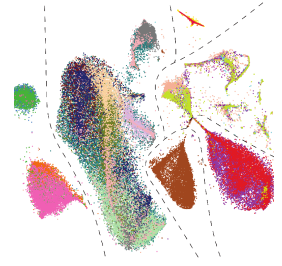


Nov 18, 2019

## Scanorama

DOI

[dx.doi.org/10.17504/protocols.io.9gch3sw](https://dx.doi.org/10.17504/protocols.io.9gch3sw)



Brian Hie<sup>1</sup>, Bryan Bryson<sup>1</sup>, Bonnie Berger<sup>1</sup>

<sup>1</sup>Massachusetts Institute of Technology

Human Cell Atlas Metho...



Brian Hie

OPEN  ACCESS



DOI: [dx.doi.org/10.17504/protocols.io.9gch3sw](https://dx.doi.org/10.17504/protocols.io.9gch3sw)

External link: <http://scanorama.csail.mit.edu>

**Protocol Citation:** Brian Hie, Bryan Bryson, Bonnie Berger 2019. Scanorama. **protocols.io**  
<https://dx.doi.org/10.17504/protocols.io.9gch3sw>

**Manuscript citation:**

Brian Hie, Bryan Bryson & Bonnie Berger. Efficient integration of heterogeneous single-cell transcriptomes using Scanorama. Nature Biotechnology 37:685–691 (2019).

**License:** This is an open access protocol distributed under the terms of the **Creative Commons Attribution License**, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

**Protocol status:** Working

**We use this protocol and it's working**

**Created:** November 18, 2019

**Last Modified:** November 18, 2019

**Protocol Integer ID:** 29924



**Keywords:** single cell RNA-seq, integration,

## Abstract

Scanorama enables efficient integration of heterogeneous scRNA-seq data sets.

