VERSION 2

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Imaging Mass Cytometry Modality Overview V.2

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Protocol status: Working
We use this protocol and it's working

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36915

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- 1 Process donor organs into samples for analysis.
Lymph Node: [dx.doi.org/10.17504/protocols.io.bbgnijve](https://doi.org/10.17504/protocols.io.bbgnijve)
Thymus: [dx.doi.org/10.17504/protocols.io.bbgmiju6](https://doi.org/10.17504/protocols.io.bbgmiju6)
Spleen: [dx.doi.org/10.17504/protocols.io.bc3kiykw](https://doi.org/10.17504/protocols.io.bc3kiykw)
- 2 Register organ donor, organs received, and common coordinate region information in the HuBMAP UUID generator at
<https://uuid.hubmapconsortium.org>
- 3 Prepare paraffin blocks from tissue samples.
Cassette Processing: [dx.doi.org/10.17504/protocols.io.8nzhvf6](https://doi.org/10.17504/protocols.io.8nzhvf6)
Paraffin Embedding: [dx.doi.org/10.17504/protocols.io.bam9ic96](https://doi.org/10.17504/protocols.io.bam9ic96)
- 4 Package and send paraffin blocks to the Bodenmiller lab:
[dx.doi.org/10.17504/protocols.io.bf5njq5e](https://doi.org/10.17504/protocols.io.bf5njq5e)
- 5 Conjugate primary antibodies using the Maxpar Antibody Labeling Kit:
[dx.doi.org/10.17504/protocols.io.bf5jjq4n](https://doi.org/10.17504/protocols.io.bf5jjq4n)
- 6 Cut and mount paraffin sections for staining and analysis.
Sectioning: [dx.doi.org/10.17504/protocols.io.bfz4jp8w](https://doi.org/10.17504/protocols.io.bfz4jp8w)
- 7 Antibody staining of paraffin sections for Imaging Mass Cytometry:
[dx.doi.org/10.17504/protocols.io.bfz8jp9w](https://doi.org/10.17504/protocols.io.bfz8jp9w)
- 8 Prepare a slide to use for compensation: [dx.doi.org/10.17504/protocols.io.bf2djqa6](https://doi.org/10.17504/protocols.io.bf2djqa6)
- 9 Tune the Image Mass Cytometer for acquisition: [dx.doi.org/10.17504/protocols.io.bf2gjqbw](https://doi.org/10.17504/protocols.io.bf2gjqbw)

- 10 Data Acquisition by Image Mass Cytometry: dx.doi.org/10.17504/protocols.io.bf2jjqce
- 11 Compensation Slide Acquisition: dx.doi.org/10.17504/protocols.io.bf2jjqcn
- 12 Image Processing and Segmentation:
<https://github.com/BodenmillerGroup/ImcSegmentationPipeline>
- 13 Load Imaging Mass Cytometry Datasets onto Hipergator:
☐ IMC_Transfer Data Zurich to HPG.docx
- 14 Prepare and upload data to the HuBMAP HIVE Globus landing pad using Hipergator.
☐ IMC Transfer data from Hipergator to HuBMAP HIVE Globus.docx