Research Methods Deserve Credit and Recognition as a Valuable Research Output

Munin Conference on Scholarly Publishing – Nov 2020

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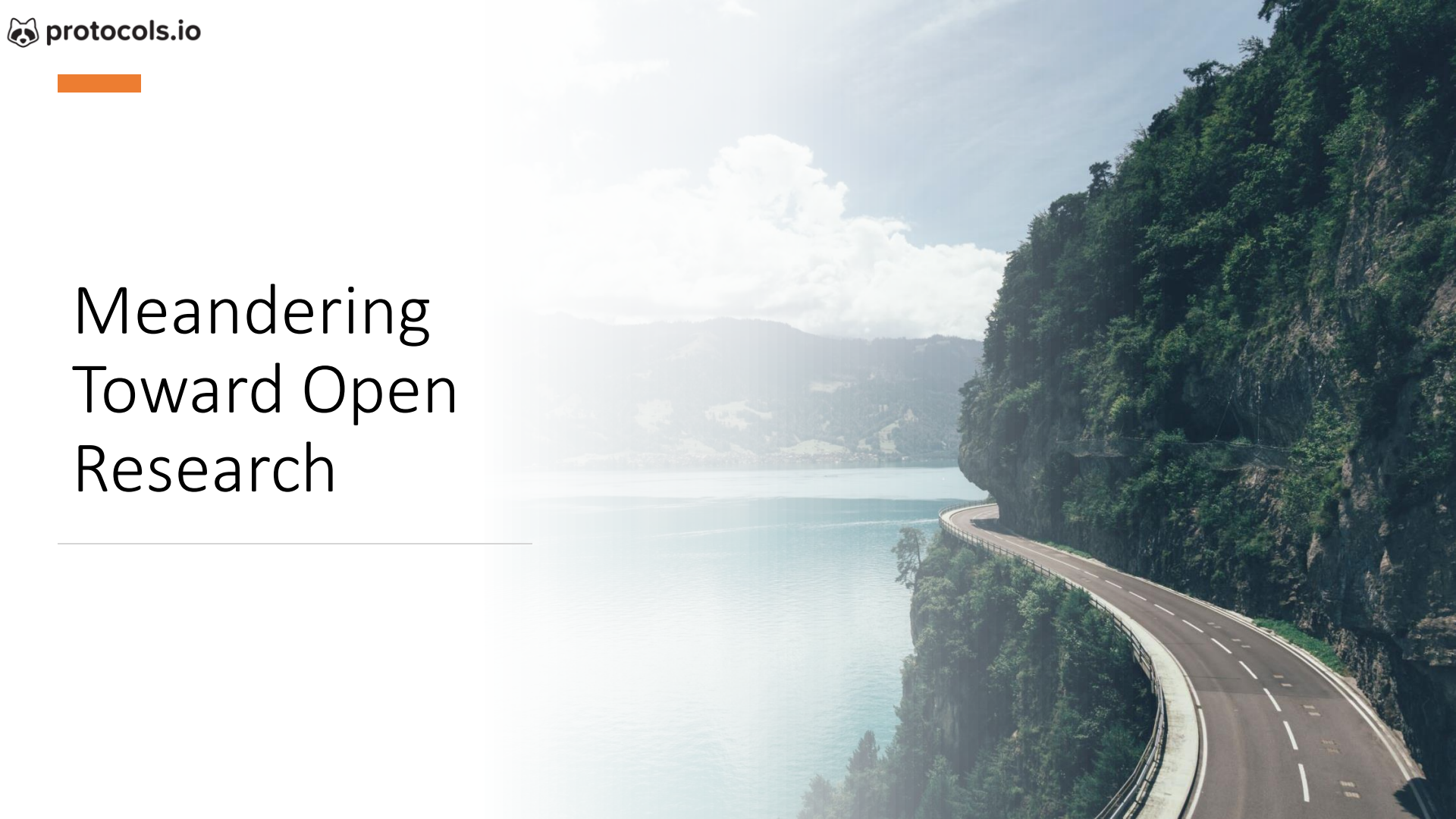
Meandering Toward Open Research



