Methods Sharing with protocols.io

Mon 11th May, 2020

protocols.io

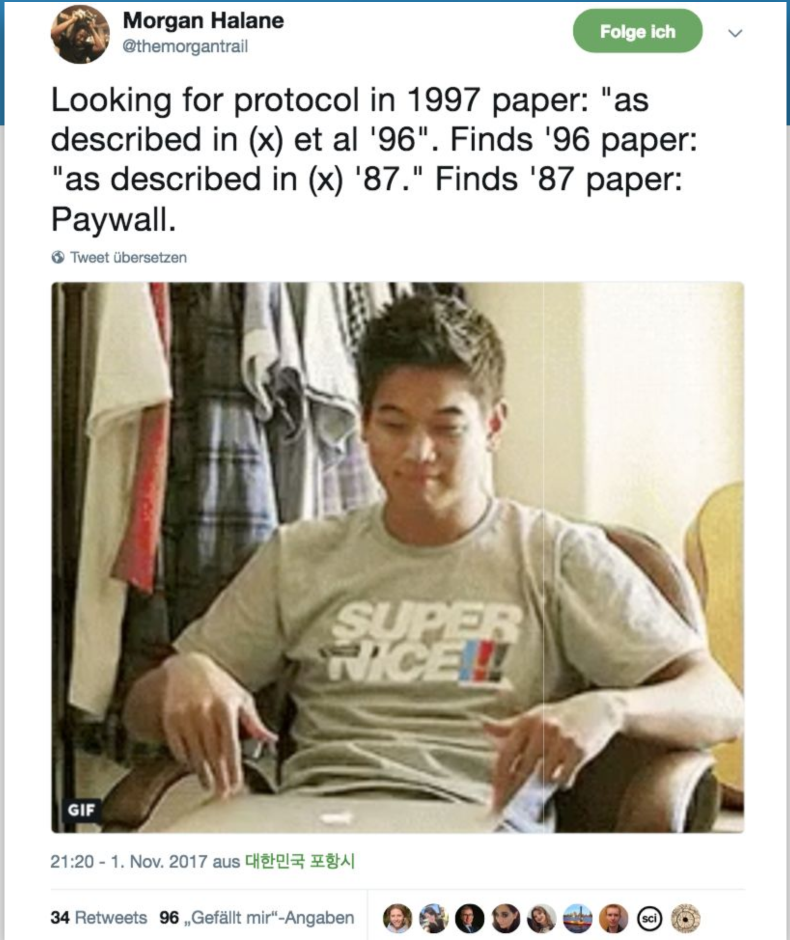
Overview

1. Introduction to protocols.io
2. Relationship with publishers, funders & institutions
3. Linking method development to publication
4. protocols.io during the current crisis

Q&A

Reproducibility

Lab Notebook
From
Previous
Postdoc



Morgan Halane
@themorgantrail

Looking for protocol in 1997 paper: "as described in (x) et al '96". Finds '96 paper: "as described in (x) '87." Finds '87 paper: Paywall.

21:20 - 1. Nov. 2017 aus 대한민국 포항시

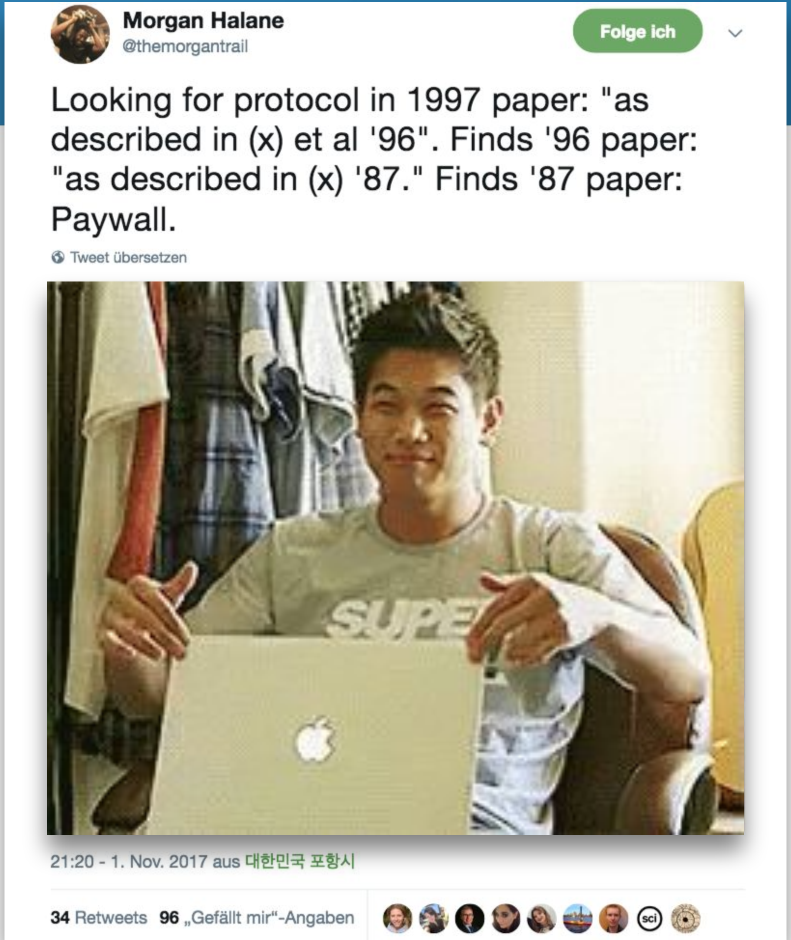
34 Retweets 96 „Gefällt mir"-Angaben

Researchers unable to…

- find
- access
- replicate

Reproducibility

Lab Notebook
From
Previous
Postdoc



Morgan Halane
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34 Retweets **96** „Gefällt mir"-Angaben

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The Problem – Method Communication

Repeating and building on previously published work is extremely hard.

