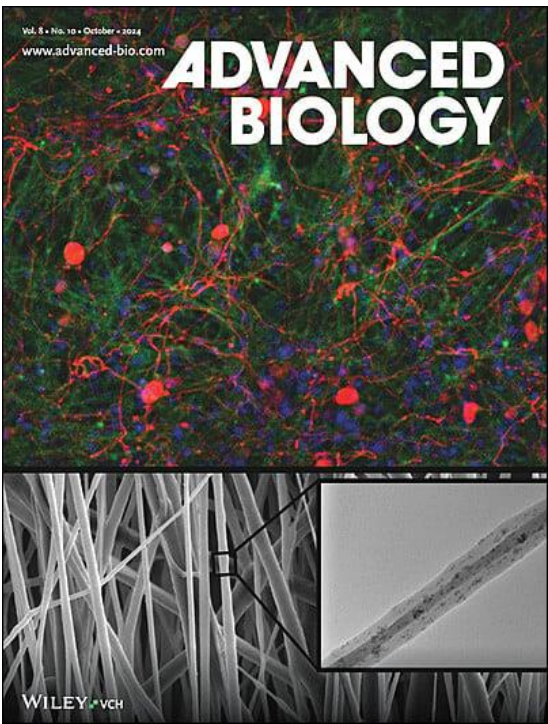


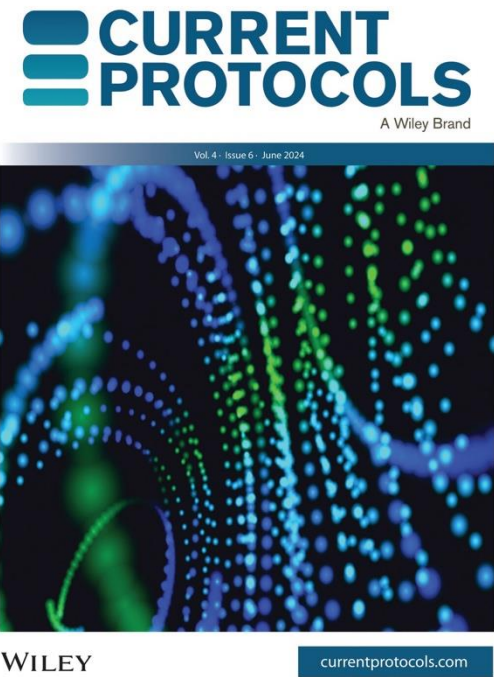
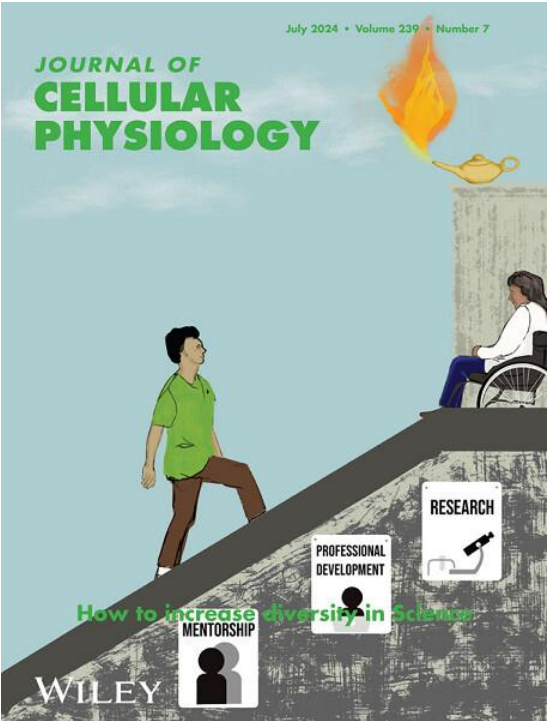
Demystifying the Publication Process and Tips for Early Career Researchers

Alexander Hutchison, PhD, Editor-in-Chief,
Current Protocols, Wiley

My time at Wiley



Aging Cell



My background

- High School math & science teacher for 7 years.
- College professor for 12 years.
- Good term paper like good submission.
- Starts by reading the instructions.

KINE 4350-0001 - Senior Seminar – Dr. Alexander Hutchison

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KINE 4350-0001: Senior Seminar
Spring 2021

[CATALOG DESCRIPTION OF COURSE](#) (will open new page)

Professor: Alexander Hutchison, PhD
Office: Metz 409D
Office Hours: MW 9:30-10:30 AM, TTh 11:00 AM-12:30 PM ONLINE ONLY (e-mail me with requested times and dates and we will meet via Microsoft Teams)
Telephone: 210-528-7057
Email: athutchison@ollusa.edu
Class Times: TTH 9:30am-10:45am
Classroom: PWSR

COURSE OVERVIEW
The purpose of this class is to provide our students with an introduction to research design. They will learn how to search for peer-reviewed published research that is of interest to them. They will then learn how to read, comprehend, and present scientific papers. Finally, the students will learn how to develop a testable research question, collect and analyze data, and present their findings.

READING AND INSTRUCTIONAL MATERIALS [OLLU bookstore](#) (will open new page).
All papers used in class will come from the Journal of Strength and Conditioning Research, published by the National Strength and Conditioning Association, (NSCA).

