preLights – a community platform for preprint highlights

Mate Palfy, PhD

Community Manager, The Company of Biologists

CNIC PhDay, 22 November 2019, Madrid

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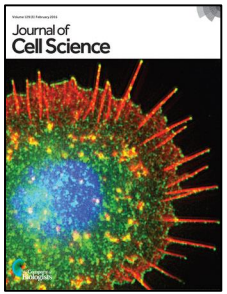
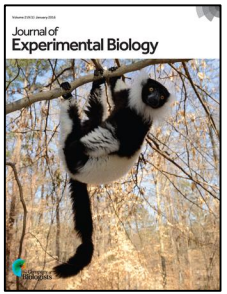
Supporting biologists, inspiring biology





Charitable grants

Meetings and Workshops

Community building

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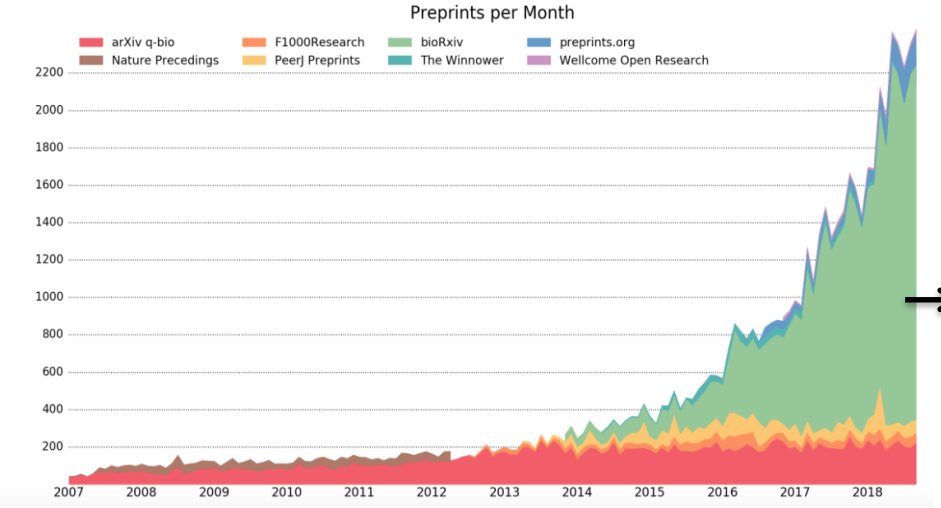
Growth of preprints in the biological sciences

Preprint: version of a scientific paper that precedes publication in a peer-reviewed journal and is uploaded to a public server.



bioRχiv

(Source: PrePubmed.org)

Some benefits of preprints

- Earlier access to new findings & technologies (and negative results, confirmatory/contradictory results)
- Freely accessible
- Help transparency & reproducibility
- Open up dialogue about work

Scientific community

- Rapid dissemination of results
- Establishment of ‘priority’ for a particular finding
- Preprint can be referenced
- Early feedback on work from community

Authors

The Company of Biologists

Preprints are also an opportunity for publishers

Inviting interesting studies

Innovation in peer review

ASAPbio

EMBO excellence in life sciences

Review COMMONS

eLIFE JCB EMBO JOURNAL EMBO reports EMBO Molecular Medicine molecular systems biology

MBoC Biology Open Journal of Cell Science Development Disease Models & Mechanisms

PLOS ONE PLOS GENETICS PLOS PATHOGENS PLOS COMPUTATIONAL BIOLOGY

PLOS BIOLOGY

Community Comments and Peer Review: A preprint commenting pilot at PLOS

eLIFE

Authors should control the decision to publish

The peer-review trial was right to aspire to give control of publishing decisions to authors. But inserting an editorial selection process in between authors and publishing is much more about empowering editors than it is about empowering authors.

