

Open Research: Moving beyond open access

Open in Practice 2019

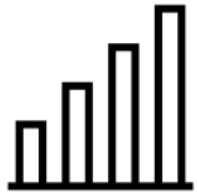
Demitra Ellina – Editorial Community Manager

Outline

- What do we mean by Open Research?
- What is F1000Research?
- How does it work?
- What are the benefits of publishing on this platform?
- Why are funders adopting our publishing model?

Open Research is more than Open Access

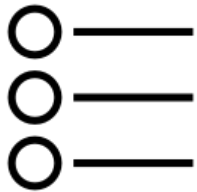
Open Data



Open Source



Open Methods



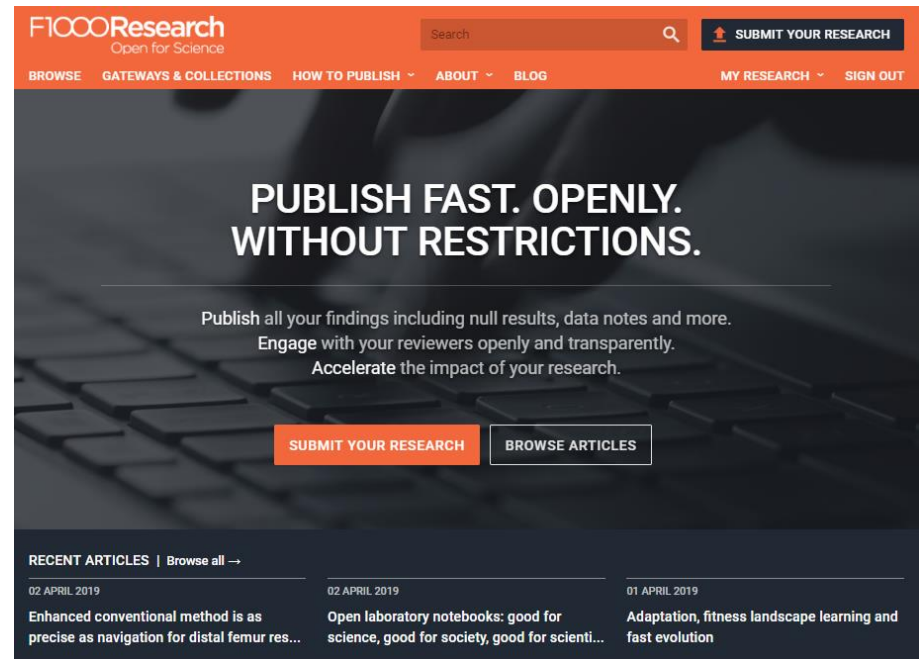
Open Peer Review



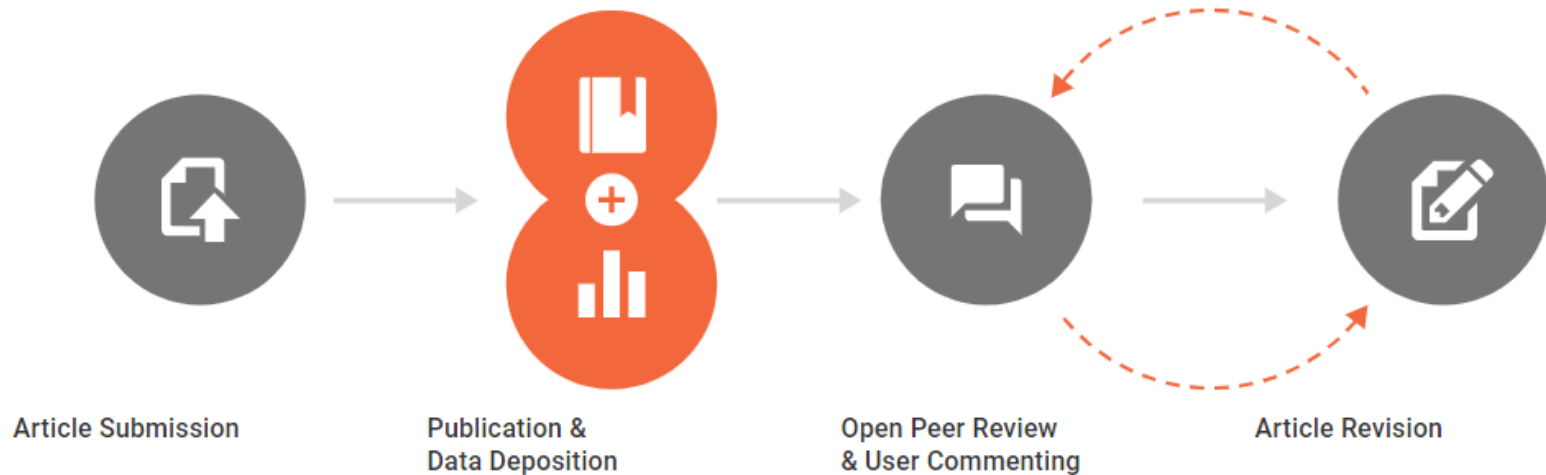
What is F1000Research?