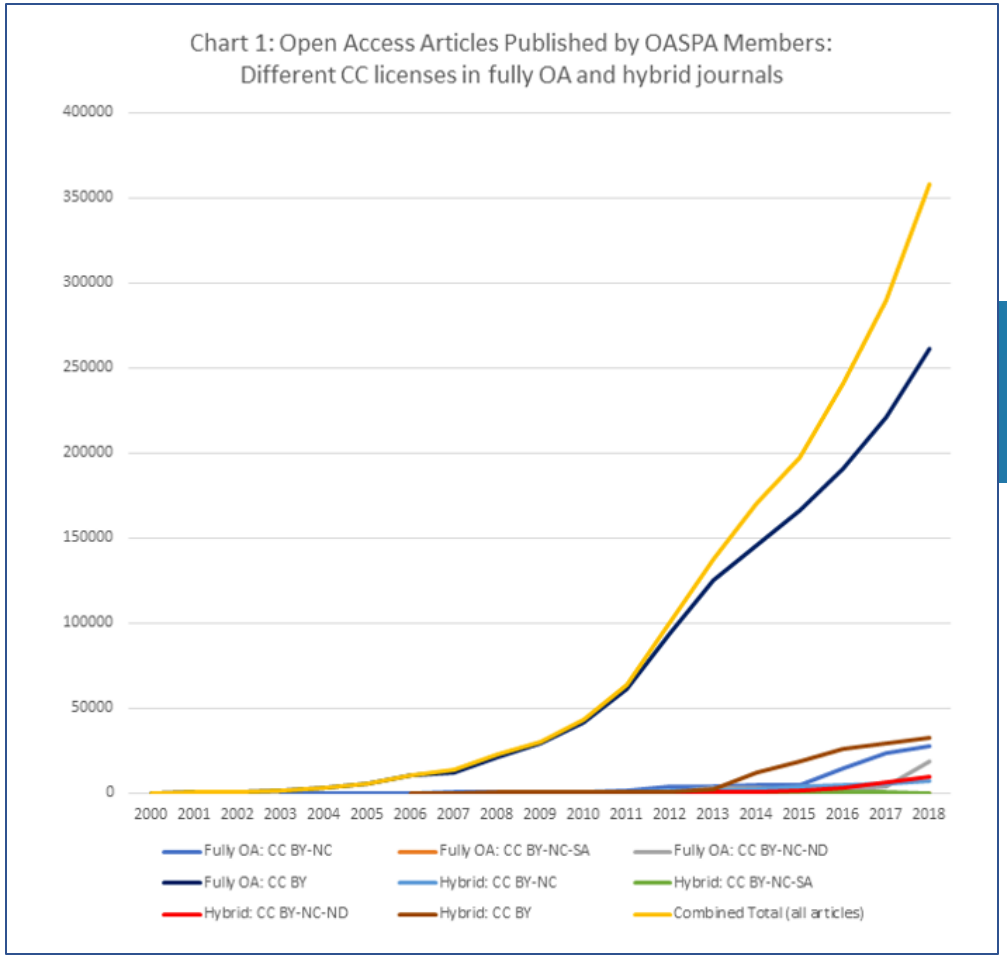
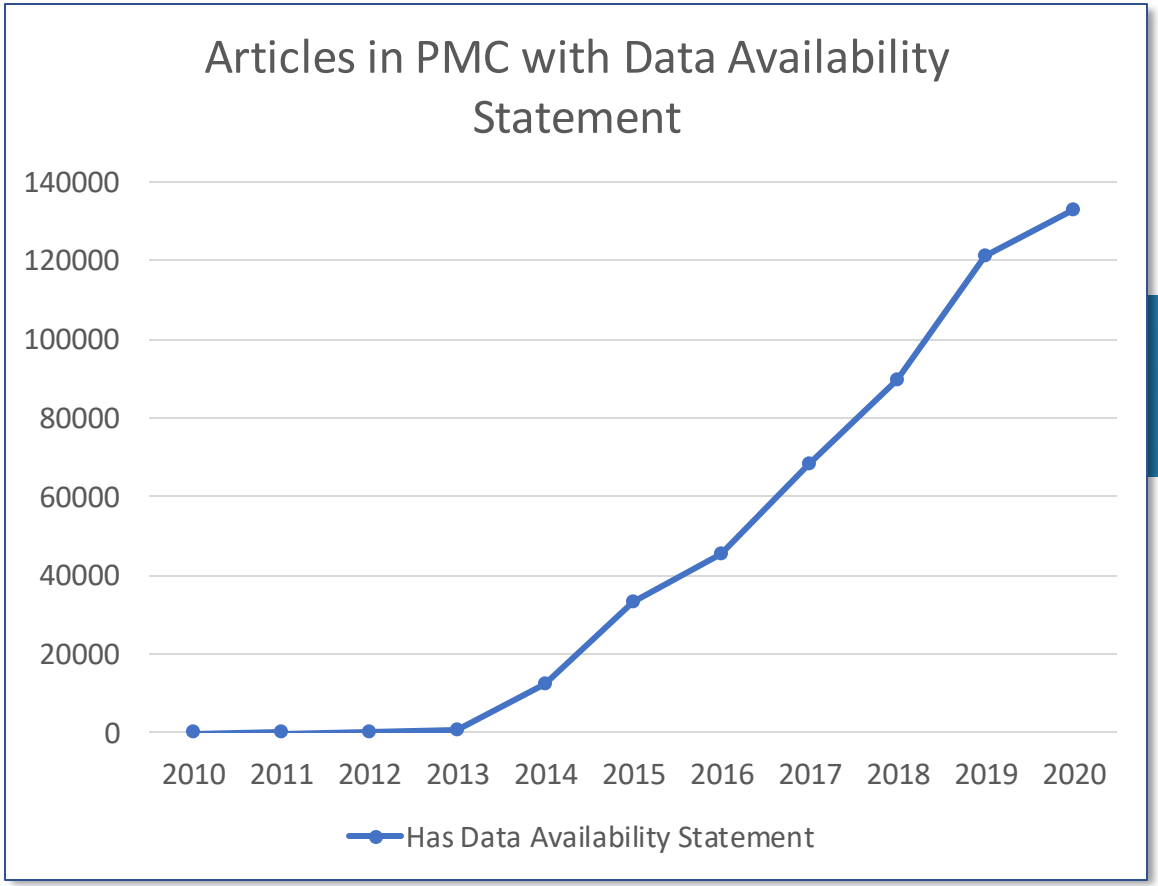


Chart 1: Open Access Articles Published by OASPA Members:
Different CC licenses in fully OA and hybrid journals
400000
350000
300000
250000
200000
150000
100000
50000
0
2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018
Fully OA: CC BY-NC
Fully OA: CC BY-NC-SA
Fully OA: CC BY-NC-ND
Fully OA: CC BY
Hybrid: CC BY-NC
Hybrid: CC BY-NC-SA
Hybrid: CC BY-NC-ND
Hybrid: CC BY
Combined Total (all articles)