Fortunately, eLife does not have to solve this problem anymore. It has already been solved by bioRxiv (and other preprint servers), which makes it possible for scientists to share their work when they feel ready to do so. In many corners of biology, papers

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Authors

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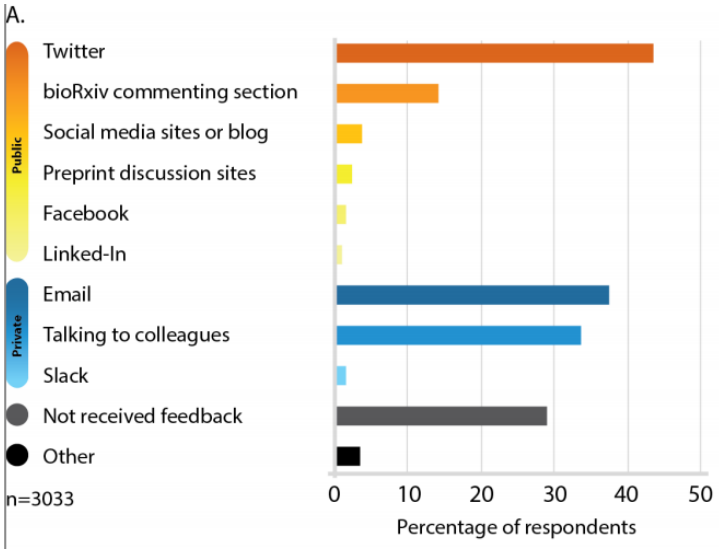
Most authors get personal feedback via email, or comments via Twitter



(Sever et al. 2019 *bioRxiv*)

Public commenting on preprints is still relatively rare

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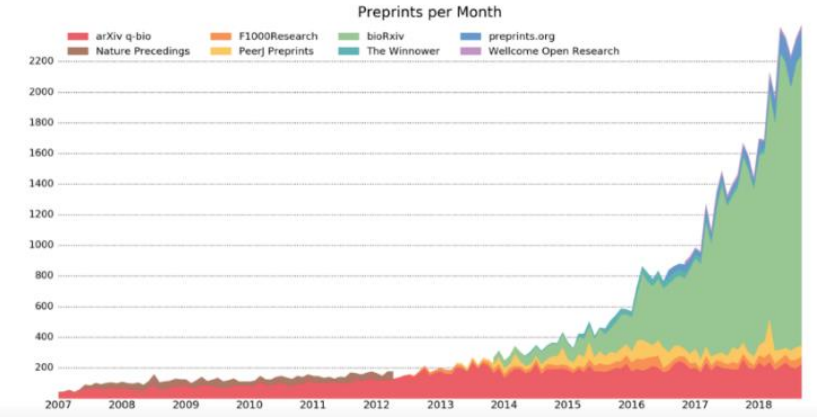
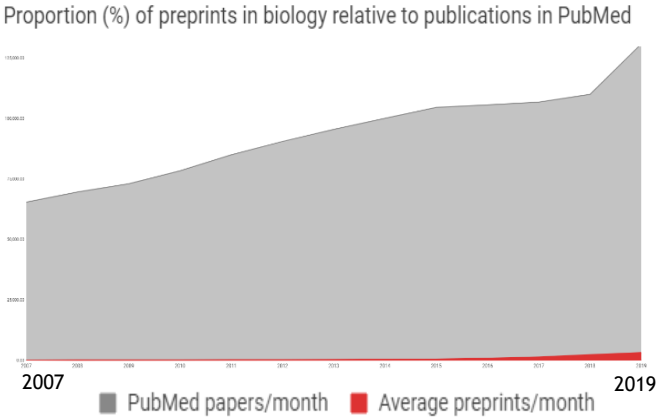
Another challenge with preprints for readers: growing volume

