OPEN BIOLOGY

**Completed by:**

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# *Open Biology* reproducibility reporting form

Authors are expected to complete this form to ensure good reporting standards and reproducibility in your paper. The form is intended for publication alongside accepted manuscripts. The table will serve as an overview of the key reagents, cell lines, source data and software used in the study should provide all the experimental and statistical details to allow others to replicate their study. The form is based on the NIH Principles and Guidelines for Reporting Preclinical Research and is intended to help ensure high standards for reporting and to aid reproducibility. Items in the table must also be reported in the 'methods' section of the manuscript within the context of their use. Any references cited in the reporting form must be included in the References list of the manuscript.

If you have any questions, please consult our author information or publishing polices page - or contact us: openbiology@royalsociety.org.

Definitions:

| | | |
|---|---|---|
| **Resource or reagent type -** Provide full descriptive names of items so can be identified (include version number for software, host source for antibody, strain name etc) | **Source** – *report the stockist, manufacturer, company, lab (name of principle investigator)* | **Identifier** - *include the catalogue number, accession or database number* |

*Open Biology recommends RRIDs as the identifier (in particular for antibodies and organisms, but also for software tools and databases). For more details on how to obtain or generate an RRID for existing or newly generated resources, please search for RRIDs.*

## Please indicate if the following were used in the study:

**Cell lines**

- [●] Yes (please provide further details in table below)
- [ ] Not applicable

| Resource or reagent type | Source | Identifier |
|---|---|---|
| Trypanosoma brucei brucei, procyclic form | Keith Gull lab | SmOxP9 |

**Antibodies**

*For antibodies, provide a citation, catalogue number and/or clone number and batch number. We recommend using RRIDs as the identifier; more details on how to obtain or generate an RRID for existing or newly generated resources, please search for RRIDs.*

- [✔] Yes (please provide further details in table below)
- [ ] Not applicable

| Resource or reagent type | Source | Identifier |
|---|---|---|
| monoclonal anti-GFP antibodies | Roche | 11814460001 |

**Plasmids**

☑ Yes (please provide further details in table below)

☐ Not applicable

| Resource or reagent type | Source | Identifier |
|---|---|---|
| All details are listed in Table S3 | | |

**Bacterial or viral strains**

☐ Yes (please provide further details in table below)

☑ Not applicable

| Resource or reagent type | Source | Identifier |
|---|---|---|
| | | |

**Recombinant proteins**

☐ Yes (please provide further details in table below)

☑ Not applicable

| Resource or reagent type | Source | Identifier |
|---|---|---|
| | | |

**Primers**

☑ Yes (please provide further details in table below)

☐ Not applicable

| Resource or reagent type | Source | Identifier |
|---|---|---|
| All details are listed in Table S4 | | |

**Recombinant DNA**

☐ Yes (please provide further details in table below)

☑ Not applicable

| Resource or reagent type | Source | Identifier |
|---|---|---|
| | | |

**Commercial assays**

☐ Yes (please provide further details in table below)

☑ Not applicable

| Resource or reagent type | Source | Identifier |
|---|---|---|
| | | |

**Biological samples**

☐ Yes (please provide further details in table below)

☑ Not applicable

| Resource or reagent type | Source | Identifier |
|---|---|---|
| | | |

## Animal participants

*Please report species, strain, age and sex for laboratory animals (or age, sex and species for field animals). See our guidelines on research ethics - follow ARRIVE guidelines*

☑ Not applicable

## Human participants

*Please provide relevant data on human research participants including age, gender, genotypic information. See our guidelines on research ethics - follow ARRIVE guidelines*

☑ Not applicable

## Software

Describe the software used to analyse the data in this study. For manuscripts using custom algorithms or software not yet described in the published literature, software must be made available to editorial office and reviewers upon request.

☑ Not applicable

## Availability of Materials

*Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a third party.*

☑ No restrictions

☐ Restrictions apply (please provide further details below):

## Sample size

*Describe the statistical methods that were used to predetermine sample size or how sample sizes were chosen*

### Statistical analyses and parameters

*All figures and tables that use statistical methods, please confirm that the following items are present in relevant figure legends:*

- exact sample size (n) for each experimental group or condition, given as a number, not a range.
- A description of the sample collection that allows the reader to understand whether the samples represent technical or biological replicates (including how many animals, cultures, etc.).
- A statement of how many times the experiment shown was replicated in the laboratory.
- A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range) -

Statistical test results, e.g. P values.

- Details of statistical method.

☐ I/we confirm

☑ Not applicable

Additional relevant information not included in the above: