

CyTOF & Helios Publications

CyTOF 质谱流式技术近年来越来越多地被应用于肿瘤、免疫、生物标志物、干细胞诸多研究领域和方向。作为基础研究和临床诊疗中不可或缺的技术手段，其高参数检测、提高数据准确性、平行性和实验效率等方面所表现出来的优势和不可替代性也被越来越多的研究成果所证明。

在此，我们按照应用方向为您收集了 Helios 的文献，并特别整理了部分 2018 年最新文献，供您参考。



目 录

1. 2018 NEW	3
2. BIOMARKER SCREENING	4
3. DATA ANALYSIS METHODS	4
4. I/O	8
5. IMMUNOLOGY	9
6. IMMUNOPHENOTYPING	18
7. INHERITED DISEASE	21
8. METHOD DEVELOPMENT	21
9. MICROBIOLOGY/PATHOGEN DETECTION (VIRAL)	30
10. ONCOLOGY	32
11. PHARMACOGENOMICS	37
12. STEM CELL	37
13. OTHER	38

2018 NEW

- 1 [Unsupervised trajectory analysis of single-cell RNA-seq and imaging data reveals alternative tuft cell origins in the gut](#)
Herring, C.A., Banerjee, A., McKinley, E.T. et al. *Cell Systems* (2018): 37–51.e9
- 2 [CyteGuide: visual guidance for hierarchical single-cell analysis](#)
Holt, T., Pezzotti, N., van Unen, V. et al. *IEEE Transactions on Visualization and Computer Graphics* (2018): 739–48
- 3 [High throughput automated analysis of big flow cytometry data](#)
Rahim, A., Meskas, J., Drissler, S. et al. *Methods* (2018): doi: 10.1016/j.jymeth.2017.12.015
- 4 [A beginner's guide to analyzing and visualizing mass cytometry data](#)
Kimball, A.K., Oko, L.M., Bullock, B.L. et al. *Journal of Immunology* (2018): 3–22
- 5 [Commonly Occurring Cell Subsets in High-Grade Serous Ovarian Tumors Identified by Single-Cell Mass Cytometry](#)
Gonzalez, V.D., Samusik, N., Chen, T.J. et al. *Cell Reports* (2018): 1,875-88
- 6 [Immune activation underlies a sustained clinical response to Yttrium-90 radioembolisation in hepatocellular carcinoma](#)
Chew, V., Lee, Y.H., Nasir, N.J.M. et al. *Gut*(2018): doi: 10.1136/gutjnl-2017-315485
- 7 [High-dimensional single-cell analysis predicts response to anti-PD-1 immunotherapy](#)
Krieg, C., Nowicka, M., Guglietta, S. et al. *Nature Medicine* (2018): doi: 10.1038/nm.4466
- 8 [Clinical response to PD-1 blockade correlates with a sub-fraction of peripheral central memory CD4+ T cells in patients with malignant melanoma](#)
Takeuchi, Y., Tanemura, A., Tada, Y. et al. *International Immunology* (2018): 13-22
- 9 [Technology to watch in 2018: boosting cancer vaccines](#)
Mardis, E. *Nature* (2018): 532
- 10 [Identity and Diversity of Human Peripheral Th and T Regulatory Cells Defined by Single-Cell Mass Cytometry](#)
Kunicki, M.A., Amaya Hernandez, L.C., Davis, K.L. et al. *Journal of Immunology* (2018): 336-46
- 11 [High-Dimensional Phenotyping Identifies Age-Emergent Cells in Human Mammary Epithelia](#)
Pelissier Vatter et al., 2018, *Cell Reports* 23, 1205–1219
- 12 [Differences Between Pediatric and Adult T Cell Responses to In Vitro Staphylococcal Enterotoxin B Stimulation](#)
Mark E. Rudolph et al., *Frontiers in Immunology* 2018

- 13 [Development of a Click-Chemistry Reagent Compatible with Mass Cytometry](#)
Jessica Shaklee et al., *Scientific Reports* 2018

BIOMARKER SCREENING

- 14 [Mass Cytometry Identifies Distinct Lung CD4+ T Cell Patterns in Löfgren's Syndrome and Non-Löfgren's Syndrome Sarcoidosis](#)
Kaiser, Y., Lakshmikanth, T., Chen, Y., et al. *Frontiers in Immunology* (2017): 1,130
- 15 [A Frameshift in CSF2RB Predominant Among Ashkenazi Jews Increases Risk for Crohn's Disease and Reduces Monocyte Signaling via GM-CSF](#)
Chuang, L.S., Villaverde, N., Hui, K.Y. et al. *Gastroenterology* (2016): 710–23.e2
- 16 [A time to amaze, a time to settle down, and a time to discover](#)
Cosma, A. *Cytometry Part A* (2015): 795–6
- 17 [A High-Sensitivity Lanthanide Nanoparticle Reporter for Mass Cytometry: Tests on Microgels as a Proxy for Cells](#)
Lin, W., Hou, Y., Lu, Y. et al. *Langmuir*(2014): 3,142–53
- 18 [Immune cell profiling to guide therapeutic decisions in rheumatic diseases](#)
Ermann, J., Rao, D.A., Teslovich, N.C. et al. *Nature Reviews Rheumatology* (2015): 541–51
- 19 [Signaling effects of sodium hydrosulfide in healthy donor peripheral blood mononuclear cells](#)
Sulen, A., Gullaksen, S.E., Bader, L. et al. *Pharmacological Research* (2016): 216–27

DATA ANALYSIS METHODS

- 20 [Average Overlap Frequency: a simple metric to evaluate staining quality and community identification in high dimensional mass cytometry experiments](#)
Amir, E.D., Guo, X.V., Mayovska, O. et al. *Journal of Immunological Methods* (2017): doi:10.1016/j.jim.2017.08.011
- 21 [Automated identification of stratifying signatures in cellular subpopulations](#)
Bruggner, R.V., Bodenmiller, B., Dill, D.L. et al. *Proceedings of the National Academy of Sciences of the United States of America* (2014): E2770–E2777
- 22 [OpenCyto: an open source infrastructure for scalable, robust, reproducible, and automated, end-to-end flow cytometry data analysis](#)
Finak, G., Frelinger, J., Jiang, W. et al. *PLoS Computational Biology* (2014): e1003806

- 23 [Conditional density-based analysis of T cell signaling in single-cell data](#)
Krishnaswamy, S., Spitzer, M.H., Mingueneau, M. et al. *Science* (2014): 1,250,689
- 24 [Visual analysis of mass cytometry data by hierarchical stochastic neighbour embedding reveals rare cell types](#)
Van Unen, V., Höllt, T., Pezzotti, N. et al. *Nature Communications* (2017): 1,740
- 25 [Mass cytometry: blessed with the curse of dimensionality](#)
Newell, E.W., Cheng, Y. *Nature Immunology* (2016): 890-5
- 26 [Cytosplore: Interactive Immune Cell Phenotyping for Large Single-Cell Datasets](#)
Höllt, T., Pezzotti, N., van Unen, V. et al. *Computer Graphics Forum* (2016): 171-80
- 27 [Gating mass cytometry data by deep learning](#)
Li, H., Shaham, U., Stanton, K.P. et al. *Bioinformatics* (2017): 3,423-30
- 28 [Extracting a Cellular Hierarchy from High-dimensional Cytometry Data with SPADE](#)
Qiu, P., Simonds, E.F., Bendall, S.C. et al. *Nature Biotechnology* (2011): 886–91
- 29 [Integrated inference and analysis of regulatory networks from multi-level measurements](#)
Poultney, C.S., Greenfield, A., Bonneau, R. *Methods in Cell Biology* (2012): 19–56
- 30 [RchyOptimyx: cellular hierarchy optimization for flow cytometry](#)
Aghaeepour, N., Jalali, A., O'Neill, K. et al. *Cytometry, Part A* (2012): 1,022–30
- 31 [Automatic Classification of Cellular Expression by Nonlinear Stochastic Embedding \(ACCENSE\)](#)
Shekhar, K., Brodin, P., Davis, M.M. et al. *Proceedings of the National Academy of Sciences* (2014): 202–7
- 32 [Enhanced flowType/RchyOptimyx: a BioConductor pipeline for discovery in high-dimensional cytometry data](#)
O'Neill, K., Jalali, A., Aghaeepour, N. et al. *Bioinformatics* (2014): 1,329–30
- 33 [Bayesian Hierarchical Models for Protein Networks in Single-Cell Mass Cytometry](#)
Mitra, R., Müller, P., Qiu, P. et al. *Cancer Informatics* (2014): 79–89
- 34 [FlowSOM: Using self-organizing maps for visualization and interpretation of cytometry data](#)
Van Gassen, S., Callebaut, B., Van Helden, M.J. et al. *Cytometry Part A* (2015): 636–45

- 35 [An Interactive Reference Framework for Modeling a Dynamic Immune System](#)
Spitzer, M.H., Gherardini, P.F., Fragiadakis, G.K. et al. *Science* (2015):
1,259,425
- 36 [immunoClust—An automated analysis pipeline for the identification of immunophenotypic signatures in high-dimensional cytometric datasets](#)
Sørensen, T., Baumgart, S., Durek, P. et al. *Cytometry, Part A* (2015): 603–15
- 37 [NetworkPainter: dynamic intracellular pathway animation in Cytobank](#)
Karr, J.K., Guturu, H., Chen, E.Y. et al. *BMC Bioinformatics* (2015): 172
- 38 [Computationally efficient multidimensional analysis of complex flow cytometry data using second order polynomial histograms](#)
Zaunders, J., Jing, J., Leipold, M. et al. *Cytometry, Part A* (2015): 44–58
- 39 [Processing, visualising and reconstructing network models from single-cell data](#)
Woodhouse, S., Moignard, V., Göttgens, B., Fisher, J. *Immunology and Cell Biology*(2015): 256–65
- 40 [Comparison of clustering methods for high-dimensional single-cell flow and mass cytometry data](#)
Weber, L.M., Robinson, M.D. *Cytometry Part A* (2016): 1,084–96
- 41 [Wishbone identifies bifurcating developmental trajectories from single-cell data](#)
Setty, M., Tadmor, M.D., Reich-Zeliger, S. et al. *Nature Biotechnology* (2016):
637–45
- 42 [Automated mapping of phenotype space with single-cell data](#)
Samusik, N., Good, Z., Spitzer, M.H. et al. *Nature Methods* (2016): 493–6
- 43 [Computational flow cytometry: helping to make sense of high-dimensional immunology data](#)
Saeys, Y., Gassen, S.V., Lambrecht, B.N. *Nature Reviews Immunology* (2016):
449–62
- 44 [The end of gating? An introduction to automated analysis of high dimensional cytometry data](#)
Mair, F., Hartmann, F.J., Mrdjen et al. *European Journal of Immunology* (2015):
34–43
- 45 [Mapping the effects of drugs on the immune system](#)
Kidd, B.A., Wroblewska, A., Boland, M.R. et al. *Nature Biotechnology* (2015):
47–54
- 46 [densityCut: an efficient and versatile topological approach for automatic clustering of biological data](#)
Ding, J., Shah, S., Condon, A. *Bioinformatics* (2016): 2,567–76
- 47 [Categorical Analysis of Human T Cell Heterogeneity with One-Dimensional Soli-Expression by Nonlinear Stochastic Embedding](#)

