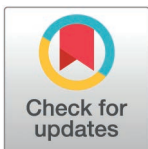


COMMUNITY PAGE

The IBEX Knowledge-Base: A central resource for multiplexed imaging techniques

Andrea J. Radtke¹*, Ifeanyichukwu U. Anidi², Leanne Arakkal³, Armando J. Arroyo-Mejias³, Rebecca T. Beuschel^{3,4}, Katy Börner⁴, Colin J. Chu⁵, Beatrice Clark³, Menna R. Clatworthy⁶, Jake Colautti⁷, Fabian Coscia⁸, Joshua Croteau⁹, Saven Denha⁷, Rose Dever¹⁰, Walderez O. Dutra¹¹, Sonja Fritzsche⁹, Spencer Fullam¹², Michael Y. Gerner¹³, Anita Gola¹⁴, Kenneth J. Gollob¹⁵, Jonathan M. Hernandez¹⁶, Jyh Liang Hor³, Hiroshi Ichise³, Zhixin Jing³, Danny Jonigk^{17,18}, Evelyn Kandov^{3,9}, Wolfgang Kastenmüller¹⁹, Joshua F. E. Koenig⁷, Rosa K. Kortekaas²⁰, Aanandita Kothurkar⁵, Alexandra Y. Kreins^{21,22}, Ian T. Lamborn³, Yuri Lin¹⁶, Katia Luciano Pereira Morais¹⁵, Aleksandra Lunich², Jean C. S. Luz²³, Ryan B. MacDonald⁵, Chen Makranz²⁴, Vivien I. Maltez²⁵, John E. McDonough²⁰, Ryan V. Moriarty²⁶, Juan M. Ocampo-Godinez^{21,27,28}, Vitoria M. Olyntho⁷, Annette Oxenius²⁹, Kartika Padhan¹, Kirsten Remmert¹⁶, Nathan Richoz⁶, Edward C. Schrom³, Wanjing Shang³, Lihong Shi³⁰, Rochelle M. Shih³, Emily Speranza³¹, Salome Stierli³², Sarah A. Teichmann^{33,34}, Tibor Z. Veres³, Megan Vierhout⁷, Brianna T. Wachter³⁵, Adam K. Wade-Vallance³, Margaret Williams², Nathan Zangger²⁹, Ronald N. Germain^{1,3,*}, Ziv Yaniv^{36,*}



OPEN ACCESS

Citation: Radtke AJ, Anidi IU, Arakkal L, Arroyo-Mejias AJ, Beuschel RT, Börner K (2025) The IBEX Knowledge-Base: A central resource for multiplexed imaging techniques. *PLoS Biol* 23(3): e3003070. <https://doi.org/10.1371/journal.pbio.3003070>

Published: March 19, 2025

Copyright: © 2025. This is an open access article, free of all copyright, and may be freely reproduced, distributed, transmitted, modified, built upon, or otherwise used by anyone for any lawful purpose. The work is made available under the [Creative Commons CC0](https://creativecommons.org/licenses/by/4.0/) public domain dedication.

Funding: This work was supported by the Division of Intramural Research, The National Institute of Allergy and Infectious Diseases (NIAID), National Institutes of Health (NIH), Center for Cancer Research, National Cancer Institute (NCI), NIH, The National Heart, Lung, and Blood Institute (NHLBI), NIH, and The National Institute of Arthritis and Musculoskeletal and Skin Diseases (NIAMS), NIH under the following grants: 1ZIAAI000758-26 and 1ZIAAI000545-35. KB is supported by the NIH Common Fund through the Office of Strategic Coordination/Office of the NIH Director under award OT20D033756,

