were surface-stained as described above, fixed and permeabilized using FoxP3/transcription factors staining buffer set (eBioscience) following the manufacturer's instructions and stained with anti-mouse/rat/human FoxP3-PE (Biolegend).

Instrument	BD FACSCalibur, BD FACS Aria II, Beckman Coulter CytoFLEX S
Software	BD CellQuest Pro5.2, BD FACS Diva software or Beckman Coulter CytExpert2.3 were used for acquisition of flow cytometry data, Flowjo-V10 and Beckman Coulter CytExpert2.3 for data analysis.
Cell population abundance	For sequencing analysis of CD11b- CD45- CD31+ endothelial cells isolated ex-vivo from brain dura and brain leptomeninges of naïve animals, 10,000–20,000 cells were sorted for each replicate. Each sample was re-analysed after sorting for assessing cell population abundance and purity. Just samples with a purity > 98% were further processed. For sequencing analysis of TbSYN cells isolated from brain (dura, leptomeninges and parenchyma), blood, CSF, ingLNs and dcLNs on day 3.5 p.t. Between 10,000–100000 TbSYN cells were sorted from each sample. Each sample was re-analysed after sorting for assessing cell population abundance and purity. Just samples with a purity > 98% were further processed.
Gating strategy	Gating strategy, with representative gating, is reported in Supplementary Fig. 1. Briefly, singlets were gated using the height, area and the pulse width of the forward and side scatter. The boundaries between "positive" and "negative" were determined by the clear cell subpopulations and unstained negative controls.

☒ 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	Structural descriptive brain MRI in anesthetized rats
Design specifications	No functional MRI was performed
Behavioral performance measures	No behavioural measures were analysed

Acquisition

Imaging type(s)	Structural
Field strength	9.4 T
Sequence & imaging parameters	T2-weighted axial MRI with repetition time (TR) of 9286 ms, echo time (TE) of 11 ms, RARE factor of 12, 60 slices, in-plane resolution of 120×120 µm, slice thickness of 480 µm, and total acquisition time (TA) of 195 s as well as sagittal MRI (TR/TE = 4333/11 ms, RARE factor = 12, 28 slices, field-of-view = 30.72×30.72 mm, matrix size = 256×256, in-plane resolution = 120×60 µm, slice thickness = 480 µm, and TA = 182 s) were performed with the use of multislice fast spin-echo MRI.
Area of acquisition	Brain

Diffusion MRI

☐ Used☒ Not used

Preprocessing

Preprocessing software

Provide detail on software version and revision number and on specific parameters (model/functions, brain extraction, segmentation, smoothing kernel size, etc.).

Normalization

If data were normalized/standardized, describe the approach(es): specify linear or non-linear and define image types used for transformation OR indicate that data were not normalized and explain rationale for lack of normalization.

Normalization template

Describe the template used for normalization/transformation, specifying subject space or group standardized space (e.g. original Talairach, MNI305, ICBM152) OR indicate that the data were not normalized.

Noise and artifact removal

Describe your procedure(s) for artifact and structured noise removal, specifying motion parameters, tissue signals and physiological signals (heart rate, respiration).

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.