- Cheng, Y., Wong, M.T., van der Maaten, L., Newell, E.W. *Journal of Immunology* (2016): 924–32
- 48 [Cytofit: A Bioconductor Package for an Integrated Mass Cytometry Data Analysis Pipeline](#)
Chen, H., Lau, M.C., Wong, M.T. et al. *PLoS Computational Biology* (2016): e1005112
- 49 [AirLab: a cloud-based platform to manage and share antibody-based single-cell research](#)
Catena, R., Özcan, A., Jacobs, A. et al. *Genome Biology* (2016): 142
- 50 [destiny: diffusion maps for large-scale single-cell data in R](#)
Angerer, P., Haghverdi, L., Büttner, M. et al. *Bioinformatics* (2016): 1,241–3
- 51 [Visualization and cellular hierarchy inference of single-cell data using SPADE](#)
Anchang, B., Hart, T.D., Bendall, S.C. et al. *Nature Protocols* (2016): 1,264–79
- 52 [Predicting Causal Relationships from Biological Data: Applying Automated Causal Discovery on Mass Cytometry Data of Human Immune Cells](#)
Triantafillou, S., Lagani, V., Heinze-Deml, C. et al. *Scientific Reports* (2017): 12,724
- 53 [Toward deterministic and semiautomated SPADE analysis](#)
Qiu, P. *Cytometry Part A* (2017): 281–9
- 54 [A computational approach for phenotypic comparisons of cell populations in high-dimensional cytometry data](#)
Platon, L., Pejoski, D., Targat, B. et al. *Methods* (2017): doi: 10.1016/j.ymeth.2017.09.005
- 55 [CyTOF workflow: differential discovery in high-throughput high-dimensional cytometry datasets](#)
Nowicka, M., Krieg, C., Weber, L.M. et al. *F1000 Research* (2017): 748
- 56 [Cluster stability in the analysis of mass cytometry data](#)
Melchioni, R., Gracio, F., Kordasti, S. et al. *Cytometry Part A* (2017): 73–84
- 57 [Testing for differential abundance in mass cytometry data](#)
Lun, A.T.L., Richard, A.C., Marioni, J.C. *Nature Methods* (2017): 707–9
- 58 [SPADEVizR: an R package for visualization, analysis and integration of SPADE results](#)
Gautreau, G., Pejoski, D., Le Grand, R. et al. *Bioinformatics* (2017): 779–81
- 59 [Characterizing cell subsets in heterogeneous tissues using marker enrichment modeling](#)
Diggins, K.E., Greenplate, A.R., Leelatian, N. et al. *Nature Methods* (2017): 275-8
- 60 [Exploring Glucocorticoid Receptor Agonists Mechanism of Action through Mass Cytometry and Radial Visualizations](#)

Abraham, Y., Gerrits, B., Ludwig, M.G. et al. *Cytometry Part B Clinical Cytometry*(2016): 42–56

I/O

- 61 [Integrated functional and mass spectrometry-based flow cytometric phenotyping to describe the immune microenvironment in acute myeloid leukemia](#)
Lamble, A.J., Dietz, M., Laderas, T. et al. *Journal of Immunological Methods* (2017): doi: 10.1016/j.jim.2017.11.010
- 62 [Immunotherapy-induced sarcoidosis in patients with melanoma treated with PD-1 checkpoint inhibitors: Case series and immunophenotypic analysis](#)
Lomax, A.J., McGuire, H.M., McNeil, C. et al. *International Journal of Rheumatic Diseases* (2017): 1,277–85
- 63 [Intratumoral HPV16-specific T-cells constitute a type 1 oriented tumor microenvironment to improve survival in HPV16-driven oropharyngeal cancer](#)
Welters, M.J.P., Ma, W., Santegoets, S.J. et al. *Clinical Cancer Research* (2017): DOI: 10.1158/1078-0432.CCR-17-2140
- 64 [Delineation of an immunosuppressive gradient in hepatocellular carcinoma using high-dimensional proteomic and transcriptomic analyses](#)
Chew, V., Lai, L., Pan, L. et al. *Proceedings of the National Academy of Sciences of the United States of America* (2017): E5900–9
- 65 [T-cell invigoration to tumour burden ratio associated with anti-PD-1 response](#)
Huang, A.C., Postow, M.A., Orlowski, R.J. et al. *Nature* (2017): 60–5
- 66 [Mitochondrial dysregulation and glycolytic insufficiency functionally impair CD8 T cells infiltrating human renal cell carcinoma](#)
Siska, P.J., Beckerman, K.E., Mason, F.M. et al. *JCI Insight* (2017): e93411
- 67 [VISTA is an inhibitory immune checkpoint that is increased after ipilimumab therapy in patients with prostate cancer](#)
Gao, J., Ward, J.F., Pettaway, C.A. et al. *Nature Medicine* (2017): 551–5
- 68 [Natural Killer Defective Maturation Is Associated with Adverse Clinical Outcome in Patients with Acute Myeloid Leukemia](#)
Chretien, A.S., Fauriat, C., Orlanducci, F. et al. *Frontiers in Immunology* (2017): 573
- 69 [An immune atlas of clear cell renal cell carcinoma](#)
Chevrier, S., Levine, J.H., Zanotelli, V.R.T. et al. *Cell* (2017): 736–49
- 70 [Systems immune monitoring in cancer therapy](#)
Greenplate, A.R., Johnson, D.B., Ferrell, P.B. Jr., Irish, J.M. *European Journal of Cancer*(2016): 77–84

- 71 Combined targeting of BCL-2 and BCR-ABL tyrosine kinase eradicates chronic myeloid leukemia stem cells
Carter, B.Z., Mak, P.Y., Mu, H. et al. *Science Translational Medicine* (2016): 355ra117

IMMUNOLOGY

- 72 Single-cell mass cytometry of TCR signaling: amplification of small initial differences results in low ERK activation in NOD mice
Mingueneau, M., Krishnaswamy, S., Spitzer, M.H. et al. *Proceedings of the National Academy of Sciences of the United States of America* (2014): 16,466–71
- 73 Unique transcriptome signatures and GM-CSF expression in lymphocytes from patients with spondyloarthritis
Al-Mossawi, M.H., Chen, L., Fang, H. et al. *Nature Communications* (2017): 1,510
- 74 Humanized mouse model supports development, function, and tissue residency of human natural killer cells
Herndler-Brandstetter, D., Shan, L., Yao, Y. et al. *Proceedings of the National Academy of Sciences of the United States of America* (2017): doi: 10.1073/pnas.1705301114
- 75 Multiplex peptide-MHC tetramer staining using mass cytometry for deep analysis of the influenza-specific T-cell response in mice
Fehlings, M., Chakarov, S., Simoni, Y. et al. *Journal of Immunological Methods* (2017): doi: 10.1016/j.jim.2017.09.010
- 76 Unique phenotypes and clonal expansions of human CD4 effector memory T cells re-expressing CD45RA
Tian, Y., Babor, M., Lane, J. et al. *Nature Communications* (2017): doi: 10.1038/s41467-017-01728-5
- 77 Single-cell mass cytometry and transcriptome profiling reveal the impact of graphene on human immune cells
Orecchioni, M., Bedognetti, D., Newman, L. et al. *Nature Communications* (2017): doi: 10.1038/s41467-017-01015-3
- 78 Mass Cytometry and Topological Data Analysis Reveal Immune Parameters Associated with Complications after Allogeneic Stem Cell Transplantation
Lakshmikanth, T., Olin, A., Chen, Y. et al. *Cell Reports* (2017): 2,238–50
- 79 A Liver Capsular Network of Monocyte-Derived Macrophages Restricts Hepatic Dissemination of Intraperitoneal Bacteria by Neutrophil Recruitment
Sierra, F., Evrard, M., Rizzetto, S. et al. *Immunity* (2017): 374–86

- 80 [High-dimensional, single-cell characterization of the brain's immune compartment](#)
Korin, B., Ben-Shaanan, T.L., Schiller, M. et al. *Nature Neuroscience* (2017): 1,300–9
- 81 [By CyTOF: Heterogeneity of Human Monocytes](#)
Loke, P. and Niewold, T.B. *Arteriosclerosis, Thrombosis, and Vascular Biology* (2017): 1,423–4
- 82 [Distinct Cellular Mechanisms Underlie Anti-CTLA-4 and Anti-PD-1 Checkpoint Blockade](#)
Wei, S.C., Levine, J.H., Cogdill, A.P. et al. *Cell* (2017): 1,120–33.e17
- 83 [Phenotyping the Immune Response to Trauma: A Multiparametric Systems Immunology Approach](#)
Seshadri, A., Brat, G.A., Yorkgitis, B.K. et al. *Critical Care Medicine* (2017): 1,523–30
- 84 [Mass cytometry deep phenotyping of human mononuclear phagocytes and myeloid-derived suppressor cells from human blood and bone marrow](#)
Roussel, M., Ferrell Jr., P.B., Greenplate, A.R. et al. *Journal of Leukocyte Biology*(2017): 437–47
- 85 [A cluster of immunoresolvents links coagulation to innate host defense in human blood](#)
Norris, P.C., Libreros, S., Chiang, N. et al. *Science Signaling* (2017): eaan1471
- 86 [Systems approach to uncover signaling networks in primary immunodeficiency diseases](#)
Choi, J., Fernandez, R., Maecker, H.T., Butte, M.J. *Journal of Allergy and Clinical Immunology* (2017): 881–4.e8
- 87 [An immune clock of human pregnancy](#)
Aghaeepour, N., Ganio, E.A., Mcilwain, D. et al. *Science Immunology* (2017): eaan2946
- 88 [Mapping the human DC lineage through the integration of high-dimensional techniques](#)
See, P., Dutertre, C.A., Chen, J. et al. *Science* (2017): doi: 10.1126/science.aag300
- 89 [SOX2 immunity and tissue resident memory in children and young adults with glioma](#)
Vasquez, J.C., Huttner, A., Zhang, L. et al. *Journal of Neuro-Oncology* (2017): 41–53
- 90 [NKG2D ligand expression in Crohn's disease and NKG2D-dependent stimulation of CD8+ T cell migration](#)

- Vadstrup, K., Galsgaard, E.D., Jensen, H. et al. *Experimental and Molecular Pathology*(2017): 56–70
- 91 [Human Blood Monocyte Subsets: A New Gating Strategy Defined Using Cell Surface Markers Identified by Mass Cytometry](#)
Thomas, G.D., Hamers, A.A.J., Nakao, C. et al. *Arteriosclerosis, Thrombosis and Vascular Biology* (2017): 1,548–58
- 92 [High Dimensional Cytometry of Central Nervous System Leukocytes During Neuroinflammation](#)
Mrdjen, D., Hartmann, F.J., Becher, B. *Methods in Molecular Biology* (2017): 321–32
- 93 [Class I HLA haplotypes form two schools that educate NK cells in different ways](#)
Horowitz, A., Djaoud, Z., Nemat-Gorgani, N. et al. *Science Immunology* (2016): eaag1672
- 94 [Systemic innate immune activation in food protein-induced enterocolitis syndrome](#)
Goswami, R., Blazquez, A.B., Kosoy, R. et al. *Journal of Allergy and Clinical Immunology* (2017): 1,885–96.e9
- 95 [Informatics-Based Discovery of Disease-Associated Immune Profiles](#)
Delmas, A., Oikonomopoulos, A., Lacey, P.N. et al. *PLoS One* (2016): e0163305
- 96 [The newborn human NK cell repertoire is phenotypically formed but functionally reduced](#)
Strauss-Albee, D.M., Liang, E.C., Ranganath, T. et al. *Cytometry Part B, Clinical Cytometry* (2017): 33–41
- 97 [Single-Cell Mass Cytometry Analysis of the Human Endocrine Pancreas](#)
Wang, Y.J., Golson, M.L., Schug, J. et al. *Cell Metabolism* (2016): 616–26
- 98 [Detection, phenotyping, and quantification of antigen-specific T cells using a peptide-MHC dodecamer](#)
Huang, J., Zeng, X., Sigal, N. et al. *Proceedings of the National Academy of Sciences of the United States of America*(2016): 113
- 99 [Mapping the human DC lineage through the integration of high-dimensional techniques](#)
See, P., Dutertre, C.A., Chen, J. et al. *Science* (2017): eaag3009
- 100 [Assessing basophil activation by using flow cytometry and mass cytometry in blood stored 24 hours before analysis](#)
Mukai, K., Gaudenzio, N., Gupta, S. et al. *Journal of Allergy and Clinical Immunology* (2017): 889–99.e11