1 Lymphocyte Biology Section and Center for Advanced Tissue Imaging, Laboratory of Immune System Biology, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, Maryland, United States of America, **2** Critical Care Medicine and Pulmonary Branch, National Heart, Lung and Blood Institute, National Institutes of Health, Bethesda, Maryland, United States of America, **3** Lymphocyte Biology Section, Laboratory of Immune System Biology, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, Maryland, United States of America, **4** Department of Intelligent Systems Engineering, Indiana University, Bloomington, Indiana, United States of America, **5** UCL Institute of Ophthalmology and NIHR Moorfields Biomedical Research Centre, London, United Kingdom, **6** Molecular Immunity Unit, Laboratory of Molecular Biology, Cambridge Institute for Therapeutic Immunology and Infectious Diseases, University of Cambridge Department of Medicine, Cambridge, United Kingdom, **7** Department of Medicine, McMaster Immunology Research Centre, Schroeder Allergy and Immunology Research Institute, Faculty of Health Sciences, McMaster University, Hamilton, Canada, **8** Max-Delbrueck-Center for Molecular Medicine in the Helmholtz Association (MDC), Spatial Proteomics Group, Berlin, Germany, **9** Department of Business Development, BioLegend Inc., San Diego, California, United States of America, **10** Functional Immunogenomics Unit, National Institute of Arthritis and Musculoskeletal and Skin Diseases, National Institutes of Health, Bethesda, Maryland, United States of America, **11** Laboratory of Cell-Cell Interactions, Department of Morphology, Institute of Biological Sciences, Universidade Federal de Minas Gerais, Belo Horizonte, Brazil, **12** Division of Rheumatology, Rush University Medical Center, Chicago, Illinois, United States of America, **13** Department of Immunology, University of Washington School of Medicine, Seattle, Washington, United States of America, **14** Robin Chemers Neustein Laboratory of Mammalian Cell Biology and Development, The Rockefeller University, New York, New York, United States of America, **15** Center for Research in Immunooncology (CRIO), Hospital Israelita Albert Einstein, São Paulo, Brazil, **16** Surgical Oncology Program, National Cancer Institute, National Institutes of Health, Bethesda, Maryland, United States of America, **17** Institute of Pathology, Aachen Medical University, RWTH Aachen, Aachen, Germany, **18** German Center for Lung Research (DZL), Biomedical Research in Endstage and Obstructive Lung Disease Hannover (BREATH), Hannover, Germany, **19** Würzburg Institute of Systems Immunology, Max Planck Research Group at the Julius-Maximilians-Universität Würzburg, Würzburg, Germany, **20** Department of Medicine, McMaster University, Firestone Institute for Respiratory Health, St Joseph's Healthcare, Hamilton, Canada, **21** Infection Immunity and Inflammation Research and Teaching Department, University College London Great Ormond Street Institute of Child Health, London, United Kingdom, **22** Department of Immunology and Gene Therapy, Great Ormond Street Hospital for Children NHS Foundation Trust, London, United Kingdom, **23** Viral Vector Laboratory, Cancer Institute of São Paulo, University of São Paulo, São Paulo, Brazil, **24** Neuro-Oncology Branch, National Cancer Institute, National Institutes of Health, Bethesda, Maryland, United States of America, **25** Division of Allergy, Immunology and Rheumatology, Department of Pediatrics, University of California San Diego, La Jolla, California, United States of America, **26** Department of Cellular and Developmental Biology, Northwestern University, Chicago, Illinois, United

the SenNet CODCC under award number U24CA268108, National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK) under award U24DK135157, the Kidney Precision Medicine Program (KPMP) grant U2CDK114886, and the CIFAR MacMillan Multiscale Human program. CJC is supported as a Wellcome Trust Clinical Research Career Development Fellow (224586/Z/21/Z). MRC and the Clatworthy lab (NR) are supported by a Wellcome Investigator Award (220268/Z/20/Z), the National Institute of Health Research (NIHR) Cambridge Biomedical Research Centre (NIHR203312), and the NIHR Blood and Transplant Research Unit in Organ Donation and Transplantation (NIHR203332), a partnership between NHS Blood and Transplant, the University of Cambridge and Newcastle University. The views expressed are those of the authors and not necessarily those of the NIHR or the Department of Health and Social Care. JC, SD, VMO, and JFEK are supported by a peer-reviewed Food Allergy Research Grant jointly funded by the Canadian Institutes of Health Research (CIHR) Institute of Infection and Immunity (CIHR-III), CIHR Institute of Circulatory and Respiratory Health (CIHR-ICRH), and the Canadian Allergy, Asthma and Immunology Foundation (CAAIF), the Walter and Maria Schroeder Foundation, and the J.P. Bickell Foundation. F.C. and S.F. acknowledge funding support by the Federal Ministry of Education and Research (BMBF), as part of the National Research Initiatives for Mass Spectrometry in Systems Medicine, under grant agreement No. 161L0222. WOD is supported by Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), Fundação de Amparo à Pesquisa do Estado de Minas Gerais (FAPEMIG), and National Institute of Science and Technology for Tropical Diseases (INCT-DT). SF is supported by NIH grant NIHR01AR077019. MYG is supported by NIH grant R01AI134713 and NIH contract 75N93019C00070. AG is funded by Damon Runyon Cancer Research Foundation (National Mah Jongg League Fellowship (DRG 2409-20)). KJG and KLPM are supported by CNPq, FAPEMIG, FAPESP (#2021/00408-6), Instituto Nacional de Ciencia e Tecnologia em Doenças Tropicais (INCT-DT). DJ is supported by the grant of the European Research Council (ERC); European Consolidator Grant, XHale (Reference #771883). WK is supported by the European Research Council (ERC) (819329-STEP2). AK and RBM are supported by a Biotechnology and Biological Sciences Research Council (BBSRC) David Phillips