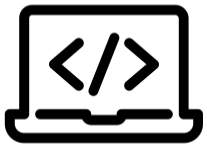
OA Growth


Articles in PMC with Data Availability Statement
140000
120000
100000
80000
60000
40000
20000
0
2010
2011
2012
2013
2014
2015
2016
2017
2018
2019
2020
Has Data Availability Statement

Open Data

Amanda Wray, US

Code



Gregor Cresnar

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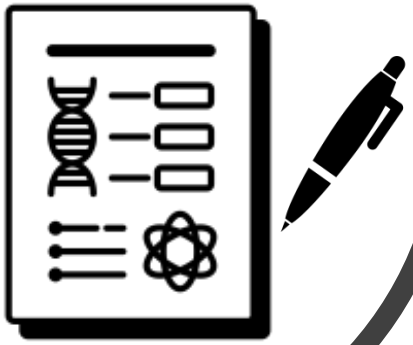
Data

Research Articles



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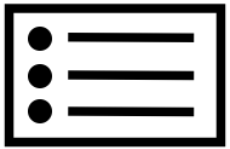

tom, GB

Citations (& Abstracts)

Becris

Methods??

Icons from https://thenounproject.com/

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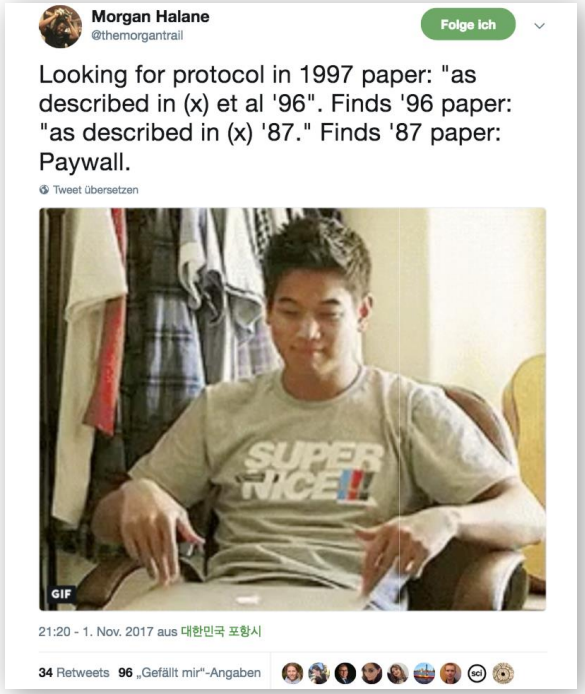
Methods for Reproducible Research



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The Brick Wall / Wild Goose Chase

Researchers cannot:

- find,
- access, or
- replicate…

… the methods

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The Methods Status Quo

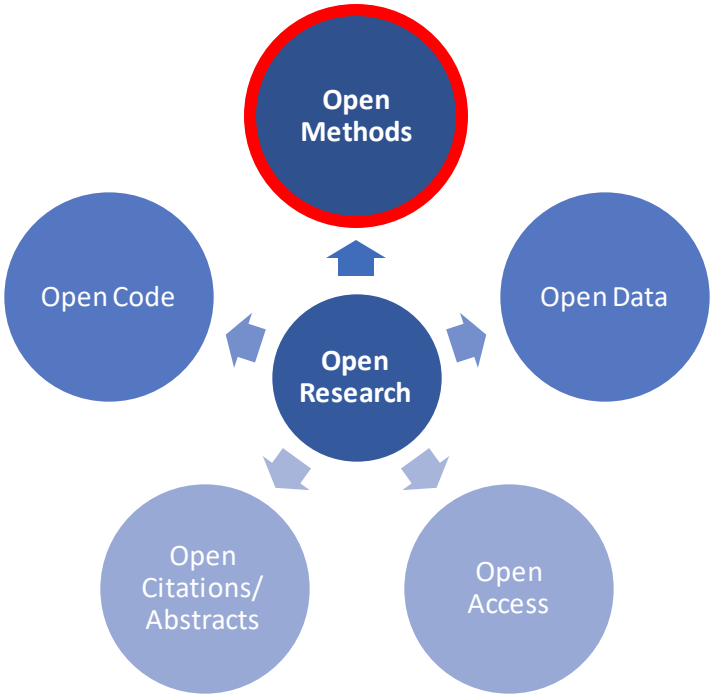
The Cancer Reproducibility Project

- Planned to Replicate 50 Cancer Studies
- Replication of Only 18/50 Attempted
- A “Hopeless Slog”
- Insufficient Methods Details Available

The Cancer Reproducibility Project

"The hardest part, by far, was figuring out exactly what the original labs actually did. Scientific papers come with methods sections that theoretically ought to provide recipes for doing the same experiments. ***But often, those recipes are incomplete, missing out important steps, details, or ingredients. In some cases, the recipes aren't described at all****; researchers simply cite an earlier study that used a similar technique."*

Open Research Requires Open Methods



Methods are potentially **the single most important element needed to replicate and reproduce research**, and they must be available for research to truly be Open Research.