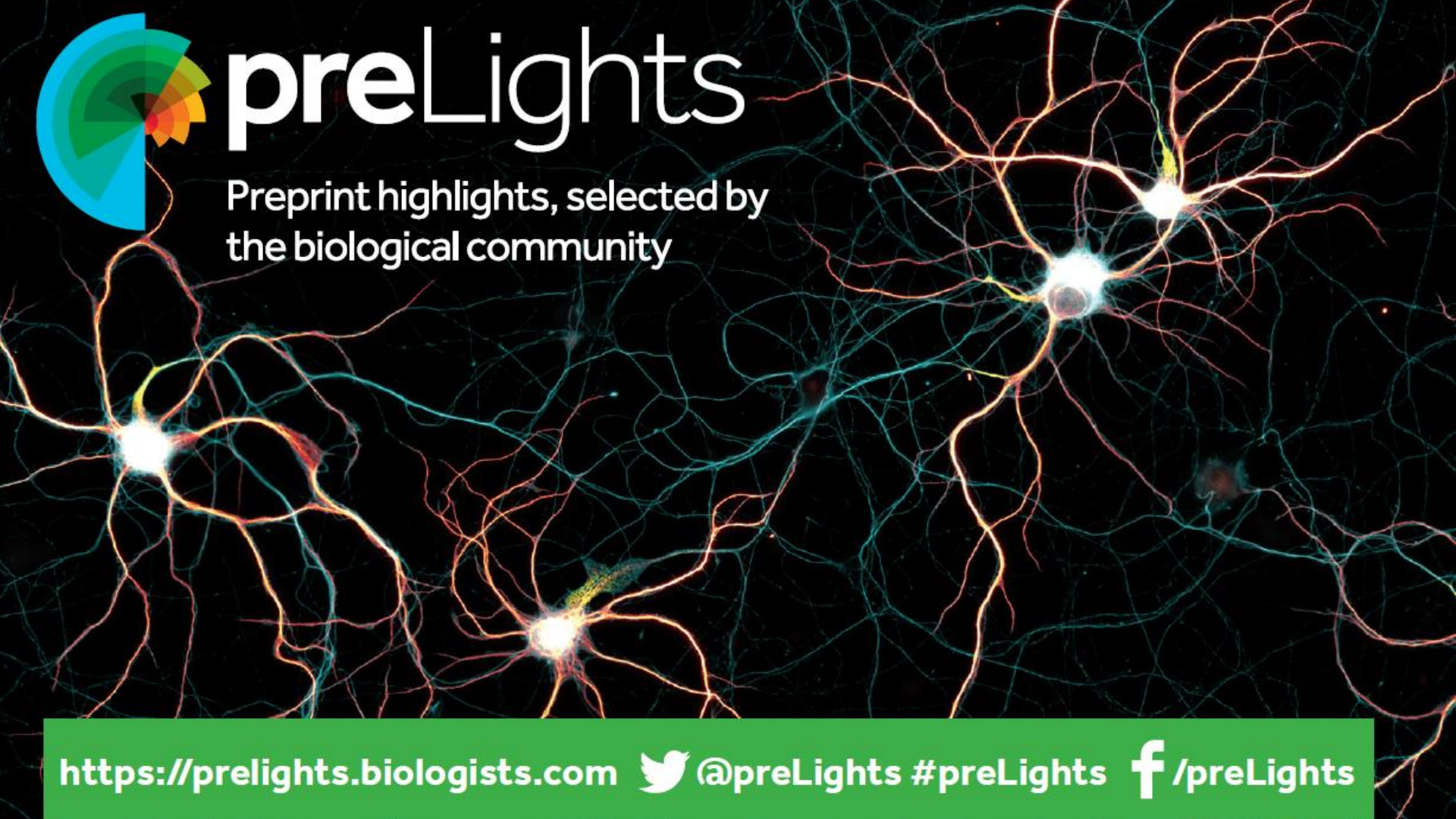


(Source: PrePubmed.org)



(Source: ASAPbio)

Difficult to keep up with preprint literature


preLights
Preprint highlights, selected by the biological community
https://prelights.biologists.com
@preLights #preLights
/preLights

preLighters

Mariana De Niz 	Theresa Pohlkamp 	Berrak Ugur 	Kiran Gurung 
Ramona Jühlen 	Romain F. Laine 	Sina Knapp 	Neetha Iyer 
Martin Balcerowicz 	Jonny Coates 	Martim Dias Gomes 	Leeba Ann Chacko 
Nidhi Kanwal 	Debbie Ho 	Pavithran Ravindran 	Emily Graves 

preLights: preprint highlights (‘News & Views for preprints’)

EGFR signaling coordinates patterning with cell survival during *Drosophila* epidermal development

Samuel Henry Crossman, Sebastian J Streichan, Jean-Paul Vincent

Preprint posted on August 28, 2018 https://www.biorxiv.org/content/early/2018/08/28/399865

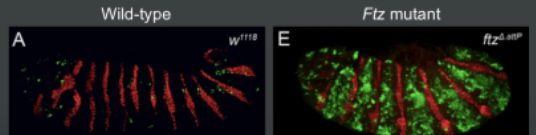
Why do cells die when they are in the "wrong" place? Preprint shows lack of EGFR signalling, rather than any cell fitness recognition event, is responsible

Selected by **Sarah Bowling**

Categories: developmental biology

Background

Cells that fail to form the correct tissue for their environment are often eliminated by apoptosis. This phenomenon has been observed across model organisms from zebrafish to mice, and is triggered by mutation of signalling pathway genes required for patterning. The phenotype is particularly evident in *Drosophila* segmentation mutants: mutation of genes that function at different steps of the segmentation cascade to define the *Drosophila* body plan leads to widespread apoptosis in the compartment where they are normally expressed (Fig. 1).