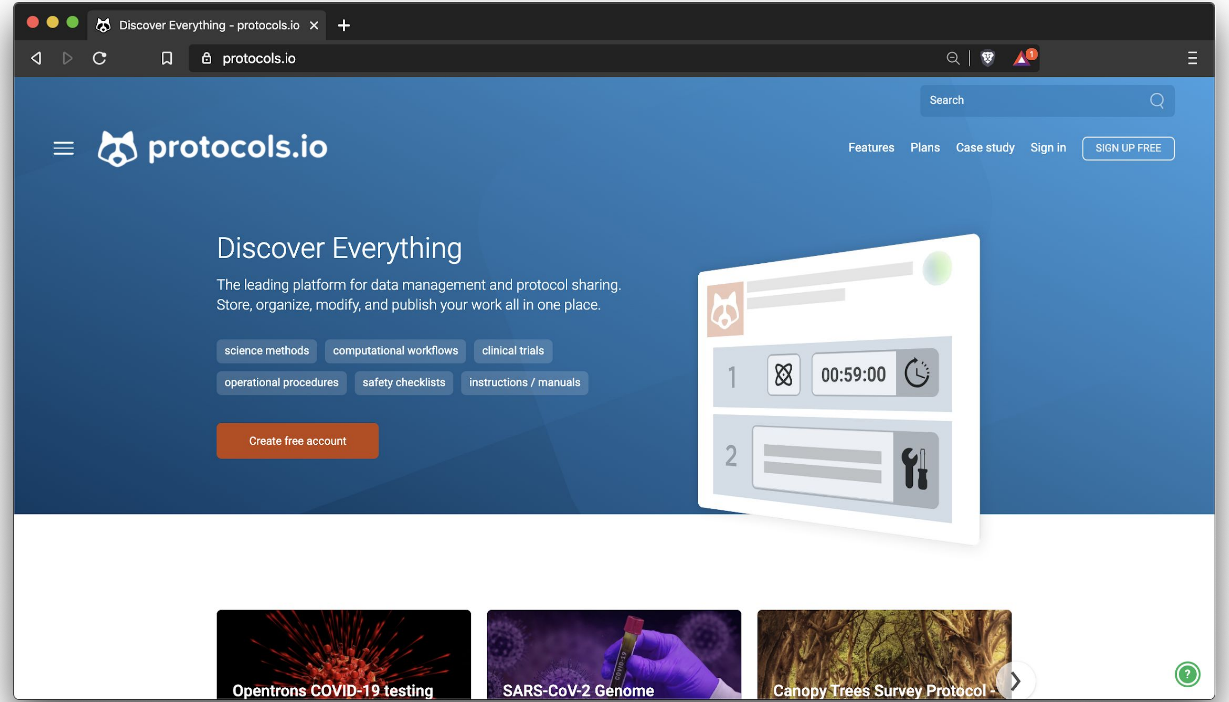
The Atlantic

How Reliable Are Cancer Studies?
January 18, 2017

> *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.*

Discover Protocols

→ Open access repository
→ ~7,000 public protocols
→ Large diversity of disciplines



Discover Everything

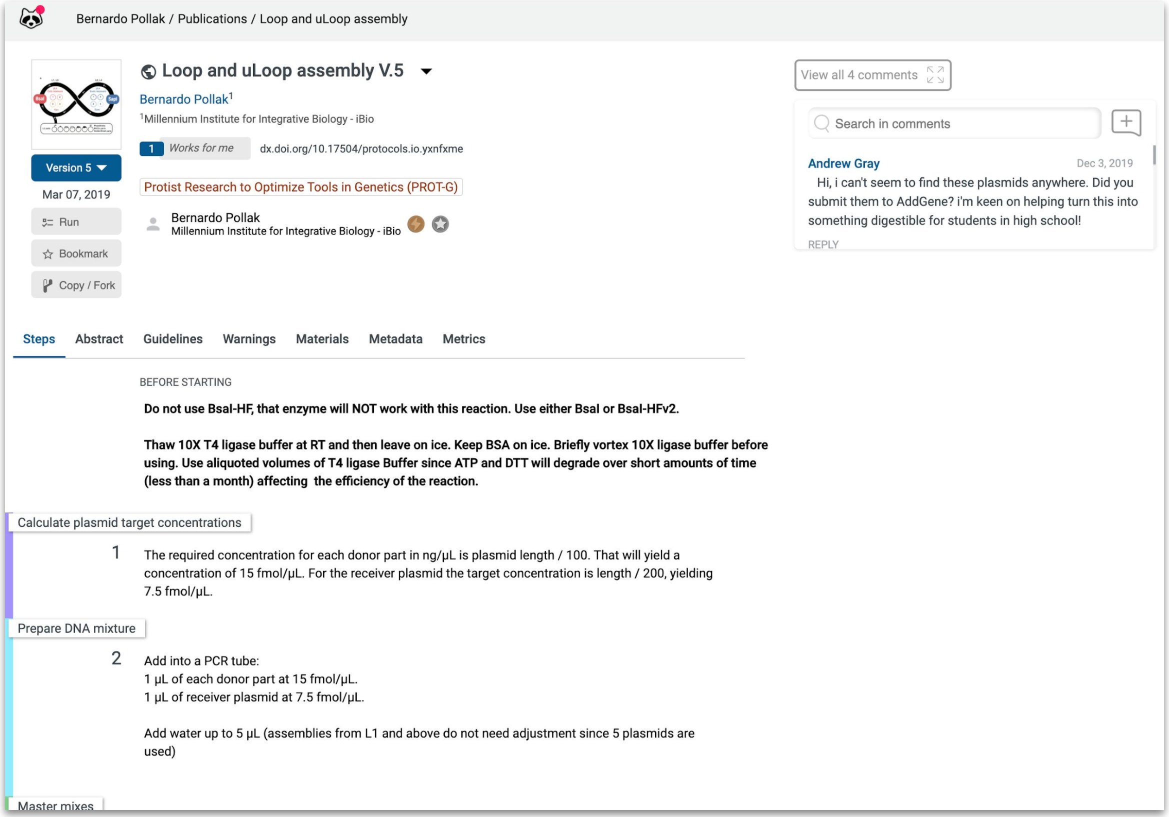
The leading platform for data management and protocol sharing. Store, organize, modify, and publish your work all in one place.

https://www.protocols.io/welcome

Overview: Mission of protocols.io

Making it easy to share method details
before, **during** and **after publication**.

Protocol



Loop and uLoop assembly V.5

Bernardo Pollak[1]

[1]Millennium Institute for Integrative Biology - iBio

1 Works for me

dx.doi.org/10.17504/protocols.io.yxnfxme

Mar 07, 2019

Protist Research to Optimize Tools in Genetics (PROT-G)

Bernardo Pollak
Millennium Institute for Integrative Biology - iBio

Andrew Gray Dec 3, 2019

Hi, i can't seem to find these plasmids anywhere. Did you submit them to AddGene? i'm keen on helping turn this into something digestible for students in high school!

BEFORE STARTING

Do not use BsaI-HF, that enzyme will NOT work with this reaction. Use either BsaI or BsaI-HFv2.

Thaw 10X T4 ligase buffer at RT and then leave on ice. Keep BSA on ice. Briefly vortex 10X ligase buffer before using. Use aliquoted volumes of T4 ligase Buffer since ATP and DTT will degrade over short amounts of time (less than a month) affecting the efficiency of the reaction.

Calculate plasmid target concentrations

1 The required concentration for each donor part in ng/µL is plasmid length / 100. That will yield a concentration of 15 fmol/µL. For the receiver plasmid the target concentration is length / 200, yielding 7.5 fmol/µL.

