

# The eLife research article

1 Department of Production, eLife, Cambridge , United Kingdom

2 Department of Technology, eLife, Cambridge , United Kingdom

† These authors contributed equally to this work

‡ These authors also contributed equally to this work

§ Department of Wellcome Trust, Sanger Institute, London, United Kingdom

# Deceased (not really!!)

¶ This footnote text must work in isolation as nothing is processed on the html view to make it "work"

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## Abstract

This is the abstract. This article will describe the eLife article and the process. An abstract can contain any formatting, such as *italics*, **bold**, <sup>superscript</sup>, <sub>subscript</sub> or small caps. MathML is also allowed:  $m p m = 0$ .

eLife does not structure abstracts into sub headings expect in a clinical trial article, but the abstract can have multiple paragarahs. The sub DOI is always .001 as it is the first asset in any article. I have added an unmatched > bracket as this has been an issue for PubMed deposits in the past.

If this was a clinical trial the clinical trial details would be listed at the end of the abstract:

Clinical trial Registration: EudraCT2004-000446-20.

## Abstract

### eLife digest

eLife digest are now optional and not every research article will contain one. These are layman abstracts, designed for non-specialists in this field to be able to understand this article, as well as the general public.

Here is paragraph 2 of the digest.

## Introduction (Level 1 heading)

This article is a guide to the tagging and display of eLife articles and will encompass all the elements that can possibly be contained in an eLife article. It will also include information from the author guide. For this reason, it is colloquially known as the eLife 'kitchen sink'.

### The eLife editorial process (level 2 heading)

eLife publishes the most highly influential research across the life sciences and biomedicine. Before you submit your work, please note that eLife is a very selective journal that aims to publish work of the highest scientific standards and importance. Leading academic researchers evaluate new submissions and approximately two-thirds are returned to the authors without further peer review. See [DeLano \(2002\)](#) and [Department of Education and Morgan \(2016\)](#). Approximately half of the articles that are selected for peer review go on to be published ([Brettar et al., 2004a](#)). If other researchers publish similar findings after submission, this will not be a reason for rejection. The eLife editorial process broadly occurs in three phases ([Turlings and Wäckers, 2004a](#); [Turlings and Wäckers, 2004b](#); [Wolski et al., 2008](#); [Walker, 1994](#); [Tanaka et al., 2016](#)). If you are interested in submitting your work to eLife, please review the guidelines relating to initial submissions. If you have received an encouraging response to your initial submission, please review the guidelines relating to full submissions. If your full submission has been peer reviewed and you have been asked to make revisions, please review our guidelines for revised submissions ([Brettar et al., 2004b](#)).

#### Initial submission (level 3 heading)

eLife publishes research of the very highest ([Bricogne et al., 2011](#)) standard and significance, so many manuscripts are returned to the authors without in-depth peer review. During the initial submission phase, members of eLife's senior editorial team rapidly assess new submissions, often in consultation with members of the Board of Reviewing Editors or with external guest editors where necessary, to identify the ones that are appropriate for in-depth peer review ([Cardé and Millar, 2004](#); [Cartwright, 2016](#); [Chmeil, 2008](#)). To simplify the submission process, authors should submit their full manuscript as a single PDF. Limited additional information is collected via the submission screen questions to complete the submission ([Brettar et al., 2004b](#)).

#### Full submission (level 3 heading)

For manuscripts that are invited for in-depth peer review, see [Coyne and Orr \(1989\)](#) and [Du et al. \(2014\)](#), we request detailed information about the work to support the peer review process, to ensure that the work meets appropriate standards for the reporting of new findings, and, if accepted, to assist in rapid publication and further dissemination of the work in relevant indexes and repositories. Authors are asked to agree to publish their work under the terms of the Creative Commons Attribution license (PDF of the agreement), or the Creative Commons CC0 public domain dedication (PDF of the agreement) if one or more authors are US-government employees ([Hubbard and Thornton, 1993](#); [GlaxoSmithKline UK, 2016](#); [Jain et al., 2010](#)).

#### Revised submission (level 3 heading)

We will require a response to the essential revision requirements outlined in the decision letter. A response to minor comments is optional. In the event of acceptance, the substantive revision requests and the authors' response will be published, under the terms of the Creative Commons Attribution license. In preparation for submission, authors should ensure they have all the materials and information necessary to expedite the submission and assessment of their work ([Eisen, 2016](#); [Ferry et al., 2014](#); [Gavrilov et al., 2014](#); [Goodstadt, 2010](#); [Hoang et al., 2015](#)).

### The eLife production process (level 2 heading)

#### Immediate publication (accepted manuscript) (level 3 heading)

On acceptance an eLife article can be published in accepted manuscript form immediately. The mean time from acceptance to publication at this stage is 1 day. Using SQL, basic metadata is exported from the submission system to an AWS bucket as CSV files. The author files are exported to another AWS bucket and an eLife process generates a package of this information and the author files to deliver to the online platform, Continuum.

#### Publication of the full version (version of record) (level 3 heading)

The production process includes an author proofing cycle, the output of which is the final full text version of the article online, as well as a typeset PDF.

#### Publication of versions (level 3 heading)

eLife allows the publication of updates to an article after the full version has been produced. These are treated as new versions of the article. All previous versions of the article will continue to exist online and will be accessible from the latest live version.

#### level 4 heading

eLife allows up to four levels of headings and no more. This is a demonstration of a level 4 heading.

## Results

This section will be used to demonstrate the majority of eLife XML tagging and editorial policies. However, the Introduction section was used to demonstrate heading levels. See [Appendix 1.1](#) and [2](#).