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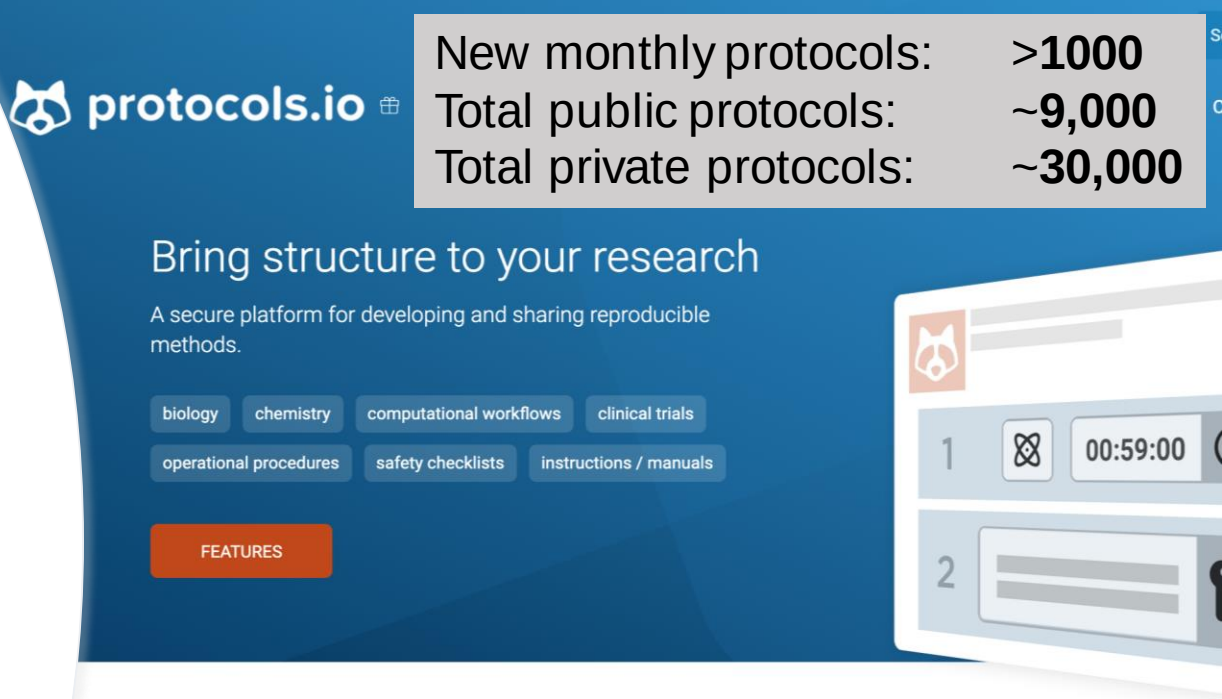
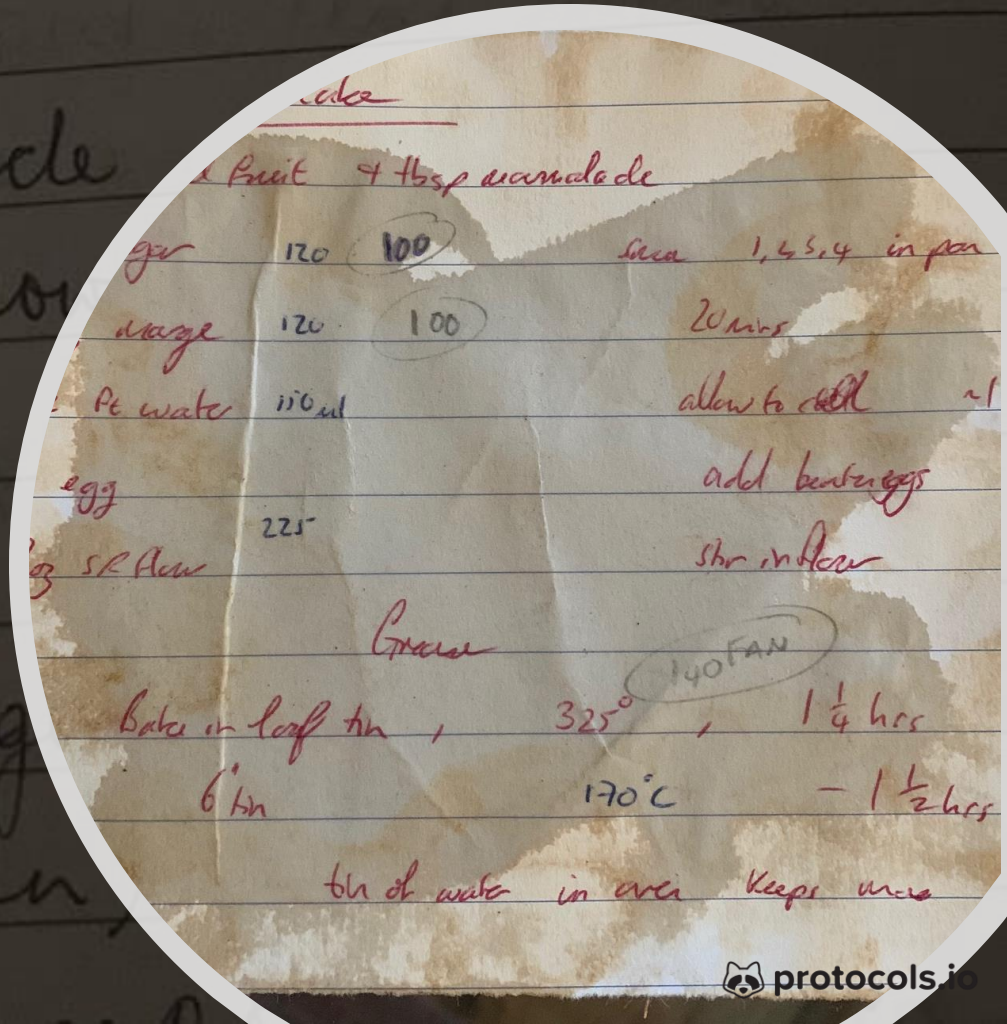
Methods for Methods

→ OA Repository (CC BY)
→ Free to Publish
→ Diversity of Disciplines
→ Archived & Mirrored
→ Public API
→ PDF and JSON



From Old Handwritten Recipes...