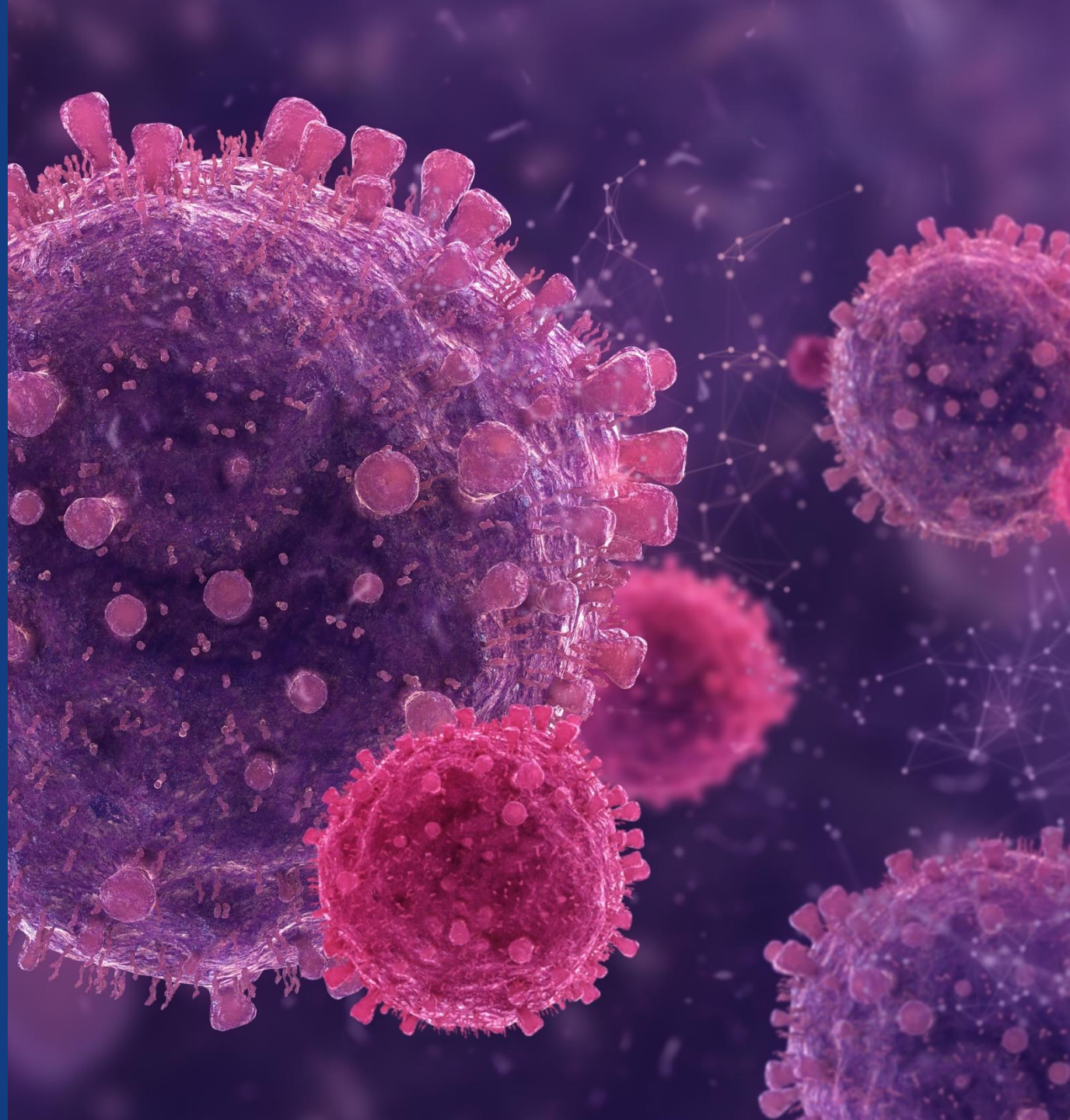
The professor will utilize the Blackboard online course management system. All course materials, including the syllabus, course schedule, lecture notes, instructions for all assignments, assignment submissions, and the grade book, will be accessed through this system. Blackboard may be accessed through your OLLU portal.

STUDENT LEARNING OUTCOMES
Kinesiology Program Goals

1. **Kinesiology majors will master course content.**
Kinesiology majors will master course content by understanding:
 - 1.1 Exercise Physiology
 - 1.2 Health and Wellness
 - 1.3 Movement Science.
2. **Kinesiology majors will develop proficient Kinesiology-related skills.**
Kinesiology majors will develop proficient kinesiology-related skills by:
 - 2.1 Assessing the health, fitness, and performance ability of individuals.
 - 2.2 Developing and implementing plans for improvement.
 - 2.3 Evaluating the effectiveness of those plans.
 - 2.4 Students will be able to demonstrate movements to improve health, fitness, and performance improvement.

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**Journal of
Cellular
Physiology**



Aims & Scope (What we want)

The ***Journal of Cellular Physiology*** publishes high-quality original research articles and reviews in areas of eukaryotic cell biology and physiology, focusing on those articles that adopt a mechanistic approach to investigate cell structure and function. There is appreciation for the application of cellular, biochemical, molecular and in vivo genetic approaches, as well as the power of genomics, proteomics, bioinformatics, and systems biology. Research articles must have a clear hypothesis and present novel and significant findings as well as perspectives on topics of cellular science, including molecular biology, biochemistry, pathobiochemistry, and molecular medicine.

Aims & Scope (What we don't want)

Merely descriptive manuscripts that do not go beyond correlations are not the focus of the Journal. Examples include associations of sequencing and omics data, RNA data (mRNA, non-coding RNA, microRNA), in silico analysis, and mere tests of compounds (including natural extracts) in cellular and animal models without mechanistic insights. Studies that are primarily bioinformatic in nature or focus on identifying novel biomarkers are considered outside of the scope of the Journal.

2023 Submissions

Total Submissions	Bioinformatics	Long non-coding RNA	Micro RNA	In silico	Nutraceuticals
2370					

53.7%

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Manuscript title

Synthesis and Application of a Caged Bioluminescent Probe for the Immunoproteasome

Manuscript abstract

iCP probe developed that incorporates a luminescent reporter that could be applied to a variety of different applications. The protocols presented here describe the synthesis of a cleavable activity-based bioluminescent probe that is selective for the iCP, and the application of the synthesized probe in immunoproteasome activity assays by luminescent plate reader. Having this bioluminescent reporter, a better understanding of how the iCP is implicated in disease progression, as well as identification of small molecule interactors can be achieved.