States of America, **27** Laboratorio de Bioingeniería de Tejidos, Departamento de Estudios de Posgrado e Investigación, Universidad Nacional Autónoma de México, Mexico City, Mexico, **28** Laboratorio de Inmunquímica I, Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Mexico City, Mexico, **29** Institute of Microbiology, ETH Zurich, Zurich, Switzerland, **30** Laboratory of Immune System Biology, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, Maryland, United States of America, **31** Florida Research and Innovation Center, Cleveland Clinic Lerner Research Institute, Port Saint Lucie, Florida, United States of America, **32** Institute of Anatomy, University of Zurich, Zurich, Switzerland, **33** Cambridge Stem Cell Institute, Jeffrey Cheah Biomedical Centre, Puddicombe Way, Cambridge Biomedical Campus, Cambridge, United Kingdom, **34** Department of Medicine, University of Cambridge, Cambridge, United Kingdom, **35** Laboratory of Clinical Immunology and Microbiology, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, Maryland, United States of America, **36** Bioinformatics and Computational Bioscience Branch, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, Maryland, United States of America

✉a Current address: Leica Microsystems, Wetzlar, Germany

✉b Current address: Division of Rheumatology, Inflammation, and Immunity, Department of Medicine, Brigham and Women's Hospital and Harvard Medical School, Boston, Massachusetts, United States of America

✉c Current address: Department of Pharmacology, Vanderbilt Brain Institute, Vanderbilt Center for Addiction Research, Vanderbilt University, Nashville, Tennessee, United States of America

* andrea.radtke@leica-microsystems.com (AJR); rgermain@niaid.nih.gov (RNG); zivyaniv@nih.gov (ZY)

Multiplexed imaging is a powerful approach in spatial biology, although it is complex, expensive and labor-intensive. Here, we present the IBEX Knowledge-Base, a central resource for reagents, protocols and more, to enhance knowledge sharing, optimization and innovation of spatial proteomics techniques.

Introduction

Multiplexed imaging is a powerful approach for studying the spatial organization and cellular composition of intact tissues at single-cell resolution. The last decade has seen a rapid expansion in the development and commercialization of spatial biology techniques. These methods include technologies that probe RNA molecules using imaging-based approaches or spatial barcoding techniques. In addition, proteins may be targeted with antibodies applied to thin sections as well as thick tissue volumes using a variety of approaches [1]. These methods vary in the optical resolution, tissue volume, and number and type of targets (RNA, protein, or both) that can be imaged in a specimen [2]. As with any rapidly evolving field, the technical specifications of a given method are constantly improving, enhancing the value of these approaches. Spatial proteomics, recently named Method of the Year by *Nature Methods* [3], has been especially informative for quantifying cell–cell interactions, identifying rare cells, evaluating spatial relationships among cells, and providing new insights into higher level tissue organization. These technologies have been foundational for the construction of single-cell atlases and the study of naturally occurring cancers. However, several challenges prevent their widespread adoption. The majority of these methods require expensive equipment and consumables that may not be available in all research settings. Extensive expertise is also needed to optimize tissue collection, validate reagents, acquire images, and analyze data [1].

