

Oct 06, 2020

## MPAPASS Software Collection

 In 1 collection

DOI

[dx.doi.org/10.17504/protocols.io.bm3gk8jw](https://dx.doi.org/10.17504/protocols.io.bm3gk8jw)



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**Collection Citation:** Joshua A Welsh, Sean M Cook, Jennifer Jones 2020. MPAPASS Software Collection. **protocols.io** <https://dx.doi.org/10.17504/protocols.io.bm3gk8jw>

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**Protocol status:** Working

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

**Created:** October 06, 2020

**Last Modified:** October 06, 2020

**Collection Integer ID:** 42824



## Disclaimer

This protocol summarizes key steps for a specific type of method, which is one of a collection of methods and assays used for EV analysis in the NCI Translational Nanobiology Section at the time of submission of this protocol. Appropriate use of this protocol requires careful, cohesive integration with other methods for EV production, isolation, and characterization.

## Abstract

This collection contains the protocols required for each step in the mpapass software pipeline for performing stitched multiplex analysis. This is one of a number of protocols in the pipeline for using the mpapass software package and is applicable to the latest release of the software.

## Before start

MPAPASS software can be found at <https://nano.ccr.cancer.gov/mpapass>.

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This protocol summarizes key steps for a specific type of method, which is one of a collection of methods and assays used for EV analysis in the NCI Translational Nanobiology Section at the time of submission of this protocol. Appropriate use of this protocol requires careful, cohesive integration with other methods for EV production, isolation, and characterization.

## Files

### Protocol



NAME

**MPAPASS - Gating flow cytometry multiplex data**

VERSION 1

CREATED BY



**Jennifer Jones**  
NIH

**OPEN** →

### Protocol



NAME

**MPAPASS - Creating an MPAPASS database**

VERSION 1

CREATED BY



**Jennifer Jones**  
NIH

**OPEN** →