- 101 [Novel Resolvin D2 Receptor Axis in Infectious Inflammation](#)
Chiang, N., de la Rosa, X., Libreros, S. et al. *Journal of Immunology* (2017): 842–51
- 102 [Combining Flow and Mass Cytometry in the Search for Biomarkers in Chronic Graft-versus-Host Disease](#)
Stikvoort, A., Chen, Y., Rådestad, E. et al. *Frontiers in Immunology* (2017): 717
- 103 [Immune Checkpoint Function of CD85j in CD8 T Cell Differentiation and Aging](#)
Gustafson, C.E., Qi, Q., Hutter-Saunders, J. et al. *Frontiers in Immunology* (2017): 692
- 104 [RNA-Seq and CyTOF immuno-profiling of regenerating lacrimal glands identifies a novel subset of cells expressing muscle-related proteins](#)
Hawley, D., Ding, J., Thotakura, S. et al. *PLoS One* (2017): e0179385
- 105 [Deep immune profiling by mass cytometry links human T and NK cell differentiation and cytotoxic molecule expression patterns](#)
Bensch, B., Ohtani, T., Herati, R.S. et al. *Journal of Immunological Methods* (2017): doi: 10.1016/j.jim.2017.03.009
- 106 [Interferon Gamma Induces Changes in Natural Killer \(NK\) Cell Ligand Expression and Alters NK Cell-Mediated Lysis of Pediatric Cancer Cell Lines](#)
Aquino-López, A., Senyukov, V.V., Vlastic, Z. et al. *Frontiers in Immunology* (2017): 391
- 107 [Dissecting the Molecular Mechanisms of the Tropism of Varicella-Zoster Virus for Human T Cells](#)
Sen, N., Arvin, A.M. *Journal of Virology*(2016): 3,284–7
- 108 [Single-cell technologies for monitoring immune systems](#)
Chattopadhyay, P.K., Gierahn, T.M., Roederer, M., Love, J.C. *Nature Immunology* (2014): 128–35
- 109 [Multiparameter analysis of stimulated human peripheral blood mononuclear cells: a comparison of mass and fluorescence cytometry](#)
Nicholas, K.J., Greenplate, A.R., Flaherty, D.K. et al. *Cytometry Part A* (2015): 271–80
- 110 [Regulation of adaptive NK cells and CD8 T cells by HLA-C correlates with allogeneic hematopoietic cell transplantation and with cytomegalovirus reactivation](#)
Horowitz, A., Guethlein, L.A., Nemat-Gorgani, N. et al. *Journal of Immunology*(2015): 4,524–36
- 111 [Age-related aspects of human IgM+ B cell heterogeneity](#)
Martin, V., Wu, Y.C., Kipling, D., Dunn-Walters, D.K. *Annals of the New York Academy of Sciences* (2015): 153–63

- 112 Implementing mass cytometry at the bedside to study the immunological basis of human diseases: distinctive immune features in patients with a history of term or preterm birth
Gaudillière, B., Ganio, E.A., Tingle, M. et al. *Cytometry, Part A* (2015): 817–29
- 113 Application of mass cytometry (CyTOF®) for functional and phenotypic analysis of natural killer cells
Kay, A.W., Strauss-Albee, D.M., Blish, C.A. *Methods in Molecular Biology* (2016): 13–26
- 114 Heparin reduces nonspecific eosinophil staining artifacts in mass cytometry experiments
Rahman, A.H., Tordesillas L., Berin M.C. *Cytometry Part A* (2016): 601–7
- 115 Single-cell states versus single-cell atlases—two classes of heterogeneity that differ in meaning and method
Janes, K.A. *Current Opinion in Biotechnology* (2016): 120–5
- 116 Mapping the diversity of follicular helper T cells in human blood and tonsils using high-dimensional mass cytometry analysis
Wong, M.T., Chen, J., Narayanan, S. et al. *Cell Reports* (2015): 1,822–33
- 117 Cutting Edge: Redox Signaling Hypersensitivity Distinguishes Human Germinal Center B Cells
Polikowsky, H.G., Wogsland, C.E., Diggins, K.E. et al. *Journal of Immunology* (2015): 1,364–7
- 118 Single-cell systems-level analysis of human Toll-like receptor activation defines a chemokine signature in patients with systemic lupus erythematosus
O’Gorman, W.E., Hsieh, E.W., Savig, E.S. et al. *Journal of Allergy and Clinical Immunology* (2015): 1,326–36
- 119 Phenotypic complexity of the human regulatory T cell compartment revealed by mass cytometry
Mason, G.M., Lowe, K., Melchiotti, R. et al. *The Journal of Immunology* (2015): 2,030–7
- 120 A small molecule screen for enhanced homing of systemically infused cells
Levy, O., Mortensen, L.J., Boquet, G. et al. *Cell Reports* (2015): 1,261–8
- 121 Phenotype and function of nasal dendritic cells
Lee, H., Ruane, D., Law, K. et al. *Mucosal Immunology* (2015): 1,083–98
- 122 Beneficial Effects of CpG-Oligodeoxynucleotide Treatment on Trauma and Secondary Lung Infection
Wanke-Jellinek, L., Keegan, J.W., Dolan, J.W. et al. *The Journal of Immunology*(2016): 767–77

- 123 [Mass Cytometry of the Human Mucosal Immune System Identifies Tissue- and Disease-Associated Immune Subsets](#)
van Unen, V., Li, N., Molendijk, I. et al. *Immunity* (2016): 1,227–39
- 124 [A High-Dimensional Atlas of Human T Cell Diversity Reveals Tissue-Specific Trafficking and Cytokine Signature](#)
Wong, M.T., Ong, D.E., Lim, F.S, et al. *Immunity* (2016): 442–56
- 125 [Mass cytometry profiling the response of basophils and the complete peripheral blood compartment to peanut](#)
Tordesillas, L., Rahman, A.H., Hartmann, B.M. et al. *Journal of Allergy and Clinical Immunology* (2016): 1741–4.e9
- 126 [Cytometry by time-of-flight immunophenotyping identifies a blood Sjögren's signature correlating with disease activity and glandular inflammation](#)
Mingueneau, M., Boudaoud, S., Haskett, S. et al. *The Journal of Allergy and Clinical Immunology* (2016): 1,809–21
- 127 [Increased lymphocyte apoptosis in mouse models of colitis upon ABT-737 treatment is dependent upon BIM expression](#)
Lutz, C., Mozaffari, M., Tosevski, V. et al. *Clinical and Experimental Immunology*(2015): 343–56
- 128 [Single-cell mass cytometry of differential immune and drug responses across a human hematopoietic continuum](#)
Bendall, S.C., Simonds, E.F., Qiu, P. et al. *Science* (2011): 687–96
- 129 [Human CD4+ lymphocytes for antigen quantification: characterization using conventional flow cytometry and mass cytometry](#)
Wang, L., Abbasi, F., Ornatsky, O. et al. *Cytometry, Part A* (2012): 567–75
- 130 [The transcriptional landscape of \$\alpha\beta\$ T cell differentiation](#)
Mingueneau, M., Kreslavsky, T., Gray, D. et al. *Nature Immunology* (2013): 619–32
- 131 [Genetic and environmental determinants of human NK cell diversity revealed by mass cytometry](#)
Horowitz, A., Strauss-Albee, D.M., Leipold, M. et al. *Science Translational Medicine*(2013): 208ra145
- 132 [Antigen-dependent integration of opposing proximal TCR-signaling cascades determines the functional fate of T lymphocytes](#)
Wolchinsky, R., Hod-Marco, M., Oved, K. et al. *Journal of Immunology* (2014): 2,109–19
- 133 [Clinical recovery from surgery correlates with single-cell immune signatures](#)
Gaudillière, B., Fragiadakis, G.K., Bruggner, R.V. et al. *Science Translational Medicine*(2014): 255ra131

- 134 Single-cell mass cytometry analysis of human tonsil T cell remodeling by varicella zoster virus
Sen, N., Mukherjee, G., Sen, A. et al. *Cell Reports* (2014): 633–45
- 135 CD161 defines a transcriptional and functional phenotype across distinct human T cell lineages
Fergusson, J.R., Smith, K.E., Fleming, V.M. et al. *Cell Reports* (2014): 1,075–88
- 136 Human skin is protected by four functionally and phenotypically discrete populations of resident and recirculating memory T cells
Watanabe, R., Gehad, A., Yang, C. et al. *Science Translational Medicine* (2015): 279ra39
- 137 Pregnancy Does Not Attenuate the Antibody or Plasmablast Response to Inactivated Influenza Vaccine
Kay, A.W., Bayless, N.L., Fukuyama, J. et al. *The Journal of Infectious Diseases* (2015): 861–70
- 138 Single-cell trajectory projection uncovers progression and regulatory coordination in human B cell development
Bendall, S.C., Davis, K.L., Amir, E.D. et al. *Cell* (2014): 714–25
- 139 Adenoviral Vector Vaccination Induces a Conserved Program of CD8+ T Cell Memory Differentiation in Mouse and Man
Bolinger, B., Sims, S., Swadling, L. et al. *Cell Reports* (2015): 1,578–88
- 140 Large-Scale and Comprehensive Immune Profiling and Functional Analysis of Normal Human Aging
Whiting, C.C., Siebert, J., Newman, A.M. et al. *PLoS One* (2015): e0133627
- 141 Expansion of inflammatory innate lymphoid cells in patients with common variable immune deficiency
Cols, M., Rahman, A., Maglione, P.J. et al. *Journal of Allergy and Clinical Immunology* (2016): 1,206–15
- 142 Reversibility of Defective Hematopoiesis Caused by Telomere Shortening in Telomerase Knockout Mice
Raval, A., Behbehani, G.K., Nguyen, L.X.T. et al. *PLoS One* (2015): e0131722
- 143 Deep Profiling Human T Cell Heterogeneity by Mass Cytometry
Cheng, Y., Newell, E.W. *Advances in Immunology* (2016): 101–34
- 144 Expression of specific inflammasome gene modules stratifies older individuals into two extreme clinical and immunological states
Furman, D., Chang, J., Lartigue, L. et al. *Nature Medicine* (2017): 174–84
- 145 Mass spectrometry goes with the flow: mass cytometry and its potentials in regenerative medicine
Agnetti, G. *Circulation: Cardiovascular Genetics* (2012): 379–80