### eLife controlled lists

## Article types

This is an example of a list where the prefix character is a lowercase roman numeral. eLife Article Types are taken from a controlled list:

- i. Research article
- ii. Short Report
- iii. Tools and Resources
- iv. Research Advance
- v. Registered Report
- vi. Replication Study

## Article types (XML only, not display) (level 4 heading)

This is an example of a list where the prefix character is an uppercase roman numeral. This is a controlled list from the JATS DTD

- I. article-commentary (used for Insights)
- II. correction
- III. discussion (used for Feature 1 and Feature 2)
- IV. editorial
- V. research-article (all research content)

Nested lists are allowed and these are very common in Registered Reports. Below is an example of a nested list to 3 levels.

Genus: Plasmodium; following species are known to infect humans

- I.
  - i. *P. falciparum*
  - ii. *P. vivax*
  - iii. *P. ovale*
  - iv. *P. malariae*
  - v. *P. knowlesi*

Genus: Leishmania. There are 3 subgenus of Leishmania:

- II.
  - i. Leishmania
  - ii. Sauroleishmania
  - iii. Viannia
  - iv. Within Viannia subgenus, there are 11 species:
    - *L. braziliensis*
    - *L. colombiensis*
    - *L. equatorensis*
    - *L. guyanensis*
    - *L. lainsoni*
    - *L. naiffi*
    - *L. panamensis*
    - *L. peruviana*
    - *L. pifanoi*
    - *L. shawi*
    - *L. utingensis*

## Major Subject Areas

This is an example of a bulleted list. eLife Major subject areas are taken from a controlled list:

- Biochemistry
- Biophysics and Structural Biology
- Cell Biology
- Computational and Systems Biology
- Developmental Biology and Stem Cells
- Ecology
- Epidemiology and Global Health
- Genes and Chromosomes
- Genomics and Evolutionary Biology
- Human Biology and Medicine
- Immunology
- Microbiology and Infectious Disease
- Neuroscience
- Plant Biology

## Multi-lists

1. Here is an example of a list with multiple paragraphs and equations.

A discrete three-dimensional model space was generated (represented as a three-dimensional matrix; [Figure 2—figure supplement 1A](#), left), with dimensions corresponding to population  $\mu$ , population  $\sigma$ , and  $f$  value. Any given value in the matrix indicates  $P(f|\mu,\sigma)$ , that is, the probability of a given frequency given a particular  $\mu$  and  $\sigma$ . The columns (all  $f$  values for a given  $\mu$  and  $\sigma$  combination; [Figure 2—figure supplement 1](#), upper-right) thus constitute the forward model (by which stimuli are generated), and the planes (all combinations of  $\mu$  and  $\sigma$  for a given  $f$  value; [Figure 2—figure supplement 1](#), lower-middle) constitute the inverse model (by which hidden parameters can be estimated from observed  $f$  values).

2. 2) For each segment, the model was inverted for its particular  $f$  value, yielding a two-dimensional probability distribution for the hidden parameters ([Figure 2—figure supplement 1](#), lower-

3. These probability distributions, for each segment subsequent to the most recent estimated population change (as defined later), were multiplied together, and scaled to a sum of 1. The resulting probability distribution ([Figure 2—figure supplement 1](#), lower-right) thus reflects parameter probabilities taking into account all relevant f values
4. This combined parameter probability distribution was then scalar multiplied with the full model space, in order to weight each of the forward model columns (each corresponding to a particular parameter combination) by the probability of that parameter combination being in effect. The resulting weighted model space was then averaged across parameter dimensions, to yield a one-dimensional (forward) probability distribution, constituting an optimal prediction about the f value of the next stimulus segment, provided a population change did not occur before then. A probability distribution applicable if a population change were to occur was calculated the same way, but without weighting the forward model columns (so as to encompass every possible parameter combination).
5. It was assumed that a population change occurred immediately prior to the first stimulus segment. To infer subsequent population changes, for each segment the probability of observing the present f value was compared for the two probability distributions (the distribution assuming a population change, and the distribution assuming no change), that is,  $P(f|c)$  and  $P(f|\sim c)$ , respectively, with c denoting a population change. The probabilities were compared, in conjunction with the known prior probability of a population change (1/8), using Bayes' rule, as stated in Equation 2:  $P(c|f) = P(f|c)P(c)/P(f)$

6. For each segment, the above calculation of  $P(c|f)$  was made not only with respect to the immediately preceding segment, but also a number of segments preceding that, up to a maximum of 4. Therefore, for segment  $t$ , it was possible to conclude that a population change had occurred immediately prior to  $t$ ,  $t-1$ ,  $t-2$ ,  $t-3$ , or none of the above. A population change was judged to have occurred at the time point with the highest value of  $P(c|f)$ , provided this value was greater than 0.5. Using more than 4 lags did not appreciably alter the estimates obtained by model inversion. Importantly, any retrospective inference of population changes did not retrospectively alter any prior predictions generated by the model (e.g. at time  $t$ , if a population change were inferred to have occurred at time  $t-3$  then the priors for  $t-2$ ,  $t-1$  and  $t$  were not affected, but only the priors for  $t+1$  onwards).

## Research Organisms

1. *Arabidopsis*
2. *B. subtilis*
3. *C. elegans*
4. *C. intestinalis*
5. Chicken
6. *D. melanogaster*
7. *Dictyostelium*
8. *E. coli*
9. Frog
10. Human
11. *M. mulatta*
12. Maize
13. Mouse
14. *M. thermophila*
15. *M. crassa*
16. *Neurospora*
17. None
18. Other
19. *O. fasciatus*
20. *P. falciparum*
21. *P. dumerilii*
22. Rat
23. *S. cerevisiae*
24. *S. pombe*
25. *S. entericaserovar Typhi*
26. *S. pyogenes*
27. Virus
28. *Volvox*
29. *Xenopus*
30. *P. cynocephalus*
31. Zebrafish