Prepare DNA mixture

2 Add into a PCR tube:
1 µL of each donor part at 15 fmol/µL.
1 µL of receiver plasmid at 7.5 fmol/µL.

Add water up to 5 µL (assemblies from L1 and above do not need adjustment since 5 plasmids are used)

Master mixes

Versions

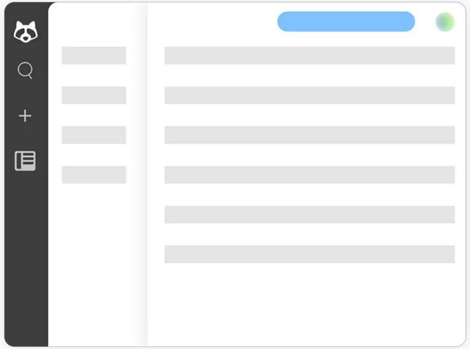
Works for me

DOI (or keep private)

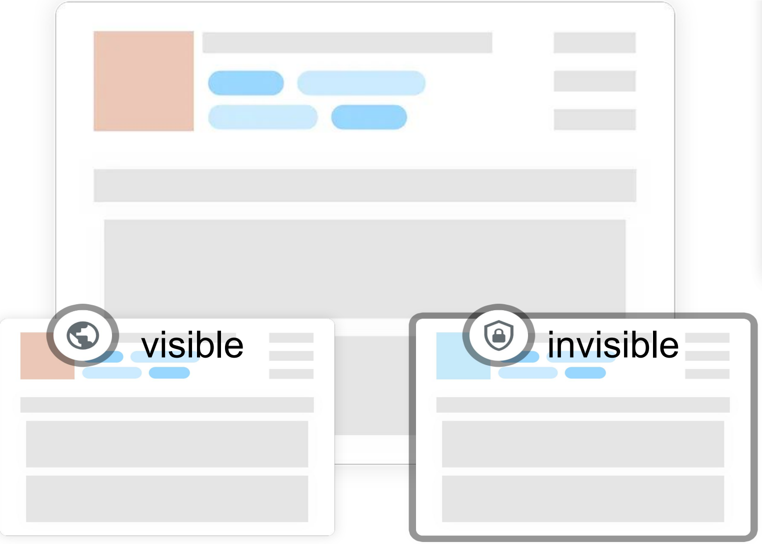
Comments

Elements of protocols.io

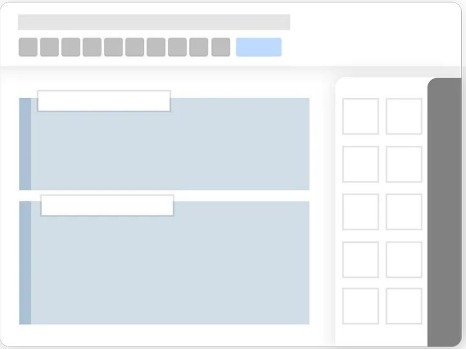
File Manager



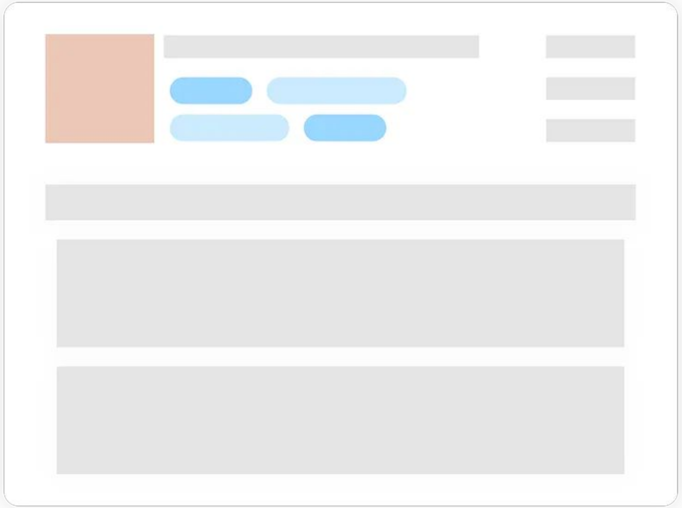
Workspaces



Editor



Workspaces



- Group management
- Everything in one place
- Secure file sharing

Fully integrated task manager

☑ Prevent from sharing files outside of the group
☑ Prevent from moving files outside of the group
☑ Prevent from removing files
☐ Disable ability to get DOI
☐ Disable ability to publish
☐ Disable ability to copy files to other storage providers

Key Insights

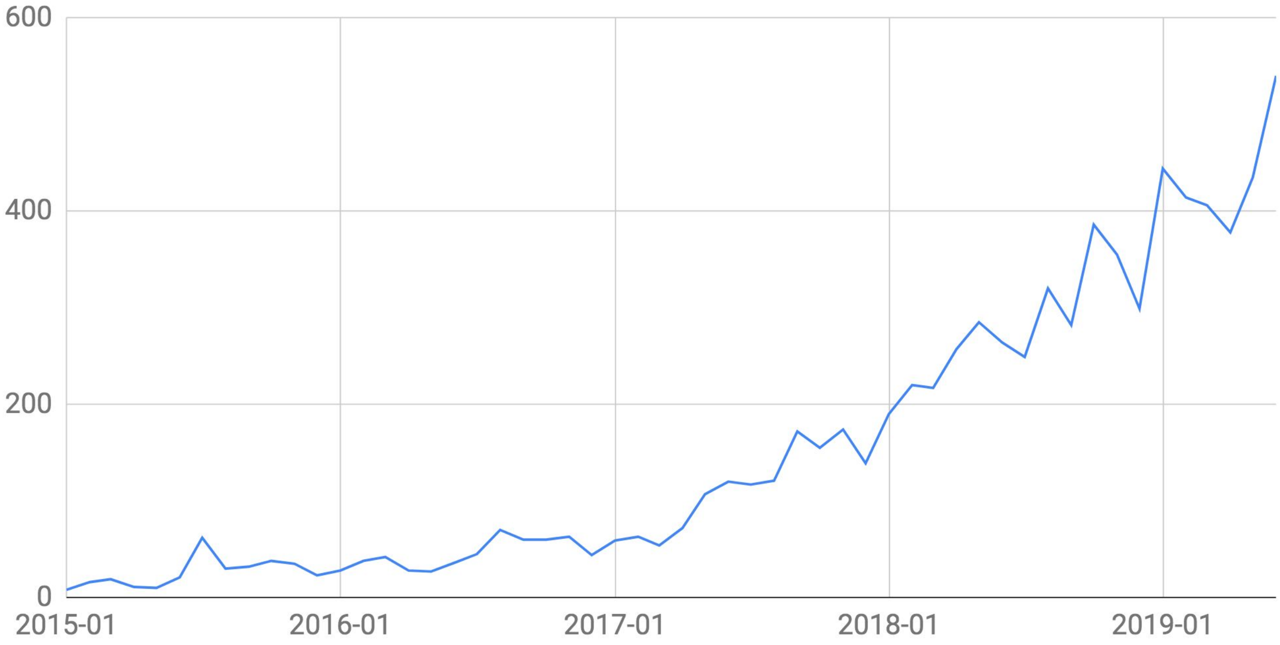
Manage and share research data and protocols

Simplify teamwork and improve collaboration

Saving time and keep work organized

Adoption

Monthly users creating new protocols



Total public protocols: >**7,000**
Total private protocols: >**24,000**

New monthly protocols: >**1000**

Organizations encouraging use of protocols.io

Journals & Publishers

Recommend protocols.io during manuscript submission

AACR American Association for Cancer Research

PLOS

GSA Genetics Society of America

eLIFE

500+ journals

Funders

Require or recommend protocols.io in grant guidelines/policies

The Leona M. and Harry B. Helmsley Charitable Trust

Alex's Lemonade Stand

CZ

Gordon and Betty Moore Foundation

NIH

wellcome

Institutions

Campus licenses for more reproducible research and publications.

