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 STRANGE 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' section.	

Antibodies	**Indicate where provided: section/figure legend**	**N/A**
For commercial reagents, provide supplier name, catalogue number and RRID, if available.	'SDS-PAGE, protein transfer, and western blotting' section in 'Materials & Methods'.	

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.	All DNA sequences are provided in 'Supplementary File 2'.	

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.		X
Primary cultures: Provide species, strain, sex of origin, genetic modification status.		X

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.	Information about species, sex, and age is provided in the '*C. elegans* strain maintenance' section in 'Materials & Methods' on p44. 'Supplementary file 1A' provides strain and genetic modification status information.	
Animal observed in or captured from the field: Provide species, sex, and age where possible.		X

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).		X
Microbes: provide species and strain, unique accession number if available, and source.	Microbe information is provided in the '*C. elegans* strain maintenance' and 'Biotin treatment' sections in 'Materials & Methods'.	

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.		X

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.		X

Laboratory protocol	Indicate where provided: section/figure legend	N/A

Provide DOI OR other citation details if detailed step-by-step protocols are available.	***C. elegans* strain maintenance:** in 'Materials & Methods'. **Proteomics:** Step-by-step details for all TurboID experiments are provided in 'Materials & Methods'. This includes biotin treatment, protein extraction and quantification, SDS-PAGE, protein transfer, and western blotting, and mass spectrometry (including sample preparation and data analysis). **Behavioural tests:** All protocols are outlined in 'Materials & Methods'. A step-by-step protocol for salt aversive learning is also provided in reference RAHMANI, A., MCMILLEN, A., ALLEN, E., MINERVINI, C. & CHEW, Y. L. 2024. Behavioral Tests for Associative Learning in Caenorhabditis elegans. In: DWORKIN, S. (ed.) Neurobiology: Methods and Protocols. New York, NY: Springer US.	

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	**Mass spectrometry experiments:** We state in-text: "We performed five biological replicates, in line with other *C. elegans* studies (Artan et al., 2022, Holzer et al., 2021)." **Behavioural experiments:** We state in-text: "For behavioural experiments, we performed 3–5 biological replicates for most genotypes, consistent with similar high-quality studies (Kitazono et al., 2017, Lim et al., 2018, Sakai et al., 2017, Stein and Murphy, 2014)."	
Randomisation	**Behavioural experiments:** We state in-text: "Randomisation was not applied because experimental groups were defined by genotype or condition."	

Blinding	**Behavioural experiments:** We state in-text: “Quantification of chemotaxis assays was conducted without blinding to genotype or condition.”	
Inclusion/exclusion criteria	**Behavioural experiments:** We state in-text: “Exclusion criteria were pre-determined: Groups were excluded only if bacterial contamination was evident or if fewer than 20 individual animals were present in a technical replicate.”	

Sample definition and in-laboratory replication	**Indicate where provided: section/figure legend**	**N/A**
State number of times the experiment was replicated in the laboratory.	**Mass spectrometry experiments:** We state in-text: “We performed five biological replicates, in line with other *C. elegans* studies (Artan et al., 2022, Holzer et al., 2021).” **Behavioural experiments:** Replication number is provided for every figure generated from behavioural experiments in their respective figure legend. A summary of this data is also provided in the ‘Statistical analysis’ section.	
Define whether data describe technical or biological replicates.	**Mass spectrometry experiments:** We state in-text: “We performed five biological replicates, in line with other *C. elegans* studies (Artan et al., 2022, Holzer et al., 2021).”. **Behavioural experiments:** All graphs for behavioural experiments plot biological replicate data. All figure legends define the number of biological replicates, number of technical replicates, and number of animals per technical replicate. We also provide a summary for this information in-text in the ‘Statistical analysis’ section.	

Ethics	**Indicate where provided: section/submission form**	**N/A**

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

Dual Use Research of Concern (DURC)	**Indicate where provided: section/submission form**	**N/A**
If study is subject to dual use research of concern regulations, state the authority granting approval and reference number for the regulatory approval.		X

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.	**Behavioural experiments:** We state in-text: “Exclusion criteria were pre-determined: Groups were excluded only if bacterial contamination was evident or if fewer than 20 individual animals were present in a technical replicate.”	

Statistics	**Indicate where provided: section/figure legend**	**N/A**
Describe statistical tests used and justify choice of tests.	**Behavioural experiments:** We state in-text: “This statistical analysis was chosen given that it aligns with recent publications that employ similar experimental designs and data structures (Beets et al., 2020, Jang et al., 2019, Kitazono et al., 2017, Lim et al., 2018, Lin et al., 2010).” Supplementary File 1I reports results from all statistical tests done in this work.	

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' section.	
When newly created datasets are publicly available, provide accession number in repository OR DOI and licensing details where available.	'Data availability' section.	
If reused data is publicly available provide accession number in repository OR DOI, OR URL, OR citation.	This study reuses existing transcriptome data from several studies (including St. Ange et al., 2024, Ghaddar et al., 2023, Kaletsky et al. 2016, Princeton University, 2025, & Taylor et al., 2021), all cited in-text.	

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.	'Data availability' section.	
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.	'Data availability' section.	
If reused code is publicly available provide accession number in repository OR DOI OR URL, OR citation.	We state in-text: "The source data from this publication, including mass spectrometry data (files from MASCOT search) and raw data from learning assays have been uploaded to Dryad at https://doi.org/10.5061/dryad.1c59zw43k. Custom Python code is available through GitHub (https://github.com/ChewWormLab/Chew-Worm-Lab-Post-Mass-Spectrometry-Peptide-processing). *C. elegans* strains used in this study are available upon request." on p56. We also cite existing code Anaconda, BioPython 1.78, and pandas software used in our custom python code.	

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.		X

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* 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