

Method development, sharing and publication at core facilities

WACD 2022

Gabriel Gasque, PhD
Head of Outreach



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Agenda



- protocols.io's mission
- protocols.io's platform
- protocols.io and core facilities
 - Methods
 - Equipment
 - Collaborations
 - Credit
- Training resources
- Q&A

Agenda



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



Cancer Biology Reproducibility Project



← → ↻ cos.io/rpcb

🔒 ☆ 📄 📱 🌐

When preparing replications of **193 experiments** from **53 papers** there were a number of challenges.

2%

experiments with open data

70%

of experiments required asking for key reagents

69%

of experiments needing a key reagent original authors were willing to share

0%

of protocols completely described

32%

of experiments the original authors were not helpful (or unresponsive)

41%

of experiments the original authors were very helpful



1. Experimental reproducibility
2. Scientific integrity and accountability
3. Data interpretability
4. Credit for method development
5. Method-based collaboration
6. Method preservation

Agenda

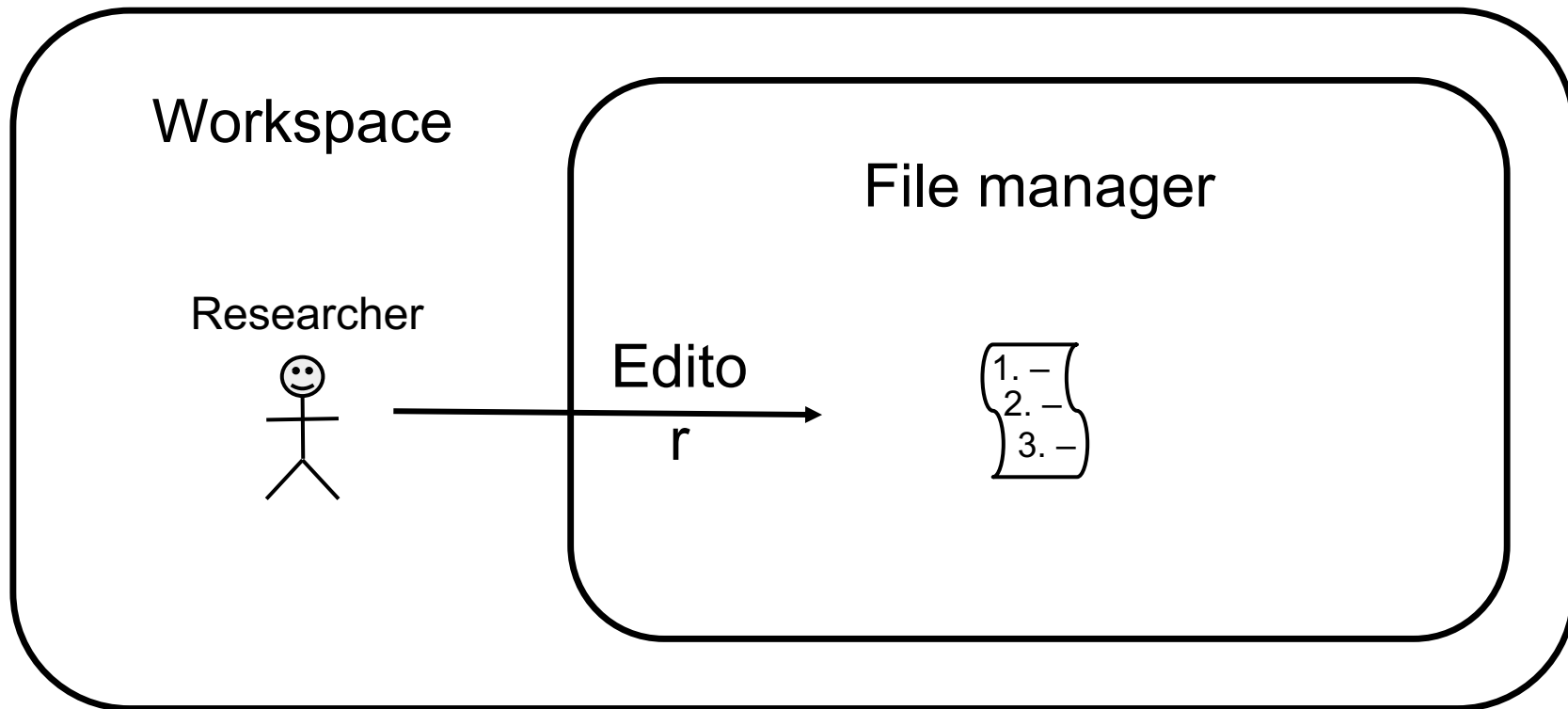


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- Collaborative development and refinement of detailed, interactive and dynamic experimental protocols.
- Archiving, organizing, exporting and copying/forking.
- Sharing and publishing.
- Protocol repository
- Collaborative workspaces