## Tables

Genotype	GLVs (percent IS plant <sup>-1</sup> )				TPS10 products (percent IS plant <sup>-1</sup> )				Non-target volatiles (percent IS plant <sup>-1</sup> )							
	(Z)-Hexen-3-ol				TAB		TBF		α-Duprezianene		Germacrene A					
	Day	Night	Day	Night	Day	Night	Day	Night	Day	Night	Day	Night				
WT	8	8	0.99% ± 0.99%	7.96% ± 4.25%	a	0.37% ± 0.29%	a	—	a	—	a	—	2.13% ± 0.85%	0.96% ± 0.42%	1.68% ± 0.98%	—
TPS10	7	7	2.37% ± 1.55%	2.84% ± 0.63%	a	18.97% ± 6.03%	b	0.94% ± 0.53%	a	—	b	0.20% ± 0.20%	9.47% ± 5.26%	0.94% ± 0.26%	2.78% ± 1.52%	—
lox2/3	7	8	0.13% ± 0.13%	1.06% ± 0.64%	b	—	a	0.15% ± 0.15%	b	—	a	—	2.75% ± 1.12%	0.60% ± 0.19%	1.68% ± 1.49%	—
lox2/3xTPS10	7	7	0.07% ± 0.07%	1.24% ± 0.84%	b	7.39% ± 2.56%	b	2.08% ± 0.84%	TPS	4.47% ± 1.70%	b	0.40% ± 0.40%	3.02% ± 1.42%	0.73% ± 0.31%	0.66% ± 0.37%	—

WT, wild type.

[Table 2](#) is an example of a standard table that will be the width of the text column in the PDF. It does not contain any unusual styling. It does have footnotes linked to content in the table using the prescribed symbols.

Table 2.: This table contains references and footnotes and is sized to the text column width in the PDF.

Protein	Molar ratio of lipid:protein in RPL reactions*	Molar ratio of lipid:protein on vacuoles		References†
		BJ3505	DKY6218	
Vam7p	2 × 10 <sup>3</sup>	30 × 10 <sup>4</sup>	6.5 × 10 <sup>4</sup>	<a href="#">DeLano, 2002</a>
Vam3p	2 × 10 <sup>3</sup>	11 × 10 <sup>4</sup>	22 × 10 <sup>4</sup>	<a href="#">Department of Education and Morgan, 2016</a>
Vti1p	2 × 10 <sup>3</sup>	10 × 10 <sup>4</sup>	13 × 10 <sup>4</sup>	<a href="#">Zhong et al., 2013</a>
Nyv1p	2 × 10 <sup>3</sup>	4.3 × 10 <sup>4</sup>	8.1 × 10 <sup>4</sup>	<a href="#">Ferry et al., 2014</a>
<b>Protein Molar ratio of lipid:protein in RPL reactions* Molar ratio of lipid:protein on vacuoles References†</b>				
Ypt7p	4 × 10 <sup>3</sup>	1.9 × 10 <sup>4</sup>	1.8 × 10 <sup>4</sup>	<a href="#">Zhong et al., 2013</a>
Sec17p	7 × 10 <sup>3</sup>	41 × 10 <sup>4</sup>	13 × 10 <sup>4</sup>	<a href="#">Wolski et al., 2008</a>
Sec18p	1 × 10 <sup>3</sup>	10 × 10 <sup>4</sup>	13 × 10 <sup>4</sup>	This article ( <a href="#">Figure 1</a> )
Vps33p	6 × 10 <sup>3</sup>	17 × 10 <sup>4</sup>	31 × 10 <sup>4</sup>	<a href="#">Zhong et al., 2013</a>

\* Footnotes can be used to highlight properties of data reported in a table such as statistical significance. They are separate from the table caption and appear afterwards. They are hyperlinked to allow easy navigation. Footnotes in tables use the same standard set of symbols used for authors footnotes.  
† Authors are fully allowed to cite references and figures in tables. There is no difference in citation style between the main text and tables.

Order: Designated footnotes (e.g. \*, †, ‡, §, #, ¶, \*\*, and so on), p value footnotes (\*p, \*\*p, \*\*\*p), undesigned footnotes and abbreviations.

[Table 3](#) is an example of a narrow table that will appear at half the text column width in the PDF. It also has source data.

Table 3.:

**Representative curves of steady-state kinetic analyses for each IGF1R protein characterized.**

Each data point was performed in duplicate and is shown separately.

DOI: [10.7554/eLife.00666.006](#)

[Download](#)

Data collection	
Space group	P6 <sub>2</sub>
Cell dimensions (Å)	a = b = 78.33, c = 62.32
	α = β = 90°, γ = 120°
Wavelength (Å)	0.9794
R <sub>sym</sub> or R <sub>merge</sub> (%)	8.4
Resolution (Å)	50–2.05 (2.09–2.05)
I/σI	19.19 (3.23)
Completeness (%)	99.8 (97.3)
Redundancy	6.2 (5.4)
Refinement	
No. reflections	12,206
Resolution (Å)	39.17–2.06 (2.14–2.06)
R <sub>work</sub> /R <sub>free</sub>	0.17/0.21 (0.16/0.19)
No. atoms	
Protein	1608
Ligand/ion	3
Water	61
R.m.s. deviations	
Bond lengths (Å)	0.0077
Bond angles (°)	0.932

The following unnamed table is an example of an inline table that has no heading.

