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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	X-ray data collection: MXCube; Electrophysiology: Clampex 10.6; UV-spectroscopy measurements: UVProbe 2.33; Ion translocation: Logger Lite 1.7.
Data analysis	Crystallography: XDS5, AIMLESS, REFMAC553, PHENIX, Coot, MoRDa, PyMOL, HOLLOW, PPM server. Electrophysiology: Multiclamp 700B. Time-resolved absorption spectra: MEXFIT, Origin. Molecular dynamics: GROMACS 2018, CHARMM36m, MDAnalysis.

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

The protein coordinates and atomic structure factors have been deposited in the Protein Data Bank (PDB) under accession numbers 7AKW (O1O2 mutant), 7AKX (OLPVR1 in P1 space group) and 7AKY (OLPVR1 in P21212 space group) respectively. All other data are available from corresponding author upon reasonable request.

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

Life sciences study design

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

Sample size	Sample sizes were determined based on prior literature and practices in the field, such as Nagel et. al 2003, Govorunova et. al 2015, Kato et. al 2018. We did not use statistical methods a predetermine sample size. The sample size for electrophysiology recordings was typically four or greater measurements.
Data exclusions	No data were excluded.
Replication	All attempts at replication were successful. For electrophysiological experiments multiple measurements with different cells were done. Crystallization attempts were succesful for n = 2-5 independent trials for each crystal structure reported.
Randomization	The samples were not allocated into different groups, therefore the randomization was not required.
Blinding	Animal experiments were not performed in this study, so Investigators were not blinded to the experiment. No other experiments in this study involved blinding.

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	Anti-Map2, Abcam, ab32454, polyclonal; Alexa Fluor goat anti-rabbit 647 IgG, Invitrogen, A21244
Validation	The primary antibodies for immunostaining were validated by the manufacturer as descibed in the product datasheet: Anti-Map2: https://www.thermofisher.com/order/genome-database/dataSheetPdf?producttype=antibody&productsubtype=antibody_primary&productId=PA5-17646&version=122 Alexa IgG: https://www.thermofisher.com/order/genome-database/dataSheetPdf?producttype=antibody&productsubtype=antibody_secondary&productId=A-21244&version=122

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	SH-SY5Y human neuroblastoma cells were purchased from Sigma
Authentication	Cells have been authenticated by the vendors (STR-profiling, DNA barcoding, etc) https://www.sigmaaldrich.com/catalog/product/sigma/cb_94030304?lang=de&region=DE
Mycoplasma contamination	All cell lines tested negative for mycoplasma

Commonly misidentified lines (See ICLAC register)	Cells are not listed in the database