Workspace, file manager, and editor



Workspace, file manager, and editor



Gabriel Gasque / Bio

Timeline Bio Publications 5 Workspaces 7 Posts 6 Following Bookmarks 4

iental integrity. With over nine years of experience in the L.

npany whose goals are to foster scientific te experimental transparency, reproducibility, integrity tal protocols. Before joining protocols.io, I was Senior Public Library of Science (PLOS), an open access

iversity of Mexico (UNAM) and was awarded the :toral thesis in 2006. I did postdoctoral studies at a PEW Latin American fellow.

Gabriel Gasque ▼
protocols.io

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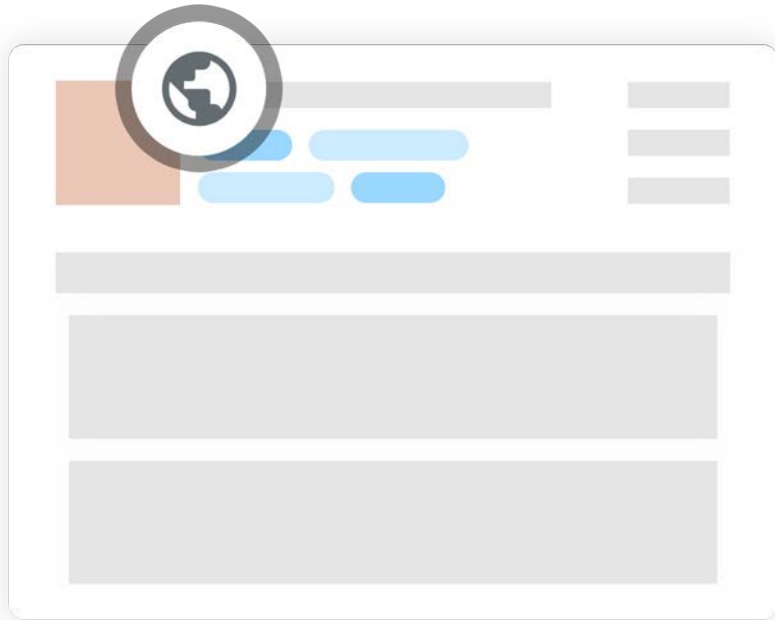
Messages

Manage categories

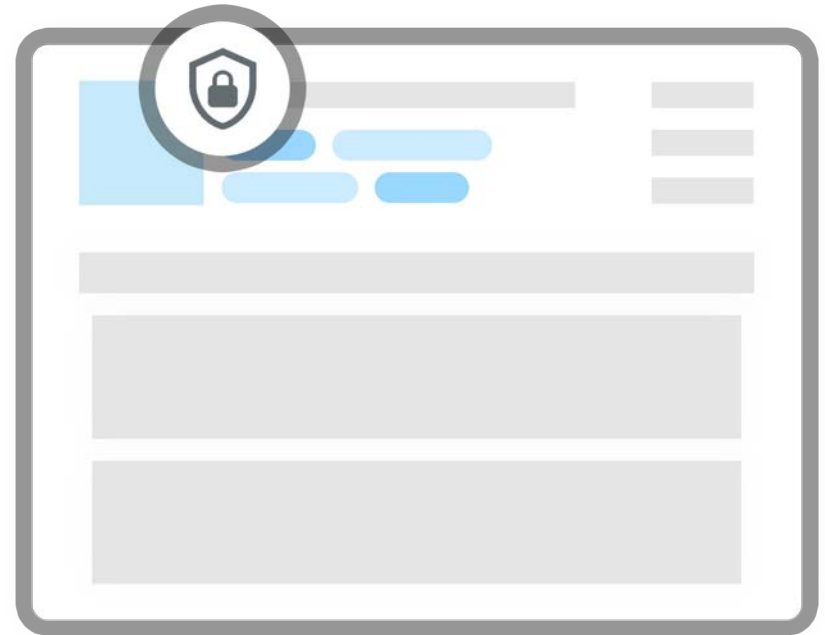
Workspaces can be public or private



Public workspaces



Private workspaces



Workspace membership is customizable



Group profile page visibility ⓘ

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The group profile page is visible on the site and search results