	pY Experiment	Concentration (μM)
IGF1R-fl + IGF1	+ <i>K<sub>m</sub></i> ATP	500, 400, 300, 250, 125, 62.5, 31.3, 15.6, 7.8
IGF1R-fl + IGF1	+ <i>K<sub>m</sub></i> Peptide	600, 300, 150, 75, 37.5, 18.8, 9.4
IGF1R-fl + IGF1	– <i>K<sub>m</sub></i> ATP	2000, 1000, 500, 250, 125, 62.5, 31.3, 15.6, 7.8
IGF1R-fl + IGF1	– <i>K<sub>m</sub></i> Peptide	500, 250, 125, 62.5, 31.3, 15.6, 7.8, 3.9
IGF1R-fl	+ <i>K<sub>m</sub></i> ATP	500, 400, 300, 250, 125, 62.5, 31.3, 15.6, 7.8
IGF1R-fl	+ <i>K<sub>m</sub></i> Peptide	500, 400, 250, 125, 62.5, 31.3, 15.6, 7.8
IGF1R-fl	– <i>K<sub>m</sub></i> ATP	1000, 500, 250, 125, 62.5, 31.3, 15.6, 7.8
IGF1R-fl	– <i>K<sub>m</sub></i> Peptide	1000, 500, 250, 125, 62.5, 31.3, 15.6
IGF1R-icd	+ <i>K<sub>m</sub></i> ATP	500, 250, 125, 62.5, 31.3, 15.6, 7.8, 3.9
IGF1R-icd	+ <i>K<sub>m</sub></i> Peptide	1000, 500, 250, 125, 62.5, 31.3, 15.6, 7.8
IGF1R-icd	– <i>K<sub>m</sub></i> ATP	1000, 500, 250, 125, 62.5, 31.3
IGF1R-icd	– <i>K<sub>m</sub></i> Peptide	1000, 500, 250, 125, 62.5, 31.3
IGF1R-kin	– <i>K<sub>m</sub></i> Peptide	1250, 625, 312.5, 156.3, 78.1, 39.1

This is an unmarked footnote for an anchored/inline table

**Maths**

Content can contain inline formulae or display formulae. Below is an example of a mixture of inline and display formula. MathML is used in all instances.

We propose a Bayesian scheme for BCV (see [equation 1](#)) that accommodates the influence of context on incentive value. BCV focuses on scenarios (i) where incentive value depends on contextual information (either represented by cues or by previous rewards) provided before options or rewards are presented, and (ii) where reward is defined by a single attribute (e.g., reward amount). To describe the basic principles of BCV, we adopt the formalism of Bayesian graphs ( [The Shigella Genome Sequencing Consortium, 2015c](#)) where a generative model is described by nodes or circles, representing random variables (shaded and white circles refer to observed and non-observed variables respectively), and arrows, representing causal relationships among variables. A simple generative model hypothesized by BCV is shown in Figure 1A of another article (not linked here), where C represents prior beliefs about the average reward expected in a given context. Formally, this corresponds to a (Gaussian) prior belief (with mean  $\mu_c$  and variance  $\sigma_c^2$  over the mean of a (Gaussian) distribution of reward options R (with variance  $\sigma_R^2$ ). When R is observed, a posterior expectation about the context is obtained by application of Bayes rule ( [The Shigella Genome Sequencing Consortium, 2015b](#) ):  $(3) \mu_C | R = \mu_C + \sigma_C^2 \sigma_C^2 + \sigma_R^2 (R - \mu_C)$  where text following on from this equation but still within the same paragraph should not be indented in the PDF. This is usually used by authors wanting to explain the terms used in the maths.

Additional to maths, eLife articles can also contain code blocks for the display of computer code snippets. For example:

```
<MotifGraft name="motif_grafting"
context_structure="%%context%"
motif_structure="truncatedBH3.pdb"
RMSD_tolerance="3.0"
NC_points_RMSD_tolerance="2.0"
clash_score_cutoff="0"
clash_test_residue="ALA"
hotspots="9:12:13:14:16:17"
combinatory_fragment_size_delta="0:0"
max_fragment_replacement_size_delta="0:0"
full_motif_bb_alignment="1"
allow_independent_alignment_per_fragment="0"
graft_only_hotspots_by_replacement="0"
only_allow_if_N_point_match_aa_identity="0"
only_allow_if_C_point_match_aa_identity="0"
revert_graft_to_native_sequence="1"
allow_repeat_same_graft_output="1"/>
```

Figures

This section of the article shows how figures should be presented and will include examples of single figures and figures arranged with a variety of additional assets.

Figure 1 is an example of a single figure.



Figure 1.: Single figure: The header of an eLife article example on the HTML page. In the Pdf this is represented as a single column.

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DOI: [10.7554/eLife.00666.007](#)

Figure 2 is an example of a figure with figure supplements, Figure 2—figure supplement 1 and Figure 2—figure supplement 2.



Figure 2.: Figure with figure supplements. In the PDF this asset box will take full column width.

This is the basic information provided about an article. Figure 1 shows an expanded view (Kok et al., 2015; National Institute of Mental Health, 1990).  
[Download full-size image](#)  
DOI: [10.7554/eLife.00666.008](#)



Figure 2—figure supplement 1.: The representation of the Major Subject Areas, Research Organisms and author keywords on the eLife HTML page

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Figure 2—figure supplement 2.: Representation of figure with figure supplements on the HTML view.

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Figure 3 is an example of a figure with a figure supplement (Figure 3—figure supplement 1) with two sub-assets, Figure 3—figure supplement 1—source data 1 and Figure 3—video 1 (see Zhang et al., 2010, Zhong et al., 2013; World Health Organization, 2016).



Figure 3.: Figure with figure supplements and figure supplement with source data and a video (see Koch, 1959) .

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Figure 3—figure supplement 1.: Title of the figure supplement

Title of the figure supplement source data.

Legend of the figure supplement source data.

DOI: [10.7554/eLife.00666.013](#)  
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DOI: [10.7554/eLife.00666.012](#)

Figure 3—video 1.

A description of the eLife editorial process.

Figure 4 is an example of a figure with source code (Figure 4—source code 1).



Figure 4.: Single figure with source code.

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Title of the source code.

Legend of the source code.

DOI: [10.7554/eLife.00666.015](#)  
[Download](#)

Videos

Video 1 shows the editorial process and Animation 1 shows how we represent animated gif files.

Video 1.

A description of the eLife editorial process.

Title of the source code.

Legend of the source code.

DOI: [10.7554/eLife.00666.037](#)  
[Download](#)  
Animation 1.

A demonstration of how to tag an animated gif file to ensure it is autolooped when on the eLife website.

Other stuff

Boxes

It is rare for eLife research articles to contain boxes; however they are common in Feature content. Box 1 is a simple box that contains very little text and Box 2 is larger.