1217 of 3000 characters

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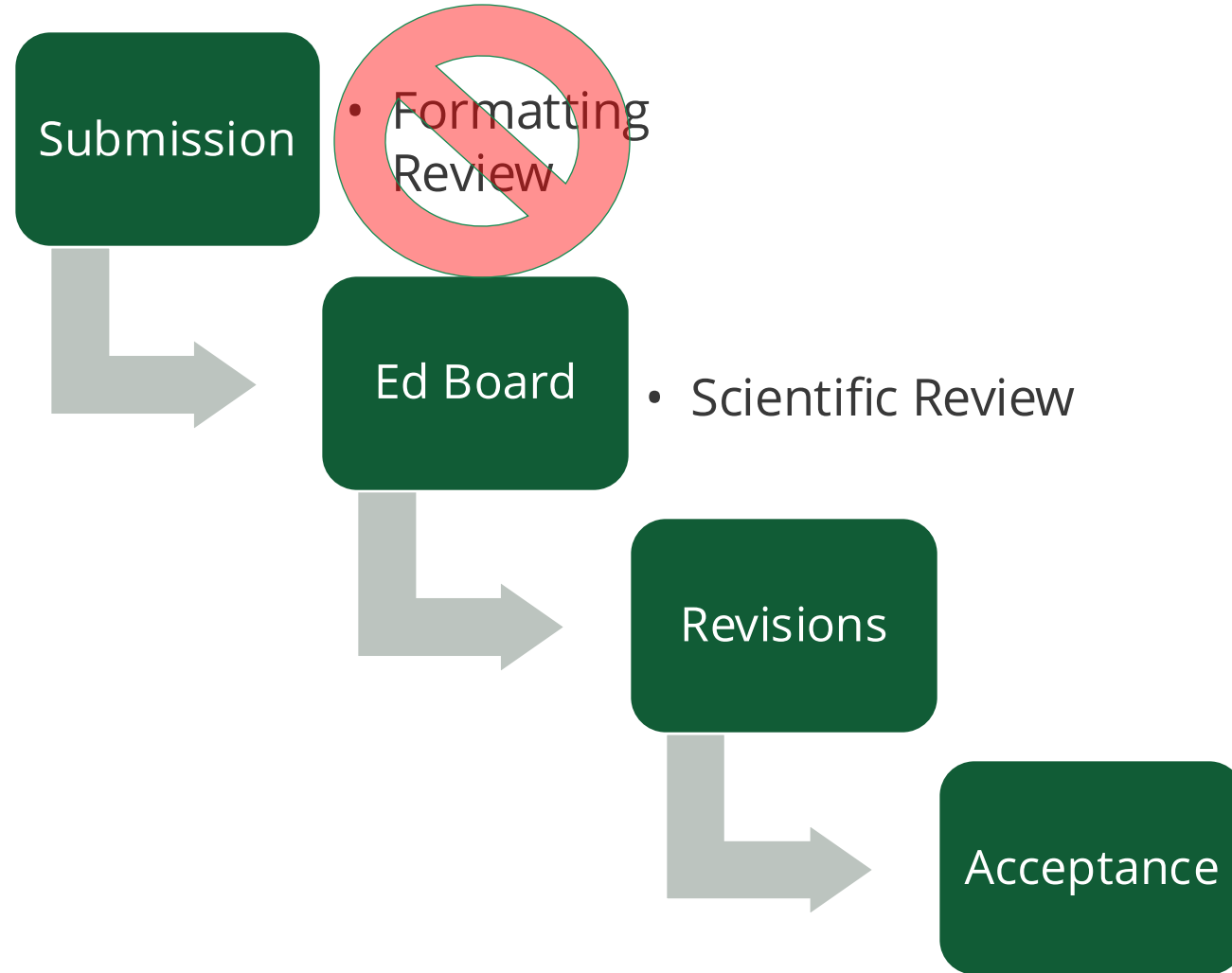
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Current Protocols



Current Protocols Workflow



Deepak S. Atri,^{1,2,3} Vivian S. Lee-Kim,^{1,2,3} Shamsudheen K. Vellarikkal,^{1,2} Oscar Sias-Garcia,^{1,2} Mounica Yanamandala,^{1,2} Gavin R. Schnitzler,^{1,2} and Rajat M. Gupta^{1,2,4}

¹Division of Cardiovascular Medicine and Department of Genetics, Brigham and Women's Hospital, Boston, Massachusetts
²Broad Institute of MIT and Harvard, Cambridge, Massachusetts
³These authors contributed equally to this work
⁴Corresponding author: rgupta@broadinstitute.org

Genome editing of primary human cells with CRISPR-Cas9 is a powerful tool to study gene function. For many cell types, there are efficient protocols for editing with optimized plasmids for Cas9 and sgRNA expression. Vascular cells, however, remain refractory to plasmid-based delivery of CRISPR machinery for *in vitro* genome editing due to low transfection efficiency, poor expression of the Cas9 machinery, and toxic effects of the selection antibiotics. Here, we describe a method for high-efficiency editing of primary human vascular cells *in vitro* using nucleofection for direct delivery of sgRNA-Cas9-NLS ribonucleoprotein complexes. This method is more rapid and its high editing efficiency eliminates the need for additional selection steps. The edited cells can be employed in diverse applications, such as gene expression measurement or functional assays to assess various genetic perturbation effects *in vitro*. This method proves effective in vascular cells that are refractory to standard genome manipulation techniques using viral plasmid delivery. We anticipate that this technique will be applied to other non-vascular cell types that face similar barriers to efficient genome editing. © 2021 Wiley Periodicals LLC.