IBEX: An open and versatile method for multiplexed imaging

To provide a robust and widely usable solution for highly multiplexed imaging, we developed the Iterative Bleaching Extends multipleXity (IBEX) method [4,5]. This method achieves high

fellowship (BB/S010386/1). AYK is supported by the Wellcome Trust (222096/Z/20/Z). All research at GOSH is supported by the National Institute of Health Research (NIHR) GOSH Biomedical Research Centre (BRC). JCSL is supported by the Sao Paulo Research Foundation (FAPESP fellowship 2023/01697-7). VIM is supported by the National Institute of General Medical Sciences (NIGMS) MOSAIC K99/R00 4R00GM147841-02. JMOG is supported by the National Polytechnic Institute (IPN) of Mexico (ID: DRI/DII/0445/2024) and the National Council of Humanities, Science and Technology (Conahcyt) (ID: B210344 and CVU: 10008) with fundings for research at UCL-Great Ormond Street Institute Child Health (UCL-GOSH). MV was supported by the Canadian Institutes of Health Research (CIHR) Doctoral Award (Grant No. 170793) and the Ontario Graduate Scholarship (OGS) Program. Z.Y. is supported by the Bioinformatics and Computational Biosciences Branch (BCBB) Support Services Contract HHSN316201300006W/75N93022F00001 to Guidehouse Inc. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Competing interests: I have read the journal's policy and the authors of this manuscript have the following competing interests: SAT is a remunerated Scientific Advisory Board member of Qiagen, Foresite Labs, OMass Therapeutics, and a consultant and equity holder of TransitionBio and EnsoCell, and a non-executive board director of 10x Genomics, as well as part-time employee of GlaxoSmithKline. JC is an employee and stakeholder of BioLegend (revvity inc.). AJR is now an employee of Leica Microsystems. All other authors declare no competing interests.

parameter imaging (>65 markers) in a single tissue section (5–30 μm) using cyclic rounds of antibody labeling and dye inactivation. Following image acquisition, individual images are registered, pixel-to-pixel, into one composite image using open-source software. IBEX has been adopted by scientists from fields as diverse as immunology, developmental biology, comparative anatomy, and cancer biology [6–8]. Furthermore, IBEX has been used to evaluate tissues obtained from humans, mice, non-human primates, canines, and zebrafish. These advances reflect the community's ability to both adopt and expand the original IBEX method to different applications and laboratory settings. As a result, we have collectively overcome common challenges, developed workflows for automated imaging and immunolabeling, and incorporated new reagents to acquire high-quality imaging datasets for a variety of studies.

Motivation and design for the IBEX Knowledge-Base

From the beginning, we have strived to share knowledge related to each stage of the multiplexed imaging workflow: sample preparation, antibody selection, antibody validation, panel design, image alignment, image processing, data analysis, and publication of results via open data repositories and scholarly publications. This effort was born out of a desire to reduce the significant time, resources, and expertise required to implement IBEX and other multiplexed imaging techniques [1,9]. To achieve this aim, we established the IBEX Knowledge-Base [10], a central resource for reagents, protocols, data, software, and information related to IBEX and other spatial biology methods; these include non-iterative, standard tissue imaging (Multiplexed 2D Imaging), IBEX imaging with Opal dyes (Opal-plex), thick volume imaging achieved through clearing enhanced 3D (Ce3D) [11], and integration of Ce3D and IBEX (Ce3D-IBEX) to obtain highly multiplexed imaging of thick samples (>300 μm) [12]. We anticipate the number of methods supported by the community to grow and include unique extensions of the protocol for the detection of novel chemistries and nucleic acid probes as well as inclusion of other open source and commercial methods employing fluorescently conjugated antibodies. This next phase of growth, the IBEX++ Knowledge-Base, is a nod to our inspiration from the software development world and the C++ origin story [13].

