



protocols.io is the centralized platform for the collaborative creation, management and sharing of research methods. Now, you can deliver a platform to your researchers, faculty and students to work better and smarter; you can support the re-use and reproducibility of research as needed; and you gain better insight into the totality of research that is done at your institution.



## A Dynamic Environment

Give your researchers, faculty and students a dynamic environment to organize and update methods and edit these collaboratively. The protocols.io environment is interactive, enabling others to comment on entire methods or on individual steps. Methods can be easily exported locally or mirrored to Google Drive, Dropbox, and other cloud storage sites. Researchers, faculty and students can also readily view and compare different versions of the methods.

Aleksandar Janjic / Publications / mcSCR-seq protocol

**Version 2**

May 22, 2018

Run

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**mcSCR-seq protocol V.2**

Nature Communications

Johannes Bagnoli<sup>1</sup>, Christoph Ziegenhai Swati Parekh<sup>1</sup>, Johanna Geuder<sup>1</sup>, Ines H Lucas Esteban Wange<sup>1</sup>, Beate Vieth<sup>1</sup>, d<sup>1</sup>

<sup>1</sup>Ludwig-Maximilians-Universität Münch

dx.doi.org/10.17504/pro

Human Cell Atlas Method Development Co

Aleksandar Janjic  
Ludwig-Maximilians-Universität München

View 33 comments on prior versions

35 comments

Comment or ask a question.

**Mohammad-Monzoor Akinwale** Aug 16, 2019

I need suggestions and directions on what may be denaturing competent DNA specimens during Agarose gel electrophoresis and what to do to protect them from such attack and to make them show under uv transillumination as bands

**Read more**

REPLY

**Aleksandar Janjic** Aug 19, 2019  
Ludwig-Maximilians-Universi...

**Steps** Abstract Guidelines Materials Forks Metadata Metrics

BEFORE STARTING

Wipe bench surfaces with RNase Away and keep working environment clean.

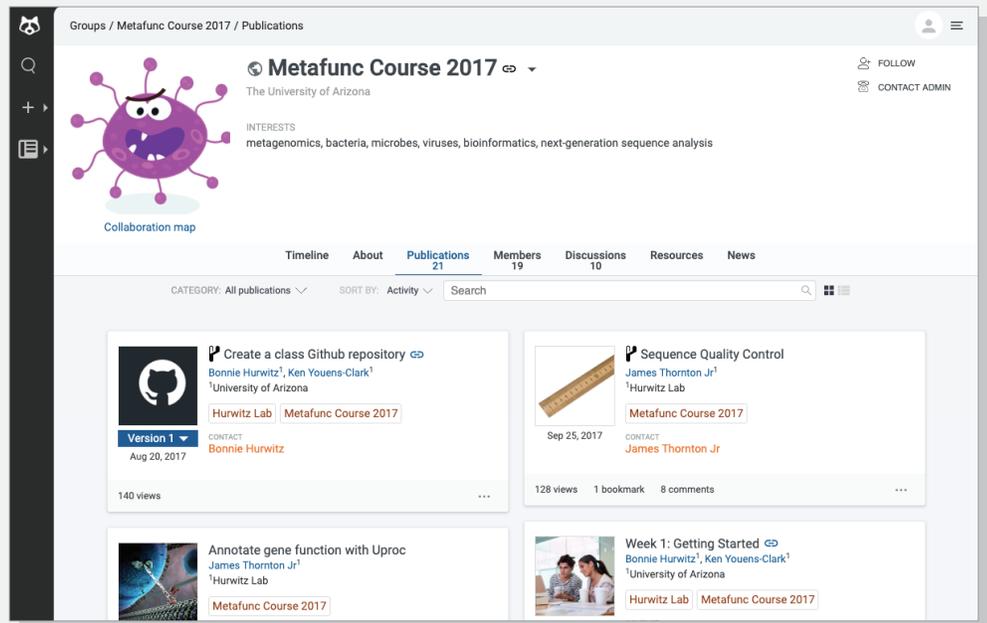
Preparation of lysis plates

1 Prepare Lysis Buffer according to the number of plates to be filled.

	A	B	C
1	Reagent	96-well plate	384-well plate
2	NEB HF Phusion buffer (5x)	1.1 µL	4.4 µL
3	Proteinase K (20 mg/mL)	27.5 µL	110 µL
4	UltraPure Water	411.4 µL	1645.6 µL
5	Total	440 µL	1760 µL