INVISIBLE
Only you and the members of the group will see the group

Group membership

OPEN TO ALL
Anyone may join this group

BY REQUEST
Anyone may ask to join but you control who gets in

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- Disable ability to publish
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Workspace, file manager, and editor



Gabriel Gasque
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<https://orcid.org/0000-0002-6062-5809>

I am an advocate for open science and for reproducibility and experimental integrity. With over nine years of experience in the field, I am expert in science outreach, communication, and publication. I current... **Show more**

- Edit profile
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Timeline Bio Publications 5 Workspaces 7 Posts 6 Following Bookmarks 4

June 3, 2022

Comment on U-251MG Spheroid Generation Using Hanging Drop Method Protocol (step 2)
Is this step supposed to be empty? Same for step 3

Protocol discussion Step 2

Gabriel Gasque
Jun 03, 2022

To test fork notification Version 2
Gabriel Gasque¹
^protocols.io
Gabriel Gasque
Jun 03, 2022 · 👁 8

Comment on Cómo hacer un protocolo nuevo (step 25)
Disregard, test comment

Protocol discussion Step 25

Gabriel Gasque
Jun 03, 2022

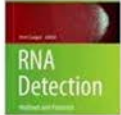
Dynamic and interactive protocols



Workspaces / Gabriel's workspace / Protocol examples / Super-Resolution Single Molecule FISH at the Drosophila Neuromuscular Junction


SHARE MORE You are currently in View mode. EDIT

3.1 Larva Neuromuscular Junction...
3.2 Fixation
3.3 Hybridization
3.4 Washing and Counterstain
3.5 Mounting
3.6 Image Acquisition on the Spin...
3.7 Image Acquisition for 3D-SIM
3.8 Image Management Using the ...
3.9 Image Analysis (See Note 7)
3.9.1 Find Foci
3.9.2 FISHQuant (Fig. 4c)
3.9.3 Imaris Spots (Fig. 4d)

 Super-Resolution Single Molecule FISH at the Drosophila Neuromuscular Junction
Forked from Super-Resolution Single Molecule FISH at the Drosophila Neuromuscular Junction

Joshua S. Titlow¹, Lu Yang¹, Richard M. Parton¹, Ana Palanca¹, Ilan Davis¹
¹Department of Biochemistry, University of Oxford, Oxford, UK

1 Works for me

 Gabriel Gasque
protocols.io

Steps Guidelines Warnings Materials Metadata

ABSTRACT

The lack of an effective, simple, and highly sensitive protocol for fluorescent in situ hybridization (FISH) at the *Drosophila* larval neuromuscular junction (NMJ) has hampered the study of mRNA biology. Here, we describe our modified single molecule FISH (smFISH) methods that work well in whole mount *Drosophila* NMJ preparations to quantify primary transcription and count individual cytoplasmic mRNA molecules in specimens while maintaining ultrastructural preservation. The smFISH method is suitable for high-throughput sample processing and 3D image acquisition using any conventional microscopy imaging modality and is compatible with the use of antibody colabeling and transgenic fluorescent protein tags in axons, glia, synapses, and muscle cells. These attributes make the method particularly amenable to super-resolution imaging. With 3D Structured Illumination Microscopy (3D-SIM), which increases spatial resolution by a factor of 2 in X, Y, and Z, we acquire super-resolution information about the distribution of single molecules of mRNA in relation to covisualized synaptic and cellular structures. Finally, we demonstrate the use of commercial and open source software for the quality control of single transcript expression analysis, 3D-SIM data acquisition and reconstruction as well as image archiving management and presentation. Our methods now allow the detailed mechanistic and functional analysis of sparse as well as abundant mRNAs at the NMJ in their appropriate cellular context.