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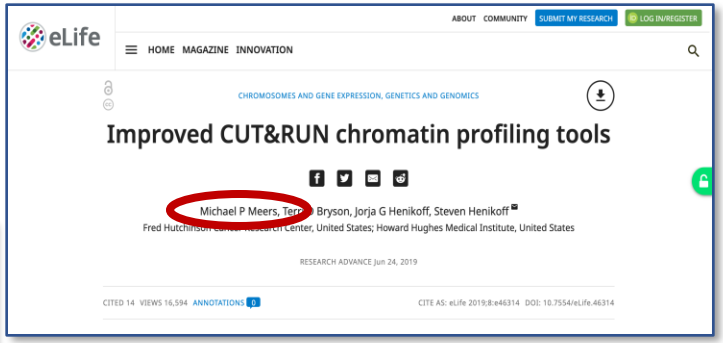
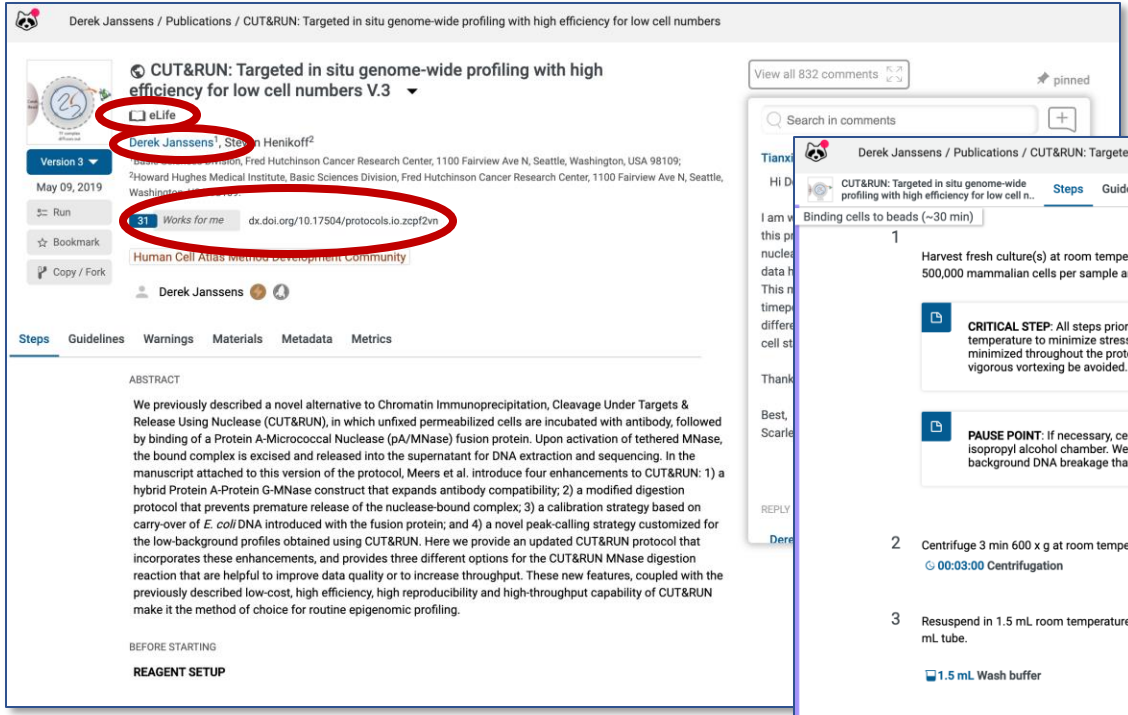
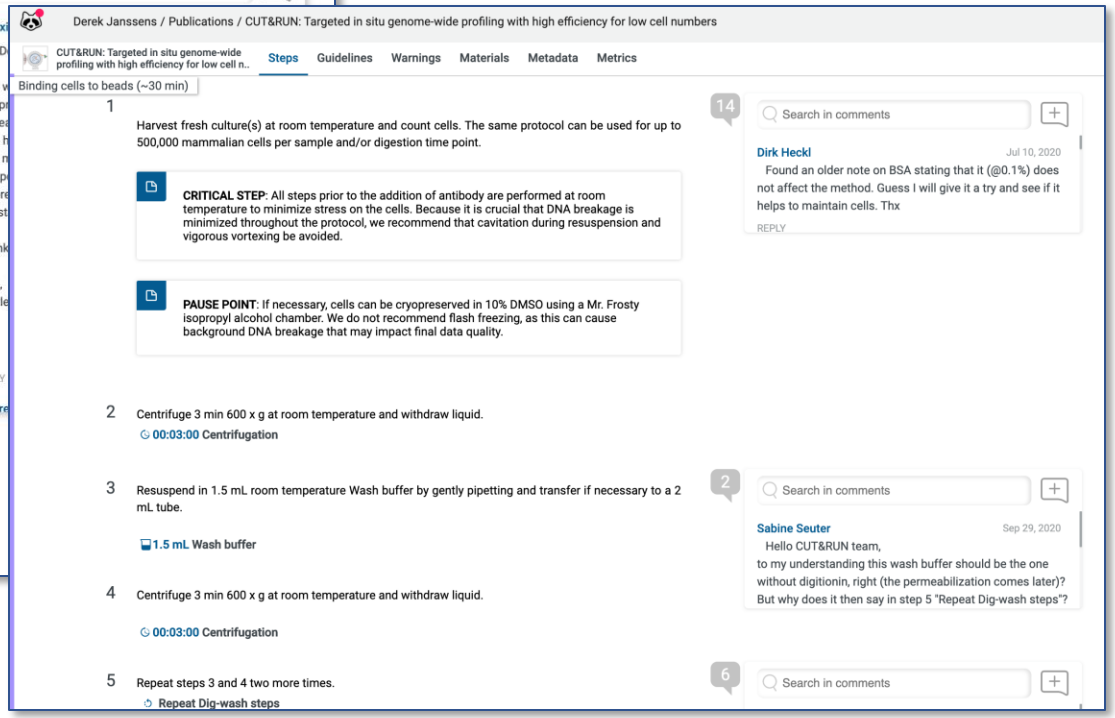
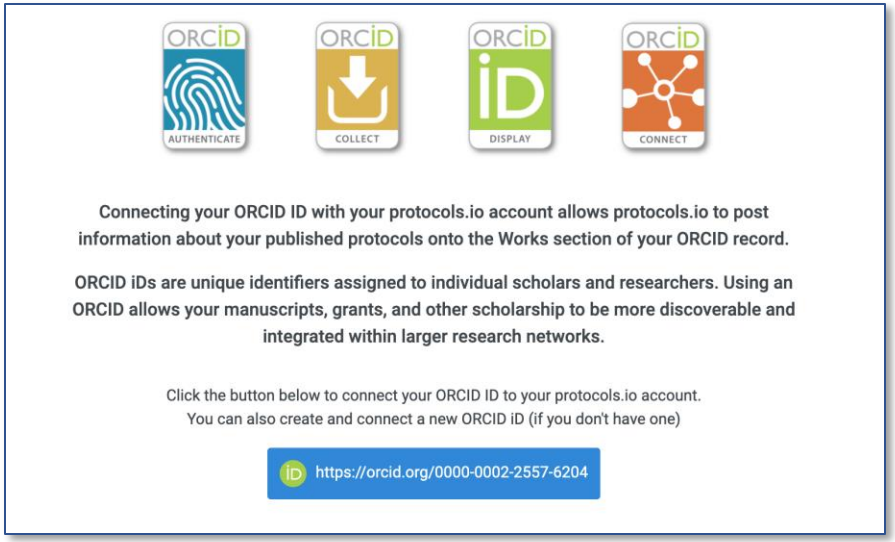
…to Structured Protocols