Preprint information & link

Short engaging summary of the preprint

preLighter (link to profile)

Background information

preLights: personal thoughts on the preprint

Conclusions and thoughts

Through a series of elegant genetics experiments and image analysis, the authors show that death of mispatterned cells in *Drosophila* segmentation mutants arises from disrupted EGFR signalling patterns. In addition, the data indicate that insufficient exposure to EGFR signalling could be a trigger of cell death in wild-type larvae.

Importantly, the preprint leads to the intriguing suggestion that as well as dictating compartment boundaries, segmentation genes could also control compartment size through tight regulation of EGFR signalling. This builds on previous studies implicating EGFR signalling in cell number regulation (Urban et al, 2004; Bergmann et al, 2002; Gioboa and Lehmann, 2006; Parker, 2006), and extends the findings by implicating the pathway in size control of whole segments in the developing larvae. This sizing mechanism, where a limited source of a growth factor supports survival of only a subset of produced cells, is reminiscent of that described for developing neurons in mice, where cells are massively overproduced and compete for limited levels of nerve growth factor (Raff, 1992). Together, the findings suggest that tight regulation of cell death, as much as proliferation, enables the establishment of normal body and organ size during development.

Questions

Death of mispatterned cells is also seen in systems with less distinct signalling compartments. For example, in mice, deletion of APC in the developing neural crest results in massive apoptosis (Hasegawa et al, 2002). Given the system differences, do the authors think that similar mechanisms are responsible in this context?

The authors make the interesting observation that apoptosis is triggered at embryonic stage 11, long after *ftz* should have fulfilled its function in segmentation and after the cessation of proliferation. It would be really interesting to know how this time-dependent sensitisation to low EGFR signalling is orchestrated – are there any contender mechanisms?

Posted on: 26th September 2018

Key findings

preLighter's take on preprint

Questions to the preprint author

preLights: author's response

Sam Crossman shared

This paper was both mine and JP's first experience with BioRxiv. The entire process was quick and easy and I don't think either of us will have any doubts when it comes to sharing pre-prints of our work in the future. We have received many great comments and suggestions since the report went online and I was very pleased when Sarah got in touch to share her excellent preLight and ask us to provide a comment.

The presence of apoptotic cells in *Drosophila* segmentation mutants was first observed over 35 years ago and yet, at the start of this project, we couldn't really explain why these cells were even dying in the first place. The patterning genes we were investigating were not survival factors and we could remove them from cells in culture with no deleterious effects. However, when we stopped them from functioning in the context of the developing embryo, we saw strong bands of cell death in the regions where the genes would normally be expressed. Initially, we thought we were looking at the output of some form of developmental quality control mechanism – where cells lacking the patterning inputs required to differentiate correctly are removed from a tissue before they can cause any harm. In hindsight, this was perhaps a bit naïve and, in fact, the answer was staring us in the face all along.

Our study is very much built on a sturdy foundation of work from a number of groups, particularly those of Matthew Freeman, Andreas Bergmann and Joe Parker/Peter Lawrence. It is, for example, well known that EGFR signalling promotes cell survival. Likewise, it is known that the major EGFR ligands are expressed in a segmental fashion in *Drosophila* embryos, with regular peaks of ligand production occurring throughout the epidermis. In many ways, the main purpose of our paper is to connect these observations. By showing that patterning errors disrupt the regular production of EGFR activating ligands and that the major consequence of this disruption is localised cell death, we were able to explain apoptosis in mis-patterned embryos and speculate on the implications this may have on size control and overall body dimensions in the process.

