



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

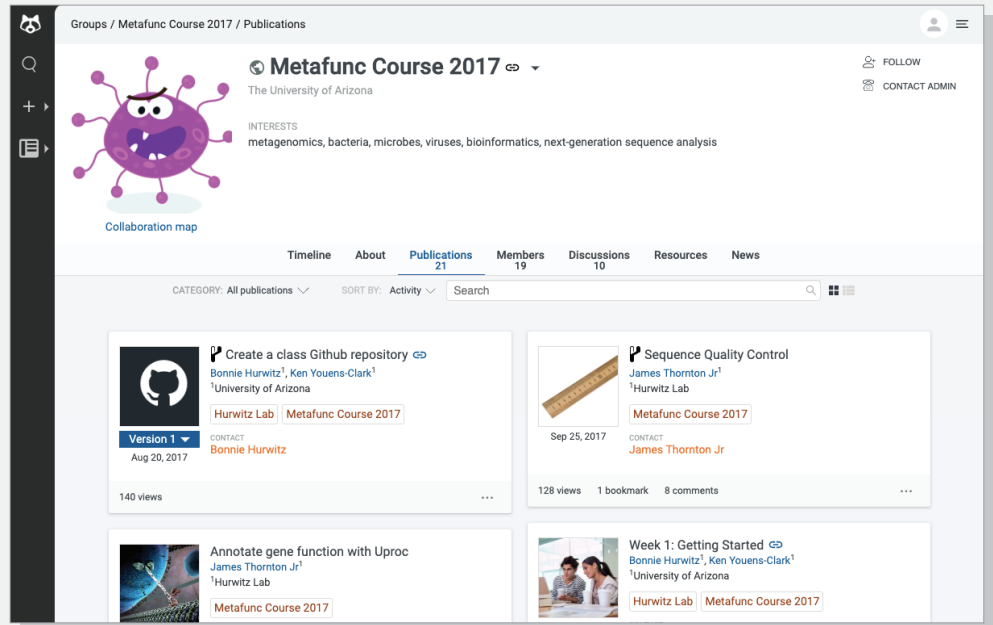
Give your researchers, faculty and students a dynamic environment to organize and update methods and edit these collaboratively. The protocols.io environment is interactive, enabling others to comment on entire methods or on individual steps. Methods can be easily exported locally or mirrored to Google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

The screenshot shows the protocols.io interface for the 'mcSCRb-seq protocol V.2'. The page includes a header with the user 'Aleksandar Janjic / Publications / mcSCRb-seq protocol', a version dropdown set to 'Version 2', and a list of authors: Johannes Bagnoli, Christoph Ziegenhain, Swati Parekh, Johanna Geuder, Ines Hoyer, Lucas Esteban Wange, and Beate Vieth. A 'Run' button is visible. A context menu is open over the 'Export' button, showing options like 'Print', 'PDF', 'JSON', 'to your computer', 'to Dropbox', 'to Google Drive', 'to Box', and 'to OneDrive'. Below the menu, there are tabs for 'Steps', 'Abstract', 'Guidelines', 'Materials', 'Forks', 'Metadata', and 'Metrics'. The 'Steps' tab is active, showing a step titled 'Preparation of lysis plates' with a table of reagents and volumes.

	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

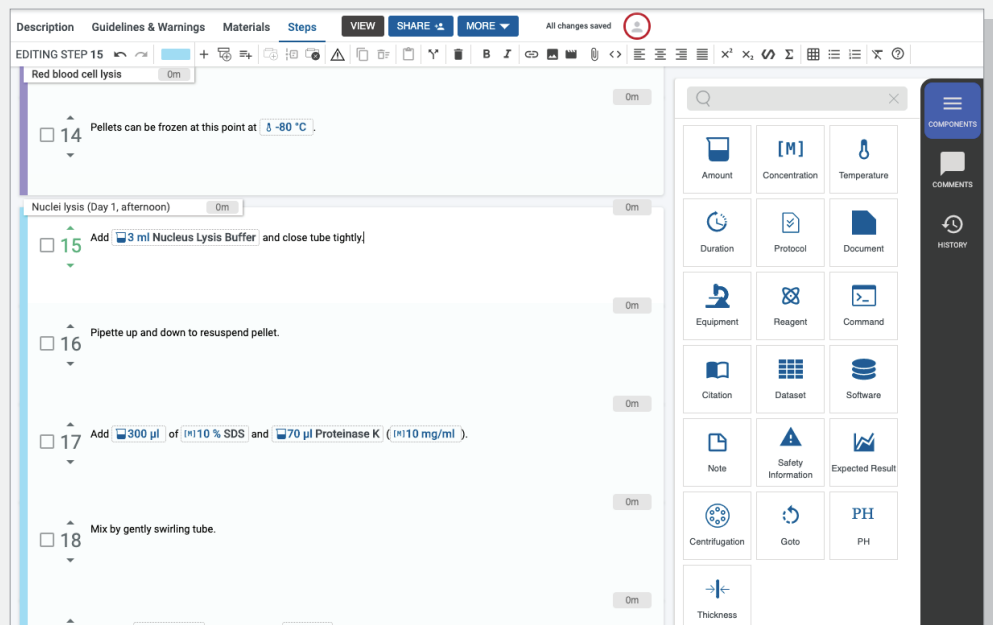
Use protocols.io in computational and lab classes, with easy sharing of class material. Students can follow instructions while also having the opportunity to directly ask questions or make comments on class content. Class content can be open for everyone, or the instructor can choose to make it only 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. The first publication is 'Create a class Github repository' by Bonnie Hurwitz and Ken Youens-Clark, dated Aug 20, 2017, with 140 views. The second is 'Sequence Quality Control' by James Thornton Jr and Hurwitz Lab, dated Sep 25, 2017, with 128 views, 1 bookmark, and 8 comments. The third is 'Annotate gene function with Uproc' by James Thornton Jr and Hurwitz Lab. The fourth is 'Week 1: Getting Started' by Bonnie Hurwitz and Ken Youens-Clark. Each publication card includes the author's name, affiliation, 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 top navigation bar includes 'Description', 'Guidelines & Warnings', 'Materials', and 'Steps'. The 'Steps' tab is active, showing a list of steps for a protocol titled 'Red blood cell lysis'. The steps are numbered 14 through 18. 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 search bar and a grid of icons for various protocol components: Amount, Concentration, Temperature, Duration, Protocol, Document, Equipment, Reagent, Command, Citation, Dataset, Software, Note, Safety Information, Expected Result, Centrifugation, Goto, PH, and Thickness. The bottom right corner has buttons for 'COMPONENTS', 'COMMENTS', and 'HISTORY'.

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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