An Open Research publishing platform where a range of research outputs can be published

<https://f1000research.com/>



How does it work?



- Open invited peer review after publication
- Open access, open data
- Transparent peer review
- Versioning

Referee report statuses

- **Approved:** No or only minor changes are required.
- **Approved with Reservations:** The article is not fully technically sound in its current version, but your criticisms could be addressed with specific, sometimes major, revisions.
- **Not Approved:** The article is of very poor quality and there are fundamental flaws in the article that seriously undermine the findings and conclusions.

Referee ratings:



Approved



Approved with reservations



Not approved

Minimal requirements for indexing:



or



Published article

- Clearly labelled as awaiting peer review
- Citable
- Grant information
- Data availability statement


The screenshot displays a research article page with the following elements:

- Check for updates** button at the top right.
- RESEARCH ARTICLE** label above the title.
- Title:** Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data [version 1; referees: awaiting peer review]
- Authors:** J. Javier Diaz-Mejia^{1,3}, Elaine C. Meng³, Alexander R. Pico⁴, Sonya A. MacParland^{5,7}, Troy Ketela¹, Trevor J. Pugh^{1,8,9}, Gary D. Bader¹⁰, and John H. Morris³. Each name is followed by an ORCID icon.
- Author details** link below the author list.
- ISCB Community Journal gateway** badge: This article is included in the International Society for Computational Biology Community Journal gateway.
- Abstract:**
 - Background:** Identification of cell type subpopulations from complex cell mixtures using single-cell RNA-sequencing (scRNA-seq) data includes automated computational steps like data normalization, dimensionality reduction and cell clustering. However, assigning cell type labels to cell clusters is still conducted manually by most researchers, resulting in limited documentation, low reproducibility and uncontrolled vocabularies. Two bottlenecks to automating this task are the scarcity of reference cell type gene expression signatures and the fact that some dedicated methods are available only as web servers with limited cell type gene expression signatures.
 - Methods:** In this study, we benchmarked four methods (CIBERSORT, GSEA, GSVA, and ORA) for the
- Metrics sidebar:**
 - METRICS:** 92
 - VIEWS:** 12
 - DOWNLOADS:** 12
 - Buttons: Get PDF, Get XML, Cite, Export, Track, Email, Share.
- Open Peer Review sidebar:**
 - Reviewer Status:** AWAITING PEER REVIEW
 - Comments on this article:** All Comments (0), Add a comment
 - Sign up for content alerts:** Input field for email address and a SIGN UP button.

Diaz-Mejia JJ, Meng EC, Pico AR et al. Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data [version 1; peer review: 3 approved with reservations]. F1000Research 2019, 8(ISCB Comm J):296 (<https://doi.org/10.12688/f1000research.18490.1>)

Published article

- Clearly labelled as awaiting peer review
- Citable
- Grant information
- Data availability statement

 Corresponding author: John H. Morris

Competing interests: No competing interests were disclosed.

Grant information: JJDM, ECM, ARP, and JHM are funded by grant number 2018-183120 from the Chan Zuckerberg Initiative DAF, an advised fund of the Silicon Valley Community Foundation. ARP, GDB and JHM are supported by the National Resource for Network Biology, P41GM103504 (NIGMS).

