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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	All equipment specifications and experimental parameters have been details in main text and method section.
Data analysis	All software and data analyses methods have been described and references appropriately cited. The following software (version number) were used: MotionCor2 1.3.2-for anisotropic correction of beam-induced motion Gctf v0.56-for defocus estimation RELION3.0-for 3D reconstraction CCP4 v7/Coot-for Crystallographic model building Phenix 1.16.1 -for refinement MolProbity4.4-for model validation Chimera1.10.1/PyMol 1.4-Molecular graphics software ResMap1.1.4-for local resolution Image J 1.50i-for measured integrated densities of different western blot bands Prism 8-for data plotting and analysis Leica DM6B microscope-for photobodies observation POVME 2.0-for volume calculation

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

Atomic coordinates and structure factors of blue light activated CRY2 tetramer have been deposited in the Protein Data Bank under accession codes PDB 6M79. The cryo-EM map of this tetramer has been deposited in the EM Database with accession code EMD-30128. Source data for Fig. 1b, Extended Data Figs.6, 7, 9, and Supplementary Fig.4 are provided with this paper online. The structures of CRY2N monomer under darkness (PDB accession code 6K8I), BIC2-CRY2N complex (PDB accession code 6k8k), and ZmCRY1cW368A tetramer (PDB accession code 6LZ3) used in this study had been reported (https://doi.org/10.1038/s41594-020-0410-z and https://doi.org/10.1038/s41594-020-0420-x).

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	In the experiments of Extended Data Fig.7a, Expi293F™ Cells transfected with corresponding proteins were incubated in dark condition. 48 hr post transfections, cells were observed under Leica DM6B microscope. Cells were uniformly distributed under coverslip. Under microscope, we randomly choose a field of view at lower magnification. Samples sizes were not statistically predetermined. Cells numbers with and without photobodies in this field of view were calculated. Cell numbers (n>=80 per mutant) were chosen to allow for more than 20 samples were analyzed, which is comparable with previous studies (e.g Hahm et al. 2020, Nat Commun.;).
Data exclusions	No exclusion of the data was performed in this study.
Replication	All experimental findings were repeated at least 3 times with similar results.
Randomization	In the experiments of Extended Data Fig.7a, Expi293F™ Cells transfected with corresponding proteins were incubated in dark condition. 48 hr post transfections, cells were observed under Leica DM6B microscope. Under microscope, we randomly choose a field of view at lower magnification. Pictures of all cells in this field were obtained at 100* oil-immersion lens under blue light. Then the percent of cells with photobodies were caculated.
Blinding	There is no allocation of samples into groups.

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	StrepII tag antibody: Abbkine, ABB-A02230-50ul; Myc tag antibody mouse mono: Proteintech, 60003-2-Ig.
Validation	StrepII tag and Myc tag antibodies were purchased from Abbkine and Proteintech. StrepII tag antibody was previously used (Ma et

Validation	al. 2020, Nature Structural & Molecular Biology). These two antibodies was validated by manufacturer using western blot analysis of StrepII-tagged and Myc-tagged fusion proteins (see http://www.amyjet.com/featured/strep-tag-ii-antibody.shtml; https://www.ptgcn.com/Products/MYC-Antibody-60003-2-Ig.htm)

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	sf9, purchased from ThermoFisher (12659017); Expi293F™ Cells, purchased from ThermoFisher (A14527).
Authentication	The cell lines were not authenticated.
Mycoplasma contamination	We did not perform further Mycoplasma contamination test for this commercial cell line.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used.