Basic Protocol: CRISPR-Cas9 genome editing of primary human vascular cells *in vitro*

Keywords: CRISPR • Cas9 • endothelial cells • genome editing • vascular smooth muscle cells

How to cite this article:

Atri, D. S., Lee-Kim, V. S., Vellarikkal, S. K., Sias-Garcia, O., Yanamandala, M., Schnitzler, G. R., & Gupta, R. M. (2021). CRISPR-cas9 genome editing of primary human vascular cells in vitro. *Current Protocols*, 1, e291. doi: 10.1002/cpz1.291

INTRODUCTION

CRISPR-Cas9 genome editing is a powerful tool in molecular biology and is now being employed in the treatment of disease (Frangoul et al., 2021; Gillmore et al., 2021). Cardiovascular disease has the highest burden of mortality worldwide, and progress in the research of cardiovascular disease may be accelerated via a rapid technique for CRISPR editing in relevant cell types. Primary human vascular cells, particularly vascular smooth muscle cells (VSMCs), are notoriously refractory to genetic manipulation using typical cellular methods such as lipid-based transfection, and typically require labor-intensive viral transduction. Such methods are limited by low transfection efficiency, potential

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List all authors and affiliations. Denote corresponding author and include contact details (email and phone number).

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The abstract should be 300 words or less. Beneath the abstract, please list the titles of **all** of the protocols in the order in which they appear (as shown below) – this text counts towards the word limit of your abstract.

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Support Protocol 1: [Title], etc.

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Describe the method, why it is performed, and what data you can obtain. The introduction should provide:

- general statement and background about biological process under study or biochemistry of any reactions
- knowledge gap/limitations of current methods
- discussion of the theory, how the technique has evolved, and applications of your protocol
- information about the type of data that can be obtained
- the central advantages (and disadvantages) of the technique and comparison with other methods currently in use
- descriptions of the protocols. If Alternate Protocols are included, explain how to choose which protocol to use.

The final paragraph of the introduction should, in sentence form, list all the protocols in the document and provide a [brief summary](#) of each one.

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Notes or cautionary statements that apply to **all** of the protocols in the article should follow the introduction, while cautions specific to an individual protocol can be placed following that protocol's introduction. For example:

CAUTION: All reactions must be run in a suitable fume hood with efficient ventilation. Many of the reactions in this article are highly exothermic; safety glasses and reagent-impermeable protective gloves should be worn.

CAUTION: <organism name> is a Biosafety Level [2, 3] ([BSL-2, -3]) pathogen. Follow all appropriate guidelines and regulations for the use and handling of pathogenic microorganisms.

Multiplexed Single-Nucleus RNA Sequencing Using Lipid-Oligo Barcodes

Qi Zhang,^{1,4} Seong Won Kim,^{1,4,5} Joshua M. Gorham,¹ Daniel M. DeLaughter,¹ Tarsha Ward,¹ Christine E. Seidman,^{1,2,3} and Jonathan G. Seidman¹

¹Department of Genetics, Harvard Medical School, Boston, Massachusetts, USA
²Cardiovascular Division, Brigham and Women's Hospital, Boston, Massachusetts, USA
³Howard Hughes Medical Institute, Chevy Chase, Maryland, USA
⁴These authors contributed equally to this work.
⁵Corresponding author: seongwon_kim@g.harvard.edu

Published in the Human Genetics section

This protocol describes a robust pipeline for simultaneously analyzing multiple samples by single-nucleus (sn)RNA-seq. cDNA obtained from each single sample are labeled with the same lipid-coupled oligonucleotide barcode (10X Genomics). Nuclei from as many as 12 individual samples can be pooled together and simultaneously processed for cDNA library construction and subsequent DNA sequencing. While previous protocols using lipid-coupled oligonucleotide barcodes were optimized for analysis of samples consisting of viable cells, this protocol is optimized for analyses of quick-frozen cell samples. The protocol ensures efficient recovery of nuclei both by incorporating high sucrose buffered solutions and by including a tracking dye (trypan blue) during nuclei isolation. The protocol also describes a procedure for removing single nuclei 'artifacts' by removing cell debris prior to single nuclear fractionation. This protocol informs the use of computational tools for filtering poorly labeled nuclei and assigning sample identity using barcode unique molecular identifier (UMI) read counts percentages. The computational pipeline is applicable to either cultured or primary, fresh or frozen cells, regardless of their cell types and species. Overall, this protocol reduces batch effects and experimental costs while enhancing sample comparison. © 2022 Wiley Periodicals LLC.

Basic Protocol 1: Labeling cells with lipid oligo barcodes and generating multiplexed single-nucleus RNA-seq libraries
Basic Protocol 2: Bioinformatic deconvolution of the multiplexed snRNAseq libraries

Keywords: lipid oligo barcode • multiplex • nuclei isolation • single-nucleus RNA sequencing

How to cite this article:

Zhang, Q., Kim, S. W., Gorham, J. M., DeLaughter, D. D., Ward, T., Seidman, C. E., & Seidman, J. G. (2022). Multiplexed single-nucleus RNA sequencing using lipid-oligo barcodes. *Current Protocols*, 2, e579. doi: 10.1002/cpz1.579

INTRODUCTION

The advent of transcription profiling at single-cell resolution has become a powerful approach to reveal diverse cell populations and states within biological systems (Hwang, Lee, & Bang, 2018). Advances in droplet-microfluidic technology, which



Current Protocols e291, Volume 1
Published in Wiley Online Library (wileyonlinelibrary.com).
doi: 10.1002/cpz1.291

