# Materials Design Analysis Reporting (MDAR)

## Checklist for Authors

The [MDAR framework](#) establishes a minimum set of requirements in transparent reporting mainly applicable to studies in the life sciences.

*eLife* asks authors to **provide detailed information within their article** to facilitate the interpretation and replication of their work. Authors can also upload supporting materials to comply with relevant reporting guidelines for health-related research (see [EQUATOR Network](#)), life science research (see the [BioSharing Information Resource](#)), or animal research (see the [ARRIVE Guidelines](#) and the [STRANG Framework](#); for details, see *eLife*’s [Journal Policies](#)). Where applicable, authors should refer to any relevant reporting standards materials in this form.

For all that apply, please note **where in the article** the information is provided. Please note that we also collect information about data availability and ethics in the submission form.

### Materials:

| Newly created materials | Indicate where provided: section/figure legend | N/A |
|--------------------------|-----------------------------------------------|-----|
| The manuscript includes a dedicated "materials availability statement" providing transparent disclosure about availability of newly created materials including details on how materials can be accessed and describing any restrictions on access. | Data availability. The xye-GFP maps and coordinate models have been deposited in the Electron Microscopy Data Bank with the deposit codes EMD-55083 (EMD-55083). DNA libraries with the accession code EMBL-EMBL-965686. | N/A |

| Antibodies | Indicate where provided: section/figure legend | N/A |
|-----------|-----------------------------------------------|-----|
| For commercial reagents, provide supplier name, catalogue number and RRID, if available. | None used. | N/A |

| DNA and RNA sequences | Indicate where provided: section/figure legend | N/A |
|-----------------------|-----------------------------------------------|-----|
| Short novel DNA or RNA including primers, probes: Sequences should be included or deposited in a public repository. | None used. | N/A |

| Cell materials | Indicate where provided: section/figure legend | N/A |
|----------------|-----------------------------------------------|-----|
| Cell lines: Provide species information, strain. Provide accession number in repository OR supplier name, catalog number, clone number, OR RRID. | Methods. NuR and SAGA were purified from Saccharomyces cerevisiae using a modified TAP purification as described. A strain modified with a TAP tag on the C terminus of EM4 or SPT7 (G4 Ormazabal) was grown at 30°C in YPD. | N/A |
| Primary cultures: Provide species, strain, sex of origin, genetic modification status. | None used. | N/A |
| **Experimental animals** | Indicate where provided: section/figure legend | N/A |
|--------------------------|-----------------------------------------------|-----|
| Laboratory animals or Model organisms: Provide species, strain, sex, age, genetic modification status. Provide accession number in repository OR supplier name, catalog number, clone number, OR RRID. | | None used. |
| Animal observed in or captured from the field: Provide species, sex, and age where possible. | | None used. |

| **Plants and microbes** | Indicate where provided: section/figure legend | N/A |
|-------------------------|-----------------------------------------------|-----|
| Plants: provide species and strain, ecotype and cultivar where relevant, unique accession number if available, and source (including location for collected wild specimens). | | None used. |
| Microbes: provide species and strain, unique accession number if available, and source. | | None used. |

| **Human research participants** | Indicate where provided: section/figure legend or state if these demographics were not collected | N/A |
|------------------------------|-----------------------------------------------|-----|
| If collected and within the bounds of privacy constraints report on age, sex, gender and ethnicity for all study participants. | | None used. |

**Design:**

| **Study protocol** | Indicate where provided: section/figure legend | N/A |
|--------------------|-----------------------------------------------|-----|
| If the study protocol has been pre-registered, provide DOI. For clinical trials, provide the trial registration number OR cite DOI. | | None used. |

| **Laboratory protocol** | Indicate where provided: section/figure legend | N/A |
|------------------------|-----------------------------------------------|-----|
| Provide DOI OR other citation details if detailed step-by-step protocols are available. | | None used. |
## Experimental study design (statistics details) *

| For in vivo studies: State whether and how the following have been done | Indicate where provided: section/figure legend. If it could have been done, but was not, write “not done” | N/A |
|---|---|---|
| Sample size determination | None used. | |
| Randomisation | None used. | |
| Blinding | None used. | |
| Inclusion/exclusion criteria | None used. | |

## Sample definition and in-laboratory replication

| State number of times the experiment was replicated in the laboratory. | Methods dCypher binding assays All binding interactions were performed in duplicate. | N/A |
|---|---|---|
| Define whether data describe technical or biological replicates. | Technical | |

## Ethics

| Studies involving human participants: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval. | None used. | |
|---|---|---|
| Studies involving experimental animals: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval. | None used. | |
| Studies involving specimen and field samples: State if relevant permits obtained, provide details of authority approving study; if none were required, explain why. | None used. | |

## Dual Use Research of Concern (DURC)

| If study is subject to dual use research of concern regulations, state the authority granting approval and reference number for the regulatory approval. | None used. | |

