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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

mcSCR-seq protocol V.2 [↗](#)

Nature Communications

Johannes Bagnoli¹, Christoph Ziegenhain, Swati Parekh¹, Johanna Geuder¹, Ines H... Lucas Esteban Wange¹, Beate Vieth¹, ...¹

¹Ludwig-Maximilians-Universität München

Version 2
May 22, 2018

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8 Works for me dx.doi.org/10.17504/pro...
Human Cell Atlas Method Development Co...

Aleksandar Janjic
Ludwig-Maximilians-Universität München

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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.

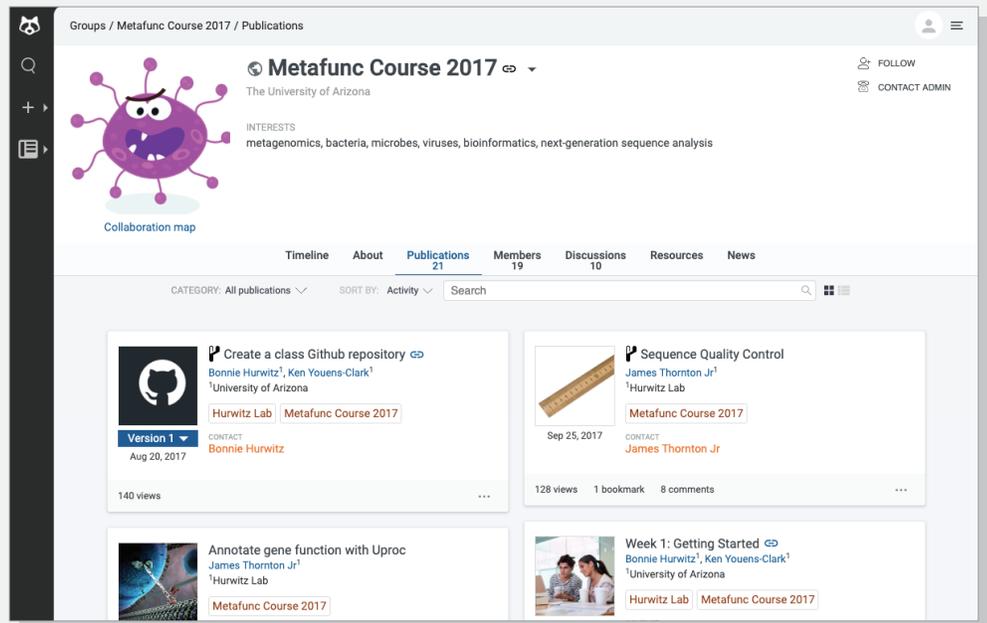
Preparation of lysis plates

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

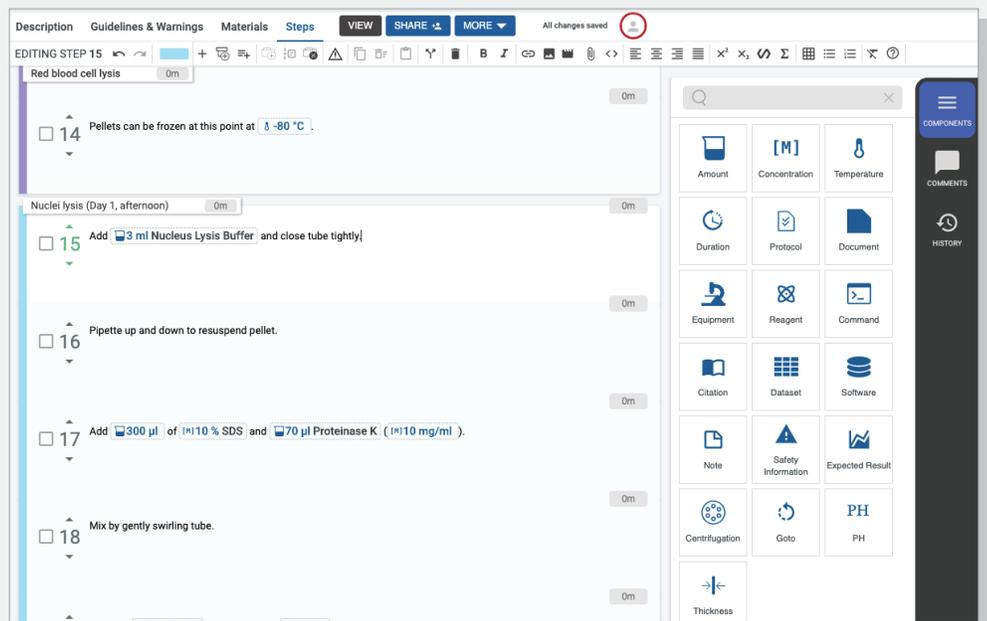
Use protocols.io in computational and lab classes, with easy sharing of class material. Students can follow instructions while also having the opportunity to directly ask questions or make comments on class content. Class content can be open for everyone, or the instructor can choose to make it only 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 like '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 also present. The main content area displays several 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 workspace displays a protocol titled 'Red blood cell lysis' with several steps. Step 14: 'Pellets can be frozen at this point at -80 °C'. Step 15: 'Add 3 ml Nucleus Lysis Buffer and close tube tightly'. Step 16: 'Pipette up and down to resuspend pellet.'. Step 17: 'Add 300 µl of 10% SDS and 70 µl Proteinase K (10 mg/ml)'. Step 18: '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. The top navigation bar includes 'Description', 'Guidelines & Warnings', 'Materials', 'Steps', 'VIEW', 'SHARE', and 'MORE'.

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

PDF
<https://protocols.io/view/mcscr-b-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

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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