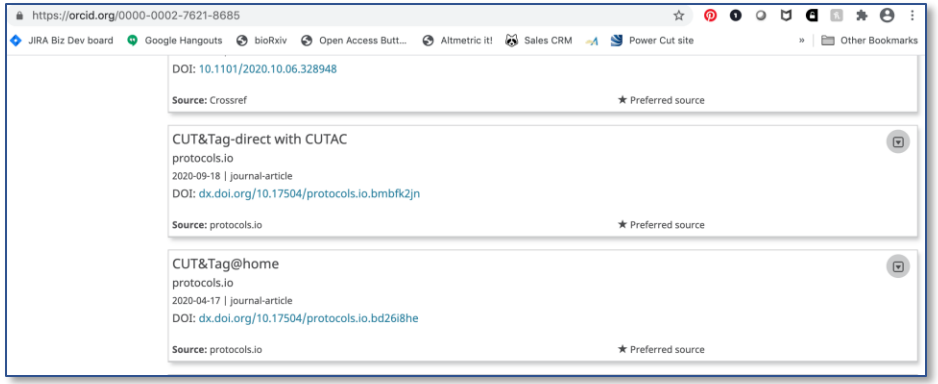




Published Protocols Appear on your ORCiD Record



https://www.protocols.io/orcid



https://orcid.org/0000-0002-7621-8685

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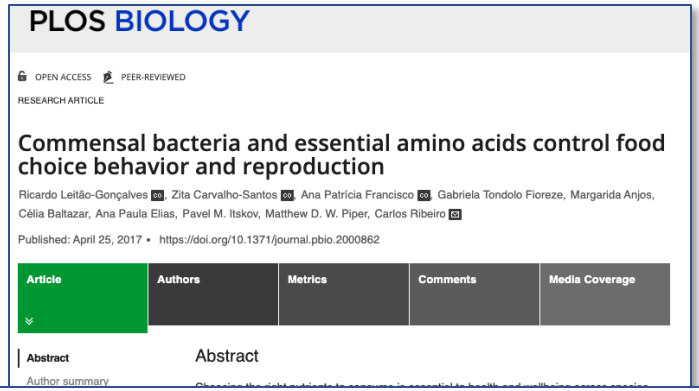
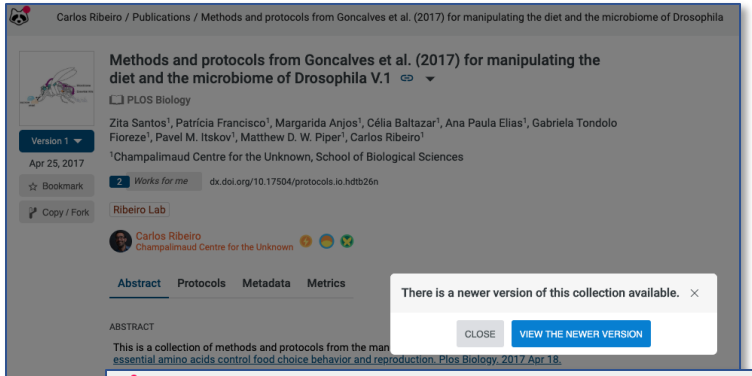
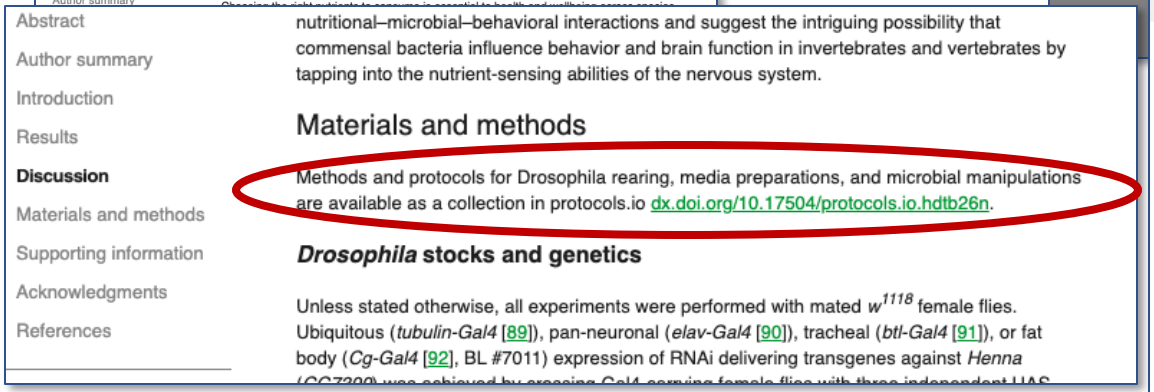
Dynamic Permanence of Published Protocols