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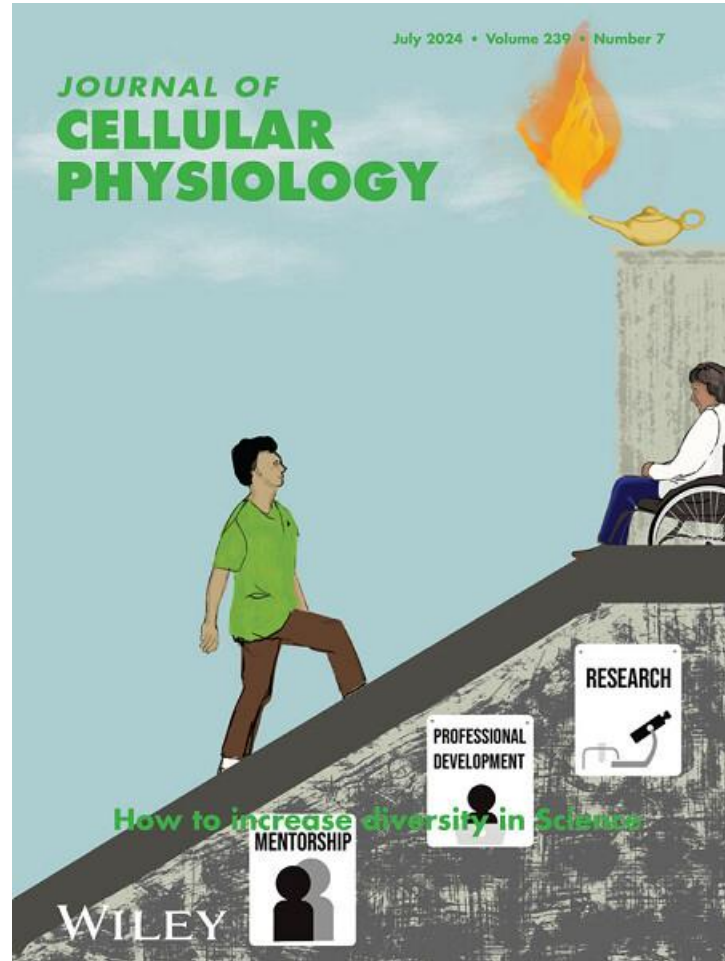
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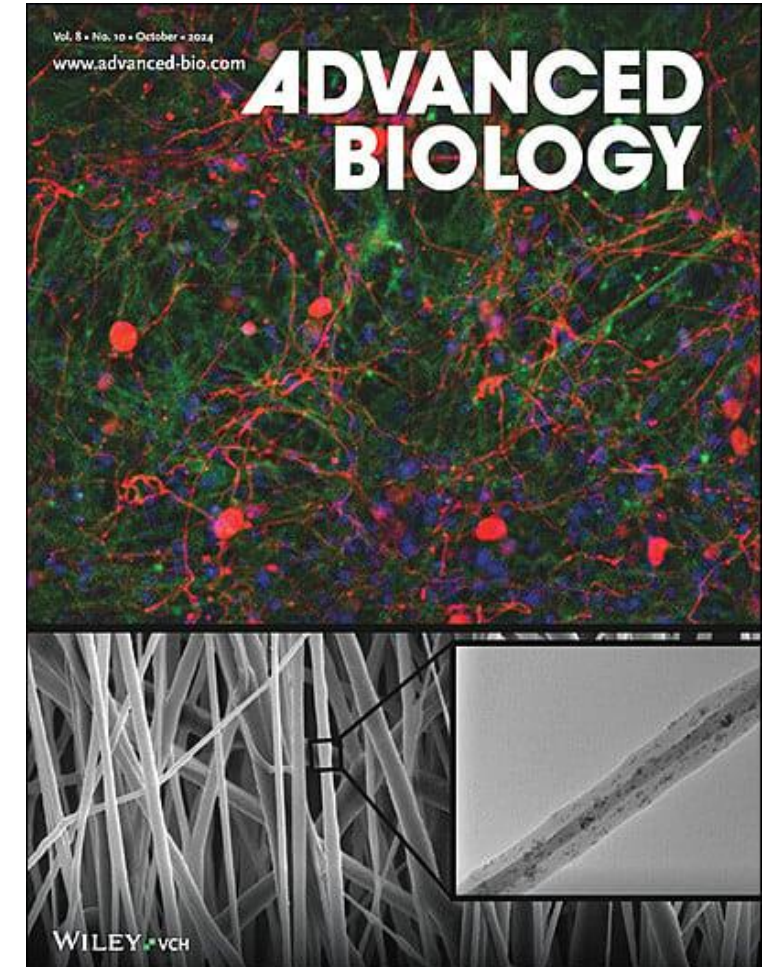
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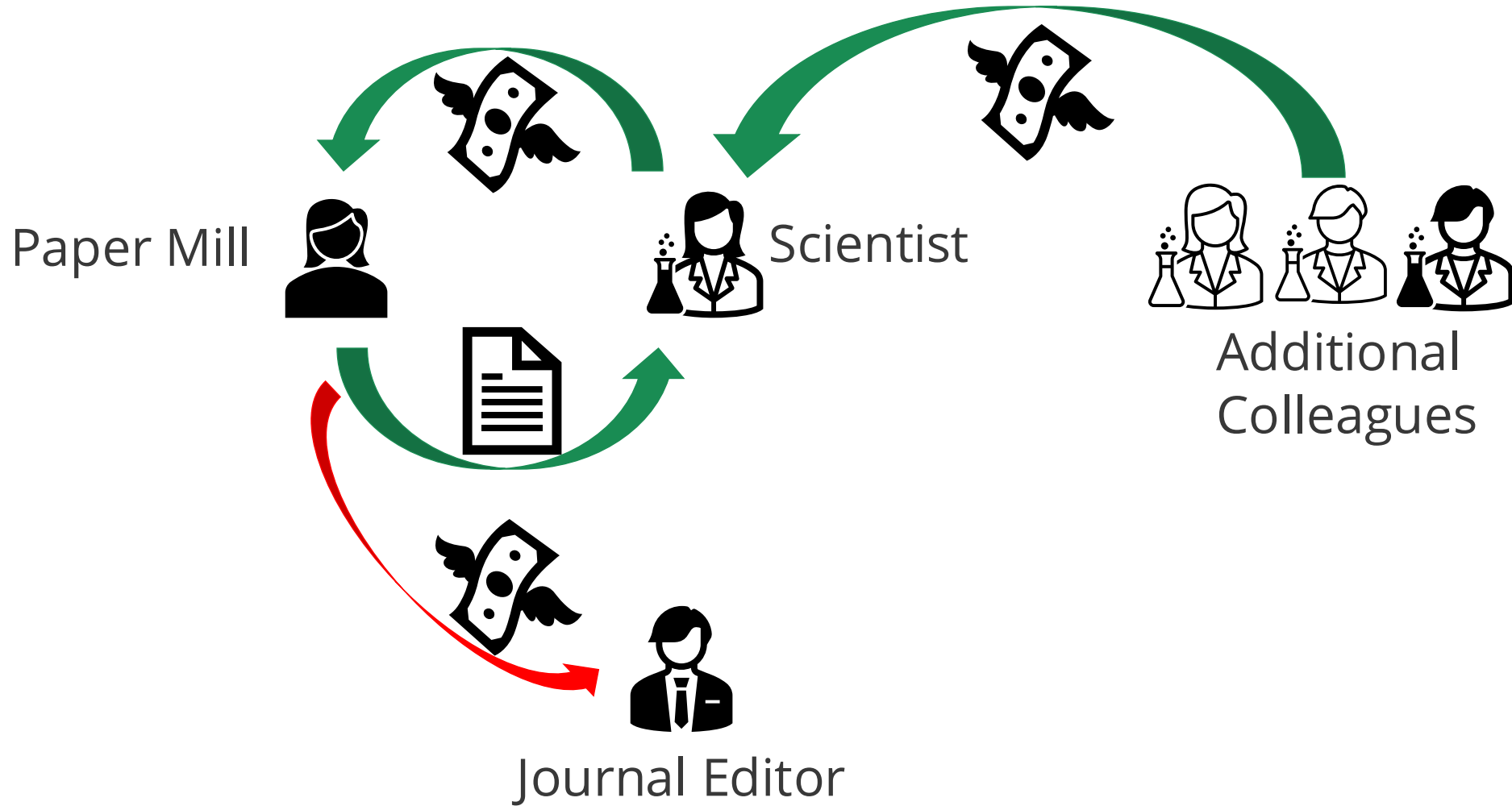
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Warning signs we look for