The IBEX Knowledge-Base is designed around three facets common to FAIR (findability, accessibility, interoperability, and reusability) data and open-source software development: a source/data repository, a static website, and an archive for source data [10]. The first facet, the IBEX Knowledge-Base GitHub repository, stores source data and scripts used to generate the static website (https://github.com/IBEXImagingCommunity/ibex_imaging_knowledge_base). Furthermore, the GitHub ecosystem provides support for automatic data validation, website creation and hosting, issue reporting, as well as a discussion forum. These latter two utilities provide an open, transparent venue for discussing issues and questions related to the IBEX Knowledge-Base and multiplexed tissue imaging, respectively. The second facet, the static website (https://ibeximagingcommunity.github.io/ibex_imaging_knowledge_base), is automatically generated with every update to the IBEX Knowledge-Base via a GitHub pull request. The IBEX Imaging Community website was designed to provide a user-friendly platform for browsing the current stage of knowledge and, unlike scientific publications, is constantly evolving with each contribution. The third and final facet of the IBEX Knowledge-Base is publication of an authoritative, citable, archival version through the generalist repository Zenodo [14]. By publishing through Zenodo, the IBEX Knowledge-Base is assigned a persistent digital object identifier, providing a mechanism for members to be rewarded with authorship for their contributions.

Guiding principles of the IBEX Knowledge-Base

The IBEX Knowledge-Base was founded on five guiding principles (Fig 1). First, we are better together and, importantly, achieve more together by adopting a mindset of shared ownership.