University of California

Carnegie Mellon University

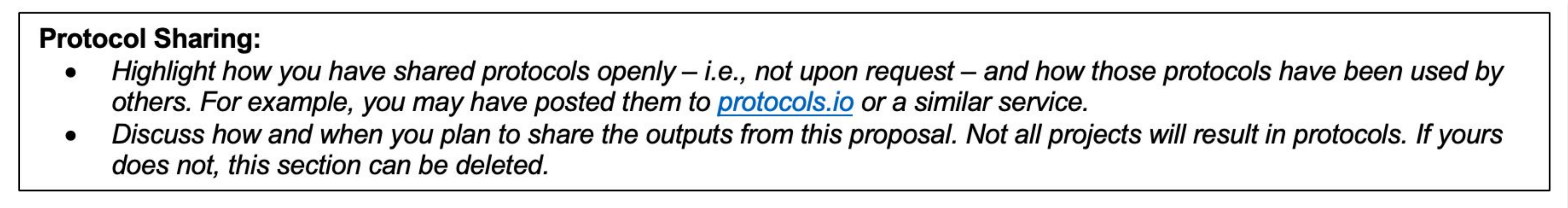
The University of Edinburgh

FRED HUTCH CURES START HERE®

\+ more

Funder examples

Alex's Lemonade Stand
FOUNDATION



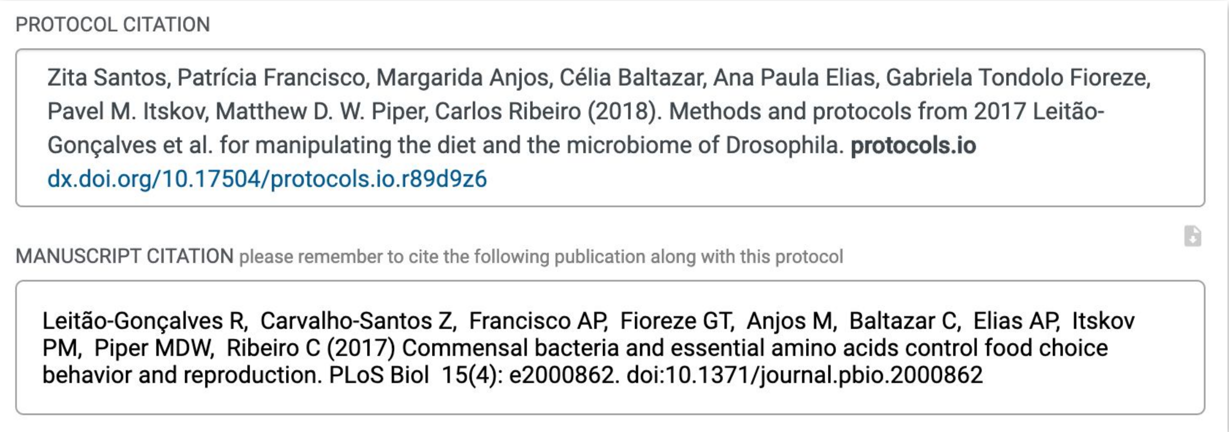
Protocol Sharing:

- *Highlight how you have shared protocols openly – i.e., not upon request – and how those protocols have been used by others. For example, you may have posted them to protocols.io or a similar service.*
- *Discuss how and when you plan to share the outputs from this proposal. Not all projects will result in protocols. If yours does not, this section can be deleted.*

Practicalities & Preservation

- Archived in CLOCKSS
- Daily backups
- All public protocols mirrored at https://github.com/protocolsio/protocols

