COMING SOON

GATES OPEN RESEARCH

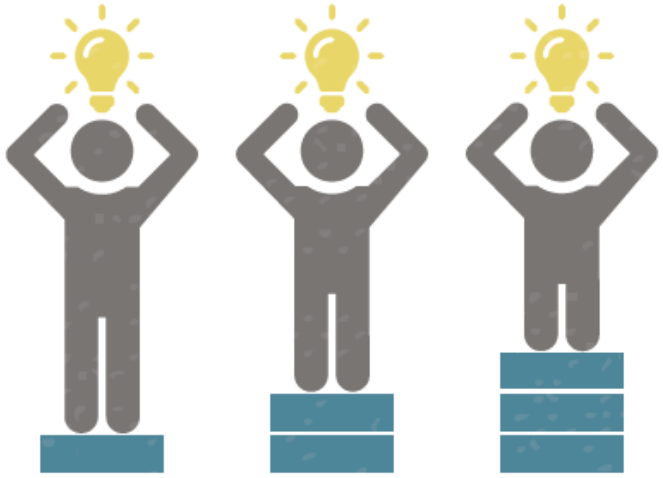
CEGA
May 26, 2017

Ashley Farley, Associate Officer, Knowledge & Research Services, Bill & Melinda Gates Foundation

Phil Dooner, Associate Publisher, F1000

Gates Commitment to Open Access is Mission Driven

Barrier-free access to foundation-funded research advances innovation and helps create a world where everyone has the opportunity to lead a healthy and productive life.



Open Access Policy: Four requirements and a commitment

The Gates Foundation's Open Access Policy enables the unrestricted access and reuse of all its peer-reviewed published research funded, in whole or in part, by the foundation, including any underlying data sets.

REQUIREMENT #1: Publications are discoverable and accessible online

REQUIREMENT #2: Publications will be on Open Access terms, i.e., published under a CC-BY license

REQUIREMENT #3: Publication will be accessible and open immediately, i.e., no embargo

REQUIREMENT #4: Underlying data supporting the published research must also be accessible and open immediately

COMMITMENT: Foundation will pay reasonable fees to publish on the above requirements*

*Special Issues/Supplements – only the APC's will be covered

What does this mean for Gates Foundation grantees?

- All grant agreements signed after January 1st, 2015 contain the following clause:

PUBLICATION IN PEER-REVIEWED JOURNALS

If You seek publication of Funded Developments in a peer-reviewed journal, such publication shall be under "open access" terms and conditions consistent with the Foundation's Open Access Policy available at: http://www.gatesfoundation.org/How-We-Work/General-Information/Open-Access-Policy, which may be modified from time to time.

- This clause is non-negotiable – no exceptions will be made
- Grantee who have signed agreements prior to January 1, 2015, can opt-in to publish on open access terms and the foundation will pay the necessary fees to do so.
- Our goal is to reach 100% compliancy so that all Gates funded research is freely available without barrier or restriction.

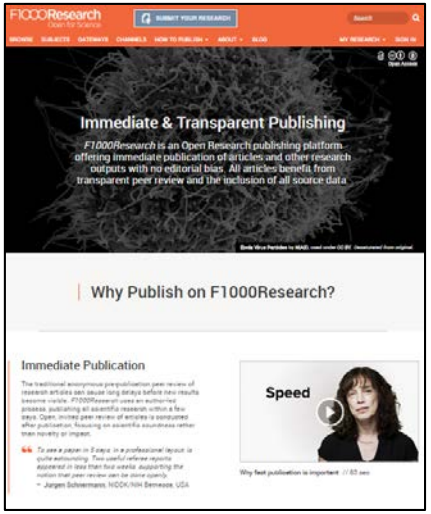
Introducing Gates Open Research

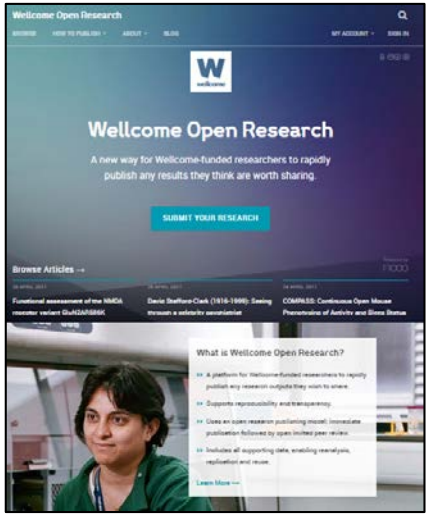
An open access publishing platform where Gates-funded researchers can publish any results they think are worth sharing.