Box 1.  
Example of a small box

Donec rhoncus in odio non vulputate. Donec vitae enim at erat tincidunt tincidunt in nec arcu. Pellentesque habitant morbi tristique senectus et netus et malesuada fames ac turpis egestas. Aliquam id nunc id arcu maximus rutrum. Praesent bibendum nisl orci, ac sollicitudin purus aliquam in. Duis eu fermentum arcu. Fusce eget dolor augue. Nulla facilisi. Suspendisse eu nisl vitae neque ullamcorper imperdiet (see [Nellåker, 2014](#); [Pages et al., 2014](#); and [Palmer et al., 2007](#)). Boxes, like main text, can contain [hyperlinks](#) at any point. Etiam in sem augue.

This box contains a [figure](#). Lorem ipsum dolor sit amet, consectetur adipiscing elit. Quisque vel rhoncus lorem. Suspendisse posuere non enim vel tempor. Fusce quis sem sed nulla tincidunt faucibus. Vivamus dictum magna in ante porttitor faucibus. Aenean lobortis, sem in viverra dignissim, odio purus vestibulum libero, in eleifend lacus metus id tortor. Phasellus tincidunt ipsum ut ornare hendrerit. Praesent lobortis consectetur egestas. Curabitur viverra lectus eu venenatis sagittis. Aliquam lobortis metus mauris, in tincidunt diam ullamcorper ac. Phasellus sagittis, leo eget lacinia commodo, eros justo mattis eros, quis dapibus ipsum ex sit amet sapien. Quisque consequat arcu ut efficitur tincidunt. Ut convallis, ex maximus aliquam tempor, lorem elit fermentum ipsum, nec volutpat velit sem a lectus. Morbi sed mauris vel purus interdum consectetur dapibus vel velit. Nam pellentesque, ipsum vel euismod mattis, turpis augue mattis nunc, ac aliquam dolor massa non mi. Vestibulum sit amet elit a augue semper facilisis interdum quis nibh. Mauris consectetur nisi aliquam urna lobortis, eu efficitur nisl lobortis; [Bates et al., 2016](#) and [Patterson et al., 2011](#).



Box 2—Figure 1.: Box figure

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DOI: [10.7554/eLife.00666.036](#)

Donec rhoncus in odio non vulputate. Donec vitae enim at erat tincidunt tincidunt in nec arcu. Pellentesque habitant morbi tristique senectus et netus et malesuada fames ac turpis egestas. Aliquam id nunc id arcu maximus rutrum. Praesent bibendum nisl orci, ac sollicitudin purus aliquam in. Duis eu fermentum arcu. Fusce eget dolor augue. Nulla facilisi. Suspendisse eu nisl vitae neque ullamcorper imperdiet. Vestibulum ultrices vehicula nibh, a ullamcorper dui semper suscipit. Etiam in sem augue.

RRIDs

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Coloured text

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References

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Discussion

The function of the Discussion is to interpret your results in light of what was already known about the subject of the investigation, and to explain our new understanding of the problem after taking your results into consideration. The Discussion will always connect to the Introduction by way of the question(s) or hypotheses you posed and the literature you cited, but it does not simply repeat or rearrange the Introduction. Instead, it tells how your study has moved us forward from the place you left us at the end of the Introduction ([Schneider, 2006](#); [Schwartz, 1993](#)).

Materials and methods

Reagent type (species) or resource	Designation	Source or reference	Identifiers	Additional information
gene ( <i>Drosophila melanogaster</i> )	nito	NA	FLYB:FBgn0027548	
gene ( <i>D. melanogaster</i> )	Sxl	NA	FLYB:FBgn0264270	
genetic reagent ( <i>D. melanogaster</i> )	MTD-Gal4	Bloomington Drosophila Stock Center	BDSC:31777; FLYB:FBtp0001612; RRID: <a href="#">BDSC_31777</a>	FlyBase symbol: P{GAL4-nos.NGT}
genetic reagent ( <i>D. melanogaster</i> )	ap-Gal4	Bloomington Drosophila Stock Center	BDSC:3041; FLYB:FBti0002785; RRID: <a href="#">BDSC_3041</a>	FlyBase symbol: P{GawB}ap[md544]
genetic reagent ( <i>D. melanogaster</i> )	nub-Gal4	PMID:20798049	FLYB:FBti0016825	FlyBase symbol: P{GawB}nubbin-AC-62
genetic reagent ( <i>D. melanogaster</i> )	dome-Gal4	PMID:12403714	FLYB:FBti0022298	FlyBase symbol: P{GawB}dome[PG14]
genetic reagent ( <i>D. melanogaster</i> )	UAS-2xEYFP	PMID:12324968	FLYB:FBtp0016537	FlyBase symbol: P{UAS-2xEYFP}
genetic reagent ( <i>D. melanogaster</i> )	nito[HP25329]	Bloomington Drosophila Stock Center	BDSC:22092; FLYB:FBal0238892; RRID: <a href="#">BDSC_22092</a>	Genotype: w[1118]; P{w[+mC]=EPg}nito[HP25329]/CyO
genetic reagent ( <i>D. melanogaster</i> )	nito[1]	this paper		Progenitor = nito[HP25329]; imprecise excision; lethal
genetic reagent ( <i>D. melanogaster</i> )	nito shRNA (HMJ02081)	Bloomington Drosophila Stock Center	TRiP:HMJ02081; BDSC:56852; RRID: <a href="#">BDSC_56852</a>	FlyBase symbol: P{TRiP.HMJ02081}attP40
genetic reagent ( <i>D. melanogaster</i> )	nito dsRNA (VDRC 20942)	Vienna Drosophila RNAi Center	VDRC:20942	
genetic reagent ( <i>D. melanogaster</i> )	FRT[G13]	Bloomington Drosophila Stock Center	BDSC:1956; FLYB:FBti0001247	FlyBase symbol: P{FRT(whs)}G13
genetic reagent ( <i>D. melanogaster</i> )	"y w hsflp; ubiGFP FRT[G13]"	PMID:18160348		
cell line ( <i>D. melanogaster</i> )	S2	other	FLYB:FBtc0000181; RRID: <a href="#">CVCL_Z992</a>	Cell line maintained in N. Perrimon lab; FlyBase symbol: S2-DRSC.
antibody	anti-Nito	this paper		Rabbit polyclonal; against aa 479-500; used YZ3137 (1:500)
antibody	anti-alpha-Spectrin (mouse monoclonal)	Developmental Studies Hybridoma Bank	DSHB:3A9; RRID: <a href="#">AB_528473</a>	(1:10)
antibody	anti-Vasa (rabbit polyclonal)	Santa Cruz Biotechnology	Santa Cruz:sc-30210; RRID: <a href="#">AB_793874</a>	(1:250)
antibody	anti-Sxl (mouse monoclonal)	Developmental Studies Hybridoma Bank	DSHB:M18; RRID: <a href="#">AB_528464</a>	(1:10)
antibody	anti-GFP (rabbit polyclonal)	Molecular Probes	Molecular Probes:A-6455; RRID: <a href="#">AB_221570</a>	(1:1000)
antibody	anti-GFP (mouse monoclonal)	Molecular Probes	Molecular Probes:A-11120; RRID: <a href="#">AB_221568</a>	(1:200)
antibody	anti-HA (rat monoclonal)	Roche	Roche:3F10; RRID: <a href="#">AB_2314622</a>	
antibody	Alexa 488- or 555- secondaries	Molecular Probes		(1:1000)
other	DAPI stain	Molecular Probes		(1:1000)
recombinant DNA reagent	pAGW (Gateway vector)	Drosophila Genomics Resource Center	DGRC:1071	
recombinant DNA reagent	pAHW (Gateway vector)	Drosophila Genomics Resource Center	DGRC:1095	
recombinant DNA reagent	GH11110 (cDNA)	Drosophila Genomics Resource Center	DGRC:5666	
recombinant DNA reagent	GFP-Nito (plasmid)	this paper		Progenitors: GH11110 (cDNA); Gateway vector pAGW
recombinant DNA reagent	HA-Sxl (plasmid)	PMID:16207758		Progenitors: PCR, UAS-Sxl flies; Gateway vector pAHW
recombinant DNA reagent	GFP-Sxl (plasmid)	PMID:16207758		Progenitors: PCR, UAS-Sxl flies; Gateway vector pAGW