- Public APIs
- Export (PDF, JSON)
- Citable



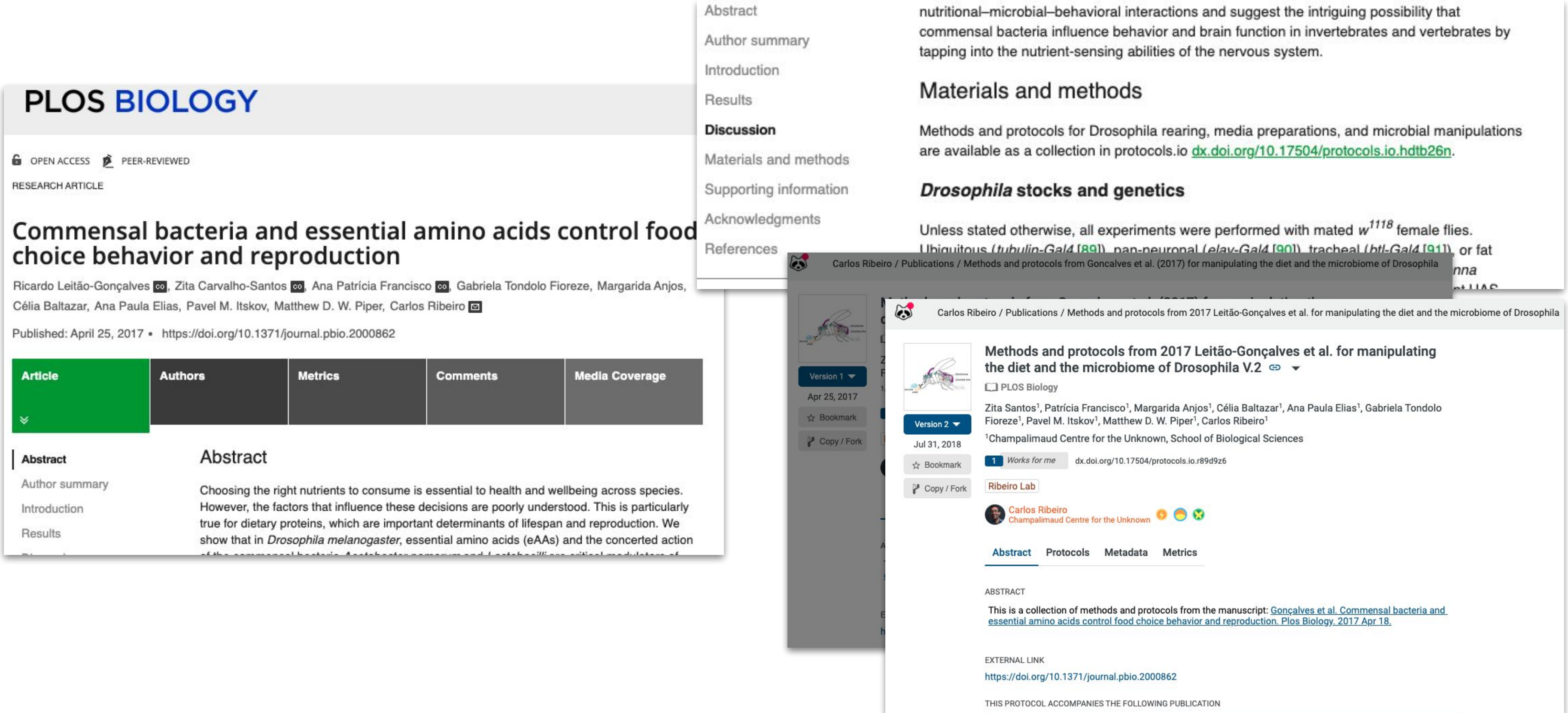
PROTOCOL CITATION

Zita Santos, Patrícia Francisco, Margarida Anjos, Célia Baltazar, Ana Paula Elias, Gabriela Tondolo Fioreze, Pavel M. Itskov, Matthew D. W. Piper, Carlos Ribeiro (2018). Methods and protocols from 2017 Leitão-Gonçalves et al. for manipulating the diet and the microbiome of Drosophila. **protocols.io** dx.doi.org/10.17504/protocols.io.r89d9z6

MANUSCRIPT CITATION please remember to cite the following publication along with this protocol

Leitão-Gonçalves R, Carvalho-Santos Z, Francisco AP, Fioreze GT, Anjos M, Baltazar C, Elias AP, Itskov PM, Piper MDW, Ribeiro C (2017) Commensal bacteria and essential amino acids control food choice behavior and reproduction. PLoS Biol 15(4): e2000862. doi:10.1371/journal.pbio.2000862

Dynamic Permanence



PLOS BIOLOGY

OPEN ACCESS PEER-REVIEWED

RESEARCH ARTICLE

Commensal bacteria and essential amino acids control food choice behavior and reproduction

Ricardo Leitão-Gonçalves, Zita Carvalho-Santos, Ana Patrícia Francisco, Gabriela Tondolo Fioreze, Margarida Anjos, Célia Baltazar, Ana Paula Elias, Pavel M. Itskov, Matthew D. W. Piper, Carlos Ribeiro

Published: April 25, 2017 • https://doi.org/10.1371/journal.pbio.2000862

Abstract

Choosing the right nutrients to consume is essential to health and wellbeing across species. However, the factors that influence these decisions are poorly understood. This is particularly true for dietary proteins, which are important determinants of lifespan and reproduction. We show that in *Drosophila melanogaster*, essential amino acids (eAAs) and the concerted action

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nutritional–microbial–behavioral interactions and suggest the intriguing possibility that commensal bacteria influence behavior and brain function in invertebrates and vertebrates by tapping into the nutrient-sensing abilities of the nervous system.

Materials and methods

Methods and protocols for Drosophila rearing, media preparations, and microbial manipulations are available as a collection in protocols.io dx.doi.org/10.17504/protocols.io.hdtb26n.

Drosophila stocks and genetics

Unless stated otherwise, all experiments were performed with mated w^{1118} female flies. Ubiquitous (*tubulin-Gal4* [89]), pan-neuronal (*elav-Gal4* [90]), tracheal (*btl-Gal4* [91]), or fat

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Carlos Ribeiro / Publications / Methods and protocols from Goncalves et al. (2017) for manipulating the diet and the microbiome of Drosophila

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Carlos Ribeiro / Publications / Methods and protocols from 2017 Leitão-Gonçalves et al. for manipulating the diet and the microbiome of Drosophila

Methods and protocols from 2017 Leitão-Gonçalves et al. for manipulating the diet and the microbiome of Drosophila V.2

PLOS Biology

Zita Santos[1], Patrícia Francisco[1], Margarida Anjos[1], Célia Baltazar[1], Ana Paula Elias[1], Gabriela Tondolo Fioreze[1], Pavel M. Itskov[1], Matthew D. W. Piper[1], Carlos Ribeiro[1]

[1]Champalimaud Centre for the Unknown, School of Biological Sciences

dx.doi.org/10.17504/protocols.io.r89d9z6

Ribeiro Lab

Carlos Ribeiro
Champalimaud Centre for the Unknown

ABSTRACT

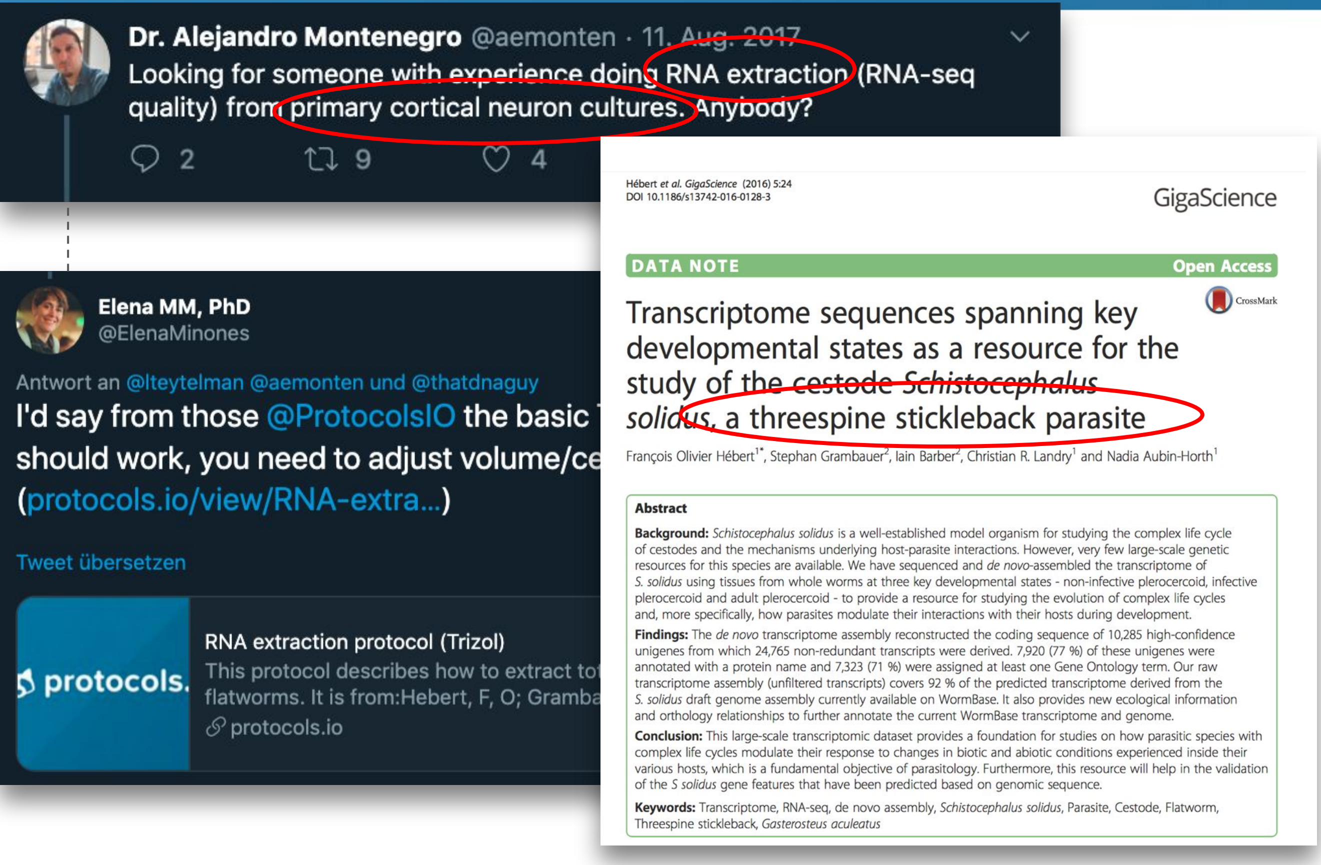
This is a collection of methods and protocols from the manuscript: Gonçalves et al. Commensal bacteria and essential amino acids control food choice behavior and reproduction. Plos Biology. 2017 Apr 18.