## Teaching and Learning

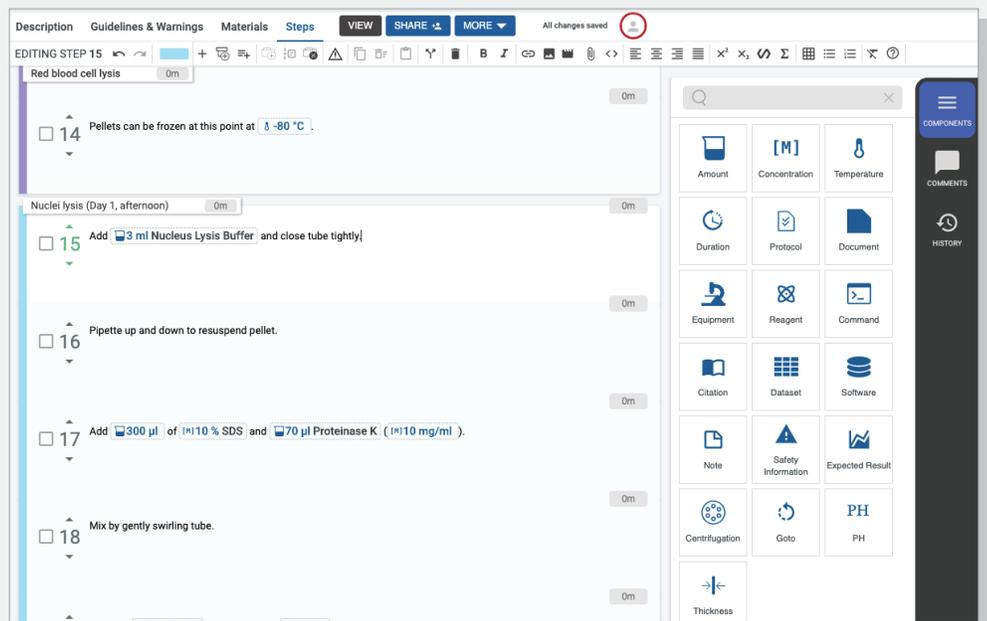
Use protocols.io in computational and lab classes, with easy sharing of class material. Students can follow instructions while also having the opportunity to directly ask questions or make comments on class content. Class content can be open for everyone, or the instructor can choose to make it only accessible for the students.



The screenshot shows the 'Metafunc Course 2017' group page on protocols.io. The page header includes the group name, 'The University of Arizona', and interests: 'metagenomics, bacteria, microbes, viruses, bioinformatics, next-generation sequence analysis'. Below the header are navigation tabs for 'Timeline', 'About', 'Publications' (21), 'Members' (19), 'Discussions' (10), 'Resources', and 'News'. A search bar is located below the tabs. The main content area displays a grid of publications, including 'Create a class Github repository', 'Sequence Quality Control', and 'Annotate gene function with Uproc'. Each publication card shows the author, date, and view/comment counts.

## Reproducibility and Re-use

With protocols.io, the research community can readily reproduce and re-use research methods in support of open science goals and mandates. The protocols.io editor feature makes it simple and easy to enter detailed procedures, supporting open communication with authors and facilitating reproducibility and refinement. As a result, protocols.io also speeds the time in which research is produced and disseminated, as researchers can collaborate and iterate on methods in real-time.



The screenshot shows the protocols.io protocol editor interface. The main editing area displays a protocol titled 'Red blood cell lysis' with several steps: 'Pellets can be frozen at this point at -80 °C', 'Add 3 ml Nucleus Lysis Buffer and close tube tightly', 'Pipette up and down to resuspend pellet', 'Add 300 µl of 10% SDS and 70 µl Proteinase K (10 mg/ml)', and 'Mix by gently swirling tube'. The right sidebar contains a 'COMPONENTS' panel with various icons for protocol elements like Amount, Concentration, Temperature, Duration, Protocol, Document, Equipment, Reagent, Command, Citation, Dataset, Software, Note, Safety Information, Expected Result, Centrifugation, Goto, PH, and Thickness.

## Increased Citations

protocols.io supports the minting of a DOI for each published method, which can be associated with the published paper. As a result, researchers can be cited for more than just their article

Aleksandar Janjic / Publications / mcSCRb-seq protocol

Steps Abstract Guidelines Materials Forks Metadata Metrics

DOI  
[dx.doi.org/10.17504/protocols.io.p9kdr4w](https://dx.doi.org/10.17504/protocols.io.p9kdr4w)

PDF  
<https://protocols.io/view/mcscrb-seq-protocol-p9kdr4w.pdf>

PROTOCOL CITATION

Johannes Bagnoli, Christoph Ziegenhain, Aleksandar Janjic, Lucas Esteban Wange, Beate Vieth, Swati Parekh, Johanna Geuder, Ines Hellmann, Wolfgang Enard (2018). mcSCRb-seq protocol. protocols.io [dx.doi.org/10.17504/protocols.io.p9kdr4w](https://dx.doi.org/10.17504/protocols.io.p9kdr4w)

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

Johannes W. Bagnoli, et al (2018) Sensitive and powerful single-cell RNA sequencing using mcSCRb-seq. *Nature Communications*9:2937. doi: [10.1038/s41467-018-05347-6](https://doi.org/10.1038/s41467-018-05347-6)

KEYWORDS  
molecular crowding, scRNA-seq, SCRb-seq

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## Institutional Stewardship

When you provide a centralized platform to your researchers, you gain much-needed insight over the research methods that are created in your institution, ran and copied (forked). You can also readily collect research methods for inclusion in the (institutional) repository, preserve it, and understand its impact through in-depth analytics. All methods are archived in CLOCKSS for long-term preservation.

## Enterprise Benefits

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- Dedicated training webinars
- 1-on-1 video demonstrations for researchers
- Dedicated customer service and technical support
- Reporting on published output
- Integration with the institutional repository and long-term preservation
- Team administration
- For researchers: unlimited number of private protocols, shared notebook records, dedicated technical support, training and protocol import