

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

- ☐ ☒ 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 pClamp10, SerialEM

Data analysis GraphPad Prism 8, SerialEM, Coot 0.8.9.2-pre-revision-7884, Phenix 1.17.1-3660, Relion 3.0.8_cu8.0, Relion 3.1-beta_cu8.0, MotionCor2, GCTF, CTFFIND4, crYOLO, Chimera 1.14, ResMap, Pymol 2.3.2_79, Hole2, GROMACS 2019.4, CHARMM-GUI, VMD, MDAnalysis, MDTraj, eBDIMS

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

Data availability: Atomic model coordinates for bicuculline, GABA + propofol, GABA + flumazenil, GABA + etomidate, GABA + phenobarbital, GABA + diazepam, GABA, and GABA + picrotoxin-bound structures have been deposited in the Protein Data Bank with accession codes 6X3S, 6X3T, 6X3U, 6X3V, 6X3W, 6X3X, 6X3Z and 6X40, respectively, and the cryo-EM density maps have been deposited in the Electron Microscopy Data Bank with accession codes EMD-22031, EMD-22032, EMD-22033, EMD-22034, EMD-22035, EMD-22036, EMD-22037 and EMD-22038, respectively.

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	No statistical methods were used to estimate appropriate sample size.
Data exclusions	RELION-based 2D and 3D classification of single particle datasets were used to remove false positives and particles with disordered domains.
Replication	Attempts to replicate/reproduce the data were successful as detailed in the MD simulation and electrophysiology replicates.
Randomization	EM particle sets were randomly split for the purposes of estimating overall resolution.
Blinding	No blinding was performed.

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
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

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

Antibodies

Antibodies used	1F4 Fab fragment was used in EM studies, published previously in PMID: 29950725.
Validation	Binding was validated by gel filtration and structural analysis; sequence was verified by sequencing of hybridoma line and by experimental density map.

Eukaryotic cell lines

Policy information about [cell lines](#)

Cell line source(s)	ATCC CRL-3022; ATCC CRL-1711
Authentication	Purchased from commercial supplier. Not further tested.
Mycoplasma contamination	Not tested.
Commonly misidentified lines (See ICLAC register)	n/a