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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 Authors & Referees and the Editorial Policy Checklist.

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
☐	☒	An indication of 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 statistics 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
☐	☒	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	For cryo-EM collection: SerialEM; for electrophysiology data: Clampex 10.6
Data analysis	Relion-2.0, Frealign, EMAN2, PyMOL, Chimera, ConSurf, GraphPad Prism, Coot, MotionCor2, CTFFIND, Gautomatch, AFFINImeter, PHENIX, HOLE, MAFFT

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/reviewers upon request. 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 3D cryo-EM density map of the Orco-Fab complex has been deposited in the Electron Microscopy Data Bank under accession number EMD-7352. The

coordinates of the atomic model of Orco have been deposited in the Protein Data Bank under accession number 6C70. Supplementary Data 1 contain the raw protein gel images used in Extended Data Fig. 3. Supplementary Data 2 and 3 contain the sequence alignments of Orco and OR proteins, respectively, used in Fig. 5 and Extended Data Fig. 11.

Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf

Life sciences study design

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

Sample size	No calculations were performed to determine sample sizes; however, the addition of more data did not alter conclusions from this study.
Data exclusions	No functional data were excluded. Some cryo-EM particles images were excluded from the final data set following established protocols, as described in the methods.
Replication	Functional experiments were repeated on different days, using independently transfected cells and independently prepared odorant solutions. Structure determination was carried out using a single data set. Cryo-EM data was split into two subsets and independently used to refine and validate the final model. Smaller Cryo-EM data sets were independently collected and lower resolution structures were determined that matched the structural features of the final Orco model.
Randomization	This study did not allocate experimental groups thus no randomization was necessary.
Blinding	No blinding was used: all functional data were analyzed using the same methods and all data were included in the results

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☐	☒ Unique biological materials
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☒	☐ Human research participants

Methods

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

Unique biological materials

Policy information about availability of materials

Obtaining unique materials	All unique materials used in the study are available from the authors upon request.

Antibodies

Antibodies used	Mouse monoclonal hybridoma antibody lines 20F7 and 9G11 against A. bakeri Orco were created in this study. Anti-GFP was from Invitrogen (cat# A11122). HRP-conjugated anti-mouse IgG and anti-rabbit IgG secondary antibodies were from Jackson Immuno Research Laboratories, Inc. (cat# 115-035-068) and Invitrogen (cat# 656120), respectively.
Validation	Monoclonal antibody lines 20F7 and 9G11 were validated against A. bakeri Orco using western blots, ELISA, and Cryo-EM data. Anti-GFP was validated against GFP-tagged Orco using western blots and ELISA data. HRP-conjugated secondary antibodies were validated by the manufacturer.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	Sf9 (ATCC CRL-1711). HEK293S GnTi– (ATCC CRL-3022)
Authentication	none were authenticated
Mycoplasma contamination	cells were not tested for mycoplasma contamination
Commonly misidentified lines (See ICLAC register)	n/a