- 146 [New tools for classification and monitoring of autoimmune diseases](#)
Maecker, H.T., Lindstrom, T.M., Robinson, W.H. et al. *Nature Reviews Rheumatology*(2012): 317–28
- 147 [Human Innate Lymphoid Cell Subsets Possess Tissue-Type Based Heterogeneity in Phenotype and Frequency](#)
Simoni, Y., Fehlings, M., Kløverpris, H.N. et al. *Immunity* (2016): 148–61
- 148 [Novel tools for primary immunodeficiency diagnosis: making a case for deep profiling](#)
Hsieh, E.W., Hernandez, J.D. *Current Opinion in Allergy and Clinical Immunology* (2016): 549–56
- 149 [The Spectrum and Regulatory Landscape of Intestinal Innate Lymphoid Cells Are Shaped by the Microbiome](#)
Gury-BenAri, M., Thaïss, C.A., Serafini, N. et al. *Cell* (2016): 1,231–46
- 150 [Deep phenotyping of Tregs identifies an immune signature for idiopathic aplastic anemia and predicts response to treatment](#)
Kordasti, S., Costantini, B., Seidl, T. et al. *Blood* (2016): 1,193–205
- 151 [Unsupervised High-Dimensional Analysis Aligns Dendritic Cells across Tissues and Species](#)
Guilliams, M., Dutertre, C.A., Scott, C.L. et al. *Immunity* (2016): 669–84
- 152 [Wild immunology assessed by multidimensional mass cytometry](#)
Japp, A.S., Hoffmann, K., Schlickeiser, S. et al. *Cytometry Part A* (2016): 85–95
- 153 [Mass cytometry analytical approaches reveal cytokine-induced changes in natural killer cells](#)
Vendrame, E., Fukuyama, J., Strauss-Albee, D.M. et al. *Cytometry Part B Clinical Cytometry* (2016): 57–67
- 154 [Comprehensive mass cytometry analysis of cell cycle, activation and coinhibitory receptors expression in CD4 T cells from healthy and HIV-infected individuals](#)
Corneau, A., Cosma, A., Even, S. et al. *Cytometry Part B Clinical Cytometry*(2016): 21–32
- 155 [Isolation and high-dimensional phenotyping of gastrointestinal immune cells](#)
David, B.A., Rubino, S., Moreira, T.G. et al. *Immunology* (2016): 56–70
- 156 [Lymphocyte enrichment using CD81-targeted immunoaffinity matrix](#)
Pelák, O., Kužílková, D., Thürner, D., et al. *Cytometry Part A* (2017): 62–72
- 157 [Activation of the reward system boosts innate and adaptive immunity](#)
Ben-Shaan, T.L., Azulay-Debby, H., Dubovik, T., et al. *Nature Medicine* (2016): 940–4

- 158 Impact of the microbial derived short chain fatty acid propionate on host susceptibility to bacterial and fungal infections in vivo
Ciarlo, E., Heinonen, T., Herderschee, J. et al. *Scientific Reports* (2016): 37,944
- 159 Identification of Novel CD4+ T Cell Subsets in the Target Tissue of Sjögren's Syndrome and Their Differential Regulation by the Lymphotoxin/LIGHT Signaling Axis
Haskett, S., Ding, J., Zhang, W. et al. *Journal of Immunology* (2016): 1,600,407
- 160 Technological advances transforming rheumatology
Robinson, W.H., Mao, R. *Nature Reviews Rheumatology* (2015): 626–8
- 161 Biomarkers to guide clinical therapeutics in rheumatology?
Robinson, W.H., Mao, R. *Current Opinion in Rheumatology* (2016): 168–75
- 162 Shooting movies of signaling network dynamics with multiparametric cytometry
Claassen, M. *Current Topics in Microbiology and Immunology* (2013): 177–89
- 163 Different subsets of natural killer T cells may vary in their roles in health and disease
Kumar, V., Delovitch, T.L. *Immunology*(2014): 321–36
- 164 Cracking the code of human T-cell immunity
Harvey, C.J., Wucherpfennig, K.W. *Nature Biotechnology* (2013): 609–10
- 165 La couleur du métal Brève introduction à la cytométrie de masse (Fr.)
Cosma, A., Le Grand, R. *Médecine/sciences* (2011): 1,072–4
- 166 Beyond model antigens: high-dimensional methods for the analysis of antigen-specific T cells
Newell, E.W., Davis, M.M. *Nature Biotechnology* (2014): 149–57
- 167 Unifying immunology with informatics and multiscale biology
Kidd, B.A., Peters, L.A., Schadt, E.E., Dudley, J.T. *Nature Immunology* (2014): 118–27
- 168 NK Cells in HIV Disease
Scully, E., Alter, G. *Current HIV/AIDS Reports* (2016): 85–94
- 169 New assays for monitoring residual HIV burden in effectively treated individuals
Strain, M.C, Richman, D.D. *Current Opinion in HIV & AIDS* (2013): 106–110
- 170 Human NK Cell Diversity in Viral Infection: Ramifications of Ramification
Strauss-Albee, D.M., Blish, C.A. *Frontiers in Immunology* (2016): 66
- 171 Analyzing the phenotypic and functional complexity of lymphocytes using CyTOF (cytometry by time-of-flight)
Chen, G., Weng, N.P. *Cellular and Molecular Immunology* (2012): 322–3
- 172 Coordinated regulation of natural killer receptor expression in the maturing human immune system

- Strauss-Albee, D.M., Horowitz, A., Parham, P., Blish, C.A. *Journal of Immunology*(2014): 4,871–9
- 173 **Challenges and Promise for the Development of Human Immune Monitoring**
Shen-Orr, S.S. *Rambam Maimonides Medical Journal* (2012): e0023
- 174 **Higher Throughput Methods of Identifying T Cell Epitopes for Studying Outcomes of Altered Antigen Processing and Presentation**
Newell, E.W. *Frontiers in Immunology*(2013): 430
- 175 **Guardians of the Gut – Murine Intestinal Macrophages and Dendritic Cells**
Gross, M., Salame, T.M., Jung, S. *Frontiers in Immunology* (2015): 254

IMMUNOPHENOTYPING

- 176 **OMIP-034: Comprehensive immune phenotyping of human peripheral leukocytes by mass cytometry for monitoring immunomodulatory therapies**
Baumgart, S., Peddinghaus, A., Schulte-Wrede, U. et al. *Cytometry Part A* (2016): 34–8
- 177 **High-dimensional single-cell analysis reveals the immune signature of narcolepsy**
Hartman, F.J., Bernard-Valnet, R., Quériault, C. et al. *Journal of Experimental Medicine*(2017): 2,621–33
- 178 **CytoFACS Measurement of Immunocompetence Across Major Immune Cell Types**
Subrahmanyam, P.B., Maecker, H.T. *Current Protocols in Cytometry* (2017): 9.54.1–12
- 179 **Deep Immune Profiling of an Arginine-Enriched Nutritional Intervention in Patients Undergoing Surgery**
Aghaepour, N., Kin, C., Ganio, E.A. et al. *Journal of Immunology* (2017): doi: 10.4049/jimmunol.1700421
- 180 **In depth comparative phenotyping of blood innate myeloid leukocytes from healthy humans and macaques using mass cytometry**
Elhmouzi-Younes, J., Palgen, J.L., Tchitchek, N. et al. *Cytometry Part A* (2017): 969–82
- 181 **Innate immune landscape in early lung adenocarcinoma by paired single-cell analyses**
Lavin, Y., Kobayashi, S., Leader, A. et al. *Cell* (2017): 750-65
- 182 **Continuous immunotypes describe human immune variation and predict diverse responses**
Kaczorowski, K.J., Shekhar, K., Nkulikiyimfura, D. et al. *Proceedings of the National Academy of Sciences of the United States of America* (2017): E6,097–106

- 183 [Application of phospho-CyTOF to characterize immune activation in patients with sickle cell disease in an ex vivo model of thrombosis](#)
Glassberg, J., Rahman, A.H., Zafar, M. et al. *Journal of Immunological Methods* (2017): doi: 10.1016/j.jim.2017.07.014
- 184 [Multiparameter single cell profiling of airway inflammatory cells](#)
Yao, Y., Welp, T., Liu, Q. et al. *Cytometry Part B, Clinical Cytometry* (2016): 12–20
- 185 [Applying mass cytometry to the analysis of lymphoid populations in transplantation](#)
Krams, S.M., Schaffert, S., Lau, A.H., Martinez O.M. *American Journal of Transplantation* (2016): 1,992–9
- 186 [Mass cytometry reveals a distinct immunoprofile of operational tolerance in pediatric liver transplantation](#)
Lau, A.H., Vitalone, M.J., Hass, K. et al. *Pediatric Transplantation* (2016): 1,072–80
- 187 [Mapping the Fetomaternal Peripheral Immune System at Term Pregnancy](#)
Fragiadakis, G.K., Baca, Q.J., Gherardini, P.F. et al. *The Journal of Immunology*(2016): 4,482–92
- 188 [The dynamic lives of T cells: new approaches and themes](#)
Yamanaka, Y.J., Gierahn, T.M., Love, J.C. *Trends in Immunology* (2013): 59–66
- 189 [Emerging single-cell technologies in immunology](#)
Herderschee, J., Fenwick, C., Pantaleo, G. et al. *Journal of Leukocyte Biology* (2015): 23–32
- 190 [Highly multiparametric analysis by mass cytometry](#)
Ornatsky, O., Bandura, D., Baranov, V. et al. *Journal of Immunological Methods* (2010): 1–20
- 191 [Mass cytometry: single cells, many features](#)
Spitzer, M.H., Nolan, G.P. *Cell* (2016): 780–91
- 192 [Patient-specific immune states before surgery are strong correlates of surgical recovery](#)
Fragiadakis, G.K., Gaudillière, B., Ganio, E.A. et al. *Anesthesiology* (2015): 1,241–55
- 193 [Mass cytometry as a platform for the discovery of cellular biomarkers to guide effective rheumatic disease therapy](#)
Nair, N., Mei, H.E., Chen, S.Y. et al. *Arthritis Research & Therapy* (2015): 127
- 194 [Variation in the human immune system is largely driven by non-heritable influences.](#)
Brodin, P., Jojic, V., Gao, T. et al. *Cell* (2015): 37–47

- 195 Distinct immunologic changes in vivo following combination versus individual PD-1 or CTLA-4 checkpoint blockade in human cancer
Dhodapkar, K., Verma, R., Sznol, M. et al. *Journal for ImmunoTherapy of Cancer*(2014): O7
- 196 Combination therapy with anti-CTLA4 and anti-PD1 leads to distinct immunologic changes in-vivo
Das, R., Verma, R., Sznol, M. et al. *Journal of Immunology* (2015): 950–9
- 197 Human NK cell repertoire diversity reflects immune experience and correlates with viral susceptibility
Strauss-Albee, D.M., Fukuyama, J., Liang, E.C. et al. *Science Translational Medicine*(2015): 297ra115
- 198 Decoupling of Tumor-Initiating Activity from Stable Immunophenotype In HoxA9-Meis1 Driven AML
Gibbs, K.D., Jager, A., Crespo, O. et al. *Cell Stem Cell* (2013): 210–7
- 199 Multicenter Systems Analysis of Human Blood Reveals Immature Neutrophils in Males and During Pregnancy
Blazkova, J., Gupta, S., Liu, Y. et al. *Journal of Immunology* (2017): 2,479–88
- 200 Targeting YAP-dependent MDSC infiltration impairs tumor progression
Wang, G., Lu, X., Dey, P. et al. *Cancer Discovery* (2016): 80–95
- 201 Immune Profiles to Predict Response to Desensitization Therapy in Highly HLA-Sensitized Kidney Transplant Candidates
Yabu, J.M., Siebert, J.C., Maecker, H.T. *PLoS One* (2016): e0153355
- 202 Protein networks and activation of lymphocytes
Helou, Y.A., Salomon, A.R. *Current Opinion in Immunology* (2015): 78–85
- 203 High-dimensional analysis of human CD8(+) T cell phenotype, function, and antigen specificity
Newell, E.W., Lin, W. *Current Topics in Microbiology and Immunology* (2013): 61–84
- 204 Characterization of lung infection-induced TCR $\gamma\delta$ T cell phenotypes by CyTOF mass cytometry
Wanke-Jellinek, L., Keegan, J.W., Dolan, J.W., Lederer, J.A. *Journal of Leukocyte Biology* (2015): 483–93
- 205 Characterizing Phenotypes and Signaling Networks of Single Human Cells by Mass Cytometry
Leelatian, N., Diggins, K.E., Irish, J.M. *Methods in Molecular Biology* (2015): 99–113
- 206 New technologies for autoimmune disease monitoring
Maecker, H.T., Nolan, G.P., Fathman, C.G. *Current Opinion in Endocrinology, Diabetes and Obesity* (2010): 322–8

- 207 **SCREENING: CyTOF—the next generation of cell detection**
Cheung, R.K., Utz, P.J. *Nature Reviews Rheumatology* (2011): 502–3