EXTERNAL LINK

https://doi.org/10.1371/journal.pbio.2000862

THIS PROTOCOL ACCOMPANIES THE FOLLOWING PUBLICATION

Why publish protocols?



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 @lteytelman @aemonten und @thatdnaguy

I'd say from those @ProtocolsIO the basic
should work, you need to adjust volume/ce
(protocols.io/view/RNA-extra...)

Tweet übersetzen

RNA extraction protocol (Trizol)
This protocol describes how to extract to
flatworms. It is from:Hebert, F, O; Gramba
protocols.io

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, Cestode, Flatworm, Threespine stickleback, *Gasterosteus aculeatus*

Accelerate Science

→ Increase Discoverability

→ Reproducibility

→ Facilitate Research Connections

→ Enable Reuse

→ Enhance Value of Research

Stewardship of Research Outputs

When researchers do not have a platform to create and share methods, the institution loses ‘stewardship’ over the research methods and their ingredients.

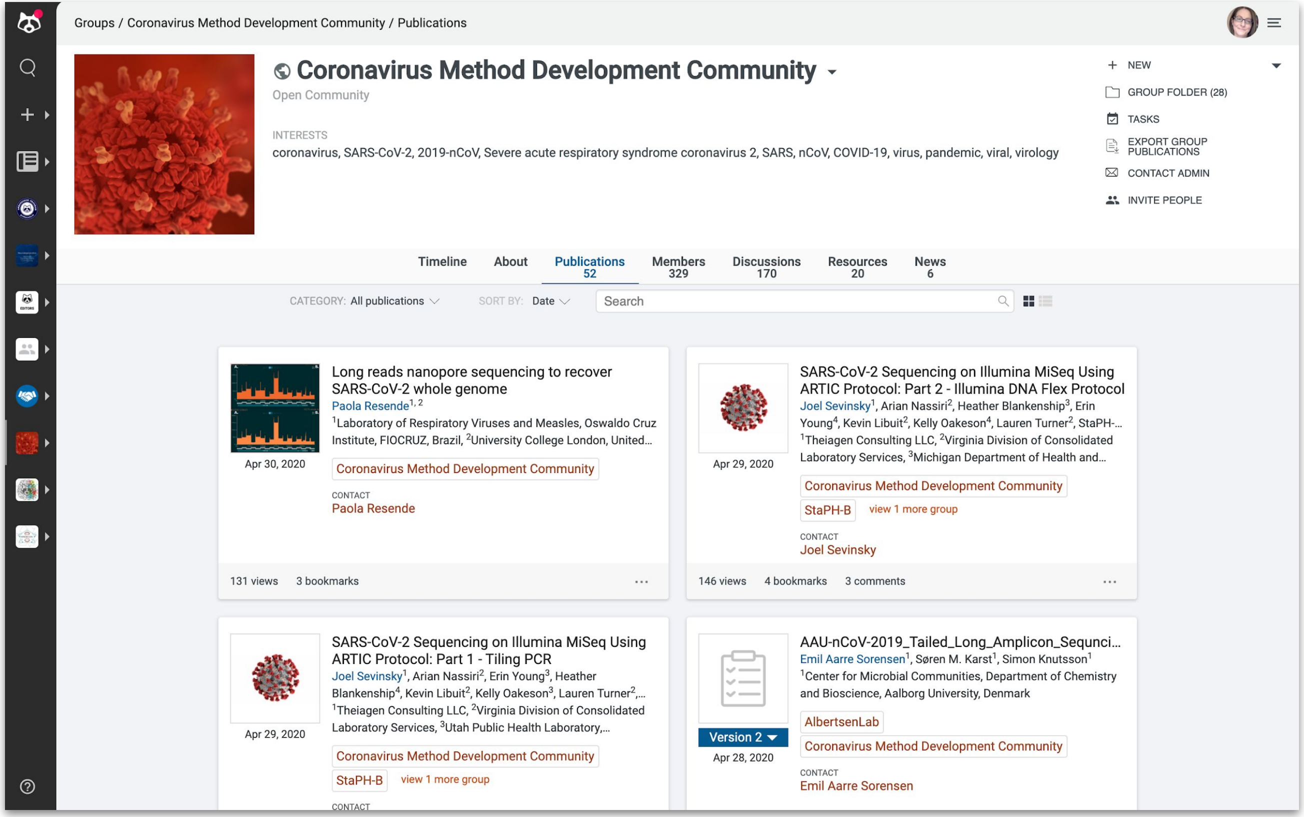
Benefits of protocols.io

Accelerate Science

- ★ Increase Discoverability
- ★ Reproducibility
- ★ Facilitate Research Connections
- ★ Enable Reuse
- ★ Enhance Value of Research
- ★ Dynamic Permanence (Versioning)
- ★ Improved Materials & Methods
- ★ Stewardship of Research Output

Vibrant Open Research Community

Coronavirus Methods Development Community



Coronavirus Method Development Community

Open Community

INTERESTS

coronavirus, SARS-CoV-2, 2019-nCoV, Severe acute respiratory syndrome coronavirus 2, SARS, nCoV, COVID-19, virus, pandemic, viral, virology

Long reads nanopore sequencing to recover SARS-CoV-2 whole genome

Paola Resende[1, 2]

[1]Laboratory of Respiratory Viruses and Measles, Oswaldo Cruz Institute, FIOCRUZ, Brazil, [2]University College London, United…

Apr 30, 2020

Coronavirus Method Development Community

CONTACT

Paola Resende

131 views 3 bookmarks

SARS-CoV-2 Sequencing on Illumina MiSeq Using ARTIC Protocol: Part 2 - Illumina DNA Flex Protocol