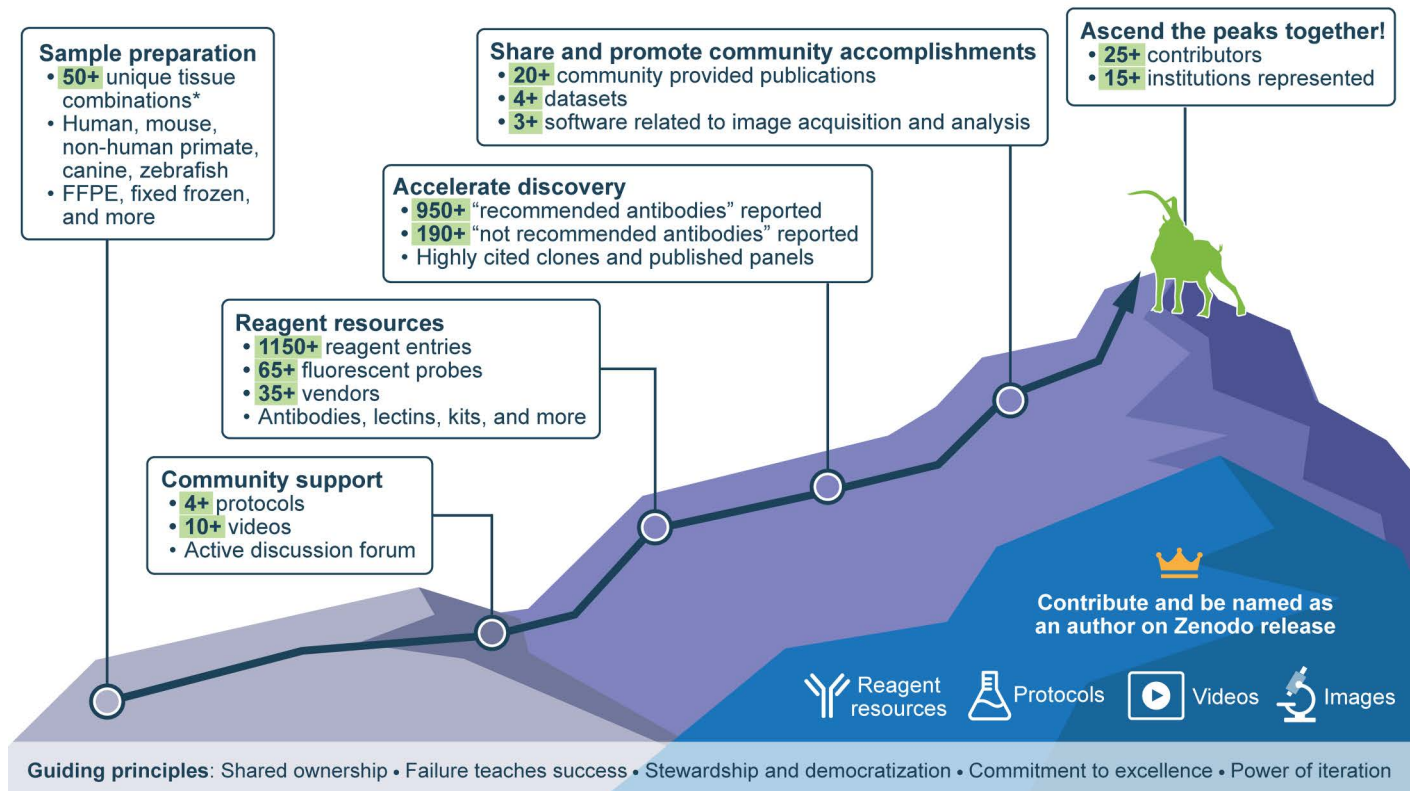


Fig 1. The IBEX Knowledge-Base is a central portal for IBEX and related multiplexed tissue imaging techniques. The IBEX Knowledge-Base is an open, global repository providing information related to IBEX and other spatial biology methods. The evolving state of knowledge is reflected by the plus signs associated with the information found here. The 50+ unique tissue combinations are calculated using details related to the target species, tissue preservation method, target tissue, and tissue state, e.g., infected with a particular pathogen. The crown denotes contributions leading to authorship on the Zenodo release (some restrictions apply). The ibex (goat) climbing the mountain is symbolic of the method’s namesake. To date, more than 25 contributors from Brazil, Canada, Germany, Mexico, Switzerland, the United Kingdom, and the United States have shared their expertise with the community.

<https://doi.org/10.1371/journal.pbio.3003070.g001>

For this reason, everyone who contributes knowledge (e.g., reagent resource, validation image(s), protocols, etc.) is named as an author on the Zenodo dataset and static website. Our second principle is failure teaches success. Unlike publications in which only successful work is described, the goal of the IBEX Knowledge-Base is to document both successful and failed work. By sharing failures, we advance science at a faster pace, reduce financial costs, and instill confidence in the resulting data. Our third principle, stewardship and democratization, is rooted in the open science principles of data sharing, equity, and inclusion. Beyond sharing recommended reagents, we actively encourage the communication of unsatisfactory reagents to prevent other researchers from wasting time and resources. Through stewardship, we make science more equitable, reduce the significant cost of validating antibodies [1,9], and empower scientists to perform multiplexed imaging. Fourth, members of the IBEX Knowledge-Base are distinguished by a commitment to excellence. To achieve this goal, we adopted the antibody metadata established by the Human BioMolecular Atlas Program [1,9], and expanded it to include additional details known to impact the performance of a reagent. We also designed a mechanism for self-correction whereby members of the community can “agree” or “disagree” with reagent entries using their Open Researcher and Contributor ID (ORCID).

Like *PLOS Biology*, we believe in the importance of being second because reproducible science is good science. Our most current state of knowledge reports 16 reagent entries

replicated by two independent authors and one reagent entry replicated by three experts. More than a year after its launch, we celebrated our first disagreement regarding an antibody that labels anticipated cell types as well as unusual cell types in the mouse lymph node. We welcome you to join the conversation in the post titled, “Our first disagreement” in the discussion forum (https://github.com/IBEXImagingCommunity/ibex_imaging_knowledge_base/discussions/174). This contribution exemplifies our fifth and final principle by demonstrating the power of iteration, particularly as it applies to refining our collective state of knowledge. With each addition to the IBEX Knowledge-Base, our knowledge about sample preparation, reagents, and many other aspects of multiplexed imaging and analysis grows (Fig 1).

An open invitation to use and contribute

The IBEX Knowledge-Base operates under the Creative Commons Attribution 4.0 license which allows anyone to use the resources collected here with attribution. Before embarking on multiplexed tissue imaging, we invite you to use the Knowledge-Base to identify the best way to prepare your samples based on protocols, videos, publications, and support offered via the discussion forum. There are several ways to use the “Reagent Resources” tab on the IBEX Imaging Community website to find suitable reagents for your study. The most common approach is to use the filter function to find community-validated antibodies that are “recommended Yes” for your target species, tissue preservation method, and antigen retrieval conditions. Another option is to use the “Reagent Resources” tab and community provided publications to identify what other members are examining in the same or similar tissues. In addition, the extensive list of vendors (35+) may help investigators find where to purchase antibodies for non-traditional experimental animal model systems. Finally, in accordance with our guiding principles we encourage you to return to the IBEX Knowledge-Base to celebrate your accomplishments and share your knowledge with others.

Acknowledgments

We are deeply appreciative of Arlene Radtke for her encouragement, proof-reading, and assistance with antibody metadata fields.