INHERITED DISEASE

- 208 **Leveraging blood and tissue CD4+ T cell heterogeneity at the single cell level to identify mechanisms of disease in rheumatoid arthritis**
Fonseka, C.Y., Rao, D.A., Raychaudhuri, S. *Current Opinion in Immunology* (2017): 27-36
- 209 **STING-associated vasculopathy develops independently of IRF3 in mice**
Warner, J.D., Irizarry-Caro, R.A., Bennion, B.G. et al. *Journal of Experimental Medicine* (2017): 3,279–92
- 210 **β -Cells are not uniform after all—Novel insights into molecular heterogeneity of insulin-secreting cells**
Avrahami, D., Wang, Y.J., Klochendler, A. et al. *Diabetes, Obesity and Metabolism*(2017): 147–52
- 211 **Dietary gluten triggers concomitant activation of CD4+ and CD8+ $\alpha\beta$ T cells and $\gamma\delta$ T cells in celiac disease**
Han, A., Newell, E.W., Glanville, J. et al. *Proceedings of the National Academy of Sciences* (2013): 13,073–8

METHOD DEVELOPMENT

- 212 **xCell: digitally portraying the tissue cellular heterogeneity landscape**
Aran, D., Hu, Z., Butte, A.J. *Genome Biology* (2017): 220
- 213 **High-dimensional single-cell analysis with mass cytometry**
Brodie, T.M., Tosevksi, V. *Current Protocols in Immunology* (2017): 5.11.1–5.11.25
- 214 **Scalable multi-sample single-cell data analysis by Partition-Assisted Clustering and Multiple Alignments of Networks**
Li, Y.H., Li, D., Samusik, N. et al. *PLoS Computational Biology* (2017): <https://doi.org/10.1371/journal.pcbi.1005875>
- 215 **Comparison of CyTOF® assays across sites: results of a six-center pilot study**
Leipold, M.D., Obermoser, G., Fenwick, C. et al. *Journal of Immunological Methods*(2017): doi:10.1016/j.jim.2017.11.008
- 216 **Lanthanide-Coordinated Semiconducting Polymer Dots Used for Flow Cytometry and Mass Cytometry**
Wu, X., DeGottardi, Q., Wu, I.C. et al. *Angewandte Chemie* (2017): 14,908-12
- 217 **viSNE enables visualization of high dimensional single-cell data and reveals phenotypic heterogeneity of leukemia**

- Amir, el-A.D., Davis, K.L., Tadmor, M.D. et al. *Nature Biotechnology* (2013): 545–52
- 218 [Silver nanoparticles for the detection of cell surface antigens in mass cytometry](#)
Schulz, A.R., Stanislawiak, S., Baumgart, S. et al. *Cytometry Part A* (2016): 25–33
- 219 [Staining of Frozen and Formalin-Fixed, Paraffin-Embedded Tissues with Metal-Labeled Antibodies for Imaging Mass Cytometry Analysis](#)
Chang, Q., Ornatsky, O., Hedley, D. *Current Protocols in Cytometry* (2017): 12.47.1–12.47.8
- 220 [Cell Cycle Analysis by Mass Cytometry](#)
Behbehani, G.K. *Methods in Molecular Biology* (2017): 105-24
- 221 [Mass Cytometric Analysis Reveals Viable Activated Caspase-3+ Luminal Progenitors in the Normal Adult Human Mammary Gland](#)
Knapp, D.J.H.F., Kannan, N., Pellacani, D. et al. *Cell Reports* (2017): 1,116–26
- 222 [High-throughput quantitation of inorganic nanoparticle biodistribution at the single-cell level using mass cytometry](#)
Yang, Y.S., Atukorale, P.U., Moynihan, K.D. et al. *Nature Communications* (2017): 14,069
- 223 [Mass Cytometry Assays for Antigen-Specific T Cells Using CyTOF](#)
Lin, D., Maecker, H.T. *Flow Cytometry Protocols* (2017): 37-47
- 224 [Analysis of Signaling Networks at the Single-Cell Level Using Mass Cytometry](#)
Bandyopadhyay, S., Fischer, D.A.C., Malkova, O. et al. *Methods in Molecular Biology* (2017): 371–92
- 225 [Preparing Viable Single Cells from Human Tissue and Tumors for Cytomic Analysis](#)
Leelatian, N., Doxie, D.B., Greenplate, A.R. et al. *Current Protocols in Molecular Biology* (2017): 25C.1.1–25C.1.23
- 226 [Mass Cytometry for Detection of Silver at the Bacterial Single Cell Level](#)
Guo, Y., Baumgart, S., Stärk, H.J. et al. *Frontiers in Microbiology* (2017): 1,326
- 227 [Dual-labelled antibodies for flow and mass cytometry: A new tool for cross-platform comparison and enrichment of target cells for mass cytometry](#)
Baumgart, S., Schulz, A.R., Peddinghaus, A. et al. *European Journal of Immunology*(2017): 1,377–85
- 228 [Optimization of mass cytometry sample cryopreservation after staining](#)
Sumatoh, H.R., Teng, K.W., Cheng, Y. et al. *Cytometry Part A* (2017): 48–61
- 229 [Influence of node abundance on signaling network state and dynamics analyzed by mass cytometry](#)

- Lun, X.K., Zanotelli, V.R., Wade, J.D. et al. *Nature Biotechnology* (2017): 164–72
- 230 [Research Techniques Made Simple: Experimental Methodology for Single-Cell Mass Cytometry](#)
Matos, T.R., Liu, H., Ritz, J. *Journal of Investigative Dermatology* (2017): e31–8
- 231 [CyTOF Mass Cytometry for Click Proliferation Assays](#)
Tosevski, V., Ulashchik, E., Trovato, A. et al. *Current Protocols in Cytometry* (2017): 7.50.1–14
- 232 [Liposome-Encapsulated NaLnF₄ Nanoparticles for Mass Cytometry: Evaluating Nonspecific Binding to Cells](#)
Pichaandi, J., Tong, L., Bouzekri, A. et al. *Chemistry of Materials* (2017): 4,980–90
- 233 [Categorizing Cells on the Basis of their Chemical Profiles: Progress in Single-Cell Mass Spectrometry](#)
Comi, T.J., Do, T.D., Rubakhin, S.S. et al. *Journal of the American Chemical Society* (2017): 3,920–9
- 234 [Next generation ligand binding assays—review of emerging technologies' capabilities to enhance throughput and multiplexing](#)
Mora, J., Chunyk, A.G., Dysinger, M. et al. *American Association of Pharmaceutical Scientists Journal* (2014): 1,175–84
- 235 [AutoGate: automating analysis of flow cytometry data](#)
Meehan, S., Walther, G., Moore, W. et al. *Immunologic Research* (2014): 218–23
- 236 [COMPASS identifies T-cell subsets correlated with clinical outcomes](#)
Lin, L., Finak, G., Ushey, K. et al. *Nature Biotechnology* (2015): 610–6
- 237 [Review of methods to probe single cell metabolism and bioenergetics](#)
Vasdekis, A.E., Stephanopoulos, G. *Metabolic Engineering* (2015): 115–35
- 238 [The influence of PEG macromonomers on the size and properties of thermosensitive aqueous microgels](#)
Pich, A., Berger, S., Ornatsky, O et al. *Colloid and Polymer Science* (2009): 269–275
- 239 [Hybrid nanogels by encapsulation of lanthanide-doped LaF₃ nanoparticles as elemental tags for detection by atomic mass spectrometry](#)
Berger, S., Ornatsky, O., Baranov, V. et al. *Journal of Material Chemistry* (2010): 5,141–50
- 240 [The means: Cytometry and mass spectrometry converge in a single cell deep profiling platform](#)

- Weis-Garcia, F., Bandura, D., Baranov, V. et al. *Journal of Biomolecular Techniques*(2013): S12
- 241 Phenotyping of live human PBMC using CyTOF mass cytometry
Leipold, M.D., Maecker, H.T. *Bio-protocol*(2015): e1382
- 242 Algorithmic tools for mining high-dimensional cytometry data
Chester, C., Maecker, H.T. *Journal of Immunology* (2015): 773–9
- 243 Mass cytometry panel optimization through the designed distribution of signal interference
Takahashi, C., Au-Yeung, A., Fuh, F. et al. *Cytometry Part A* (2016): 39–47
- 244 On the relationship between cell cycle analysis with ergodic principles and age-structured cell population models
Kuritz, K., Stöhr, D., Pollak, N., Allgöwer, F. *Journal of Theoretical Biology* (2016): 91–102
- 245 Cytokine-stimulated phosphoflow of PBMC using CyTOF mass cytometry
Fernandez, R., Maecker, H. *Bio-protocol*(2016): e1496
- 246 Meeting the challenges of measuring human immune regulation
Martino, D., Allen, K. *Journal of Immunological Methods* (2015): 1–6
- 247 Mass cytometry moving forward in support of clinical research: advantages and considerations
Nassar, A.F., Wisnewski, A.V., Raddassi, K. *Bioanalysis* (2016): 255–7
- 248 Cytokine-stimulated phosphoflow of whole blood using CyTOF mass cytometry
Fernandez, R., Maecker, H. *Bio-protocol*(2015): e1495
- 249 Multiplexed mass cytometry profiling of cellular states perturbed by small-molecule regulators
Bodenmiller, B., Zunder, E.R., Finck, R. et al. *Nature Biotechnology* (2012): 858–67
- 250 Singlet gating in mass cytometry
Lai, L., Yeo, J.G., Albani, S. *Cytometry Part A* (2017): 170–2
- 251 Cell size assays for mass cytometry
Stern, A.D., Rahman, A.H., Birtwhistle, M.R. *Cytometry Part A* (2016): 14–24
- 252 ICP-MS-based multiplex profiling of glycoproteins using lectins conjugated to lanthanide-chelating polymers
Leipold, M.D., Herrera, I., Ornatsky, O. et al. *Journal of Proteome Research* (2008): 443–9
- 253 Bio-Functional, Lanthanide-Labeled Polymer Particles by Seeded Emulsion Polymerization and their Characterization by Novel ICP-MS Detection
Thickett, S.C., Abdelrahman, A.I., Ornatsky, O. et al. *Journal of Analytical Atomic Spectrometry* (2010): 269–81

- 254 Synthetically Modified Viral Capsids as Versatile Carriers for Use in Antibody-Based Cell Targeting
ElSohly, A.M., Netirojjanakul, C., Aanei, I.L. et al. *Bioconjugate Chemistry* (2015): 1590–6
- 255 Synthesis of a functional metal-chelating polymer and steps toward quantitative mass cytometry bioassays
Majonis, D., Herrera, I., Ornatsky, O. et al. *Analytical Chemistry* (2010): 8,961–9
- 256 Multiplexed epitope-based tissue imaging for discovery and healthcare applications
Bodenmiller, B. *Cell Systems* (2016): 225–38
- 257 Mass cytometry: a highly multiplexed single-cell technology for advancing drug development
Atkuri, K.R., Stevens, J.C., Neubert, H.. *Drug Metabolism Disposition* (2015): 227–33
- 258 Another step on the path to mass cytometry standardization
Leopold, M.D. *Cytometry Part A* (2015): 380–2
- 259 Multiplexed peptide-MHC tetramer staining with mass cytometry
Leong, M.L., Newell, E.W. *Methods in Molecular Biology* (2015): 115–31
- 260 Emerging proteomic technologies for elucidating context-dependent cellular signaling events: a big challenge of tiny proportions
Parker, S.J., Raedschelders, K., Van Eyk, J.E. *Proteomics* (2015): 1,486–502
- 261 Characterization by mass cytometry of different methods for the preparation of muscle mononuclear cells
Spada, F., Fuoco, C., Pirrò, S. et al. *New Biotechnology* (2016): 514–23
- 262 Highly multiplexed simultaneous detection of RNAs and proteins in single cells
Frei, A.P., Bava, F.A., Zunder, E.R. et al. *Nature Methods* (2016): 269–75
- 263 Cytometry-based single-cell analysis of intact epithelial signaling reveals MAPK activation divergent from TNF- α -induced apoptosis in vivo
Simmons, A.J., Banerjee, A., McKinley, E.T. et al. *Molecular Systems Biology* (2015): 835
- 264 Palladium-based mass tag cell barcoding with a doublet-filtering scheme and single-cell deconvolution algorithm
Zunder, E.R., Finck, R., Amir, el-A.D. et al. *Nature Protocols* (2015): 316–33
- 265 Organotellurium scaffolds for mass cytometry reagent development
Park, H., Edgar, L.J., Lumba, M.A. et al. *Organic and Biomolecular Chemistry* (2015): 7,027–33
- 266 Barcoding of live human peripheral blood mononuclear cells for multiplexed mass cytometry

