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1. Schott, D. H., Collins, R. N. & Bretscher, A. Secretory vesicle transport velocity in living cells depends on the myosin V lever arm length. *J. Cell Biol.* **156**, 35‐39 (2002).
2. Hogan, B. *Manipulating The Mouse Embryo: A Laboratory Manual* 2nd edn (Cold Spring Harbor Laboratory Press, 1994)
3. Haines, N. & Cotter, R. in *Studies in Manic Depression* Vol. 1 (ed. Boase, N.) Ch. 2 (Oxford Univ. Press, 1982).
4. Babichev, S. A., Ries, J. & Lvovsky, A. I. Quantum scissors: teleportation of single-mode optical states by means of nonlocal single photon. Preprint at <https://arxiv.org/abs/quant-ph/0208066> (2002).
5. Gallotti, R. & Barthélemy, M. Source code for: The multilayer temporal network of public transport in Great Britain. *Figshare*<https://doi.org/10.6084/m9.figshare.1249862.v1> (2014).
6. Manaster, J. Sloth squeak. *Scientific American Blog Network*<http://blogs.scientificamerican.com/psi-vid/2014/04/09/sloth-squeak> (2014).
7. Akutsu, T. *Total Heart Replacement Device*. Report No. NIH-NHLI-69 2185-4 (National Institutes of Health, 1974).

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* [Link to biological and medical metadata template](https://figshare.com/s/9b3a9dea7eda5348eed2)
* [Link to geological sciences metadata template](https://figshare.com/s/4af59084ac4e23667cb8)
* [Link to multiple sources metadata template](https://figshare.com/s/7934068b448f33baeb42) (for datasets which are based on an aggregation or integration of multiple data sources).

We have developed the following templates for specific experimental data. If none of these are suitable, please use one of the generic templates above.

* [Link to MRI imaging metadata template](https://figshare.com/s/d8b32838204c6c56f8ea)
* [Link to flow cytometry or fluorescence-activated cell sorting (FACS) metadata template](https://figshare.com/s/22894be522b30d6ed708)
* [Link to X-ray imaging metadata template](https://figshare.com/s/5bff22afa0ac33a6491b)

Authors who are familiar with the ISA-tab format, may also choose to submit ISA-Tab metadata files instead of using the templates above. Applications for drafting ISA-Tab files are available from [ISA tools](http://isa-tools.org/). Please also refer to our detailed [ISA-tab metadata specification](https://www.nature.com/documents/scidata-isatab-specification.pdf).

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5. When supplying multiple supplementary figures, they should be merged into a single PDF file, with figure legends immediately below each figure. A table of contents should be included on the first page, listing the page number of each supplementary figure.

Statistical guidelines

Every submission that contains statistical analyses or data-processing steps must explain the statistical methods in detail either in the Methods or the relevant figure legend. Any special statistical code or software needed for scientists to reuse or reanalyse datasets should be discussed in the Usage Notes section of Data Descriptors. We encourage authors to make openly available any code or scripts that would help readers reproduce any data-processing steps (see our [code availability policy](http://www.nature.com/sdata/policies/editorial-and-publishing-policies#code-avail)). In addition, **authors must ensure that the version of the data described and analysed in the Data Descriptor is permanently available** so that others can reproduce any statistical analyses.

Authors are encouraged to summarize their datasets with descriptive statistics in the Technical Validation section, which should include the *n* value for each dataset; a clearly labelled measure of centre (such as the mean or the median); and a clearly labelled measure of variability (such as standard deviation or range). Ranges are more appropriate than standard deviations or standard errors for small datasets. Graphs should include clearly labelled error bars. Authors must state whether a number that follows the ± sign is a standard error (s.e.m.) or a standard deviation (s.d.).

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Data Descriptors should not test new hypotheses or provide extensive interpretive analysis, and therefore should not usually contain statistical significance testing. When hypothesis-based tests must be employed, authors should state the name of the statistical test; the n value for each statistical analysis; the comparisons of interest; a justification for the use of that test (including, for example, a discussion of the normality of the data when the test is appropriate only for normal data); the alpha level for all tests, whether the tests were one-tailed or two-tailed; and the actual *p*-value for each test (not merely ‘significant’ or ‘*p* < 0.05’). It should be clear what statistical test was used to generate every *p*-value. Use of the word ‘significant’ should always be accompanied by a p-value; otherwise, use ‘substantial’, ‘considerable’, etc. Multiple test correction must be used when appropriate and described in detail in the manuscript.

Please also see our specific recommendations for [figure legends](https://www.nature.com/sdata/publish/submission-guidelines#figures).

Genetic & chemical nomenclature

Molecular structures are identified by bold Arabic numerals assigned in order of presentation in the text. Once identified in the main text or a figure, compounds may be referred to by their name, by a defined abbreviation or by the bold Arabic numeral (as long as the compound is referred to consistently as one of these three).

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Authors should use approved nomenclature for gene symbols, and use symbols rather than italicized full names (for example Ttn, not titin). Please consult the appropriate nomenclature databases for correct gene names and symbols. A useful resource is [NCBI Gene](http://www.ncbi.nlm.nih.gov/gene).

Approved human gene symbols are provided by HUGO Gene Nomenclature Committee (HGNC; e-mail: hgnc@genenames.org); see also [www.genenames.org](http://www.genenames.org/). Approved mouse symbols are provided by The Jackson Laboratory (e-mail: nomen@informatics.jax.org); see also [www.informatics.jax.org/mgihome/nomen](http://www.informatics.jax.org/mgihome/nomen).

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Avoid listing multiple names of genes (or proteins) separated by a slash, as in ‘Oct4/Pou5f1’, as this is ambiguous (it could mean a ratio, a complex, alternative names or different subunits). Use one name throughout and include the other at first mention: ‘Oct4 (also known as Pou5f1)’.

Instructions for LaTeX users

To assist with formatting, we encourage authors to use the [LaTeX Data Descriptor template provided by Overleaf](http://www.overleaf.com/latex/templates/template-for-data-descriptor-submissions-to-scientific-data/qrrnhwspvgbf). Authors submitting LaTeX files may use any of the standard class files such as article.cls, revtex.cls or amsart.cls. Non-standard fonts should be avoided; please use the default Computer Modern fonts. For the inclusion of graphics, we recommend graphicx.sty. Please use numerical references only for citations. There is no need to spend time visually formatting the manuscript: the *Scientific Data* style will be imposed when the paper is prepared for publication. References should be included within the manuscript file itself as our system cannot accept BibTeX bibliography files; authors who wish to use BibTeX to prepare their references should therefore copy the reference list from the .bbl file that BibTeX generates and paste it into the main manuscript .tex file (and delete the associated \bibliography and \bibliographystyle commands). As a final precaution, authors should ensure that the complete .tex file compiles successfully on their own system with no errors or warnings before submission.

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