The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.



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How to cite: Diaz-Mejia JJ, Meng EC, Pico AR et al. Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data [version 1; peer review: 1 approved with reservations]. *F1000Research* 2019, 8(ISCB Comm J):296 (<https://doi.org/10.12688/f1000research.18490.1>)

First published: 15 Mar 2019, 8(ISCB Comm J):296 (<https://doi.org/10.12688/f1000research.18490.1>)

Latest published: 15 Mar 2019, 8(ISCB Comm J):296 (<https://doi.org/10.12688/f1000research.18490.1>)

Published article

- Clearly labelled as awaiting peer review
- Citable
- Grant information
- Data availability statement

Data availability

Underlying data

The datasets used in this study were processed from the below underlying source data:

Single-cell RNA-sequencing data from human liver cells. Accession number, [GSE115469](https://identifiers.org/geo/GSE115469).
<https://identifiers.org/geo/GSE115469>.

Single-cell RNA-sequencing data from human peripheral blood mononuclear cells. Accession number, [SRX1723926](https://identifiers.org/insdc.sra/SRX1723926).
<https://identifiers.org/insdc.sra/SRX1723926>.

Single cell RNA-sequencing of retinal bipolar cells. Accession number, [GSE81905](https://identifiers.org/geo/GSE81905). <https://identifiers.org/geo/GSE81905>.

Extended data

Zenodo: Supplementary data for "Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data". <http://doi.org/10.5281/zenodo.2575050> (Diaz-Mejia, 2019a).

This project contains the three processed scRNA-seq datasets—from liver cells (MacParland *et al.*, 2018), peripheral blood mononuclear cells (Zheng *et al.*, 2017a) and retinal neurons (Shekhar *et al.*, 2016b)—examined in this study.

Software availability

R and Perl scripts used to run and benchmark cell type labeling methods available from:
https://github.com/jdime/scRNAseq_cell_cluster_labeling.

Archived code at time of publication: <http://doi.org/10.5281/zenodo.2583161> (Diaz-Mejia, 2019b).

License: MIT license.

Version 2

- Peer review status is clear in the title and citation
- Peer review is transparent and open
- Amendments box

RESEARCH ARTICLE

REVISED Increased abundance of ADAM9 transcripts in the blood is associated with tissue damage [version 2; peer review: 3 approved]

Darawan Rinchai¹, Chidchamai Kewcharoenwong², Bianca Kessler², Ganjana Lertmemongkolkhai²,
✉ Damien Chaussabel¹

✚ Author details

This article is included in the Sidra Medicine gateway.

Abstract

Background: Members of the ADAM (a disintegrin and metalloprotease domain) family have emerged as critical regulators of cell-cell signaling during development and homeostasis. ADAM9 is consistently overexpressed in various human cancers, and has been shown to play an important role in tumorigenesis. However, little is known about the involvement of ADAM9 during immune-mediated processes.

Results: Mining of an extensive compendium of transcriptomic datasets identified important gaps in knowledge regarding the possible role of ADAM9 in immunological homeostasis and inflammation: 1) The abundance of ADAM9 transcripts in the blood was increased in patients with acute infection but, 2) changed very little after *in vitro* exposure to a wide range of pathogen-associated molecular patterns (PAMPs). 3) Furthermore it was found to increase significantly in subjects as a result of tissue injury or tissue remodeling, in absence of infectious processes.

Conclusions: Our findings indicate that ADAM9 may constitute a valuable biomarker for the assessment of tissue damage, especially in clinical situations where other inflammatory markers are confounded by infectious processes.