- Mei, H.E., Leipold, M.D., Schulz, A.R. et al. *Journal of Immunology* (2015): 2,022–31
- 267 Evaluating the efficiency of isotope transmission for improved panel design and a comparison of the detection sensitivities of mass cytometer instruments
Tricot, S., Meyrand, M., Sammiceli, C. et al. *Cytometry, Part A* (2015): 357–68
- 268 Identification of hypoxic cells using an organotellurium tag compatible with mass cytometry
Edgar, L.J., Vellanki, R.N., Halupa, A. et al. *Angewandte Chemie* (2014): 11,473–7
- 269 CyTOF supports efficient detection of immune cell subsets from small samples
Yao, Y., Liu, R., Shin, M.S. et al. *Journal of Immunological Methods* (2014): 1–5
- 270 Metal-Containing Polystyrene Beads as Standards for Mass Cytometry
Abdelrahman, A.I., Ornatsky, O., Bandura, D. et al. *Journal of Analytical Atomic Spectrometry* (2010): 260–8
- 271 Metal-chelating polymers by anionic ring-opening polymerization and their use in quantitative mass cytometry
Illy, N., Majonis, D., Herrera, I. et al. *Biomacromolecules* (2012): 2,359–69
- 272 A platinum-based covalent viability reagent for single-cell mass cytometry
Fienberg, H.G., Simonds, E.F., Fantl, W.J. et al. *Cytometry, Part A* (2012): 467–75
- 273 Flow cytometer with mass spectrometer detection for massively multiplexed single-cell biomarker assay
Tanner, S.D., Bandura, D.R., Ornatsky, O. et al. *Pure and Applied Chemistry* (2008): 2,627–41
- 274 Transient partial permeabilization with saponin enables cellular barcoding prior to surface marker staining
Behbehani, G.K., Thom, C., Zunder, E.R. et al. *Cytometry, Part A* (2014): 1,011–9
- 275 Normalization of mass cytometry data with bead standards
Finck, R., Simonds, E.F., Jager, A. et al. *Cytometry, Part A* (2013): 483–94
- 276 Single-cell mass cytometry adapted to measurements of the cell cycle
Behbehani, G.K., Bendall, S.C., Clutter, M.R. et al. *Cytometry, Part A* (2012): 552–66
- 277 Improving lanthanide nanocrystal colloidal stability in competitive aqueous buffer solutions using multivalent PEG-phosphonate ligands
Cao, P., Tong, L., Hou, Y. et al. *Langmuir*(2012): 12,861–70

- 278 Effect of pendant group structure on the hydrolytic stability of polyaspartamide polymers under physiological conditions
Lu, Y., Chau, M., Boyle, A.J. et al. *Biomacromolecules* (2012): 1,296–306
- 279 Development of mass cytometry methods for bacterial discrimination
Leipold, M.D., Ornatsky, O., Baranov, V. et al. *Analytical Biochemistry* (2011): 1–8
- 280 Synthesis and mass cytometric analysis of lanthanide-encoded polyelectrolyte microgels
Lin, W., Ma, X., Qian, J. et al. *Langmuir*(2011): 7,265–75
- 281 Surface Functionalization Methods to Enhance Bioconjugation in Metal-Labeled Polystyrene Particles
Abdelrahman, A.I., Thickett, S.C., Liang, Y. et al. *Macromolecules* (2011): 4,801–13
- 282 Element-tagged immunoassay with ICP-MS detection: evaluation and comparison to conventional immunoassays
Razumienko, E., Ornatsky, O., Kinach, R. et al. *Journal of Immunological Methods*(2008): 56–63
- 283 Development of analytical methods for multiplex bio-assay with inductively coupled plasma mass spectrometry
Ornatsky, O.I., Kinach, R., Bandura, D.R. et al. *Journal of Analytical Atomic Spectrometry* (2008): 463–9
- 284 Biocompatible Hybrid Nanogels
Pich, A., Zhang, F., Shen, L. et al. *Small*(2008): 2,171–5
- 285 Inductively coupled plasma mass spectrometry-based immunoassay: a review
Liu, R., Wu, P., Yang, L. et al. *Mass Spectrometry Reviews* (2014): 373–93
- 286 Multiple cellular antigen detection by ICP-MS
Ornatsky, O., Baranov, V.I., Bandura, D.R. et al. *Journal of Immunological Methods*(2006): 68–76
- 287 An introduction to mass cytometry: fundamentals and applications
Tanner, S.D., Baranov, V.I., Ornatsky, O.I. et al. *Cancer Immunology, Immunotherapy*(2013): 955–65
- 288 Polymer-Based Elemental Tags for Sensitive Bioassays
Lou, X., Zhang, G., Herrera, I. et al. *Angewandte Chemie* (2007): 6,111–4
- 289 Study of cell antigens and intracellular DNA by identification of element-containing labels and metallointercalators using inductively coupled plasma mass spectrometry
Ornatsky, O.I., Lou, X., Nitz, M. et al. *Analytical Chemistry* (2008): 2,539–47
- 290 Lanthanide-containing polymer nanoparticles for biological tagging applications: nonspecific endocytosis and cell adhesion

- Vancaeyzeele, C., Ornatsky, O., Baranov, V. et al. *Journal of the American Chemical Society* (2007): 13,653–60
- 291 [Synthesis of Uniform NaLnF₄ \(Ln: Sm to Ho\) Nanoparticles for Mass Cytometry](#)
Tong, L., Lu, E., Pichaandi, J. et al. *Journal of Physical Chemistry* (2016): 6,269–80
- 292 [Single cell analysis of human tissues and solid tumors with mass cytometry](#)
Leelatian, N., Doxie, D.B., Greenplate, A.R. et al. *Cytometry, Part B* (2017): 68–78
- 293 [Barcoding of live human PBMC for multiplexed mass cytometry](#)
Mei, H.E., Leipold, M.D., Schulz, A.R. et al. *The Journal of Immunology* (2015): 2,022–31
- 294 [Standardization and quality control for high-dimensional mass cytometry studies of human samples](#)
Kleinsteuber, K., Corleis, B., Rashidi, N. et al. *Cytometry Part A* (2016): 903–13
- 295 [Lanthanide-containing polymer microspheres by multiple-stage dispersion polymerization for highly multiplexed bioassays](#)
Abdelrahman, A.I., Dai, S., Thickett, S.C. et al. *Journal of the American Chemical Society* (2009): 15,276–83
- 296 [Mass cytometry: technique for real time single cell multitarget immunoassay based on inductively coupled plasma time-of-flight mass spectrometry](#)
Bandura, D.R., Baranov, V.I., Ornatsky, O.I. et al. *Analytical Chemistry* (2009): 6,813–22
- 297 [Hybrid Imaging Labels: Providing the Link Between Mass Spectrometry-Based Molecular Pathology and Theranostics](#)
Buckle, T., van der Wal, S., van Malderen, S.J.M. et al. *Theranostics* (2017): 624–33
- 298 [Automation of sample preparation for mass cytometry barcoding in support of clinical research: protocol optimization](#)
Nassar, A.F., Wisniewski, A.V., Raddassi, K. *Analytical and Bioanalytical Chemistry* (2017): 2,363–72
- 299 [Brief introduction to mass cytometry](#)
Cosma, A., Le Grand, R. *Medecine/Sciences* (2011): 1,072–4
- 300 [Multiparameter Phenotyping of Human PBMCs Using Mass Cytometry](#)
Leipold, M.D., Newell, E.W., Maecker, H.T. *Methods in Molecular Biology* (2015): 81–95
- 301 [Enhanced multiplexing in mass cytometry using osmium and ruthenium tetroxide species](#)

- Catena, R., Özcan, A., Zivanovic, N., Bodenmiller, B. *Cytometry Part A* (2016): 491–7
- 302 [Single-cell gene expression profiling and cell state dynamics: collecting data, correlating data points and connecting the dots](#)
Marr, C., Zhou, J.X., Huang, S. *Current Opinion in Biotechnology* (2016): 207–14
- 303 [The potential for elemental analysis in biotechnology](#)
Baranov, V.I., Quinn, Z.A., Bandura, D.R., Tanner, S.D. *Journal of Analytical Atomic Spectrometry* (2002): 1,148–52
- 304 [A practical guide to multiplexed mass cytometry](#)
Zivanovic, N., Jacobs, A., Bodenmiller, B. *Current Topics in Microbiology and Immunology* (2014): 95–109
- 305 [The numerology of T cell functional diversity](#)
Haining, W.N. *Immunity* (2012): 10–2
- 306 [A Deep Profiler's Guide to Cytometry](#)
Bendall, S.C., Nolan, G.P., Roederer, M., Chattopadhyay, P.K. *Trends in Immunology*(2012): 323–32
- 307 [Multiplex bio-assay with inductively coupled plasma mass spectrometry: Towards a massively multivariate single-cell technology](#)
Tanner, S.D., Ornatsky, O., Bandura, D.R., Baranov, V.I. *Spectrochimica Acta Part B: Atomic Spectroscopy* (2007): 188–95
- 308 [Development of inductively coupled plasma-mass spectrometry-based protease assays](#)
Lathia, U.S., Ornatsky, O., Baranov, V., Nitz, M. *Analytical Biochemistry* (2009): 93–8
- 309 [Twenty \(forward looking\) questions](#)
Hassell, L.A., Wagar, E.A. *Journal of Pathology Informatics* (2014): 27
- 310 [Multiplexed protease assays using element-tagged substrates](#)
Lathia, U.S., Ornatsky, O., Baranov, V., Nitz, M. *Analytical Biochemistry* (2010): 157–9
- 311 [The synthesis and characterization of lanthanide-encoded poly\(styrene-co-methacrylic acid\) microspheres](#)
Liang, Y., Abdelrahman, A.I., Baranov, V., Winnik, M.A. *Polymer* (2011): 5,040–52
- 312 [Curious results with palladium- and platinum-carrying polymers in mass cytometry bioassays and an unexpected application as a dead cell stain](#)
Majonis, D., Ornatsky, O., Kinach, R., Winnik, M.A. *Biomacromolecules* (2011): 3,997–4,010