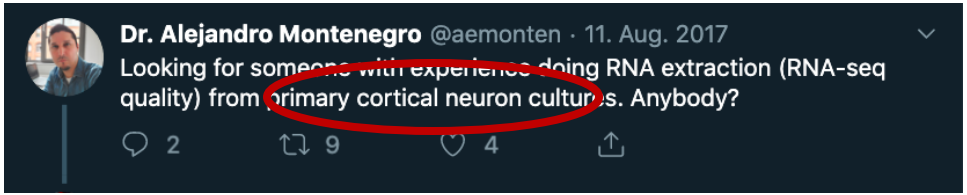


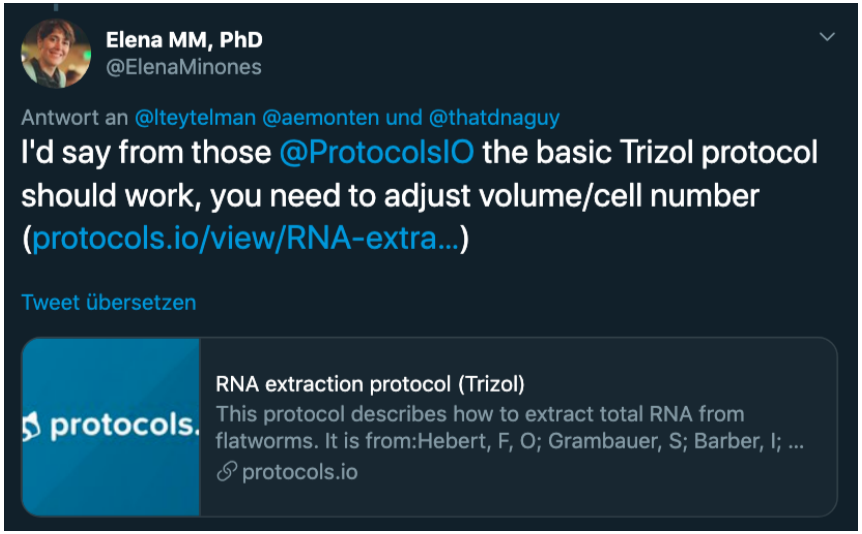
"Methods and protocols for … are available as a collection in protocols.io [DOI link]"





Connections… from brain cells to fish parasites





Hébert *et al. GigaScience* (2016) 5:24
DOI 10.1186/s13742-016-0128-3

GigaScience

DATA NOTE Open Access

Transcriptome sequences spanning key developmental states as a resource for the study of the cestode *Schistocephalus solidus*, a threespine stickleback parasite

François Olivier Hébert[1*], Stephan Grambauer[2], Iain Barber[2], Christian R. Landry[1] and Nadia Aubin-Horth[1]

Abstract

Background: *Schistocephalus solidus* is a well-established model organism for studying the complex life cycle of cestodes and the mechanisms underlying host-parasite interactions. However, very few large-scale genetic resources for this species are available. We have sequenced and *de novo*-assembled the transcriptome of *S. solidus* using tissues from whole worms at three key developmental states - non-infective plerocercoid, infective plerocercoid and adult plerocercoid - to provide a resource for studying the evolution of complex life cycles and, more specifically, how parasites modulate their interactions with their hosts during development.

Findings: The *de novo* transcriptome assembly reconstructed the coding sequence of 10,285 high-confidence unigenes from which 24,765 non-redundant transcripts were derived. 7,920 (77 %) of these unigenes were annotated with a protein name and 7,323 (71 %) were assigned at least one Gene Ontology term. Our raw transcriptome assembly (unfiltered transcripts) covers 92 % of the predicted transcriptome derived from the *S. solidus* draft genome assembly currently available on WormBase. It also provides new ecological information and orthology relationships to further annotate the current WormBase transcriptome and genome.

Conclusion: This large-scale transcriptomic dataset provides a foundation for studies on how parasitic species with complex life cycles modulate their response to changes in biotic and abiotic conditions experienced inside their various hosts, which is a fundamental objective of parasitology. Furthermore, this resource will help in the validation of the *S solidus* gene features that have been predicted based on genomic sequence.