Joel Sevinsky[1], Arian Nassiri[2], Heather Blankenship[3], Erin Young[4], Kevin Libuit[2], Kelly Oakeson[4], Lauren Turner[2], StaPH-…

[1]Theiagen Consulting LLC, [2]Virginia Division of Consolidated Laboratory Services, [3]Michigan Department of Health and…

Apr 29, 2020

Coronavirus Method Development Community

StaPH-B view 1 more group

CONTACT

Joel Sevinsky

146 views 4 bookmarks 3 comments

SARS-CoV-2 Sequencing on Illumina MiSeq Using ARTIC Protocol: Part 1 - Tiling PCR

Joel Sevinsky[1], Arian Nassiri[2], Erin Young[3], Heather Blankenship[4], Kevin Libuit[2], Kelly Oakeson[3], Lauren Turner[2],…

[1]Theiagen Consulting LLC, [2]Virginia Division of Consolidated Laboratory Services, [3]Utah Public Health Laboratory,…

Apr 29, 2020

Coronavirus Method Development Community

StaPH-B view 1 more group

CONTACT

AAU-nCoV-2019_Tailed_Long_Amplicon_Sequnci…

Emil Aarre Sorensen[1], Søren M. Karst[1], Simon Knutsson[1]

[1]Center for Microbial Communities, Department of Chemistry and Bioscience, Aalborg University, Denmark

Version 2

Apr 28, 2020

AlbertsenLab

Coronavirus Method Development Community

CONTACT

Emil Aarre Sorensen

protocols.io @protocolsIO · Mar 13

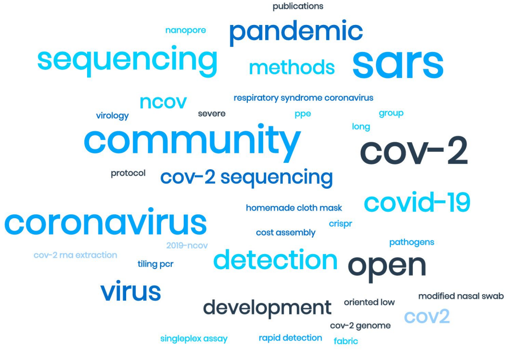
Our editorial team is ready to help import protocols into the COVID-19 group protocols.io/groups/coronav.... (Email your PDF/document to info@protocols.io. One editor enters it, another checks and we reassign privately to you for review/publishing.)

Coronavirus Method Development Community - research group on pr...

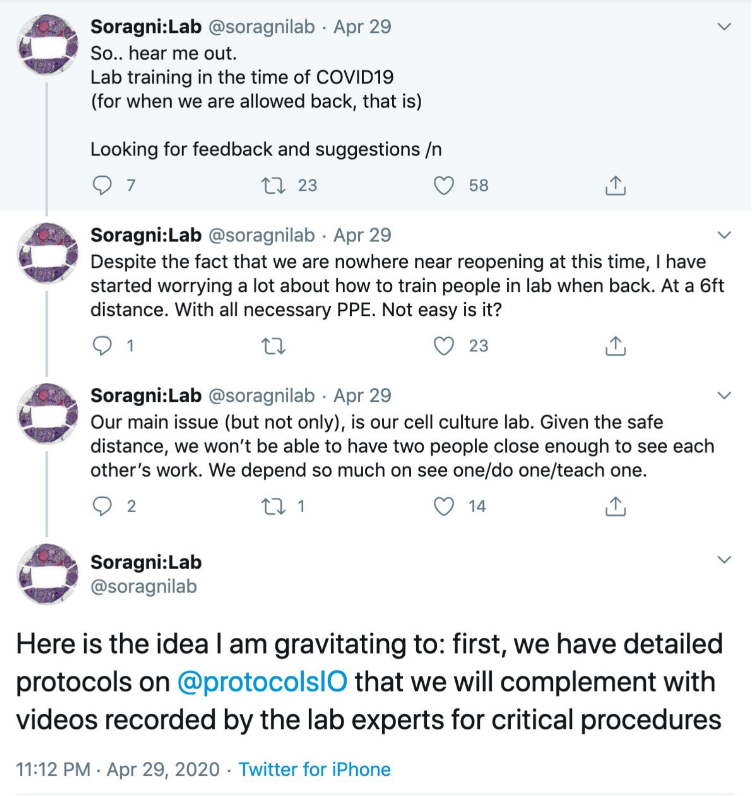
This group is for the support of researchers working on coronavirus methods, intended to facilitate method-centered collaboration and ...

protocols.io

1 66 73



Looking for a New Normal post COVID-19



Soragni:Lab @soragnilab · Apr 29
So.. hear me out.
Lab training in the time of COVID19
(for when we are allowed back, that is)

Looking for feedback and suggestions /n

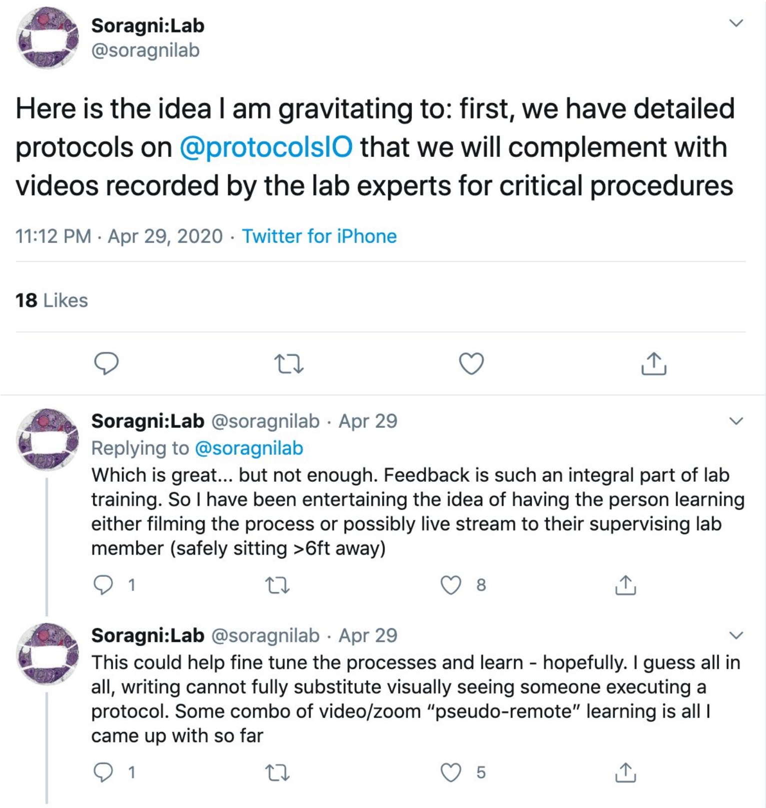
Soragni:Lab @soragnilab · Apr 29
Despite the fact that we are nowhere near reopening at this time, I have started worrying a lot about how to train people in lab when back. At a 6ft distance. With all necessary PPE. Not easy is it?