- 313 The release and extraction of lanthanide ions from metal-encoded poly (styrene-co-methacrylic acid) microspheres
Liang, Y., Abdelrahman, A.I., Baranov, V., Winnik, M.A. *Polymer* (2012): 998–1,004
- 314 A sensitive and quantitative element-tagged immunoassay with ICPMS detection
Baranov, V.I., Quinn, Z., Bandura, T.R., Tanner, S.D. *Analytical Chemistry* (2002): 1,629–36
- 315 Mass cytometry: protocol for daily tuning and running cell samples on a CyTOF mass cytometer
Leipold, M.D., Maecker, H.T. *Journal of Visualized Experiments* (2012): e4398
- 316 A CD45-based barcoding approach to multiplex mass-cytometry (CyTOF)
Lai, L., Ong, R., Li, J., Albin, S. *Cytometry, Part A* (2015): 369–74
- 317 Platinum-conjugated antibodies for application in mass cytometry
Mei, H.E., Leipold, M.D., Maecker, H.T. *Cytometry, Part A* (2015): 292–300
- 318 Single-cell methods
de Souza, N. *Nature Methods* (2012): 35
- 319 Analysis, Isolation, and Activation of Antigen-Specific CD4+ and CD8+ T Cells by Soluble MHC-Peptide Complexes
Schmidt, J., Dojcinovic, D., Guillaume, P., Luescher, I. *Frontiers in Immunology* (2013): 218
- 320 Single Cell Mass Cytometry for Analysis of Immune System Functional States
Bjornson, Z.B., Nolan, G.P., Fantl, W.J. *Current Opinion in Immunology* (2013): doi: 10.1016/j.coi.2013.07.004
- 321 Immune monitoring technology primer: flow and mass cytometry
Maecker, H.T., Harari, A. *Journal for ImmunoTherapy of Cancer* (2015): 44
- 322 Dual-purpose polymer labels for fluorescent and mass cytometric affinity bioassays
Majonis, D., Ornatsky, O., Weinrich, D., Winnik, M.A. *Biomacromolecules* (2013): 1,503–13

MICROBIOLOGY/PATHOGEN DETECTION (VIRAL)

- 323 Application and utility of mass cytometry in vaccine development
Reeves, P.M., Sluder, A.E., Paul, S.R. et al. *FASEB Journal* (2017): doi: 10.1096/fj.201700325R
- 324 High-dimensional CyTOF analysis of dengue virus-infected human DCs reveals distinct viral signatures
Hamlin, R.E., Rahman, A., Pak, T.R. et al. *JCI Insight* (2017): e92,424

- 325 Mass cytometric analysis of HIV entry, replication, and remodeling in tissue CD4+ T cells
Cavrois, M., Banerjee, T., Mukherjee, G. et al. *Cell Reports* (2017): 984-8
- 326 FHL2 Regulates Natural Killer Cell Development and Activation during *Streptococcus pneumoniae* Infection
Baranek, T., Morello, E., Valayer, A. et al. *Frontiers in Immunology* (2017): 123
- 327 Identification of vaccine-altered circulating B cell phenotypes using mass cytometry and a two-step clustering analysis
Pejoski, D., Tchitchek, N., Rodriguez, P. A. et al. *The Journal of Immunology* (2016): 4,814–31
- 328 Cytometry by time-of-flight shows combinatorial cytokine expression and virus-specific cell niches within a continuum of CD8+ T cell phenotypes
Newell, E.W., Sigal, N., Bendall, S.C. et al. *Immunity* (2012): 142–52
- 329 A human vaccine strategy based on chimpanzee adenoviral and MVA vectors that primes, boosts, and sustains functional HCV-specific T cell memory
Swadling, L., Capone, S., Antrobus, R.D. et al. *Science Translational Medicine* (2014): 261ra153
- 330 Chikungunya viral arthritis in the United States: a mimic of seronegative rheumatoid arthritis
Miner, J.J., Aw Yeang, H.X., Fox, J.M. et al. *Arthritis and Rheumatology* (2015): 1,214–20
- 331 Activation of Salmonella Typhi-Specific Regulatory T Cells in Typhoid Disease in a Wild-Type *S. Typhi* Challenge Model
McArthur, M.A., Fresnay, S., Magder, L.S. et al. *PLoS Pathogens* (2015): e1004914
- 332 High-dimensional immune profiling of total and rotavirus VP6-specific intestinal and circulating B cells by mass cytometry
Nair, N., Newell, E.W., Vollmers, C. et al. *Mucosal Immunology* (2015): 68–82
- 333 The Split Virus Influenza Vaccine rapidly activates immune cells through Fcγ receptors
O'Gorman, W.E., Huang, H., Wei, Y.L. et al. *Vaccine* (2014): 5,989–97
- 334 Combinatorial tetramer staining and mass cytometry analysis facilitate T-cell epitope mapping and characterization
Newell, E.W., Sigal, N., Nair, N. et al. *Nature Biotechnology* (2013): 623–9
- 335 Impact of CD4+ T Cell Responses on Clinical Outcome following Oral Administration of Wild-Type Enterotoxigenic *Escherichia coli* in Humans
McArthur, M.A., Chen, W.H., Magder, L. et al. *PLoS Neglected Tropical Diseases*(2017): e0005291

- 336 The natural killer cell response to West Nile virus in young and old individuals with or without a prior history of infection
Yao, Y., Strauss-Albee, D.M., Zhou, J.Q. et al. *PLoS One* (2017): e0172625
- 337 Role of immune aging in susceptibility to West Nile virus
Yao, Y., Montgomery, R.R. *Methods in Molecular Biology* (2016): 235–47
- 338 Single cell mass cytometry reveals remodeling of human T cell phenotypes by varicella zoster virus
Sen, N., Mukherjee, G., Arvin, A.M. *Methods* (2015): 85–94

ONCOLOGY

- 339 Defining Renal Neoplastic Disease, One Cell at a Time: Mass Cytometry, a New Tool for the Study of Kidney Biology and Disease
Nelson, P.J., Kretzler, M. *American Journal of Kidney Diseases* (2017): 758–61
- 340 Pregnane X receptor is associated with unfavorable survival and induces chemotherapeutic resistance by transcriptional activating multidrug resistance-related protein 3 in colorectal cancer
Dong, Y., Wang, Z., Xie, G.F. et al. *Molecular Cancer* (2017): 71
- 341 Checkpoint blockade immunotherapy reshapes the high-dimensional phenotypic heterogeneity of murine intratumoural neoantigen-specific CD8+ T cells
Fehlings, M., Simoni, Y., Penny, H.L. et al. *Nature Communications* (2017): 562
- 342 Single cell immune profiling by mass cytometry of newly diagnosed chronic phase chronic myeloid leukemia treated with nilotinib
Gullaksen, S.E., Skavland, J., Gavasso, S. et al. *Haematologica* 1,361–7
- 343 Expression of LAG-3 defines exhaustion of intratumoral PD-1+ T cells and correlates with poor outcome in follicular lymphoma
Yang, Z.Z., Kim, H.J., Villasboas, J.C. et al. *Oncotarget* (2017): 61,425–39
- 344 Novel BET protein proteolysis-targeting chimera exerts superior lethal activity than bromodomain inhibitor (BETi) against post-myeloproliferative neoplasm secondary (s) AML cells
Saenz, D.T., Fiskus, W., Qian, Y. et al. *Leukemia* (2017): 1,951–61
- 345 Colony Lysate Arrays for Proteomic Profiling of Drug-Tolerant Persisters of Cancer Cell
Kume, Kohei, Nishizuka, S.S. *Analytical Chemistry* (2017): 8,626–31
- 346 Mass cytometry analysis reveals hyperactive NF Kappa B signaling in myelofibrosis and secondary acute myeloid leukemia
Fisher, D.A., Malkova, O., Engle, E.K. et al. *Leukemia* (2017): 1,962–74

- 347 Cholesterol esterification inhibition and imatinib treatment synergistically inhibit growth of BCR-ABL mutation-independent resistant chronic myelogenous leukemia
Bandyopadhyay, S., Li, J., Traer, E. et al. *PLoS One* (2017): doi: /10.1371/journal.pone.0179558.s008
- 348 High-dimensional single cell mapping of cerium distribution in the lung immune microenvironment of an active smoker
Rahman, A.H., Lavin, Y., Kobayashi, S. et al. *Cytometry Part B: Clinical Cytometry* doi: 10.1002/cyto.b.21545
- 349 Phenotypic and functional characterization of a bortezomib-resistant multiple myeloma cell line by flow and mass cytometry
Baughn, L.B., Sachs, Z., Noble-Orcutt, K.E. et al. *Leukemia and Lymphoma* (2017): 1,931–40
- 350 PARP inhibitor upregulates PD-L1 expression and enhances cancer-associated immunosuppression
Jiao, S., Xia, W., Yamaguchi, H. et al. *Clinical Cancer Research* (2017): 3,711–20
- 351 Cytokine-induced memory-like natural killer cells exhibit enhanced responses against myeloid leukemia
Romee, R., Rosario, M., Berriern-Elliott, M.M. et al. *Science Translational Medicine*(2016): 357
- 352 The novel BMI-1 inhibitor PTC596 downregulates MCL-1 and induces p53-independent mitochondrial apoptosis in acute myeloid leukemia progenitor cells
Nishida, Y., Maeda, A., Kim, M.J. et al. *Blood Cancer Journal* (2017): e527
- 353 Overexpression of the human antigen R suppresses the immediate paradoxical proliferation of melanoma cell subpopulations in response to suboptimal BRAF inhibition
Fernandez, M., Sutterlüty-Fall, H., Schwärzler, C. et al. *Cancer Medicine*(2017): 1,652–64
- 354 Emerging understanding of multiscale tumor heterogeneity
Gerdes, M.J., Sood, A., Sevinsky, C. et al. *Frontiers in Oncology* (2014): 366
- 355 Unraveling cell populations in tumors by single-cell mass cytometry
Di Palma S., Bodenmiller B. *Current Opinion in Biotechnology* (2015): 122–9
- 356 Mass cytometric functional profiling of acute myeloid leukemia defines cell-cycle and immunophenotypic properties that correlate with known responses to therapy

- Behbahni, G.K., Samusik, N., Bjornson, Z.B. et al. *Cancer Discovery* (2015): 988–1,003
- 357 **Eradication of CML stem cells**
Carter, B.Z., Andreeff, M. *Oncoscience*(2016): 313–5
- 358 **Tissue resident memory T cells create genetically distinct immune microenvironments within melanoma metastasis**
Dhodapkar, K., Bar, N., Boddupalli, C.S. et al. *Journal for ImmunoTherapy of Cancer*(2014): O15
- 359 **NRASG12V oncogene facilitates self-renewal in a murine model of acute myelogenous leukemia**
Sachs, Z., LaRue, R.S., Nguyen, H.T. et al. *Blood* (2014): 3,274–83
- 360 **Dasatinib changes immune cell profiles concomitant with reduced tumor growth in several murine solid tumor models**
Hekim, C., Ilander, M., Yan, J. et al. *Cancer Immunology Research* (2017): 157–69
- 361 **Mutant IDH1 Downregulates ATM and Alters DNA Repair and Sensitivity to DNA Damage Independent of TET2**
Inoue, S., Li, W.Y., Tseng, A. et al. *Cancer Cell* (2016): 337–48
- 362 **PD-1 marks dysfunctional regulatory T cells in malignant gliomas**
Lowther, D.E., Goods, B.A., Lucca, L.E. et al. *Journal of Clinical Investigation* (2016): e85935
- 363 **Single-cell measurement of the uptake, intratumoral distribution and cell cycle effects of cisplatin using mass cytometry**
Chang, Q., Ornatsky, O.I., Koch, C.J. et al. *International Journal of Cancer* (2015): 1202–9
- 364 **Single-cell mass cytometry reveals intracellular survival/proliferative signaling in FLT3-ITD-mutated AML stem/progenitor cells**
Han, L., Qiu, P., Zeng, Z. et al. *Cytometry, Part A* (2015): 346–56
- 365 **Mass cytometry analysis shows that a novel memory phenotype B cell is expanded in multiple myeloma**
Hansmann, L., Blum, L., Ju, C.H. et al. *Cancer Immunology Research* (2015): 650–60
- 366 **Data-Driven Phenotypic Dissection of AML Reveals Progenitor-like Cells that Correlate with Prognosis**
Levine, J.H., Simonds, E.F., Bendall, S.C. et al. *Cell* (2015): 184–97
- 367 **Myelodysplastic Syndrome Revealed by Systems Immunology in a Melanoma Patient Undergoing Anti-PD-1 Therapy**
Greenplate, A.R., Johnson, D.B., Roussel, M. et al. *Cancer Immunology Research*(2016): 474–80