Author contributions

Conceptualization: Andrea J. Radtke, Ziv Yaniv.

Data curation: Andrea J. Radtke, Ifeanyichukwu U. Anidi, Leanne Arakkal, Armando J. Arroyo-Mejias, Rebecca T. Beuschel, Colin J. Chu, Beatrice Clark, Menna R. Clatworthy, Jake Colautti, Joshua Croteau, Saven Denha, Rose Dever, Walderez O. Dutra, Sonja Fritzsche, Spencer Fullam, Michael Y. Gerner, Anita Gola, Kenneth J. Gollob, Jonathan M. Hernandez, Jyh Liang Hor, Hiroshi Ichise, Zhixin Jing, Danny Jonigk, Evelyn Kandov, Joshua F. E. Koenig, Rosa K. Kortekaas, Aanandita Kothurkar, Ian T. Lamborn, Yuri Lin, Katia Luciano Pereira Morais, Aleksandra Lunich, Jean C.S. Luz, Ryan B. MacDonald, Chen Makranz, Vivien I. Maltez, Ryan V. Moriarty, Juan M. Ocampo-Godinez, Vitoria M. Olyntho, Kartika Padhan, Kirsten Remmert, Nathan Richoz, Edward C. Schrom, Wanjing Shang, Lihong Shi, Rochelle M. Shih, Emily Speranza, Salome Stierli, Tibor Z. Veres, Megan Vierhout, Brianna T. Wachter, Adam K. Wade-Vallance, Margaret Williams, Nathan Zangger, Ziv Yaniv.

Formal analysis: Ziv Yaniv.

Funding acquisition: Colin J. Chu, Fabian Coscia, Kenneth J. Gollob, Jonathan M. Hernandez, John E. McDonough, Annette Oxenius, Emily Speranza, Ronald N. Germain.

Investigation: Andrea J. Radtke, Ziv Yaniv.

Methodology: Andrea J. Radtke, Michael Y. Gerner, Anita Gola, Jyh Liang Hor, Hiroshi Ichise, Evelyn Kandov, Ryan V. Moriarty, Edward C. Schrom, Emily Speranza, Ronald N. Germain, Ziv Yaniv.

Project administration: Andrea J. Radtke, Katy Börner, Menna R. Clatworthy, Danny Jonigk, Wolfgang Kastenmüller, Alexandra Y. Kreins, Sarah A. Teichmann, Ronald N. Germain, Ziv Yaniv.

Resources: Andrea J. Radtke, Ifeanyichukwu U. Anidi, Colin J. Chu, Joshua Croteau, Michael Y. Gerner, Anita Gola, Jonathan M. Hernandez, Zhixin Jing, Joshua F. E. Koenig, Ronald N. Germain.

Software: Edward C. Schrom, Ziv Yaniv.

Supervision: Andrea J. Radtke, Katy Börner, Wolfgang Kastenmüller, Alexandra Y. Kreins, Ryan B. MacDonald, Sarah A. Teichmann, Ronald N. Germain, Ziv Yaniv.

Validation: Joshua F. E. Koenig, Aanandita Kothurkar, Ian T. Lamborn, Yuri Lin, Katia Luciano Pereira Morais, Aleksandra Lunich, Jean C.S. Luz, Chen Makranz, Vivien I. Maltez, Juan M. Ocampo-Godinez, Vitoria M. Olyntho, Kartika Padhan, Kirsten Remmert, Nathan Richoz, Wanjing Shang, Lihong Shi, Rochelle M. Shih, Emily Speranza, Salome Stierli, Tibor Z. Veres, Megan Vierhout, Brianna T. Wachter, Adam K. Wade-Vallance, Margaret Williams, Nathan Zangger, Ziv Yaniv.

Visualization: Andrea J. Radtke, Ziv Yaniv.

Writing – original draft: Andrea J. Radtke.

Writing – review & editing: Andrea J. Radtke, Ifeanyichukwu U. Anidi, Katy Börner, Colin J. Chu, Ronald N. Germain, Ziv Yaniv.