Editor



Example protocol

Steps Description Guidelines & Warnings Materials VIEW SHARE MORE All changes saved

EDITING STEP 1.2

FIRST SECTION NAME 0m

1 Add 200 ml reagent A to 5 ml reagent B & stir vigorously for 00:00:10

1.1 Place at 4 °C for 00:30:00

1.2 Put On Ice & leave Overnight

2 Add ethanolamine to the solution and centrifuge 100 rpm, room temperature 00:15:00

Ethanolamine (Monoethanolamine, 2-Aminoethanol) by Bio Basic Inc. Catalog #: EC6400 SIZE 1L

SECOND SECTION ... 0m

3

COMPONENTS

Amount Concentration Temperature

Duration Protocol Document

Equipment Reagent Command

Citation Dataset Software

Note Safety Information Expected Result

Centrifugation Goto PH

Thickness

Request a component

- Detailed components
- Granular editing history
- Concurrent editing
- Color coded section labels
- Step-by-step format

Copy and fork



Steven Henikoff / Publications / Bench top CUT&Tag

Bench top CUT&Tag V.2

Nature Communications
Hatice S Kaya-Okur¹, Steven Henikoff¹
¹Fred Hutchinson Cancer Research Center
Apr 21, 2019
39 Works for me dx.doi.org/10.17504/protocols.io.z6hf9b6
Human Cell Atlas Method Development Community

Steven Henikoff
Fred Hutchinson Cancer Research Center

Run Bookmarks

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Steps Guidelines Warnings Materials **Forks** Metadata Metrics

0 Private Forks Open All

Version 1
Version 2
Version 3

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Tahmineh Kandelouei Jul 19, 2020

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Version 1

Version 2

Bench top CUT&Tag with antibody
Antibodies Online GmbH
30 Comments

Version 2

Version 3

Version 4

Version 5

Bench top CUT&Tag with antibody
Antibodies Online GmbH
Version 2

Version 1

Version 3

Version 4

Version 5

Bench top CUT&RUN with antibody
Antibodies Online GmbH
25 Comments, Version 3

Version 1


Version 2

Version 4

Version comparison



Lauren Ponisio / Publications / White Water Ranch Pollinator Enhancement Study Design

 **White Water Ranch Pollinator Enhancement Study Design V.2** ▾
Lauren Ponisio¹
¹University of Oregon

1 Works for me Share [dx.doi.org/10.17504/protocols.io.b3c8qizw](https://doi.org/10.17504/protocols.io.b3c8qizw)

Version 2 ▾
Jan 02, 2022 Ponisiolab

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Lauren Ponisio
University of Oregon

Steps Forks Metadata Metrics

ABSTRACT

Field protocol for Whitewater Ranch wildflower patch enhancement study

Questions

1. Can native, flowering plants succeed (germinate and flower within 1-3 years after seeding) in clearcuts with minimal site prep?
2. What native shrubs can establish on road edges?
3. Is there an interaction between plant success and planting inside burn piles or outside burn piles?
4. Does intraspecific competition influence success?
5. Is there an effect of different site characteristics (slope, elevation, aspect, N:C ratio)?
6. Is there evidence of dispersal of seeds in subsequent years?

Study area

- 2
 - White Water Ranch ~1,700 acres of mid elevation slopes in the Cascades, along the McKenzie River (<https://g.page/whitewater-ranch?share>)
 - Area was Doug fir plantations, most burned in the 2020 Holiday farm fire
 - ~200 burn piles of varying size, easily accessible from roads, no map of locations

Share and publish



The screenshot shows a web-based protocol editor interface. At the top, the title is "Super-Resolution Single Molecule FISH at the Drosophila Neuromuscular Junction". Below the title, there are tabs for "Steps", "Description", "Guidelines & Warnings", and "Materials". A red arrow points to the "SHARE" button. To the right of "SHARE" is a "MORE" dropdown menu, which is open, showing options: "Get DOI", "Post draft", "Publish", "Export", and "Delete". A red arrow points to the "Publish" option. The main content area is titled "3.1 Larva Neuromuscular Junction Dissection" and contains a list of five numbered steps, each with a checkbox and a "0m" timer. The steps are:

- 1 Video protocols for Drosophila larva dissection are available online. Place the larva dorsal side up on a 35 mm Petri dish filled half way with Sylgard, by placing pins at the anterior ends.
- 2 Cover the larva with a few drops of saline buffer.
- 3 Use microdissection scissors to create a small incision at the centre of the dorsal midline.
- 4 Extend the incision along the dorsal midline toward the posterior end, then from the centre towards the anterior end of the larva, make the cuts as superficial as possible so as not to damage the underlying nervous system and muscle tissues.
- 5 Carefully remove gut tissue by holding the trachea with forceps and cutting the tracheal attachments at each abdominal segment. After cutting the trachea on either side the gut tissue and other organs can be carefully removed all at once, leaving the brain and nerves intact.