Keywords

ADAM9, Data mining, Transcriptomics, RNAseq, Microarray

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Open Peer Review

Reviewer Status

Reviewer Reports

Invited Reviewers

	1	2	3
Version 2 24 Oct 16	 read	 read	 read
Version 1 09 Apr 15	 read	 read	 read

1. Adaikalavan Ramasamy, University of Oxford, UK
2. Andreas Ludwig, RWTH Aachen University Hospital, Germany
Daniela Dreymüller, RWTH Aachen University Hospital, Germany
3. Caroline A. Owen, Harvard Medical School, USA

Comments on this article

All Comments (0)
Add a comment

Rinchai D, Kewcharoenwong C, Kessler B *et al.* Increased abundance of ADAM9 transcripts in the blood is associated with tissue damage [version 2; peer review: 3 approved]. *F1000Research* 2016, **4**:89
(<https://doi.org/10.12688/f1000research.6241.2>)

Version 2

- Peer review status is clear in the title and citation
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Open Peer Review			
Reviewer Status  			
Reviewer Reports			
	1	Invited Reviewers 2	3
Version 2 24 Oct 16	 read	 read	 read
	↑	↑	↑
Version 1 09 Apr 15	 read	 read	 read
<hr/> <ol style="list-style-type: none">1. Adaikalavan Ramasamy, University of Oxford, UK2. Andreas Ludwig, RWTH Aachen University Hospital, Germany Daniela Dreytmüller, RWTH Aachen University Hospital, Germany3. Caroline A. Owen, Harvard Medical School, USA			

Rinchai D, Kewcharoenwong C, Kessler B *et al*. Increased abundance of ADAM9 transcripts in the blood is associated with tissue damage [version 2; peer review: 3 approved]. *F1000Research* 2016, **4**:89
(<https://doi.org/10.12688/f1000research.6241.2>)

Version 2

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REVISED Amendments from Version 1

In response to the reviewers we added background information at the beginning of the introduction section to present the rationale behind the data mining approach that was employed as well as the purpose of diagrams that were integrated to the figures. These in essence constitute "graphical legends" and allow presentation of the data in a semi-structured format, thus diagrams were moved accordingly below the plots in each figure. We also re-plotted the result of figure 1, retaining only neutrophil and monocyte data plot as per the reviewers' suggestions. Additional data have been plotted as requested by the reviewers. We have also analyzed association of abundance of ADAM9 with degree of severity in trauma patients (GSE11375: Figure 5) and viral infections (GSE34205/GSE38900; Conclusions); and also added datasets generated in experimental models of injury *in vitro* and *in vivo* in human and mice (Supplementary figure 6) to further document the involvement of ADAM9 in tissue inflammation/injury. Finally we have also updated the title of this article.

See reviewer responses

Rinchai D, Kewcharoenwong C, Kessler B *et al*. Increased abundance of ADAM9 transcripts in the blood is associated with tissue damage [version 2; peer review: 3 approved]. *F1000Research* 2016, **4**:89 (<https://doi.org/10.12688/f1000research.6241.2>)


Reviewer report

Reviewer Report

19 Views

06 Feb 2019 | for Version 1

Matthew H. Todd , School of Pharmacy, University College London (UCL), London, UK

Edwin Tse , University of Sydney, Sydney, Australia

Marat Korsik, University of Sydney, Sydney, Australia

Mathamsanqa Bhebhe, University of Sydney, Sydney, Australia

 Cite this report

 Responses (1)

? APPROVED WITH RESERVATIONS

This opinion piece is on a timely, important topic and is clearly and engagingly written. Anecdotally, we find that many of our colleagues in science are unaware that open lab notebooks exist. This article will help.

The authors identify several important advantages and challenges associated with the near-immediate deposition of results into the public domain, online. They use examples from their own research to highlight the possibilities.

The refereeing team behind this review are seasoned users of open lab notebooks, and so are in a good position to judge the piece. We judge it to have cleared peer review from our perspective, once the following comments and suggestions have been acted upon. There are a number, which should be read not as criticism but as testament to our shared enthusiasm for this subject and its importance in the future of research.

1) **Secrecy.** In the introduction, reasons are suggested for why scientists may keep results secret. We would suggest that there are two important reasons that are not explicitly mentioned: i) that the scientist may want to patent something, and ii) that the scientist cannot be bothered to work out how to release research using atypical means. The first point is alluded to where mention is made of ownership, and the second point is alluded to by the mention of "paper" but we would argue these two factors are significant enough that they should be made explicit.

2) **Careers.** We'd be interested in whether there is a justification for the statement "Many believe that openly sharing work online will limit career opportunities." If there is none, then perhaps rephrase this more as a possibility?