References

1. Hickey JW, Neumann EK, Radtke AJ, Camarillo JM, Beuschel RT, Albanese A, et al. Spatial mapping of protein composition and tissue organization: a primer for multiplexed antibody-based imaging. *Nat Methods*. 2022;19(3):284–95. <https://doi.org/10.1038/s41592-021-01316-y> PMID: 34811556
2. Radtke AJ, Roschewski M. The follicular lymphoma tumor microenvironment at single-cell and spatial resolution. *Blood*. 2024;143(12):1069–79. <https://doi.org/10.1182/blood.2023020999> PMID: 38194685
3. Method of the year 2024: spatial proteomics. *Nat Methods*. 2024;21(12):2195–6. <https://doi.org/10.1038/s41592-024-02565-3> PMID: 39643689
4. Radtke AJ, Kandov E, Lowekamp B, Speranza E, Chu CJ, Gola A, et al. IBEX: A versatile multiplex optical imaging approach for deep phenotyping and spatial analysis of cells in complex tissues. *Proc Natl Acad Sci U S A*. 2020;117(52):33455–65. <https://doi.org/10.1073/pnas.2018488117> PMID: 33376221
5. Radtke AJ, Chu CJ, Yaniv Z, Yao L, Marr J, Beuschel RT, et al. IBEX: an iterative immunolabeling and chemical bleaching method for high-content imaging of diverse tissues. *Nat Protoc*. 2022;17(2):378–401. <https://doi.org/10.1038/s41596-021-00644-9> PMID: 35022622
6. Radtke AJ, Postovalova E, Varlamova A, Bagaev A, Sorokina M, Kudryashova O, et al. Multi-omic profiling of follicular lymphoma reveals changes in tissue architecture and enhanced stromal remodeling in high-risk patients. *Cancer Cell*. 2024;42(3):444–463.e10. <https://doi.org/10.1016/j.ccell.2024.02.001> PMID: 38428410
7. Yayan N, Kedlian VR, Boehme L, Suo C, Wachter BT, Beuschel RT, et al. A spatial human thymus cell atlas mapped to a continuous tissue axis. *Nature*. 2024;635(8039):708–18. <https://doi.org/10.1038/s41586-024-07944-6> PMID: 39567784
8. Kothurkar AA, Patient GS, Noel NCL, Krzywańska AM, Carr BJ, Chu CJ, et al. “Iterative Bleaching Extends Multiplexity” facilitates simultaneous identification of all major retinal cell types. *J Cell Sci*. 2024;137(23):jcs263407. <https://doi.org/10.1242/jcs.263407> PMID: 39540305

9. Quardokus EM, Saunders DC, McDonough E, Hickey JW, Werlein C, Surette C, et al. Organ Mapping Antibody Panels: a community resource for standardized multiplexed tissue imaging. *Nat Methods*. 2023;20(8):1174–8. <https://doi.org/10.1038/s41592-023-01846-7>
10. Ziv Y, Arakkal L, Arroyo-Mejías AJ, Beuschel RT, Börner K, Chu CJ, et al. The IBEX Imaging Knowledge-Base: a community resource enabling adoption and development of immunofluorescence imaging methods. *arXiv*. 2024;2412. <https://doi.org/10.48550/arXiv.2412.12965>
11. Li W, Germain RN, Gerner MY. Multiplex, quantitative cellular analysis in large tissue volumes with clearing-enhanced 3D microscopy (Ce3D). *Proc Natl Acad Sci U S A*. 2017;114(35):E7321–30. <https://doi.org/10.1073/pnas.1708981114> PMID: [28808033](https://pubmed.ncbi.nlm.nih.gov/28808033/)
12. Germain RN, Radtke AJ, Thakur N, Schrom EC, Hor JL, Ichise H, et al. Understanding immunity in a tissue-centric context: combining novel imaging methods and mathematics to extract new insights into function and dysfunction. *Immunol Rev*. 2022;306(1):8–24. <https://doi.org/10.1111/imr.13052> PMID: [34918351](https://pubmed.ncbi.nlm.nih.gov/34918351/)
13. Stroustrup B. A history of C++: 1979--1991. *History of programming languages---II: association for computing machinery*; 1996. p. 699–769.
14. Yaniv Z, Anidi I, Arakkal L, Arroyo-Mejias A, Beuschel RT, Börner K, Chu CJ, et al. Iterative Bleaching Extends Multiplexity (IBEX) Knowledge-Base (v0.2.0) Zenodo. 2024.