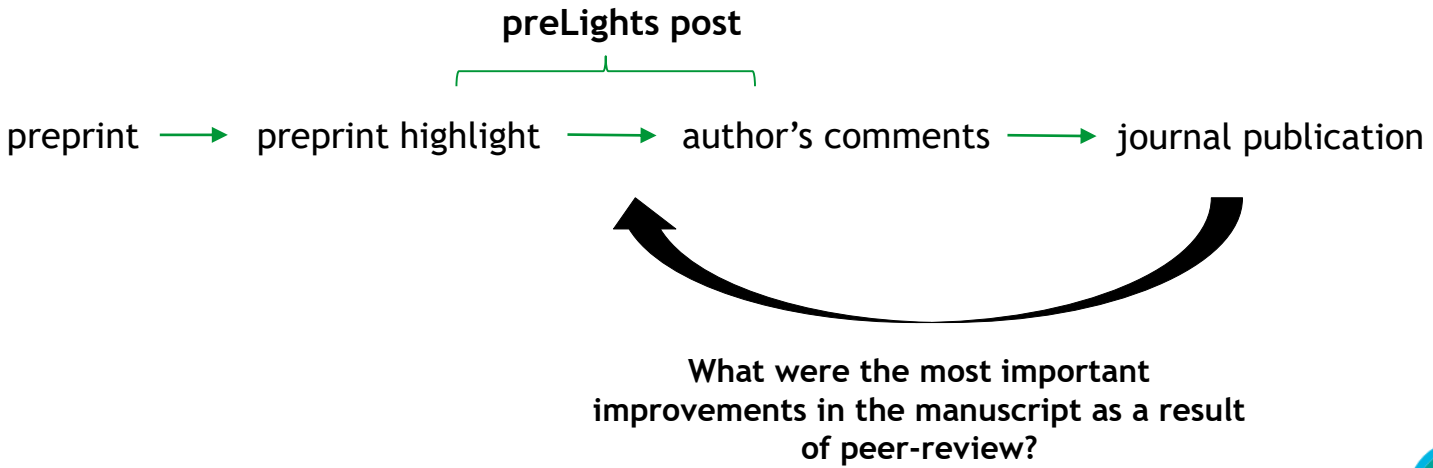
Even though we set out hoping to discover a novel mechanism of tissue homeostasis and cell fate surveillance, I am pleased that our work ended up complimenting and building on a number of excellent pre-existing studies. We are under constant pressure to discover new mechanisms or rewrite old theories in order to inflate the impact factor of our publications. However, in this instance, the simplest explanation proved to be correct and I'm very happy with the final outcome!

Author's response to questions

Authors have revised their work based on the preLights discussion

And we have seen preLights cited in published peer review reports

Commentary after journal publication to learn about peer-review process



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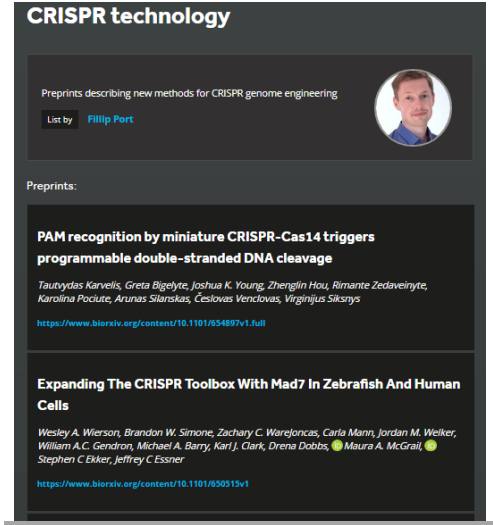
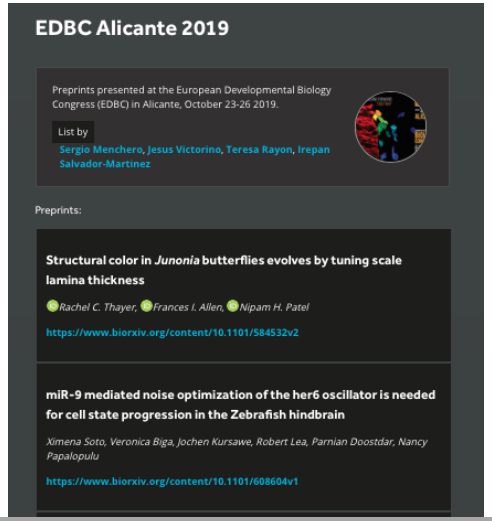
preLists: curated preprint lists

Topic-specific preprint lists



Preprint lists from conferences

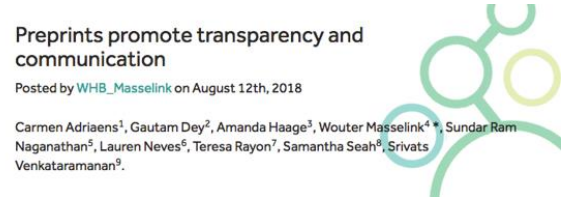


Sergio Menchero

Any scientist who registers on preLights can curate preLists!