*Experimental study design (statistics details) is a crucial aspect of scientific research that ensures the reliability and validity of the results. It involves the careful planning and execution of experiments to ensure that the data collected are meaningful and can be used to draw valid conclusions. This includes considerations such as sample size determination, randomisation, blinding, inclusion/exclusion criteria, and replication. The ethics section is equally important as it addresses the ethical considerations of involving human participants, experimental animals, and the use of specimen and field samples. Dual Use Research of Concern (DURC) is a contentious issue that requires adherence to strict regulations to prevent misuse of research results.*
## Analysis:

| Attrition | Indicate where provided: section/figure legend | N/A |
|-----------|-----------------------------------------------|-----|
| Describe whether exclusion criteria were pre-established. Report if sample or data points were omitted from analysis. If yes, report if this was due to attrition or intentional exclusion and provide justification. | Methods: Cryo-EM data processing. Erectile was extracted from the tracheae, which were cut into segments. Segments were then processed using standard cryo-EM protocols. The cryo-EM data was collected at 300 kV on a FEI Tecnai G2 F20 (FEI/ThermoFisher), and the raw data was processed using Gatan Digital Micrograph and RELION software. | |

| Statistics | Indicate where provided: section/figure legend | N/A |
|------------|-----------------------------------------------|-----|
| Describe statistical tests used and justify choice of tests. | None used. | |

| Data availability | Indicate where provided: section/submission form | N/A |
|-------------------|-----------------------------------------------|-----|
| For newly created and reused datasets, the manuscript includes a data availability statement that provides details for access (or notes restrictions on access). | Data availability: The cryo-EM maps and coordinate files have been deposited in the Electron Microscopy Data Bank with the accession codes EMD-33464 (Th1 HAT), EMD-33462 (Th1 HAT), EMD-33466 (Th1 HAT), and EMD-33465 (Th1 HAT). The protein data files with the accession files 1TPY (HATN) and 3TPY (HAT) represent the nucleated states of the Th1 HAT complexes. The N-terminal domain of the Th1 HAT complexes is represented by the PDB-1TPY (HATN) and the PDB-3TPY (HAT). Proteins for HAT and TMTIN expression have been made available through Addgene (Catalog #10000000 and #10000000). | |

| Code availability | Indicate where provided: section/figure legend | N/A |
|-------------------|-----------------------------------------------|-----|
| For any computer code/software/mathematical algorithms essential for replicating the main findings of the study, whether newly generated or re-used, the manuscript includes a data availability statement that provides details for access or notes restrictions. | Each chain segment was then inspected for stretches of high-quality density that could allow for the identification of potential side chain patterns that were then searched for within the sequences of known proteins within the complex (https://github.com/Stefan-Zukin/blobMapper). | |

| Data availability | Indicate where provided: section/submission form | N/A |
|-------------------|-----------------------------------------------|-----|
| When newly created datasets are publicly available, provide accession number in repository OR DOI and licensing details where available. | Data availability: The cryo-EM maps and coordinate files have been deposited in the Electron Microscopy Data Bank with the accession codes EMD-33464 (Th1 HAT), EMD-33462 (Th1 HAT), EMD-33466 (Th1 HAT), and EMD-33465 (Th1 HAT). The protein data files with the accession files 1TPY (HATN) and 3TPY (HAT) represent the nucleated states of the Th1 HAT complexes. The N-terminal domain of the Th1 HAT complexes is represented by the PDB-1TPY (HATN) and the PDB-3TPY (HAT). Proteins for HAT and TMTIN expression have been made available through Addgene (Catalog #10000000 and #10000000). | |

| Code availability | Indicate where provided: section/figure legend | N/A |
|-------------------|-----------------------------------------------|-----|
| Where newly generated code is publicly available, provide accession number in repository, OR DOI OR URL and licensing details where available. State any restrictions on code availability or accessibility. | None used. | |

| Code availability | Indicate where provided: section/figure legend | N/A |
|-------------------|-----------------------------------------------|-----|
| If reused code is publicly available provide accession number in repository OR DOI OR URL, OR citation. | https://github.com/Stefan-Zukin/blobMapper | MIT License |
Reporting:
The MDAR framework recommends adoption of discipline-specific guidelines, established and endorsed through community initiatives.

| Adherence to community standards | Indicate where provided: section/figure legend | N/A |
|---------------------------------|-----------------------------------------------|-----|
| State if relevant guidelines (e.g., ICMJE, MIBBI, ARRIVE, STRANGE) have been followed, and whether a checklist (e.g., CONSORT, PRISMA, ARRIVE) is provided with the manuscript. | None used. |

* We provide the following guidance regarding transparent reporting and statistics; we also refer authors to [Ten common statistical mistakes to watch out for when writing or reviewing a manuscript](#).

Sample-size estimation
- You should state whether an appropriate sample size was computed when the study was being designed
- You should state the statistical method of sample size computation and any required assumptions
- If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

Replicates
- You should report how often each experiment was performed
- You should include a definition of biological versus technical replication
- The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
- If you encountered any outliers, you should describe how these were handled
- Criteria for exclusion/inclusion of data should be clearly stated
- High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

Statistical reporting
- Statistical analysis methods should be described and justified
- Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
- For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson’s r, Cohen’s d))
- Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

Group allocation
- Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
- Indicate if masking was used during group allocation, data collection and/or data analysis