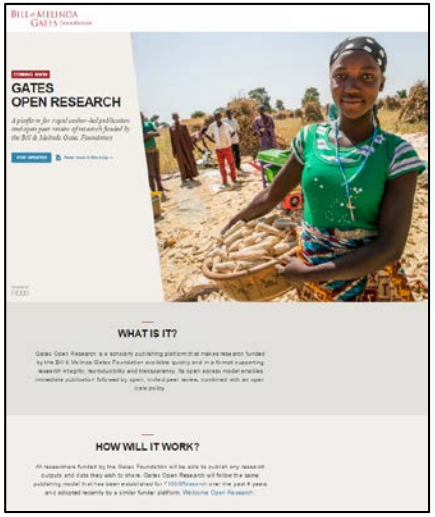
- Allow research to be disseminated without delay - especially crucial during public health emergencies
- Increase transparency and make it easier for researchers to support reproducibility

https://gatesopenresearch.org/

Open Research publishing platforms







- F1000's own platform
- Launched 2013
- More than 1,600 open access articles published

- Controlled by Wellcome, operated by F1000
- Launched Nov 2016
- More than 60 articles published since launch

- Controlled by the Gates Foundation, operated by F1000
- To be launched in Q3 2017

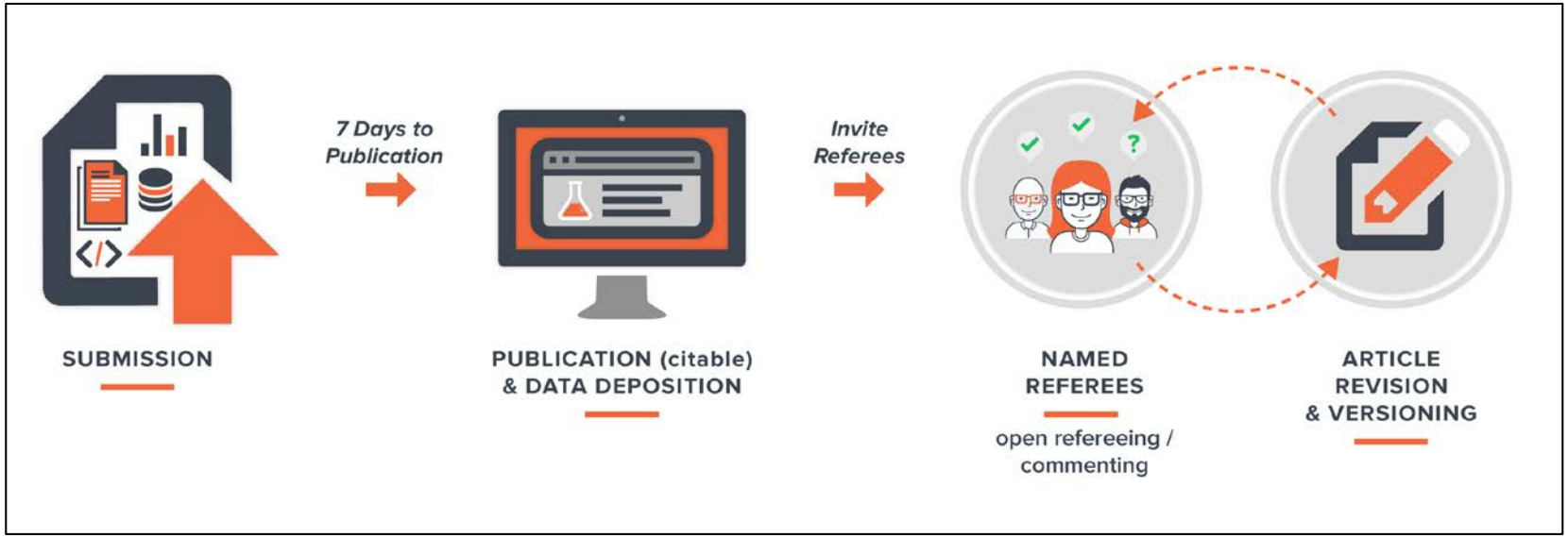
What is different about Gates Open Research?