Responses (1)

AUTHOR RESPONSE 02 Apr 2019

Matthieu Schapira, SGC, Toronto, Canada

1) **Secrecy.** In the introduction, reasons are suggested for why scientists may keep results secret. We would suggest that there are two important reasons that are not explicitly mentioned: i) that the scientist may want to patent something, and ii) that the scientist cannot be bothered to work out how to release research using atypical means. The first point is alluded to where mention is made of ownership, and the second point is alluded to by the mention of "paper" but we would argue these two factors are significant enough that they should be made explicit.

Points well taken. The following statement was added to the Introduction "...and can be compounded by constraints associated with patent protection procedures or the absence of clear mechanism to make one's data publicly available."

2) **Careers.** We'd be interested in whether there is a justification for the statement "Many believe that openly sharing work online will limit career opportunities." If there is none, then perhaps rephrase this more as a possibility?

This was not clear. The sentence was replaced as follows:

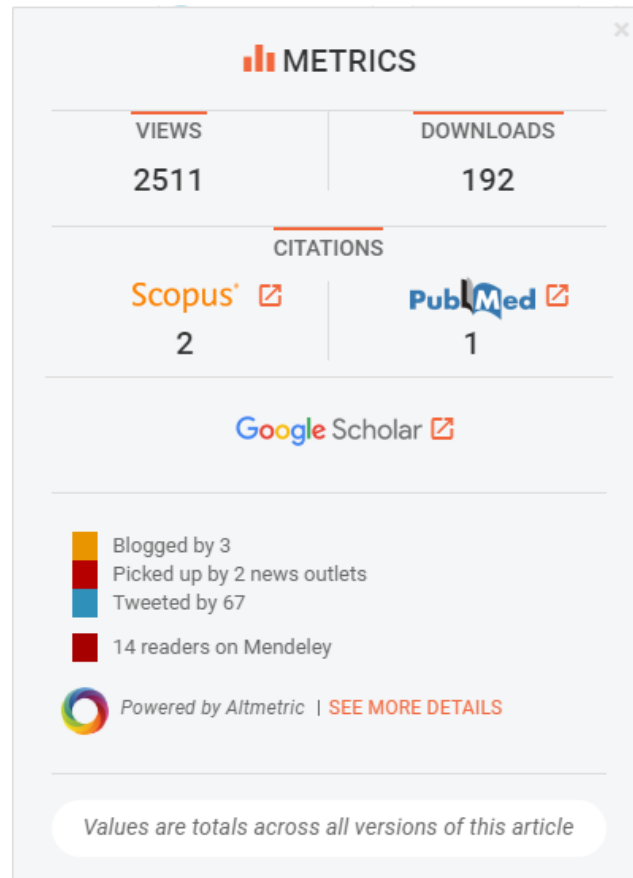
"Many believe that the chances of getting scooped before one publishes their work in a peer-reviewed journal increase when openly sharing their work online [9]"

3) **Grants.** The statement "Grant applications that highlight the use of open lab notebooks are being viewed positively" may be true (one hopes it is), but the evidence presented doesn't support that statement (the grants may have been funded because the science was so good, regardless of the dissemination plan), so again, this probably needs to be made more aspirational.

This was revised as follows:

Todd MH, Tse E, Korsik M and Bhebhe M. Referee Report For: Open laboratory notebooks: good for science, good for society, good for scientists [version 1; peer review: 2 approved with reservations]. *F1000Research* 2019, **8**:87
(<https://doi.org/10.5256/f1000research.19363.r43417>)

