Research Methods Deserve Credit and Recognition as a Valuable Research Output

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Articles in PMC with Data Availability Statement

- Has Data Availability Statement
Methods for Reproducible Research
The Brick Wall / Wild Goose Chase

Researchers cannot:
• find,
• access, or
• replicate...
... the methods
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 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.
Methods for Methods

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

New monthly protocols: >1000
Total public protocols: ~9,000
Total private protocols: ~30,000
From Old Handwritten Recipes...

- 6 eggs
- 221 g sugar
- 100 ml fruit juice
- 1 tbsp black treacle
- 1 tbsp baking powder
- 225 g self-raising flour
- 325 ml water

Mix all ingredients together, then bake in a loaf tin at 170°C for 1 1/2 hours.
...to Structured Protocols
Published Protocols Appear on your ORCiD Record

https://www.protocols.io/orcid

https://orcid.org/0000-0002-7621-8685
“Methods and protocols for ... are available as a collection in protocols.io [DOI link]”
Connections... from brain cells to fish parasites

Dr. Alejandro Montenegro @aemonten · 11. Aug. 2017
Looking for someone with experience doing RNA extraction (RNA-seq quality) from primary cortical neuron cultures. Anybody?

Elena MM, PhD @ElenaMinones
Antwort an @teytelman @aemonten und @thatghagu
I'd say from those @ProtocolsIO the basic Trizol protocol should work, you need to adjust volume/cell number (protocols.io/view/RNA-extra...)

RNA extraction protocol (Trizol)
This protocol describes how to extract total RNA from flatworms. It is from: Hebert, F; O; Grambauer, S; Barber, I; ...
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François Olivier Hébert1, Stephan Grambauer1, Iain Barber1, Christian R. Landry1 and Nadia Aubin-Horth1

Abstract
Background: Schistcephalus 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 stages - 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 24,760 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, Schistcephalus solidus, Parorchis threespine stickleback, Gasterosteus aculeatus

Transcriptome sequences spanning key developmental stages as a resource for the study of the cestode Schistcephalus solidus, a threespine stickleback parasite
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
Many Publishers, Journals, & Funders Encourage Full Protocol Sharing

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- 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
Thank you!