- **Fast** – articles published within a week
- **Inclusive** – *all* Gates-funded research outputs are suitable: traditional research articles, methods, software, data sets, protocols, negative and confirmatory results etc.
- **Open** – fulfils the foundation's OA and data sharing requirements
- **Reproducible** - source data and code published alongside article
- **Transparent** – open, author-led publishing
- **Easy** – all costs are directly covered by the Gates Foundation

BILL & MELINDA GATES foundation

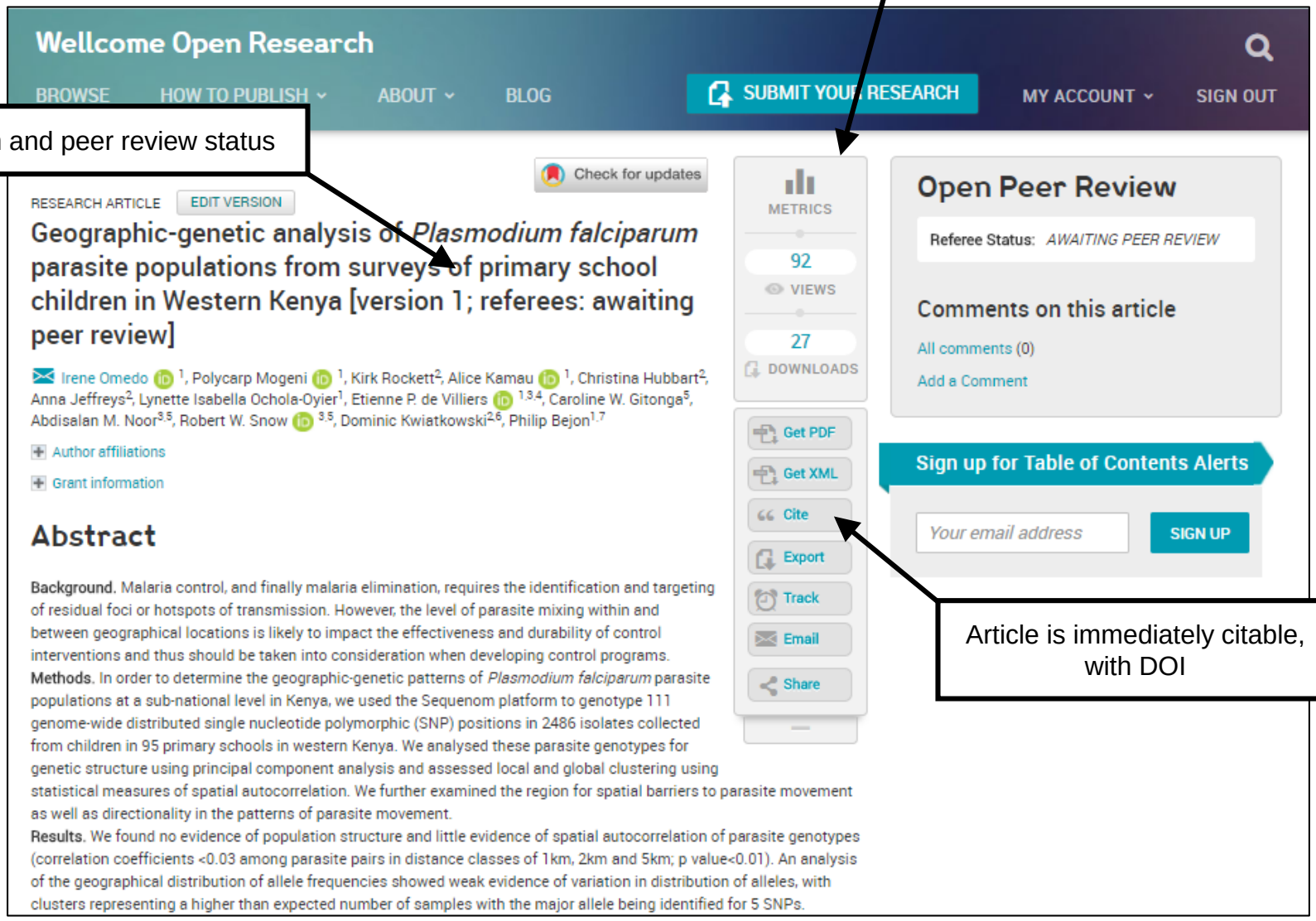
GATES
OPEN RESEARCH

How does it work?