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- Use both if need be.

Have an ORCID and keep it up to date. (Co-authors too)

Alexander Hutchison

 <https://orcid.org/0000-0001-9437-5468>  

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Assistant Professor
Department of Molecular Physiology and Biophysics
Ernest E. Just Early Career Investigator

November 23rd, 2023

Dr. Alexander Hutchison, Editor-in-Chief
Journal of Cellular Physiology

Dear Dr. Hutchison,

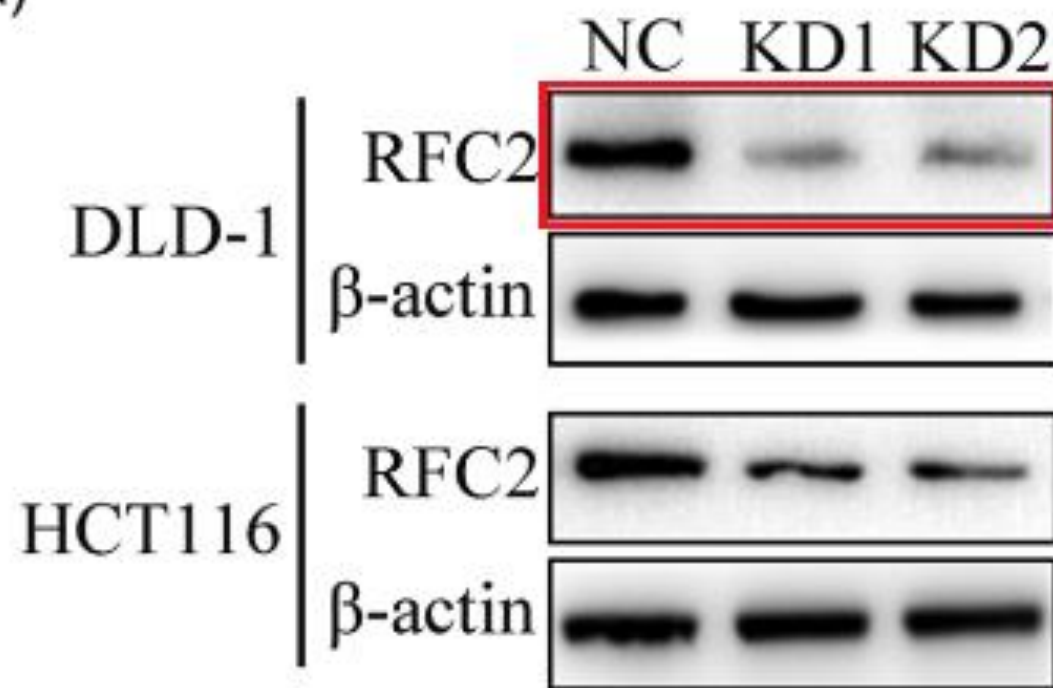
I am pleased to submit our manuscript entitled "Weaponizing Predicaments and Workplace Toxicity to Impede Minority Progress in STEAMM" for consideration for publication in *Journal of Cellular Physiology*. This article presents a comprehensive exploration of the prevalence and impact of weaponized mentoring in the context of toxic work environments within science, technology, engineering, mathematics, and medicine (STEMM) fields. Specifically, this is for the Special Issue of *Journal of Cellular Physiology* on the subject of "How to Increase Diversity in Science Under Troubling Times".

