nature portfolio

Corresponding author(s):	Alexander Sobolevsky
Last updated by author(s):	Apr 12, 2024

Reporting Summary

Nature Portfolio 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 Portfolio policies, see our <u>Editorial Policies</u> and the <u>Editorial Policy Checklist</u>.

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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.
\boxtimes	A description of all covariates tested
\boxtimes	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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
\times	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
X	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
\boxtimes	Estimates of effect sizes (e.g. Cohen's <i>d</i> , Pearson's <i>r</i>), indicating how they were calculated
	Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.

Software and code

Policy information about <u>availability of computer code</u>

Data collection

Leginon 3.5, pCLAMP 10.2

Data analysis

cryoSPARC 4.4.1, UCSF Chimera 1.16, UCSF ChimeraX 1.3, COOT 0.9.8.1, PHENIX 1.18, pyMOL 2.5.2, HOLE 2.1, Origin 2023, pCLAMP 10.2, Clampfit 10.3, DynDom 1.5, CHARMM-GUI, AmberTools20, Amber20, VMD 1.9.4

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 <u>guidelines for submitting code & software</u> for further information.

Data

Policy information about <u>availability of data</u>

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

The cryo-EM density maps have been deposited to the Electron Microscopy Data Bank (EMDB) under the accession codes EMD-44129 (GluK2Glu-2XConA-BPAM, composite map), EMD-44130 (GluK2Glu-1XConA-BPAM, composite map), EMD-44128 (GluK2Glu-ConA-BPAM, LBD-TMD), EMD-44131 (GluK2Glu-4fold), EMD-44132 (GluK2Glu-asym), EMD-44125 (ConA, Type I), EMD-44124 (ConA, Type II), EMD-44123 (GluK2Glu-ConA-BPAM, ATD), EMD-44126 (GluK2Glu-2XConA-BPAM,

reference map), and EMD-44127 (GluK2Glu-1XConA-BPAM, reference map). The atomic coordinates have been deposited to the Protein Data Bank (PDB) under the accession codes 9B36 (GluK2Glu-2XConA-BPAM), 9B37 (GluK2Glu-1XConA-BPAM), 9B35 (GluK2Glu-ConA-BPAM, LBD-TMD), 9B38 (GluK2Glu-4fold), 9B39 (GluK2Glu-asym), 9B34 (ConA, Type I), and 9B33 (ConA, Type II). The atomic coordinates under the accession codes 3ENR, 5KUF, 5WEO, 7RZ8, 7RYZ, 7TNL, 7TNM, 7TNN, 7TNO, 7TNP, 8FOO, 8FWQ and 8FWS were used for model building and structural comparisons. Source data are provided with this paper.

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		with human participants or human data. See also policy information about sex, gender (identity/presentation), thnicity and racism.
Reporting on sex and gender		N/A
Reporting on race, ethnicity, or other socially relevant groupings		N/A
Population characteristics		N/A
Recruitment		N/A
Ethics oversight		N/A
Note that full informa	ation on the appro	oval of the study protocol must also be provided in the manuscript.
- ield-spe	ecific re	porting
Please select the o	ne below that is	the best fit for your research. If you are not sure, read the appropriate sections before making your selection.
Life sciences	В	ehavioural & social sciences
For a reference copy of	the document with	all sections, see <u>nature.com/documents/nr-reporting-summary-flat.pdf</u>
_ife scier	nces stu	ıdy design
All studies must dis	sclose on these	points even when the disclosure is negative.
Sample size	healthy-looking from GluK2 pro or more biologi	-EM data collected was limited by time allocation at the microscopes. For electrophysiological experiments, we only selected cells, with contrast body and smooth membrane that also showed the fluorescent signal of GFP expressed under a different motor. No statistical approaches were used to predetermine the sample size but all measurements were performed using five cally independent measurements. Exact number of biologically independent measurements and the number of independent exported in the figure legends.
Data exclusions	No data has bee	en excluded.
Replication	sessions and we	ttempts have failed. Cryo-EM data collections were performed during two continuous two- and three-day data collection ere consistent from the beginning to the end. A replication of the cryo-EM data collection was therefore not necessary or stifiable. In electrophysiological experiments, we made at least five independent replicates for each construct.
Randomization	economically vi	ot randomized; it is not technically or practically feasible to do so for cryo-EM or patch-clamp studies. Covariant control is not able in cryo-EM data collections. Covariant control was also not possible in electrophysiological experiments due to the need in predetermind cDNAs and optimize protein expression for individual constructs.
Blinding	economically vi of cell as well as	re not blinded; it is not technically or practically feasible to do so for cryo-EM or electrophysiological experiments. It is not able to blind cryo-EM collections. For electrophysiological experiments, researchers conducting the studies were also in charge protein expression optimization for individual constructs in order to achieve recordings or transfected cells in these studies.

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 & experime	ntal sy	ystems Methods
n/a Involved in the study		n/a Involved in the study
Antibodies		ChIP-seq
Eukaryotic cell lines		Flow cytometry
Palaeontology and a	archaeol	ogy MRI-based neuroimaging
Animals and other o	organism	s
Clinical data		
Dual use research o	f concer	n
Eukaryotic cell lin	es	
Policy information about ce	ell lines	and Sex and Gender in Research
		HEK293S GnTI-, ATCC, Cat#CRL-3022
		Sf9, Gibco, Cat#12659017 HEK 293, ATCC, Cat#CRL-1573
Authentication		None of the cell lines used have been authenticated.
Authentication		Note of the cell lines used have been authenticated.
Mycoplasma contamination The cell lines used have retested in the lab.		The cell lines used have been tested for mycoplasma contamination by the providers (negative results) but have not been retested in the lab.
Commonly misidentified lines (See ICLAC register)		No commonly misidentified lines were used in this study.
Plants		
Seed stocks	N/A	
N. 1.1.	NI/A	
Novel plant genotypes	N/A	
Authorication	NI/A	
Authentication	N/A	