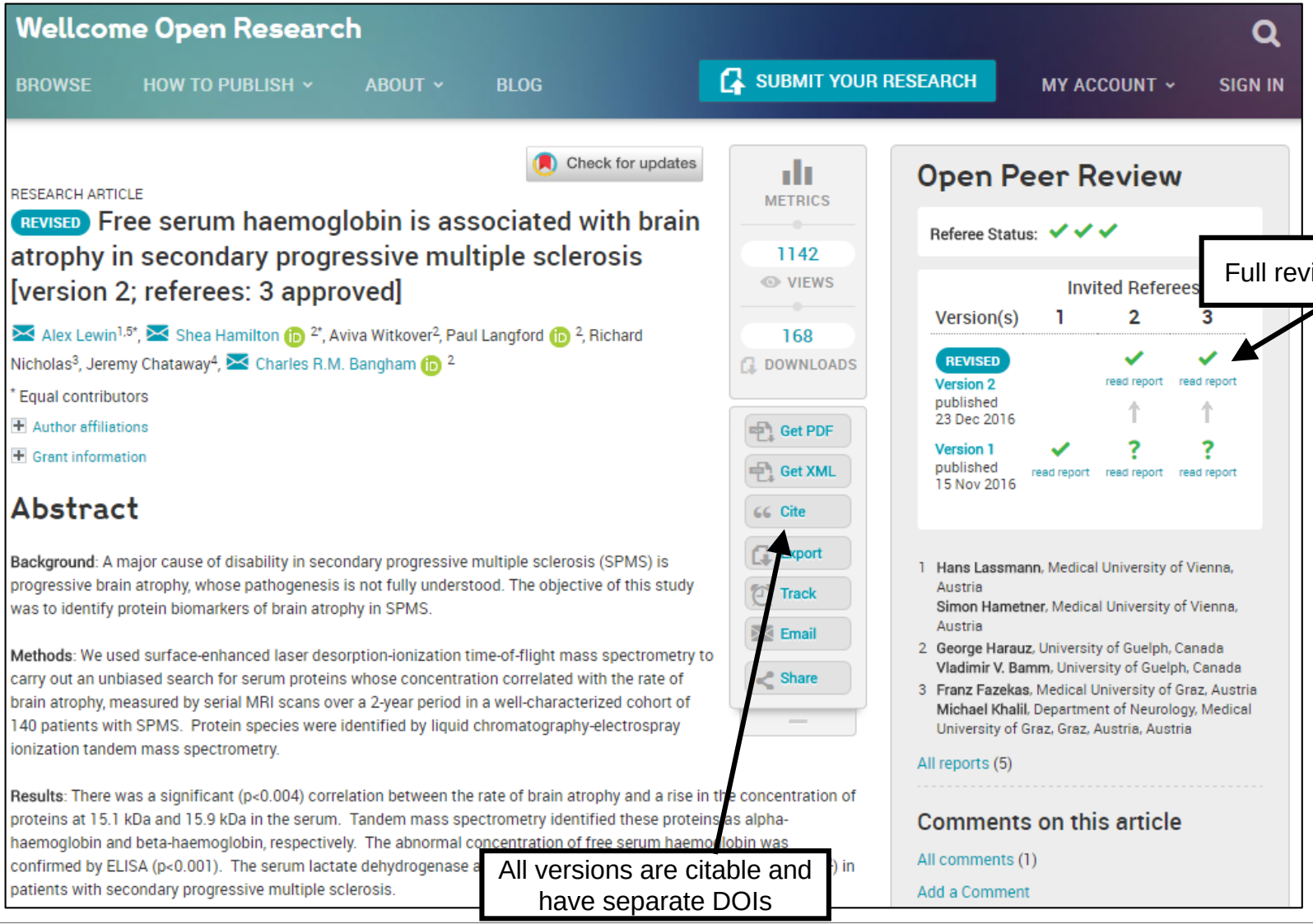


- **Peer review *after* publication** (no ‘Editor’, but in-house pre-pub checks)
- Fully transparent peer review (referee names, report and rating)
- Access to source data
- “living articles”: **Versioning** (also in PubMed) for revisions, corrections, updates

Publication without delay



Post-publication peer review and revisions



Open peer review

Referee Report 21 Nov 2016

George Harauz, Department of Molecular and Cellular Biology, University of Guelph, Guelph, ON, Canada
Vladimir V. Bamm, Department of Molecular and Cellular Biology, University of Guelph, Guelph, ON, Canada