Public content is searchable



Search microscopy

PUBLICATIONS WORKSPACES PEOPLE DISCUSSIONS REAGENTS SORT BY: RELEVANCE MORE FILTERS

234 results for microscopy

Publications

Microscopy
Ricardo Quiteres¹, Alvaro Crevenna², Zach Hense³, Federico Herrera¹
¹Faculdade de Ciências, Departamento de Química e Bioquímica, Cell Structure and Dynamics Laboratory, ²EMBL Mont e Rotondo, ³Instituto de Tecnologia Química e Biológica (ITQB NOVA)
Federico Herrera
Feb 03, 2021 · 👁 109 · 📄 88

Search microscopy

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234 results for microscopy

A growing community of users and protocols



- Open access repository
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Some Stats

Total users:

>114,000

Total public protocols:

>12,000

Total private protocols:

>40,000

Average views/month:

>200,000

<https://www.protocols.io/welcome>

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CURES START HERE®

+ more

protocols.io's business model



The screenshot shows a web browser window with the URL `protocols.io/plans/academia`. The page title is "protocols.io for Academia" with the subtitle "Public methods are always free to read and publish on protocols.io." Below this, the "Public sharing" section is highlighted, stating it is "Ideal for publishing protocols". A plan card for "Open Research" is shown, labeled "FREE". A grey box contains the text: "The protocols.io platform will always be free for published protocols." Below the card, the following features are listed: "Unlimited Public Protocols", "Unlimited public workspaces", and "Unlimited public versions and forks".

FREE (Open Access):

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protocols.io's business model



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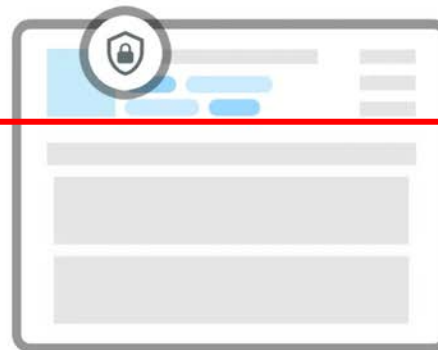
Carnegie Mellon University

Centers for Disease Control and Prevention

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Note

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[See terms and conditions for protocol entry](#)

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Agenda



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Case study: New England Biolabs



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Case study: New England Biolabs



New England Biolabs (NEB) 79  

[Timeline](#) [About](#) [Publications](#) **167** [Members](#) **17** [Discussions](#) **255** [Resources](#) [News](#)

Timeline

About

Publications **167**

Members **17**

Discussions **255**



June 10, 2022



 Lenny Teytelman

May 17, 2022

Discussions

[Comment on Step 1 of Making your own electrocompetent cells](#)

Please note: this protocol is deprecated.

 Lenny Teytelman

May 17, 2022

Case study: New England Biolabs



Isabel Gautreau / Publications / NEBNext® Ultra™ DNA Library Prep Protocol for Illumina® (E7370)

 **NEBNext® Ultra™ DNA Library Prep Protocol for Illumina® (E7370) V.3** 8

New England Biolabs¹
¹New England Biolabs

Version 3 ▼

Apr 12, 2022

Run

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dx.doi.org/10.17504/protocols.io.j8epv5edv1bz/v3

New England Biolabs (NEB)
Tech. support phone: +1(800)632-7799 email: info@neb.com

Isabel Gautreau
New England Biolabs

Steps Guidelines Warnings Materials Forks Metadata Metrics

ABSTRACT

The NEBNext®Ultra™ DNA Library Prep Kit for Illumina® contains reagents for preparation of libraries for next-generation sequencing on the Illumina platform from 5 ng – 1 µg input DNA, in a streamlined workflow. Please note that adaptors and primers are not included in the kit and are available separately.

Each kit component must pass rigorous quality control standards, and each set of reagents is functionally validated together by construction and sequencing of a library on the Illumina sequencing platform.