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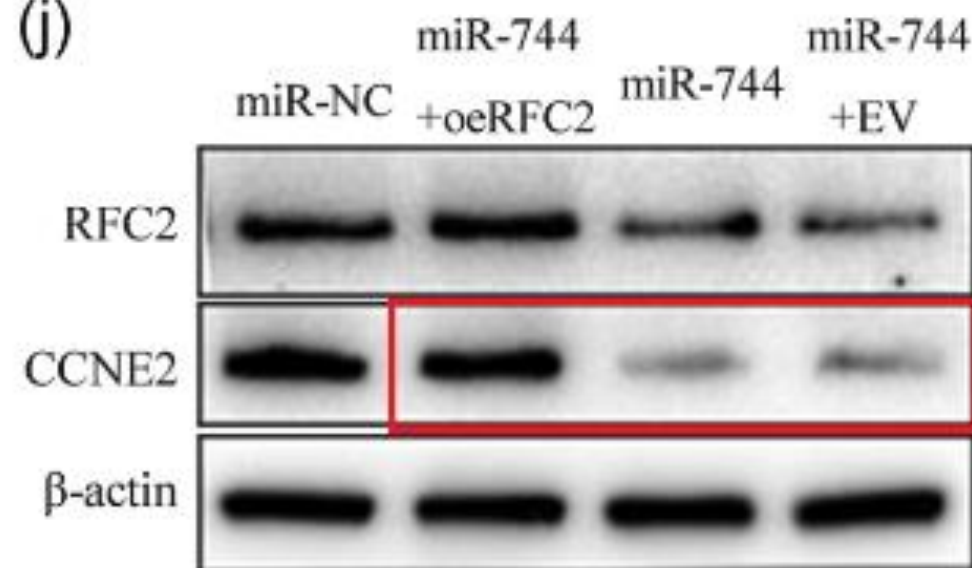
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Manipulation
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You Won't Make
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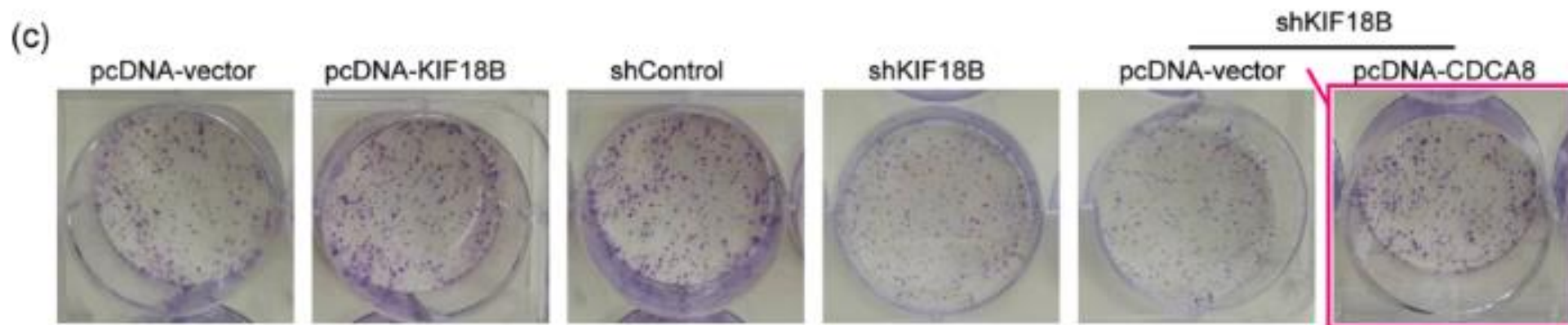
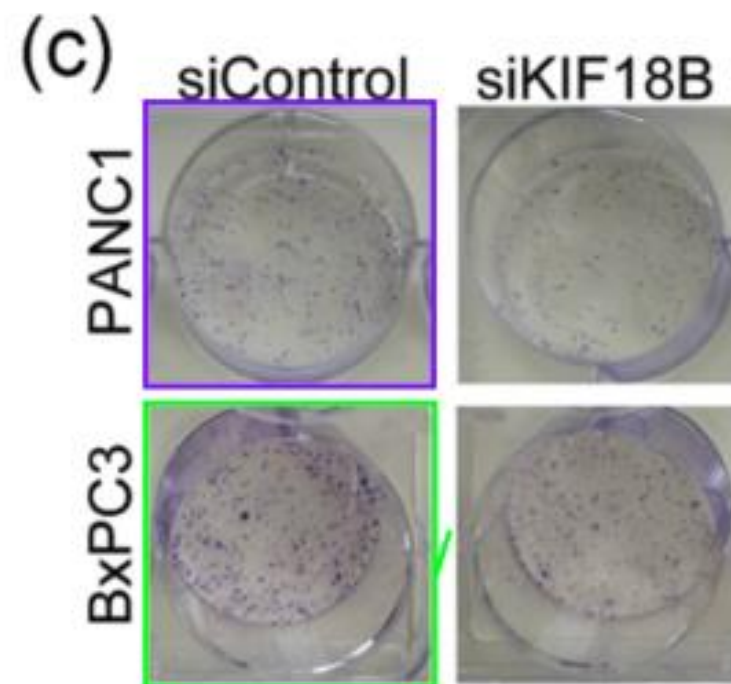
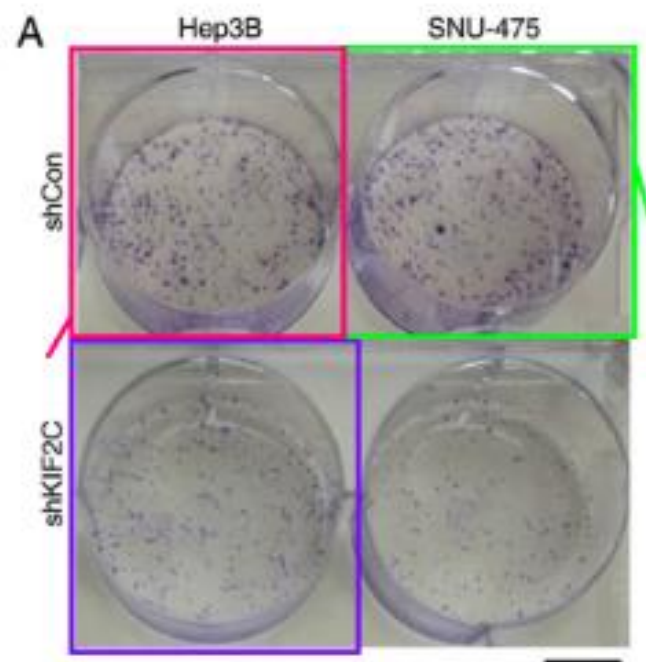


