

Materials Design Analysis Reporting (MDAR) **Checklist for Authors**

The MDAR framework establishes a minimum set of requirements in transparent reporting applicable to studies in the life sciences (see Statement of Task: [doi:10.31222/osf.io/9sm4x](https://doi.org/10.31222/osf.io/9sm4x)). The MDAR checklist is a tool for authors, editors, and others seeking to adopt the MDAR framework for transparent reporting in manuscripts and other outputs. Please refer to the MDAR Elaboration Document for additional context for the MDAR framework.

For all that apply, please note where in the manuscript the required information is provided.

Materials:

Newly created materials	indicate where provided: page no/section/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 and materials availability statement included: "All data are available in the manuscript or the supplementary material. All reagents used in this study will be shared with other researchers in academia upon receipt of a request to the corresponding author."	
Antibodies	indicate where provided: page no/section/legend)	n/a
For commercial reagents, provide supplier name, catalogue number and RRID , if available.	Materials and methods section in supplementary file: Section: Bacterial strains and growth conditions: Bacteria Type strain and antibiotics; Assessment of de novo protein synthesis: Anti-puromycin antibody; RNA isolation, library preparation and RNA seq: RNA isolation and sequence library kits; RNA isolation and quantitative RT-PCR: RNA isolation and reverse transcription kits; Northern blots: Northern blot reagents; 3' RACE: RACE reagents	
DNA and RNA sequences	indicate where provided: page no/section/legend)	n/a
Short novel DNA or RNA including primers, probes: Sequences should be included or deposited in a public repository.	All primer sequences are listed in table S6 in the supplementary file. RNA fragment sequences from RACE reactions are provided in Fig S3E and S7J.	
Cell materials	indicate where provided: page no/section/legend)	n/a
Cell lines: Provide species information, strain. Provide accession number in repository OR supplier name, catalog number, clone number, OR RRID.	-	
Primary cultures: Provide species, strain, sex of origin, genetic modification status.	Materials and methods section in supplementary file: Section: Intracellular survival	
Experimental animals	indicate where provided: page no/section/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.	Materials and methods section in supplementary file: Section: Animals and animal experiments	
Animal observed in or captured from the field: Provide species, sex, and age where possible.		n/a
Plants and microbes	indicate where provided: page no/section/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).		n/a
Microbes: provide species and strain, unique accession number if available, and source.	Materials and methods section in supplementary file: Table S5	n/a
Human research participants	indicate where provided: page no/section/legend) or state if these demographics were not collected	n/a

Design:

Study protocol	indicate where provided: page no/section/legend)	n/a
If study protocol has been pre-registered, provide DOI. For clinical trials, provide the trial registration number OR cite DOI.		n/a

Laboratory protocol	indicate where provided: page no/section/legend)	n/a
Provide DOI OR other citation details if detailed step-by-step protocols are available.		n/a

Experimental study design (statistics details)		
For in vivo studies: State whether and how the following have been done	indicate where provided: page no/section/legend. If it could have been done, but was not, write not done	n/a
Sample size determination	Details of sample sizes are listed in figure legends.	
Randomisation	All mice were randomized before treatments.	
Blinding	Investigators were NOT blinded to group allocation during data collection and analysis. Samples were blinded during histopathological analysis	
Inclusion/exclusion criteria	No data were excluded from analysis.	

Sample definition and in-laboratory replication	indicate where provided: page no/section/legend	n/a
State number of times the experiment was replicated in laboratory.	Provided in figure legends.	
Define whether data describe technical or biological replicates.	Provided in figure legends.	

Ethics	indicate where provided: page no/section/legend	n/a
Studies involving human participants: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.		n/a
Studies involving experimental animals: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.	Materials and methods section in supplementary file: Section: Animals and animal experiments	
Studies involving specimen and field samples: State if relevant permits obtained, provide details of authority approving study; if none were required, explain why.		n/a

Dual Use Research of Concern (DURC)	indicate where provided: page no/section/legend	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.		n/a

Analysis:

Attrition	indicate where provided: page no/section/legend	n/a
Describe whether exclusion criteria were preestablished. 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.	No data points were omitted from analysis.	

Statistics	indicate where provided: page no/section/legend	n/a
Describe statistical tests used and justify choice of tests.	Provided in supplemental materials and methods and in figure legends	

Data availability	indicate where provided: page no/section/legend	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.	Acknowledgements section	
If newly created datasets are publicly available, provide accession number in repository OR DOI OR URL and licensing details where available.		
If reused data is publicly available provide accession number in repository OR DOI OR URL, OR citation.	RNA seq analysis was performed on dataset from GEO database, Accession #GSE203342	n/a

Code availability	indicate where provided: page no/section/legend	n/a
For all newly generated custom computer code/software/mathematical algorithm or re-used code essential for replicating the main findings of the study, the manuscript includes a data availability statement that provides details for access or notes restrictions.		n/a
If 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.		n/a
If reused code is publicly available provide accession number in repository OR DOI OR URL, OR citation.		n/a

Reporting

MDAR framework recommends adoption of discipline-specific guidelines, established and endorsed through community initiatives. Journals have their own policy about requiring specific guidelines and recommendations to complement MDAR.

Adherence to community standards	indicate where provided: page no/section/legend	n/a
State if relevant guidelines (e.g., ICMJE, MIBBI, ARRIVE) have been followed, and whether a checklist (e.g., CONSORT, PRISMA, ARRIVE) is provided with the manuscript.		n/ a