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P<sub>NRE+AP-1</sub>: 5'- CTTCTGACTAGTCTTGACTCAGA -3'

P<sub>RAM</sub>: 5'- CTAGAAGTTTGTTCGTGACTCAGA -3'

E1: 5'- CTAGAAGTTTGTGACTACCCGA -3'

E2: 5'- CTAGAAGTTTGTGACTCATTAGA -3'

E3: 5'- CTAGAAGTTTGTGTATGACTCAGA -3'

CME: 5'- CTAGAAATTTGTACGTGCCACAGA -3'

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TAATAAGGAAGAACTGCTTATTCTTAATTATTTCTACCTACTAACTAACTAATTATCAACAAATATCATCTATTTAATAGTATATCATCACATGCGGTGTAAGAGGATGACATAAAGATTGAGAAACAGTCATCCAGTCTAATGG  
Sequences like this should be tagged during pre-editing. This tagging will also increase discoverability of gene sequences in eLife articles.

## Additional information

### Competing interests

Chair of JATS4R

No competing interests declared

Graham Nott is not an eLife employee

### Author contributions

Completed the XML mapping exercise and wrote this XML example

Contributed to the XML mapping exercise and quality checked all the tagging and content

Reviewed the PDF product

Chris Wilkinson, Performed the XML mapping exercise and generated the JSON Schema

Graham Nott, Wrote the JATSScraper

Luke Skibinski, Identified missing components from the JATSScraper

### Ethics

Human subjects: If Research Ethics Committee and Institutional Review Board approval was required for this article the details would be listed here.

Animal subjects: If there were animal subjects involved in the study the approval number for the research along with protocol approval would be listed here.

If this article was part of a clinical trial the Clinical trial registry and ID would be listed here, for example:

Clinical trial Registry: EudraCT.

Registration ID: EudraCT2004-000446-20.

### Funding

The funders had no role in study design; collection, analysis, and interpretation of data; writing the article; and or the decision to submit to the journal.

### Additional files

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A file containing underlying data.

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### Data availability

A data availability statement will generally describe how the authors have provided the source data for their work. This can list the source data files accompanying their figures, supplementary files, and/or external datasets. Hyperlinks can be included here, for example: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE102999>

The following dataset was generated:

Düsterwald KM , Currin CB , Burman RJ , Akerman CJ , Kay AR , Raimondo JV . 2018. [Data from: Biophysical models reveal the relative importance of transporter proteins and impermeant anions in chloride homeostasis](#). Dryad Digital Repository. data

The following previously published datasets were used:

Rau CD , Wang J , Wang Y , Lusi AJ . 2013. [Transcriptomes of the hybrid mouse diversity panel subjected to Isoproterenol challenge](#). NCBI Gene Expression Omnibus. data

García Miguel A . 2018. [Shear Manuscript](#). Open Science Framework. data

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## Acknowledgements

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### Sub-thanks

We need to allow authors to have sections in their acknowledgements.

- Aivazian D , Serrano RL , Pfeiffer S . 2006. [TIP47 is a key effector for Rab9 localization](#). The Journal of Cell Biology 173 :917-926
- Bates D , Maechler M , Bolker B , Walker S , Haubo Bojesen Christensen R , Singmann H , Dai B , Grothendieck G , Green P , Bolker B (Curator). 2016. [Lme4: Linear Mixed-](#)



• Effects Models Using Eigen and S4. CRAN. 1.1-12 software

• Bloss CS , Wineinger NE , Peters M , Boeldt DL , Ariniello L , Kim JL , Judy Sheard J , Komatireddy R , Barrett P , Topol EJ . 2016. [A prospective randomized trial examining health care utilization in individuals using multiple smartphone-enabled biosensors](#). bioRxiv.