Views 71 Cite

? Approved with Reservations

Summary – This article describes a proteomics analysis of serum proteins derived from 140 patients with secondary progressive multiple sclerosis (MS), 20 healthy adult volunteers, 20 patients with human T-lymphotropic virus (HTLV-1) causing symptoms resembling spinal MS, and 20 asymptomatic HTLV-1 carriers. Half of the MS patients were undergoing treatment with simvastatin, a drug used to lower blood cholesterol and shown to have immunomodulatory and anti-inflammatory properties. Protein profiling of sera was achieved by mass spectrometry of 475 serum samples collected at 0, 12, and 24 months. (A 6-month time point is mentioned in some places and is queried below). The MS patients had concurrent MRI scans at 0, 12, and 25 months to measure whole brain volume (BBSI – brain boundary shift integral), presumably amongst other measures. Serum samples were "enriched" and analysed by 1D SDS-PAGE followed by LC-MS/MS of in gel digested protein. Free haemoglobin (Hb) levels were assessed by ELISA, and activity of lactate dehydrogenase (LDH), an indicator of general tissue damage, and particularly of haemolysis was measured. The proteomics analysis suggested that a 15.1-kDa protein peak correlated with the rate of brain atrophy in seemingly all MS patients, regardless of treatment regime. Following protein enrichment, 15.1-kDa and 15.9-kDa peaks were observed and confirmed to represent the α- and β-chains of haemoglobin, respectively. In all MS patients, levels of both free Hb chains and of LDH activity were elevated compared to all controls. The results are consistent with the idea that Hb is released into serum by chronic and low-grade intravascular haemolysis, with subsequent translocation into the CNS where it has great potential to cause oxidative damage.

Comments on title and abstract –

1. We suggest that the word "associated" needs to be substituted by "correlated"

2. Conclusions in the abstract must be linked to the objectives of the study rather than be a speculative claim.

Comments on study design and data interpretation – Several points require clarification, in our view.

1. There were 140 patents, and 60 controls (3 groups of 20). So the total number is supposed to be 200 serum samples per time point. What are the other 275 samples? The question of sample numbers, both of patients and controls, arises again later when 138 patients are mentioned. Additionally, a valuable control could be a group of

Author Response 23 Dec 2016

Charles Bangham, Department of Immunology, Imperial College London, UK

Lewin *et al.* – response to reviewers
We thank the three pairs of reviewers of our article, each of whom made helpful suggestions and raised salient points for clarification or further discussion. We have revised the article in the light of these comments, and cite further relevant literature (8 references have been added). The response to individual points is given below.

4. The Top 12 Protein Depletion Spin Columns are a good way to partially fractionate the serum or to enrich the protein of interest. However, several very important proteins (haptoglobin, transferrin, and Apo AI) related to iron homeostasis will be removed by this procedure. In the context of this study, it is important to see the specific expression patterns of haptoglobin, hemopexin, and HO-1 since they represent different levels of defence mechanisms against extracellular Hb. Also, it could be beneficial to try and correlate different haptoglobin phenotypes with BBSI.

5. In the same vein, the ELISA kit will detect extracellular Hb from two sources: free Hb and haptoglobin-bound Hb. The latter form could have been removed by the spin column that was used for protein enrichment.

6. Why and how were only 20 patients selected for ELISA?

Comments on discussion – We believe that the Discussion can be augmented to give a broader picture as follows.

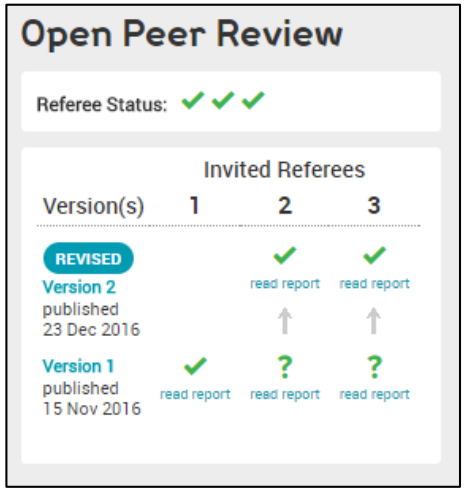
Referee ratings:

- Approved
- Approved with reservations
- Not approved

Minimal requirements for indexing:

 or

Referees can update the status:

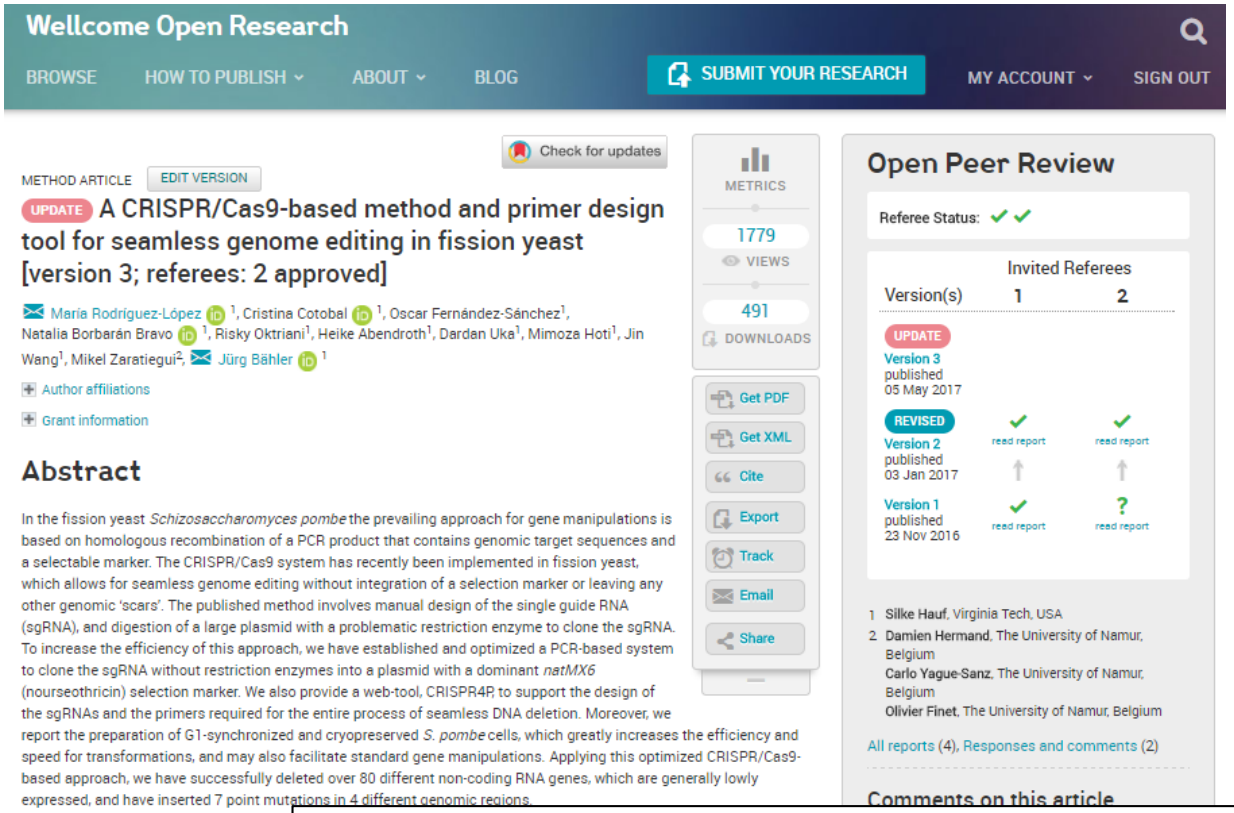


Reproducibility

Data and software policy:

- Access to source data underlying results
- Data must be hosted in a stable open repository
  (e.g. Open Science Framework, Dataverse, Zenodo)
- Data must be clearly described and formatted
- Data must be openly available (with some exceptions)
- Source code for new software must be provided (Software tool articles)

Data and software availability section



Wellcome Open Research

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METHOD ARTICLE EDIT VERSION

UPDATE A CRISPR/Cas9-based method and primer design tool for seamless genome editing in fission yeast [version 3; referees: 2 approved]

María Rodríguez-López [1], Cristina Cotobal [1], Oscar Fernández-Sánchez[1], Natalia Borbarán Bravo [1], Risky Oktriani[1], Heike Abendroth[1], Dardan Uka[1], Mimoza Hoti[1], Jin Wang[1], Mikel Zaratiegui[2], Jürg Bähler [1]

Author affiliations

Grant information

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Abstract

In the fission yeast *Schizosaccharomyces pombe* the prevailing approach for gene manipulations is based on homologous recombination of a PCR product that contains genomic target sequences and a selectable marker. The CRISPR/Cas9 system has recently been implemented in fission yeast, which allows for seamless genome editing without integration of a selection marker or leaving any other genomic 'scars'. The published method involves manual design of the single guide RNA (sgRNA), and digestion of a large plasmid with a problematic restriction enzyme to clone the sgRNA. To increase the efficiency of this approach, we have established and optimized a PCR-based system to clone the sgRNA without restriction enzymes into a plasmid with a dominant *natMX6* (nourseothricin) selection marker. We also provide a web-tool, CRISPR4P, to support the design of the sgRNAs and the primers required for the entire process of seamless DNA deletion. Moreover, we report the preparation of G1-synchronized and cryopreserved *S. pombe* cells, which greatly increases the efficiency and speed for transformations, and may also facilitate standard gene manipulations. Applying this optimized CRISPR/Cas9-based approach, we have successfully deleted over 80 different non-coding RNA genes, which are generally lowly expressed, and have inserted 7 point mutations in 4 different genomic regions.