Soragni:Lab @soragnilab · Apr 29
Our main issue (but not only), is our cell culture lab. Given the safe distance, we won't be able to have two people close enough to see each other's work. We depend so much on see one/do one/teach one.

Soragni:Lab
@soragnilab

Here is the idea I am gravitating to: first, we have detailed protocols on @protocolsIO that we will complement with videos recorded by the lab experts for critical procedures

11:12 PM · Apr 29, 2020 · Twitter for iPhone



Soragni:Lab
@soragnilab

Here is the idea I am gravitating to: first, we have detailed protocols on @protocolsIO that we will complement with videos recorded by the lab experts for critical procedures

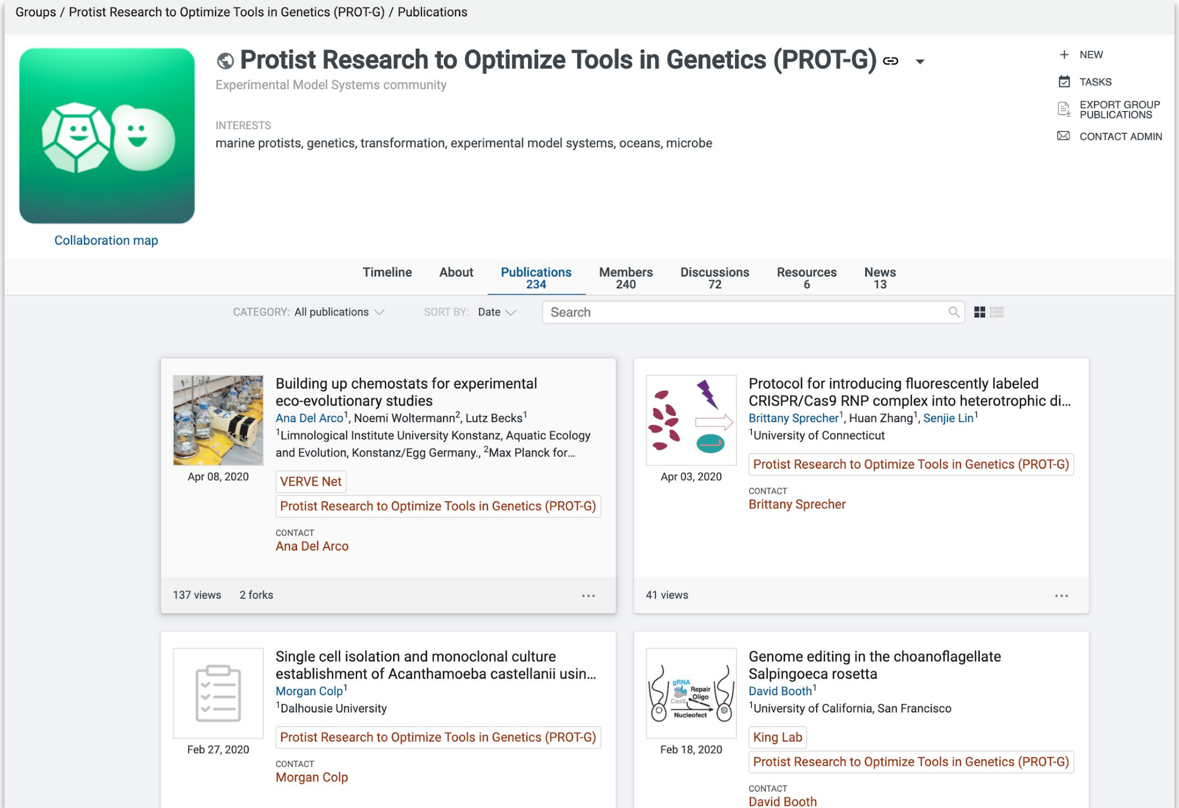
11:12 PM · Apr 29, 2020 · Twitter for iPhone

18 Likes

Soragni:Lab @soragnilab · Apr 29
Replying to @soragnilab
Which is great... but not enough. Feedback is such an integral part of lab training. So I have been entertaining the idea of having the person learning either filming the process or possibly live stream to their supervising lab member (safely sitting >6ft away)

Soragni:Lab @soragnilab · Apr 29
This could help fine tune the processes and learn - hopefully. I guess all in all, writing cannot fully substitute visually seeing someone executing a protocol. Some combo of video/zoom "pseudo-remote" learning is all I came up with so far

PROT-G



Groups / Protist Research to Optimize Tools in Genetics (PROT-G) / Publications

Protist Research to Optimize Tools in Genetics (PROT-G)

Experimental Model Systems community

INTERESTS

marine protists, genetics, transformation, experimental model systems, oceans, microbe

Building up chemostats for experimental eco-evolutionary studies

Ana Del Arco[1], Noemi Woltermann[2], Lutz Becks[1]

[1]Limnological Institute University Konstanz, Aquatic Ecology and Evolution, Konstanz/Egg Germany., [2]Max Planck for...

Apr 08, 2020

VERVE Net

Protist Research to Optimize Tools in Genetics (PROT-G)

CONTACT

Ana Del Arco

137 views 2 forks

Protocol for introducing fluorescently labeled CRISPR/Cas9 RNP complex into heterotrophic di...

Brittany Sprecher[1], Huan Zhang[1], Senjie Lin[1]

[1]University of Connecticut

Apr 03, 2020

Protist Research to Optimize Tools in Genetics (PROT-G)

CONTACT

Brittany Sprecher

41 views

Single cell isolation and monoclonal culture establishment of Acanthamoeba castellanii usin...

Morgan Colp[1]

[1]Dalhousie University

Feb 27, 2020

Protist Research to Optimize Tools in Genetics (PROT-G)

CONTACT

Morgan Colp

Genome editing in the choanoflagellate Salpingoeca rosetta

David Booth[1]

[1]University of California, San Francisco

Feb 18, 2020

King Lab

Protist Research to Optimize Tools in Genetics (PROT-G)

CONTACT

David Booth

GORDON AND BETTY MOORE FOUNDATION

- Discoverable protocols
- Q&A via Discussions
- Updates
- Resources & News

Acknowledgements


Lenny Teytelman
CEO, cofounder


Alexei Stoliartchouk
CTO, cofounder


Irina Makkaveeva
CFO, cofounder


Anita Bröllochs
Outreach


Vladimir Frolov
Development


Emma Ganley
Strategic Initiatives


Ilyas Khayrullin
Development


Monika Khassan
Project Manager


Nastia Malochka
Customer Exp.


Nick Gulev
Development


Sergey Alekseev
Development


Alex Shirazi
Design

GORDON AND BETTY MOORE FOUNDATION

CHAN ZUCKERBERG INITIATIVE

Open Philanthropy Project

GSA Genetics Society of America

(GIGA)n SCIENCE

PLOS

Q&A

protocols.io