For larger volume requirements, customized and bulk packaging is available by purchasing through the OEM/Bulks department at NEB. Please contact custom@neb.com for further information.

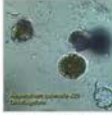
NEBNext End Prep

1 Add the following components in a sterile nuclease-free tube:

Protocols for equipment



Daniel Vaultot / Publications / Microscope video recording

 **Microscope video recording** ▼


Daniel Vaultot¹
¹Station Biologique, Roscoff, France

1 *Works for me* Share dx.doi.org/10.17504/protocols.io.k24cygw

Apr 10, 2019

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Ecology of Marine Plankton (ECOMAP) team - Roscoff Roscoff Culture Collection

 **Daniel Vaultot**
Station Biologique, Roscoff, France , Nanyang Technologica...


Steps Guidelines Metadata Metrics

ABSTRACT

Protocol to record videos on SBR Microscope

BEFORE STARTING

- Connect camera to microscope using C-mount connector
- Install Image Capture software on PC
- Connect USB cable to PC



Agenda



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Workspaces for collaborations



Anita Bröllochs / Publications / Isolation of Single Nuclei

COPY / FORK EXPORT

Isolation of Single Nuclei

Anita Bröllochs protocols.io

1 comment

Steps Abstract Metadata

Preparations 2h

1 Prepare solutions as described in the materials section.

Be sure to keep all solutions **On Ice**.

Comment or ask a question about this step.

Anita Bröllochs protocols.io Apr 18, 2020

Let's move this into the before starting section of the protocol.

Isolating Nuclei 5h

2 Add **0.5 ml** Buffer A to the tissue segments. 2m

3 Incubate at **5 °C** for **00:30:00**. 30m

Be sure to wear gloves and protective goggles.

step case

A B C


Agenda



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Published protocols are citable





ARTICLE

DOI: 10.1038/s41467-018-05347-6 **OPEN**

Sensitive and powerful single-cell RNA sequencing using mcSCRb-seq

Johannes W. Bagnoli¹, Christoph Ziegler¹, Swati Parekh^{1,3}, Johanna Geuder¹, Ines F...

Single-cell RNA sequencing (scRNA-seq) has emerged as a central genome-wide method to characterize cellular identities and processes. Consequently, improving its sensitivity, flexibility and cost-efficiency can advance many research questions. Among the flexible plate-based methods, "Single-Cell RNA-Barcoding and Sequencing" (SCRb-seq) is one of the most sensitive and efficient ones. Here, we systematically evaluated experimental conditions of this protocol and find that adding polyethylene glycol considerably increases sensitivity by enhancing cDNA synthesis. Furthermore, using Terra polymerase increases efficiency due to a more even cDNA amplification that requires less sequencing of libraries. We combined these and other improvements to a new scRNA-seq library protocol we call "molecular crowding SCRb-seq" (mcSCRb-seq), which we show to be the most sensitive and one of the most efficient and flexible scRNA-seq methods to date.

Aleksandar Janjic / Publications / mcSCRb-seq protocol

mcSCRb-seq protocol V.1

Nature Communications

Johannes JWB Bagnoli¹, Christoph Ziegenhain¹, Aleksandar Janjic¹, Lucas Esteban Wange¹, Beate Vieth¹, Swati Parekh¹, Johanna Geuder¹, Ines Hellmann¹, Wolfgang Enard¹

¹Ludwig-Maximilians-Universität München

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Human Cell Atlas Method Development Community

Aleksandar Janjic
Ludwig-Maximilians-Universität München

Steps Guidelines Materials Forks Metadata Metrics

ABSTRACT

Single-cell RNA sequencing (scRNA-seq) has emerged as a central genome-wide method to characterize cellular identities and processes. Consequently, improving its sensitivity, flexibility and cost-efficiency can advance many research questions. Among the flexible plate-based methods, "Single-Cell RNA-Barcoding and Sequencing" (SCRb-seq) is one of the most sensitive and efficient ones. Here, we systematically evaluated experimental conditions of this protocol and find that adding polyethylene glycol considerably increases sensitivity by enhancing cDNA synthesis. Furthermore, using Terra polymerase increases efficiency due to a more even cDNA amplification that requires less sequencing of libraries. We combined these and other improvements to a new scRNA-seq library protocol we call "molecular crowding SCRb-seq" (mcSCRb-seq), which we show to be the most sensitive and one of the most efficient and flexible scRNA-seq methods to date.