Open Peer Review

Referee Status: ✓ ✓

Version(s)	1	2
UPDATE Version 3 published 05 May 2017		
REVISED Version 2 published 03 Jan 2017	✓ read report	✓ read report
Version 1 published 23 Nov 2016	✓ read report	? read report

1 Silke Hauf, Virginia Tech, USA

2 Damien Hermand, The University of Namur, Belgium
Carlo Yague-Sanz, The University of Namur, Belgium
Olivier Finet, The University of Namur, Belgium

All reports (4), Responses and comments (2)

Comments on this article

[...]

At-a-glance summary:
Dataset and source code DOIs and direct citations

Data and software availability

CRISPR4P software available from: bahlerlab.info/crispr4p

Latest source code: https://github.com/Bahler-Lab/crispr4p

Archived source code: DOI: 10.5281/zenodo.164683[14]

License: MIT

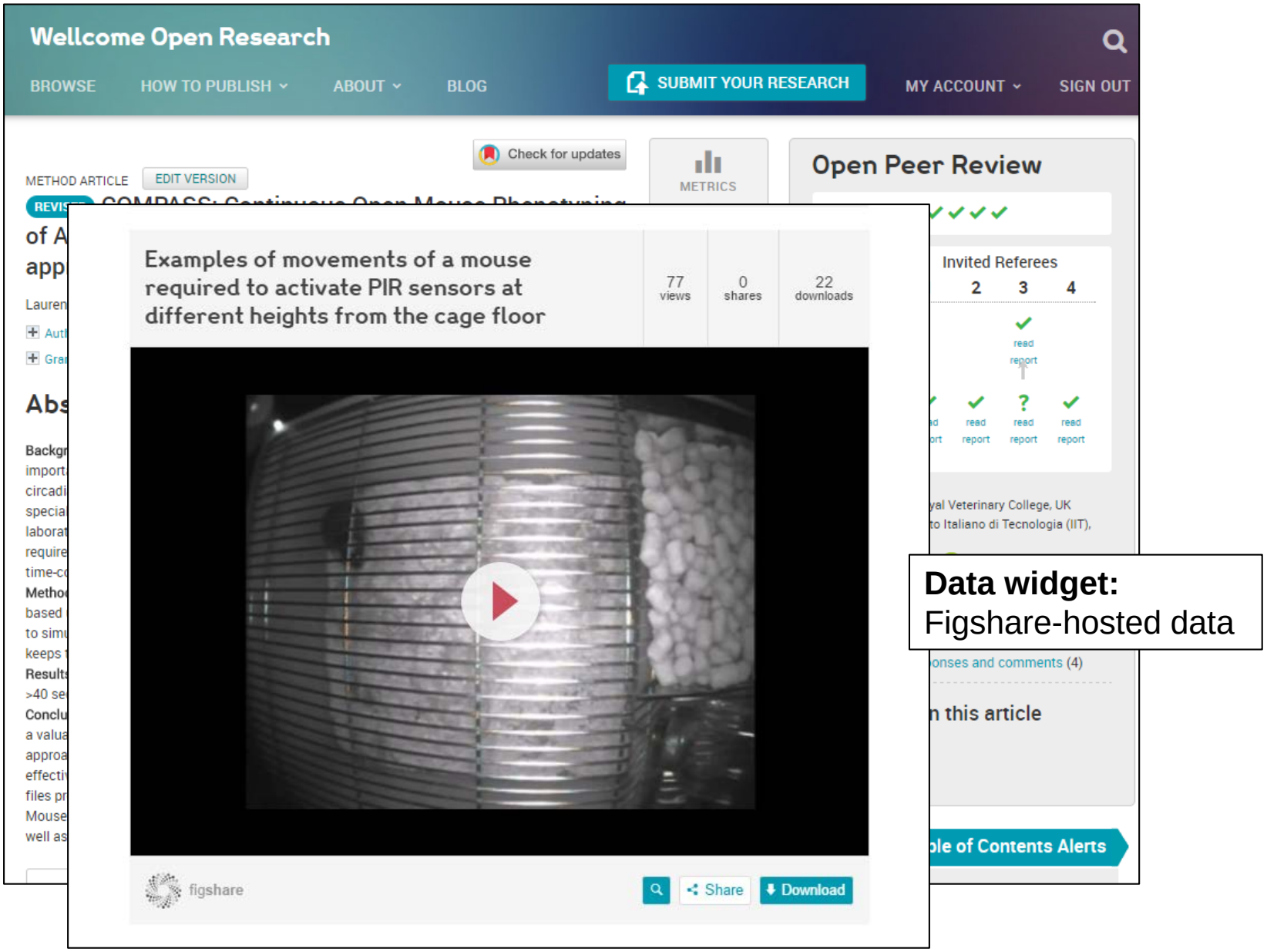
Raw data are deposited in OSF (https://osf.io/5de22/) DOI: 10.17605/OSF.IO/5DE22[28]

