

## Life Sciences Reporting Summary

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### ► Experimental design

#### 1. Sample size

Describe how sample size was determined.

In total, 267,726 particles of the RCLH1 complex were picked manually from cryoEM images. Such a number is essential to reach a good level of structural resolution, for example sub 3.0 Angstrom, where protein-protein and protein-pigment interactions can be identified.

#### 2. Data exclusions

Describe any data exclusions.

Those particles that categorized into poorly defined classes were rejected. This cleaning procedure by the use of 2D classification was repeated three times, resulting in rejection of 9.45 % of total particles. The resulting 2D classes were subjected to an initial 3D model calculation using EMAN2 for maximum-likelihood-based 3D classification. One out of four stable 3D classes, accounting for 62.3% total particles, was selected for high resolution refinement and 3D reconstruction. The resolution of each of the 3D maps from the four stable 3D classes was used as a criterion for exclusion.

#### 3. Replication

Describe whether the experimental findings were reliably reproduced.

During data processing, datasets of ~100,000 and ~167,000 particles were used independently for 3D reconstruction. They generated very similar 3D maps for the RC-LH1 complex, so they were then combined. Effectively, the final experimental result used 267,726 replicates.

#### 4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

All particles were picked as long as they were well separated in the EM images; different orientations of the complex emerge only after processing by RELION, which creates a series of 2D projections.

#### 5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

An automatic mode was used for data acquisition by the the EM. Empty and drifting images were discarded during data processing.

Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.

## 6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

n/a Confirmed

- ☐ ☒ The exact sample size ( $n$ ) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
- ☐ ☒ A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- ☒ ☐ A statement indicating how many times each experiment was replicated
- ☒ ☐ The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)
- ☒ ☐ A description of any assumptions or corrections, such as an adjustment for multiple comparisons
- ☒ ☐ The test results (e.g.  $P$  values) given as exact values whenever possible and with confidence intervals noted
- ☒ ☐ A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
- ☒ ☐ Clearly defined error bars

See the web collection on [statistics for biologists](#) for further resources and guidance.

## ► Software

Policy information about [availability of computer code](#)

## 7. Software

Describe the software used to analyze the data in this study.

MotionCorr2, RELION 2.0, ENAM2, COOT, REFMAC5

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). [Nature Methods guidance for providing algorithms and software for publication](#) provides further information on this topic.

## ► Materials and reagents

Policy information about [availability of materials](#)

## 8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.

No restrictions

## 9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

No antibodies were used in this study

## 10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.

No eukaryotic cell lines were used in this study

b. Describe the method of cell line authentication used.

No eukaryotic cell lines were used in this study

c. Report whether the cell lines were tested for mycoplasma contamination.

No eukaryotic cell lines were used in this study

d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by [ICLAC](#), provide a scientific rationale for their use.

No eukaryotic cell lines were used in this study

## ► Animals and human research participants

Policy information about [studies involving animals](#); when reporting animal research, follow the [ARRIVE guidelines](#)

## 11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.

No animals were used in this study

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.

This study did not involve human research participants.