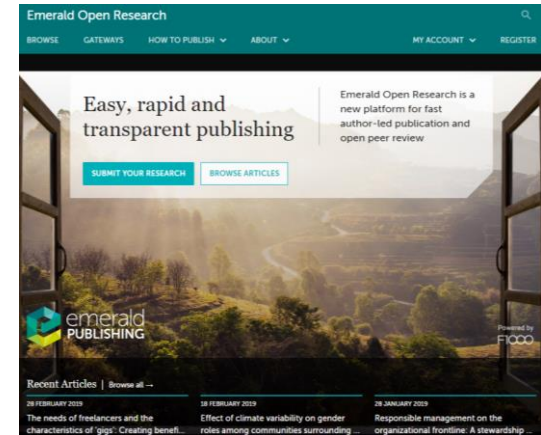
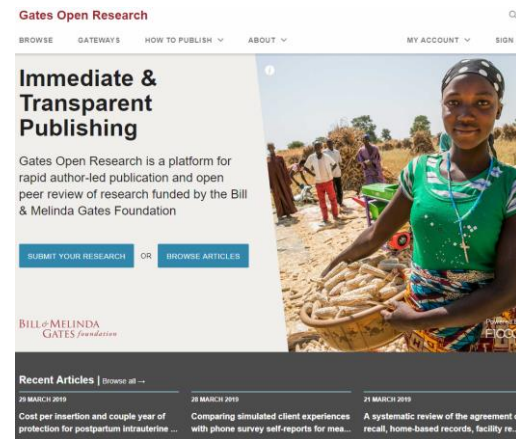
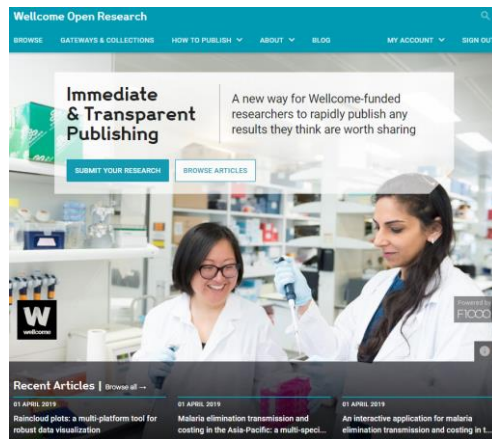
Metrics



What are the benefits?

- Fast
- Open and transparent
- Reproducible
- No editorial bias
- Inclusive
- Reduces research waste

Funder-based publishing platforms



Why are funders adopting our publishing model?

“Wellcome Open Research enables Wellcome-funded researchers to **publish all their research outputs quickly, openly and transparently and in ways which support reproducibility.**”

Prof Sir Mike Ferguson CBE FRS FRSE FMed
Governor on the Board of The Wellcome Trust

“The Gates Foundation is dedicated to the belief that all lives have equal value and everyone deserves the opportunity to lead a healthy and productive life. To solve the challenges of the 21st century, we must **accelerate open access to high-quality research on health, education, and economic development.** Gates Open Research is designed to ensure that the research we fund can be of immediate benefit to society.”

Trevor mundel
President of Global Health, Bill & Melinda Gates Foundation

Why are funders adopting our publishing model?

“HRB Open Research will help researchers to publish all findings quickly, easily and responsibly. This will **increase transparency, reduce research waste and allow reproducibility of results**. Ultimately HRB Open Research will help **build more trust in the research process**.”

Professor Declan Devane
Director of HRB-Trials Methodology Research Network
Professor of Midwifery, National University of Ireland Galway

“Emerald believes passionately in academia, policy makers and industry working together to **drive positive change**. Emerald Open Research enables our authors to publish and disseminate their research immediately and transparently, ensuring important advances in urgent areas of research reach the community quickly.

We are committed to supporting our communities in overcoming barriers to impact, working in partnership with key agencies to strengthen connections between research and society. We look to **challenge simplistic and outdated approaches to impact, shifting beyond metrics and celebrating impact of all shapes and sizes**.”

Vicky Williams
Chief Executive Officer, Emerald Publishing

Why are funders adopting our publishing model?

A service to their researchers - outlet for all research findings that is funded

Testing **new approach** to improve science & its impact:

- ***accelerate*** access & sharing of findings & data
- ***efficiency*** - to ***reduce waste*** & support ***reproducibility***
- ***alternative OA model*** - access, transparency, cost

Enable researchers get **credit & recognition** for a wider range of research outputs

Play a leading role as a funder in researcher evaluation- help shift the needle and inform new policies on researcher assessment, move away from IF

F1000 Research

Questions?

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@j_ellina