The community aspect of preLights

Commentaries and blog posts


Preprints promote transparency and communication

Posted by WHB_Masselink on August 12th, 2018

Carmen Adriaens[1], Gautam Dey[2], Amanda Haage[3], Wouter Masselink[4] *, Sundar Ram Naganathan[5], Lauren Neves[6], Teresa Rayon[7], Samantha Seah[8], Srivats Venkataramanan[9].


ascb

preLights: Preprint highlights for biology

By Amanda Haage | July 13, 2018

Preprints are a growing trend that is pushing the pace of dissemination of scientific information. preLights is a new service that selects and highlights preprints in a wide range of biological fields and can help you keep up to date!

Quick Links

Meeting up at conferences, giving talks

We help preLighters build their profile

Meet the preLighters: an interview with Carmen Adriaens

16th May 2018

Carmen Adriaens is a fourth year PhD student in the lab of Prof. Chris Marine at the Center fo Cancer Biology (VIB-KU Leuven) in Belgium. She is currently completing her final year of doctora research in the lab of Dr. Tom Misteli at the Center for Cancer Research, NCI/NIH in Bethesda, Carmen's research focuses on a long noncoding RNA that gives rise to a nuclear body called the paraspeckle. We caught up with Carmen to discuss her research, her thoughts on preprints and experience as a preLighter.

Meet the preLighters: an interview with Erik Clark

15th June 2018

Erik Clark is a postdoctoral researcher at the University of Cambridge in the lab of Michael Akam. Erik studied at Oxford and Imperial College London before starting his PhD, where he worked on segmentation patterning in Drosophila. Erik has won a number of grants and awards, among them the BSDB Beddington medal for the best PhD thesis in Developmental Biology (click here to see his Beddington lecture). We caught up with Erik at his office at the University of Cambridge Zoology Department to talk about his evo-devo research and his experience with preprints and preLights.

Meet the preLighters: an interview with Samantha Seah

26th October 2018

Samantha Seah is a PhD student at EMBL, Heidelberg in the lab of Christoph Merten. She trained as a geneticist, and now develops microfluidic technology for antibody screening. We caught up with Samantha to talk about different aspects of science, preprints and preLights.

Meet the preLighters: an interview with Heath MacMillan

22nd August 2018

Heath MacMillan is an Assistant Professor at Carleton University in Ottawa. His lab is studyin mechanisms of thermal tolerance in insects and aims to answer questions like 'Why can one survive a Canadian winter while the other cannot?' We caught up with Heath to talk about his research, lab and preprints.

Meet the preLighters: an interview with Natalie Dye

23rd April 2018

Natalie Dye is a postdoctoral scientist in Suzanne Eaton's lab at the MPI-CBG, studying growth control and tissue patterning in Drosophila. We caught up with Natalie in Dresden to talk about her career and research, her opinion on preprints, and her first impressions of being an active member of the preLights community.

Meet the preLighters: an interview with James Gagnon

8th May 2018

James Gagnon is an Assistant Professor at the University of Utah, where he started his lab at the beginning of the year. As a postdoc at Harvard, he developed methods for lineage tracing in zebrafish embryos, using CRISPR-Cas9 barcode editing. We caught up with Jamie to talk about his research, how science can be made more open, his enthusiasm for the preLights project and the fun sides of being a junior PI.

preLights - the first 20 months

- >150 'preLighters'
- 560 posts
- 1/3 of posts feature an author's response
- >2,000 views per week
- >3.8K followers on Twitter
- Feedback from community has been hugely positive

bioRxiv preprints link to preLights posts

Indexed in EuropePMC

Europe PubMed Central

"Wonderful! This is a game changer"

"It looks fantastic!"

"I do like the 'Author's Response' section"

"Great initiative"

"Showing how preprints allow for the evolution of the scientific publishing model"

ALPSP Awards for Innovation in Publishing 2019
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Thank you!

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