References

14. Sinan Shi, osfesa: Bahler-Lab/crispr4p v1.0. *Zenodo.* 2016. Data Source

28. Rodriguez-Lopez M: A CRISPR/Cas9-based method and primer design tool for seamless genome editing in fission yeast. 2016. Data Source

Data visualization

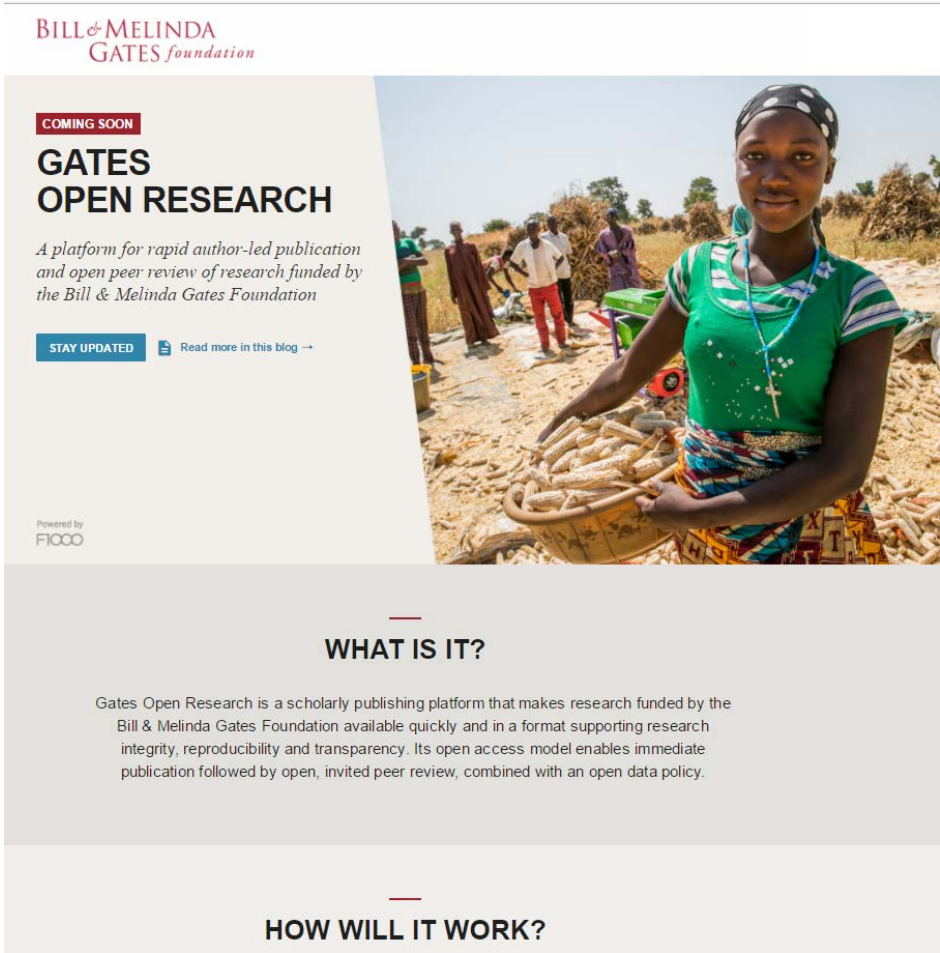


When will Gates Open Research launch?

- Instructions for authors published in July

https://gatesopenresearch.org/

- Submission system launch planned for August
- First articles published in late September



Questions?

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