Keywords: Transcriptome, RNA-seq, de novo assembly, *Schistocephalus solidus*, Parasite, Cestoda, Tapeworm, Threespine stickleback, *Gasterosteus aculeatus*

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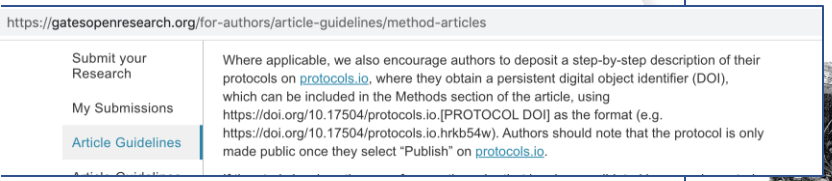
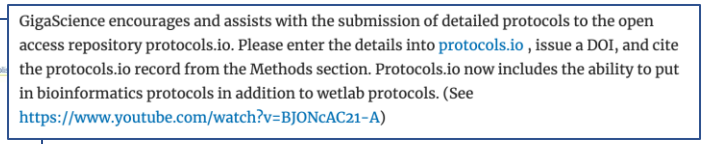
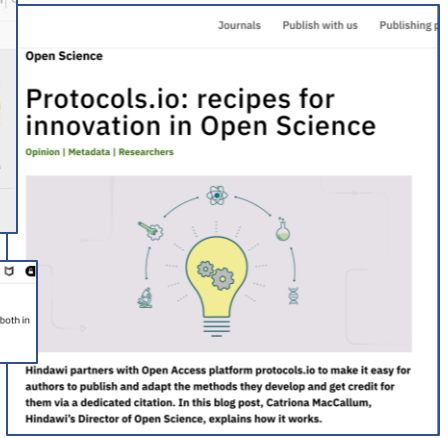
Many Publishers, Journals, & Funders Encourage Full Protocol Sharing







- Recommended by >500 journals
- Publish method into protocols.io
- Protocol DOI in materials and methods
- Dynamic commenting, Q&A discussions, and troubleshooting
- Create new versions after publication

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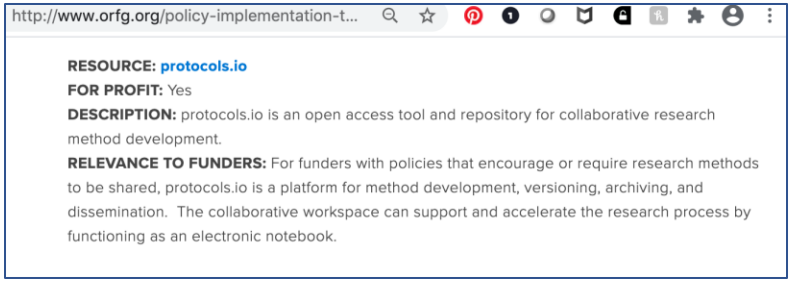
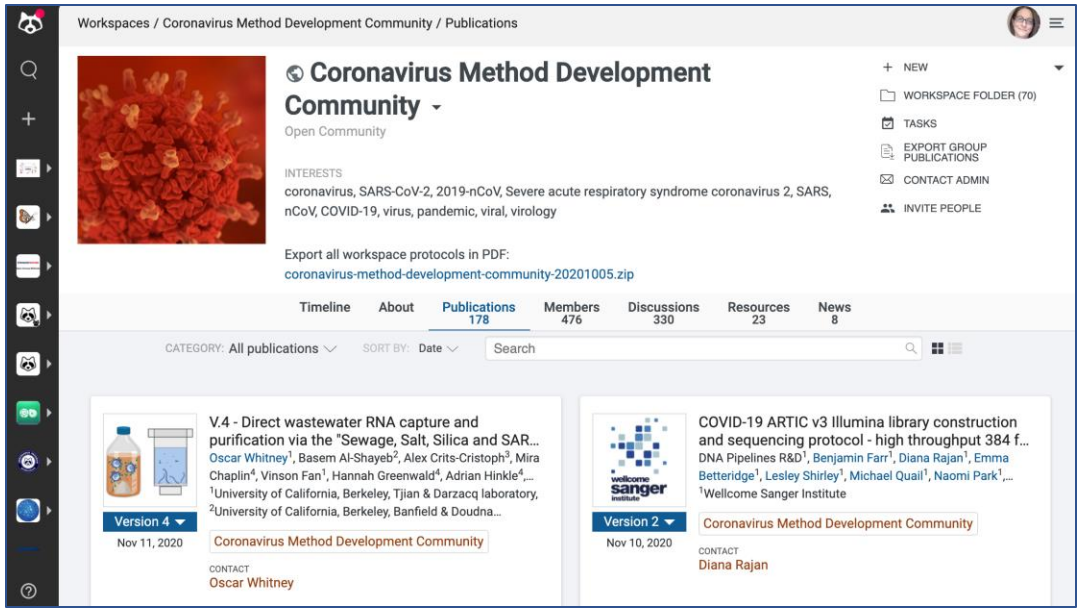
Many Publishers, Journals, & Funders Encourage Full Protocol Sharing



- Grant guidelines suggest protocols.io
- Program officers encourage
- Method sharing plan requested in DMP
- Some funders require protocol sharing
- Public or Private Workspaces for groups

Importance & Value of Method Sharing



- Increase Discoverability
- Reproducibility
- Facilitate Research Connections
- Enable Reuse
- Enhance Value of Research
- Dynamic Permanence (Versioning)
- Improved Materials & Methods
- Stewardship of Research Output
- Credit for the method developer

Accelerate & Improve Research Knowledge Dissemination

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Thank you!

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