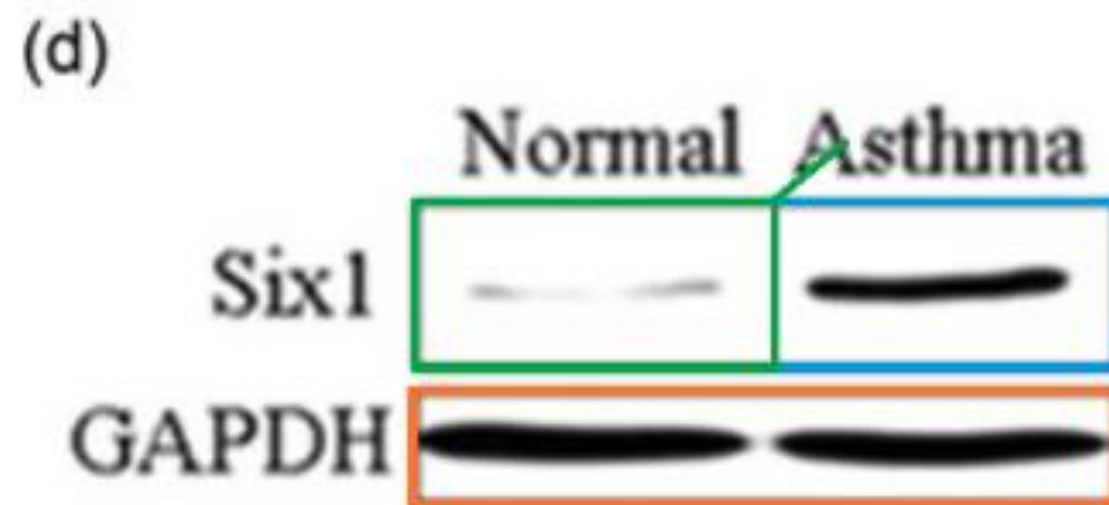
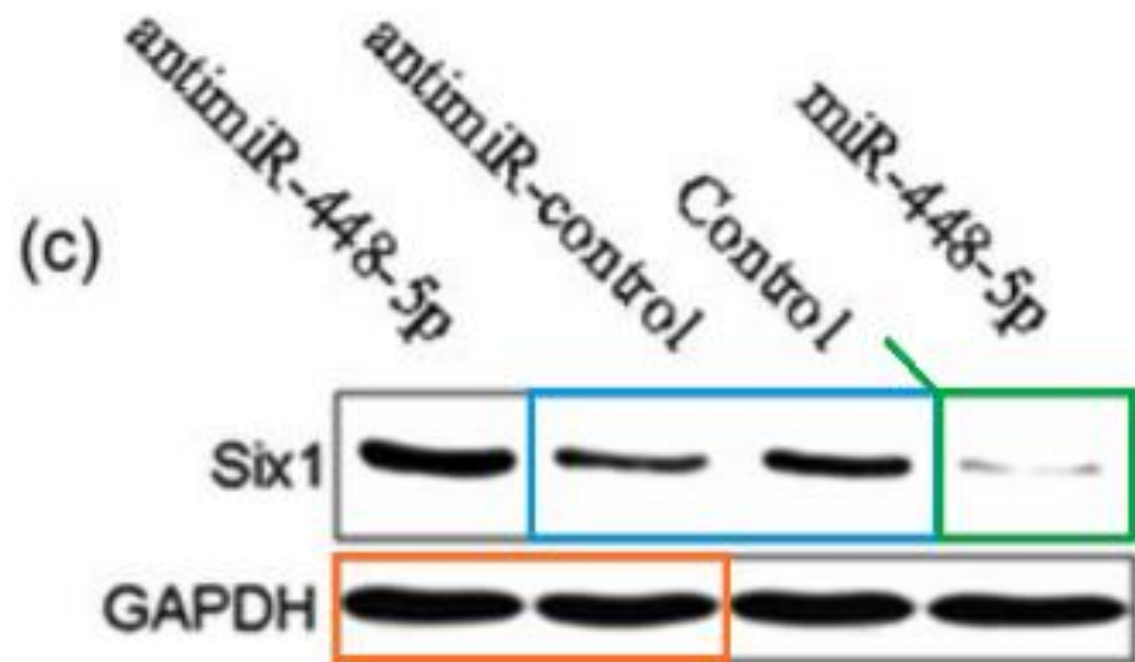
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