- 368 High-Dimensional Analysis of Acute Myeloid Leukemia Reveals Phenotypic Changes in Persistent Cells during Induction Therapy
Ferrell, P.B. Jr., Diggins, K.E., Polikowsky, H.G. et al. *PLoS One* (2016): e0153207
- 369 Anti-apoptotic ARC protein confers chemoresistance by controlling leukemia-microenvironment interactions through a NF κ B/IL1 β signaling network
Carter, B.Z., Mak, P.Y., Chen, Y. et al. *Oncotarget* (2016): 20,054–67
- 370 Expansion and Activation of CD103(+) Dendritic Cell Progenitors at the Tumor Site Enhances Tumor Responses to Therapeutic PD-L1 and BRAF Inhibition
Salmon, H., Idoyaga, J., Rahman, A. et al. *Immunity* (2016): 924–38
- 371 Messenger RNA Detection in Leukemia Cell lines by Novel Metal-Tagged in situ Hybridization using Inductively Coupled Plasma Mass Spectrometry
Ornatsky, O., Baranov, V.I., Bandura, D.R. et al. *Translational Oncogenomics* (2014): 1–9
- 372 Impaired coordination between signaling pathways is revealed in human colorectal cancer using single-cell mass cytometry of archival tissue blocks
Simmons, A.J., Scurrah, C.R., McKinley, E.T. et al. *Science Signaling* (2016): rs11
- 373 Isotopologous Organotellurium Probes Reveal Dynamic Hypoxia In Vivo with Cellular Resolution
Edgar, L.J., Vellanki, R.N., McKee, T.D. et al. *Angewandte Chemie* (2016): 13,159–63
- 374 BET protein bromodomain inhibitor-based combinations are highly active against post-myeloproliferative neoplasm secondary AML cells
Saenz, D.T., Fiskus, W., Manshour, T. et al. *Leukemia* (2016): 678–87
- 375 A Prospective Clinical Trial Combining Radiation Therapy With Systemic Immunotherapy in Metastatic Melanoma
Hiniker, S.M., Reddy, S.A., Maecker, H.T. et al. *International Journal of Radiation Oncology Biology Physics* (2016): 578–88
- 376 Mass cytometry of follicular lymphoma tumors reveals intrinsic heterogeneity in proteins including HLA-DR and a deficit in non-malignant plasmablast and germinal center B cell populations
Wogslund, C.E., Greenplate, A.R., Kolstad, A. et al. *Cytometry Part B Clinical Cytometry* (2016): 79–87
- 377 Combined inhibition of β -catenin and Bcr-Abl synergistically targets tyrosine kinase inhibitor-resistant blast crisis chronic myeloid leukemia blasts and progenitors in vitro and in vivo
Zhou, H., Mak, P.Y., Mu, H. et al. *Leukemia*(2017): doi:10.1038/leu.2017.87

- 378 [Human Melanoma-Derived Extracellular Vesicles Regulate Dendritic Cell Maturation](#)
Maus, R.L.G., Jakub, J.W., Nevala, W.K. et al. *Frontiers in Immunology* (2017): 358
- 379 [Interlesional diversity of T cell receptors in melanoma with immune checkpoints enriched in tissue-resident memory T cells](#)
Boddupalli, C.S., Bar, N., Kadaveru, K. et al. *JCI Insight* (2016): e88955
- 380 [Effect of cryopreservation on delineation of immune cell subpopulations in tumor specimens as determined by multiparametric single cell mass cytometry analysis](#)
Kadić, E., Moniz, R.J., Huo, Y. et al. *BMC Immunology* (2017): 6
- 381 [MLN0128, a novel mTOR kinase inhibitor, disrupts survival signaling and triggers apoptosis in AML and AML stem/ progenitor cells](#)
Zeng, Z., Wang, R.Y., Qiu, Y.H., et al. *Oncotarget* (2016): 55,083–97
- 382 [NCR1 Expression Identifies Canine Natural Killer Cell Subsets with Phenotypic Similarity to Human Natural Killer Cells](#)
Foltz, J.A., Somanchi, S.S., Yang, Y. et al. *Frontiers in Immunology* (2016): 521
- 383 [Comprehensive characterization of VISTA expression in patients with acute myeloid leukemia](#)
Lamble, A., Kosaka, Y., Huang, F. et al. *Journal of Clinical Oncology* (2016): e14546
- 384 [Mass Cytometry: A High-Throughput Platform to Visualize the Heterogeneity of Acute Myeloid Leukemia](#)
Do, P., Byrd, J.C. *Cancer Discovery* (2015): 912–4
- 385 [Mass cytometry to decipher the mechanism of nongenetic drug resistance in cancer](#)
Fienberg, H.G., Nolan, G.P. *Current Topics in Microbiology and Immunology* (2014): 85–94
- 386 [From single cells to deep phenotypes in cancer](#)
Bendall, S.C., Nolan, G.P. *Nature Biotechnology* (2012): 639–47
- 387 [From mass cytometry to cancer prognosis](#)
Winter, D.R., Ledegor, G., Amit, I. *Nature Biotechnology* (2015): 931–2
- 388 [Characterization of phosphorus content of biological samples by ICP-DRC-MS: potential tool for cancer research](#)
Bandura, D.R., Ornatsky, O.I., Liao, L. *Journal of Analytical Atomic Spectrometry*(2014): 96–100
- 389 [Monitoring the Immune Competence of Cancer Patients to Predict Outcome](#)
Chang, S., Kohrt, H., Maecker, H.T. *Cancer Immunology, Immunotherapy* (2014): 713–9

PHARMACOGENOMICS

- 390 **Cytometry: Measure for measure**
Kling, J. *Nature* (2015): 439–43
- 391 **Pushing the frontiers of T-cell vaccines: accurate measurement of human T-cell responses**
Saade, F., Gorski, S.A., Petrovsky, N. *Expert Review of Vaccines* (2012): 1,459–70
- 392 **Impact of recent innovations in the use of mass cytometry in support of drug development**
Nassar, A.F., Ogura, H., Wisniewski, A.V. *Drug Discovery Today* (2015): 1,169–75

STEM CELL

- 393 **MYB fusions and CD markers as tools for authentication and purification of cancer stem cells from salivary adenoid cystic carcinoma**
Panaccione, A., Zhang, Y., Ryan, M. et al. *Stem Cell Research* (2017): 160-6
- 394 **Reconstitution of immune cell populations in multiple sclerosis patients after autologous stem cell transplantation**
Karnell, F.G., Lin, D., Motley, S. et al. *Clinical and Experimental Immunology* (2017): 268–78
- 395 **Pathologically expanded peripheral T helper cell subset drives B cells in rheumatoid arthritis**
Rao, D.A., Gurish, M.F., Marshall, J.L. et al. *Nature* (2017): 110–4
- 396 **Proceedings: immune tolerance and stem cell transplantation: a CIRM mini-symposium and workshop report**
Talib, S., Millan, M.T., Jorgenson, R.L., Shepard, K.A. *Stem Cells Translational Medicine* (2015): 4–9
- 397 **Charting a map through the cellular reprogramming landscape**
Wen, L., Tang, F. *Cell Stem Cell* (2016): 215–6
- 398 **High-resolution myogenic lineage mapping by single-cell mass cytometry**
Porpiglia, E., Samusik, N., Van Ho, A.T. et al. *Nature Cell Biology* (2017): 558–67
- 399 **A continuous molecular roadmap to iPSC reprogramming through progression analysis of single-cell mass cytometry**
Zunder, E.R., Lujan, E., Goltsev, Y. et al. *Cell Stem Cell* (2015): 323–37
- 400 **Early reprogramming regulators identified by prospective isolation and mass cytometry**
Lujan, E., Zunder, E.R., Ng, Y.H. et al. *Nature* (2015): 352–6

- 401 Cell expansion during directed differentiation of stem cells toward the hepatic lineage
Raju, R., Chau, D., Cho, D.S. et al. *Stem Cells and Development* (2016): 274–84
- 402 Distinct signaling programs control human hematopoietic stem cell survival and proliferation
Knapp, D.J., Hammond, C.A., Aghaeepour, N. et al. *Blood* (2016): 307–18
- 403 Combination Of Mass Cytometry and Imaging Analysis Reveals Origin, Location, and Functional Repopulation of Liver Myeloid Cells in Mice
David, B.A., Rezende, R.M., Antunes, M.M. et al. *Gastroenterology* (2016): 1,176–91
- 404 High-dimensional analysis of the murine myeloid cell system
Becher, B., Schlitzer, A., Chen, J. et al. *Nature Immunology* (2014): 1,181–9
- 405 Low-dose IL-2 selectively activates subsets of CD4+ Tregs and NK cells
Hirakawa, M., Matos, T., Liu, H. et al. *JCI Insight* (2016): e89278
- 406 Studying hematopoiesis using single-cell technologies
Ye, F., Huang, W., Guo, G. *Journal of Hematology and Oncology* (2017): 27

OTHER

- 407 Applications of mass cytometry in clinical medicine: the promise and perils of clinical CyTOF®
Behbehani, G.K. *Clinics in Laboratory Medicine* (2017): 945–64
- 408 Diverse continuum of CD4+ T-cell states is determined by hierarchical additive integration of cytokine signals
Eizenberg-Magar, I., Rimer, J., Zaretsky, I. et al. *Proceedings of the National Academy of Sciences of the United States of America* (2017): E6447–56
- 409 Cytometry: today's technology and tomorrow's horizons
Chattopadhyay, P., Roederer, M. *Methods*(2012): 251–8
- 410 Protein Ontology: a controlled structured network of protein entities
Natale, D.A., Arighi, C.N., Blake, J.A. et al. *Nucleic Acids Research* (2013): D415–D421
- 411 Immunology. Flow cytometry, amped up
Benoist, C., Hacohen, N. *Science* (2011): 677–8
- 412 Methods for discovery and characterization of cell subsets in high dimensional mass cytometry data
Diggins, K.E., Ferrell, P.B. Jr., Irish, J.M. *Methods* (2015): 55–63
- 413 A mine is a terrible thing to waste: high content, single cell technologies for comprehensive immune analysis

- Chattopadhyay, P.K., Roederer, M. *American Journal of Transplantation* (2015): 1,155–61
- 414 [Single-cell technologies are revolutionizing the approach to rare cells](#)
Proserpio, V., Lönnberg, T. *Immunology & Cell Biology* (2016): 225–9
- 415 [Systems Biology Analysis of Heterocellular Signaling](#)
Tape, C.J. *Trends in Biotechnology* (2016): 627–37
- 416 [SWIFT—Scalable Clustering for Automated Identification of Rare Cell Populations in Large, High-Dimensional Flow Cytometry Datasets, Part 2: Biological Evaluation](#)
Mosmann, T.R., Naim, I., Rebhahn, J. et al. *Cytometry Part A* (2014): 422–33
- 417 [Coordinated Surgical Immune Signatures Contain Correlates of Clinical Recovery](#)
Gaudillière, B., Fragiadakis, G.K., Bruggner, R.V. et al. *Science Translational Medicine* (2014): 131
- 418 [The road ahead: Implementing mass cytometry in clinical studies, one cell at a time](#)
Baca, Q., Cosma, A., Nolan, G. et al. *Cytometry Part B: Clinical Cytometry* (2016): 10–11
- 419 [CyTOF analysis of anti-tumor responses](#)
Dempsey, L.A. *Nature Immunology* (2017): 254
- 420 [Next-generation flow cytometry](#)
Janes, M.R., Rommel, C. *Nature Biotechnology* (2011): 602–4
- 421 [Cycling into Future: Mass Cytometry for the Cell-Cycle Analysis](#)
Darzynkiewicz, Z. *Cytometry, Part A* (2012): 546–8
- 422 [A flow cytometry revolution](#)
Doerr, A. *Nature Methods* (2011): 531