• Bouveret R , Vaardenberg AJ , Schonrock N , Ramialison M , Doan T , de Jong D , Bondue A , Kaur G , Mohamed S , Fonoudi H , Chen C , Wouters M , Bhattacharya S , Plachta N , Dunwoodie SL , Chapman G , Blanpain C , Harvey RP . 2015. [NKX2-5 mutations causative for congenital heart disease retain functionality and are directed to hundreds of targets](#). NCBI Gene Expression Omnibus. data

• Brettar I , Christen R , Höffle M . 2004a. [Aquiflexum balticum gen. nov., sp. nov., a novel marine bacterium of the Cytophaga-Flavobacterium-Bacteroides group isolated from surface water of the central Baltic Sea](#). International journal of systematic and evolutionary microbiology **54** :2335-2341

• Brettar I , Christen R , Höffle MG . 2004b. [Belliella baltica gen. nov., sp. nov., a novel marine bacterium of the Cytophaga-Flavobacterium-Bacteroides group isolated from surface water of the central Baltic Sea](#). International journal of systematic and evolutionary microbiology **54** :65

• Bricogne G , Blanc E , Brandl M , Flensburg C , Keller P , Paciorek W , Roversi P , Sharff A , Smart OS , Vonnrhein C , Womack TO . 2011. [BUSTER](#). 2.10.0 Cambridge, UK: Global Phasing Ltd. software

• 2004. Cardé RT , Millar JG , eds. [Advances in insect chemical ecology](#). Cambridge: Cambridge University Press.

• Cartwright A . 2016. [The Venus Hypothesis](#). arXiv.org.

• 2008. Chmell N , ed. [An Introduction to Work and Organizational Psychology: A European Perspective](#) (2). Wiley-Blackwell.

• Coyne JA , Orr HA . 1989. Otte D , Endler JA , eds. [Speciation and its consequences](#). Sunderland, MA: Sinauer Associates. 1-2

• DeLano J . 2002. [The PyMol Molecular Graphics System](#). PyMol. Version 1.7.4 Schrödinger LLC. software

• Department of Education, Morgan N . 2016. Educational excellence everywhere.

• Du J , Johnson LM , Groth M , Feng S , Hale CJ , Li S , Vashisht AA , Gallego-Bartolome J , Wohlschlegel JA , Patel DJ , Jacobsen SE . 2014. [Crystal structure of KRYPTONITE in complex with mCHH DNA and SAH](#). RCSB Protein Data Bank. data

• Eisen M . 2016. [The Imprinter of All Maladies](#). it is NOT junk.

• Ferry Q , Steinberg J , Webber C , FitzPatrick DR , Ponting CP , Zisserman A , Nellåker C . 2014. [Diagnostically relevant facial gestalt information from ordinary photos database](#). Division of Clinical Neurology, University of Oxford. data

• Gall A , Treuting P , Elkon KB , Loo YM , Gale M , Barber GN . 2012. [Autoimmunity initiates in nonhematopoietic cells and progresses via lymphocytes in an interferon-dependent autoimmune disease](#). Immunity **36** :120-131

• Gavrilov S , Harvey RP , Papaioannou VE . 2014. [Mus musculus T-box 2 \(Tbx2\), mRNA](#). NCBI Nucleotide. NM\_009324.2 data

• GlaxoSmithKline UK. 2016. Augmentin 250/62 SF Suspension.

• Goodstadt L . 2010. [Ruffus: a lightweight Python library for computational pipelines](#). Bioinformatics **26** :2778-2779

• Hoang C , Swift GH , Azevedo-Pouly A , MacDonald RJ . 2015. [Effects on the transcriptome of adult mouse pancreas \(principally acinar cells\) by the inactivation of the Ptf1a gene in vivo](#). NCBI Gene Expression Omnibus. data

• Horne P , Page J . 2008. [Integrated pest management for crops and pastures](#). Victoria: Landlinks Press. 9780643092570

• Hubbard S , Thornton J . 1993. [Naccess](#). V2.1.1 Department of Biochemistry Molecular Biology, University College London. software

• Jain BV , Bollman B , Richardson M , Berger DR , Helmstaedter MN , Briggman KL , Denk W , Bowden JB , Mendenhall JM , Abraham WC , Harris KM , Kasthuri N , Hayworth KJ , Schalek R , Tapia JC , Lichtman JW , Seung HS . 2010. [Boundary learning by optimization with topological constraints](#). In: [IEEE Conference on Computer Vision and Pattern Recognition \(CVPR\)](#). 2010.

• Koch S . 1959. [Psychology A Study Of A Science](#). Mcgraw-Hill Book Company. **3: Formulations of the Person and the Social Context**

• Kok K , Ay A , Li L , Arnosti DN . 2015. [Data from: Genome-wide errant targeting by Hair1](#). Dryad Digital Repository. data

• McQuilton P , St Pierre SE , Thurmond J , FlyBase Consortium. 2012. [FlyBase 101—the basics of navigating FlyBase](#). Nucleic Acids Res **40** :D706-D714

• National Institute of Mental Health. 1990. Clinical training in serious mental illness (DHHS Publication No. ADM 90-1679).

• Nellåker C . 2014. [Clinical Face Phenotype Space Pipeline](#). Github. v1.2 software

• Pages H , Gentleman R , Aboyoun P , Biostrings DS . 2014. [String objects representing biological sequences, and matching algorithms](#). Bioconductor. R Package Version 2.30.1 software

• Palmer JA , Kreutz-Delgado K , Rao BD , Makeig S . 2007. [Probabilistic Formulation of Independent Vector Analysis Using Complex Gaussian Scale Mixtures](#) In: [Independent component analysis and signal separation](#).In: 8th International Conference, ICA 2009, Paraty, Brazil, March 15-18, 2009. 90-97

• Patterson JB (Inventor), Lonergan DG (Inventor), Flynn GA (Inventor), Qingpeng Z (Inventor), Pallai PV (Inventor), Mankind Corp. 2011. [IRE-1alpha inhibitors](#). United States patent.