ATTACHMENTS

mcSCRbseq_oligo.txt

COMMUNICATIONS | DOI: 10.1038/s41467-018-05347-6

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single-cell RNA sequencing (scRNA-seq) has emerged as a central genome-wide method to characterize cellular identities and processes. Consequently, improving its sensitivity, flexibility and cost-efficiency can advance many research questions. Among the flexible plate-based methods, "Single-Cell RNA-Barcoding and Sequencing" (SCRb-seq) is one of the most sensitive and efficient ones. Here, we systematically evaluated experimental conditions of this protocol and find that adding polyethylene glycol considerably increases sensitivity by enhancing cDNA synthesis. Furthermore, using Terra polymerase increases efficiency due to a more even cDNA amplification that requires less sequencing of libraries. We combined these and other improvements to a new scRNA-seq library protocol we call "molecular crowding SCRb-seq" (mcSCRb-seq), which we show to be the most sensitive and one of the most efficient and flexible scRNA-seq methods to date.

The authors declare no competing interests.

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protocols.io's metrics



Aleksandar Janjic / Publications / mcSCR-seq protocol

mcSCR-seq protocol V.1
Nature Communications

Johannes JWB Bagnoli¹, Christoph Ziegenhain¹, Aleksandar Janjic¹, Swati Parekh¹, Johanna Geuder¹, Ines Hellmann¹, Wolfgang Enard¹
¹Ludwig-Maximilians-Universität München

Mar 19, 2018

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Human Cell Atlas Method Development Community

Aleksandar Janjic
Ludwig-Maximilians-Universität München

Metrics

- 55,599 Views all versions
- 156 (Exports)
- 58 Steps (includes sub-steps and step cases)
- 8 Bookmarks
- 2 Forks
- 38 Comments
- 8 Protocol run records

THIS PROTOCOL IS CITED IN THE FOLLOWING PUBLICATIONS:

Nature Communications:

ABSTRACT

Single-cell RNA sequencing (scRNA-seq) has emerged as a central tool for identifying cell types and processes. Consequently, improving its sensitivity, specificity and throughput for many research questions. Among the flexible plate-based methods, "Microfluidic Cell Sorting and Sequencing" (SCR-seq) is one of the most sensitive and efficient methods for single-cell RNA sequencing. Experimental conditions of this protocol and find that adding poly(A) tail to the cDNA enhances sensitivity by enhancing cDNA synthesis. Furthermore, using Termination-Induced Capping (TIC) for more even cDNA amplification that requires less sequencing of libraries. We present improvements to a new scRNA-seq library protocol we call "molecular cloning" which we show to be the most sensitive and one of the most efficient methods for single-cell RNA sequencing.

ATTACHMENTS

mcSCRseq_oligoT.txt

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Vectorial application for the illustration of archaeological lithic artefacts using the "Stone Tools Illustrations with Vector Art" (STIVA) Method

Jacopo Niccolò Cerasoni

Published: May 11, 2021 • <https://doi.org/10.1371/journal.pone.0251466>

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Abstract

Introduction

Materials and methods

Expected results

Supporting information

Acknowledgments

References

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Jacopo Niccolò Cerasoni / Publications / Stone Tools Illustrations with Vector Art: The 'STIVA' Method

Stone Tools Illustrations with Vector Art: The 'STIVA' Method V.2

PLOS ONE Peer-reviewed method

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2 Works for me Share dx.doi.org/10.17504/protocols.io.bubqnsmw

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Jacopo Niccolò Cerasoni

Steps Guidelines Materials Forks Metadata Metrics

ABSTRACT

Lithic illustrations are often used in scientific publications to efficiently communicate the technological and morphological characteristics of stone tools. They offer invaluable information and insights not only on how stone raw materials were transformed into their final form, but also on the individuals that made them. Here, the "Stone Tools Illustrations with Vector Art" (STIVA) Method is presented, which involves the illustration of lithic artefacts using vectorial graphics software (Adobe® Illustrator®). This protocol follows an optimised step-by-step method, presenting ten major sections that constitute the creation of a lithic illustration: photography, vectorial software configuration, scale, outline, scar borders, ripples, cortex, symbols, composition, and export. This method has been developed to allow researchers, students and educators to create clear and competent illustrations for any application, from scientific publications to public outreach.