• R Development Core Team. 2015. [R: a language and environment for statistical computing](#). 3.2.2 Vienna, Austria: R Foundation for Statistical Computing. software

• Radoshevich L , Impens F , Ribet D , Quereda JJ , Nam Tham T , Nahori MA , Bierne H , Dussurget O , Pizarro-Cerdá J , Knobeloch KP , Cossart P . 2015a. [ISG15 counteracts Listeria monocytogenes infection](#). ProteomeXchange. data

• Radoshevich L , Impens F , Ribet D , Quereda JJ , Nam Tham T , Nahori MA , Bierne H , Dussurget O , Pizarro-Cerdá J , Knobeloch KP , Cossart P . 2015b. [Transcription profiling by high throughput sequencing of LoVo cells infected with Listeria for 24 hr compared to uninfected cells](#). ArrayExpress. data

• Rasband WS . 1997. [ImageJ](#). Bethesda, MA: US National Institutes of Health. software

• Roy S , Wapinski , Pfiffner J , French C , Socha A , Konieczka J , Regev A . 2013. [Arboretum: reconstruction and analysis of the evolutionary history of condition-specific transcriptional programs](#). Genome Res In press

• Schneider P . 2006. [PhD thesis: Submicroscopic Plasmodium falciparum gametocytaemia and the contribution to malaria transmission](#). thesis

• Schrödinger LLC . 2011. [The PyMOL Molecular Graphics System](#). 1.2r3pre Schrödinger LLC. software

• Schwartz J . [Obesity affects economic, social status](#). The Washington Post.

• Scripps Translational Science Institute. 2015. [Scripps Wired for Health Study](#).

• Smit A , Hubley R . 2010. [RepeatModeler](#). open-1.0 Seattle, USA: Institute for Systems Biology. software

• Staab TA , Griffen TC , Corcoran C , Evgrafov O , Knowles JA , Sieburth D . 2013. [SKN-1 from the JASPAR CORE database](#). JASPAR. data

• Tanaka Y , Hosoyama T , Mikamo A , Kurazumi H , Nishimoto A , Ueno K , Shirasawa B , Hamano K . 2016. [Hypoxic Preconditioning of Human Cardiosphere-derived Cell Sheets Enhances Cellular Functions via Activation of the PI3K/Akt/mTOR/HIF-1a Pathway](#). preprints.

• The Shigella Genome Sequencing Consortium. 2015a. [Global Diversity of Shigella Species](#). NCBI BioProject. data

• The Shigella Genome Sequencing Consortium. 2015b. [Shigella sonnei and flexneri from around the world](#). NCBI BioProject. data

• The Shigella Genome Sequencing Consortium. 2015c. [Shigella flexneri from around the world](#). NCBI BioProject . data

• Turlings TCJ , Wäckers FL . 2004a. Cardé RT , Millar JG , eds. [Advances in insect chemical ecology](#). Cambridge: Cambridge University Press. 21-75

• Turlings TCJ , Wäckers FL . 2004b. Cardé RT , Millar JG , eds. [Advances in insect chemical ecology](#). Cambridge University Press.

• Walker J . 1994. [Solar System Live](#).

• Wolski SC , Kuper J , Hanzelmann P , Truglio JJ , Croteau DL , Van Houten B . 2008. [Crystal structure of the FeS cluster-containing nucleotide excision repair helicase XPD](#). PLoS Biol **6** :e149

• World Health Organization. 2016. [Growing up unequal: gender and socioeconomic differences in young people's health and well-being. Health Behaviour in School-aged Children \(HBSC\) study \(2\).](#) World Health Organization.

• Zhang YA , Salinas I , Li J , Parra D , Bjork S , Xu Z , LaPatra SE , Bartholomew J , Sunyer JO . 2010. [Polymeric immunoglobulin receptor \[Oncorhynchus mykiss\]](#) NCBI. data

• Zhong M , Snyder M , Slightam C , Kim S , Murray J , Waterston R , Gerstein M , Niu W , Janette J , Raha D , Agarwal A , Reinke V , Sarov M , Hyman A . 2013. [ChIP-Seq Identification of C. elegans TF Binding Sites](#). modMine. data

## Appendix 1

### Preparation

In order to prepare for this Kitchen sink we reviewed our archive and found common errors or miscommunication from the archive, tagging of [Appendix 1—Figure 1](#) is a classic example and here the tagging is updated. Appendices figures can also have figure supplements, for example [Appendix 1—Figure 1—Figure Supplement 1](#) (Koch, 1959).

**Appendix 1—Figure 1.: Appendix figure title.**

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**Appendix 1—Figure 1—Figure Supplement 1.: Appendix figure supplement title.**

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### 1.1 Sub heading

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### 1.2 Sub heading

This is the text of the content of subheading 2 within appendix 2.

Appendix 1—Table 1.:

This is the title.

This is the caption: A table containing interesting formatting that is large enough to require landscape orientation in the PDF.

Genotype	GLVs (percent IS plant <sup>-1</sup> )			TPS10 products (percent IS plant <sup>-1</sup> )			Non-target volatiles (percent IS plant <sup>-1</sup> )		
	(Z)-Hexen-3-ol			TAB			α-Duprezianene		
Day	Night			TBF			Germacrene A		
	Day	Night	Day	Day	Night	Day	Day	Night	Day



			GLVs (percent IS plant <sup>-1</sup> )			TPS10 products (percent IS plant <sup>-1</sup> )			Non-target volatiles (percent IS plant <sup>-1</sup> )		
			(Z)-Hexen-3-ol			TAB			α-Duprezianene		