Photograph Artefact

- 1 Lock camera on a tripod (ideally use a macro lens with a focal length of between 90mm to 105mm) and place in light box (if available).
- 2 Place artefact flat onto the workspace.
- 2.1 If the artefact does not sit flat due to its irregular shape, use an appropriate amount of modelling clay

Vectorial application for the illustration of archaeological lithic artefacts using the "Stone Tools Illustrations with ...
Jacopo Niccolò Cerasoni

Materials and methods

The protocol described in this peer-reviewed article is published on protocols.io, dx.doi.org/10.17504/protocols.io.bubqnsmw and is included for printing [S1 File](#) with this article.

Expected results

While a variety of methods for lithic illustration already exist, with the application of the 'STIVA' method it is expected that users will produce publishable and user-friendly illustrations without

Supporting information

Summary of benefits



- protocols.io's mission
- protocols.io's platform
- protocols.io and core facilities
 - Methods
 - Equipment
 - Collaborations
 - Credit
- Training resources
- Q&A

Agenda



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Training resources



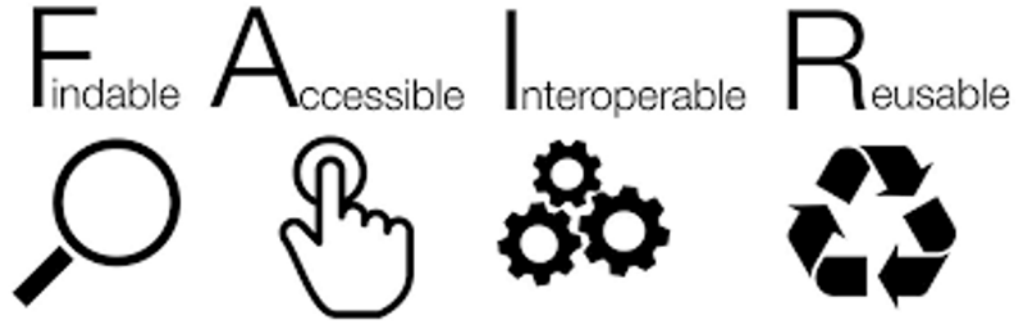
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Q/A

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FAIR principles



Every workspace has a private folder



The screenshot shows a workspace interface with a sidebar on the left containing navigation icons and a main content area. The main content area displays a workspace titled "PREMIUM Low-cost, high-quality ...". In the center, a modal window shows the workspace's folder structure: a blue folder icon labeled "Low-cost, high-quality ...", a folder icon with a white cat head logo labeled "Gabriel Gasque" (circled in red), and a trash can icon labeled "Trash". Below the modal, a table lists files:

File Name	Count	Size	Created At	Author
Ambient sample storage system of field-collected inse...	1	126KB	Dec 11, 2020 at 4:54 PM	Sam Mugford
WASP-D Field Protocol	2	151KB	Nov 13, 2020 at 12:32 PM	Greg Blonder
Low-cost tissue collection and genomic DNA extraction...	1	907KB	Jun 23, 2020 at 7:15 AM	Bradley Till
A do-it-yourself low-cost agarose gel documentation an...	1	13.9MB	Jun 23, 2020 at 7:14 AM	Rachel A Howard...



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Join this webinar to get an introduction to protocols.io and it's core functionalities. In this 30 minute webinar, you will learn more about our mission and how protocols.io can help you to make your science more reproducible. The webinar will cover the following topics: protocols.io's missi...

How to make your protocol more reproducible and discoverable

Anita Broellochs · 🐦 📘 📌

Webinar: How to make your protocol more reproducible and discoverable

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1-2-1 demos



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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 Fiozeze, Margarida Anjos, Céilia 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>

Article Authors Metrics Comments Media Coverage

Abstract

Abstract

Author summary

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 of commensal bacteria, together, control food choice behavior and reproduction.

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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 manipulation are available as a collection in protocols.io [dx.doi.org/10.17504/protocols.io/hdtb26n](https://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 (*UbiGlo-Gal4*), pan-neuronal (*elav-Gal4*), tracheal (*Trt-Gal4*), or fat (*UAS-Gal4*)

Methods and protocols for are available as a collection in protocols.io (DOI link)