Mass spectrometry

Single-Cell Proteomics Publications

Featuring Thermo Scientific™ Orbitrap™ mass spectrometers

Sample Preparation

Nanodroplet processing platform for deep and quantitative proteome profiling of 10–100 mammalian cells

Ying Zhu, Paul D. Piehowski, Rui Zhao, Jing Chen, Yufeng Shen, Ronald J. Moore, Anil K. Shukla, Vladislav A. Petyuk, Martha Campbell-Thompson, Clayton E. Mathews, Richard D. Smith, WeiJun Qian, and Ryan T. Kelly

Nat Commun 2018, 9 (1), 882
https://www.nature.com/articles/s41467-018-03367-w

High-throughput single cell proteomics enabled by multiplex isobaric labeling in a nanodroplet sample preparation platform

Maowei Dou, Geremy Clair, Chia-Feng Tsai, Kerui Xu, William B. Chrisler, Ryan L. Sontag, Rui Zhao, Ronald J. Moore, Tao Liu, Ljiljana Pasa-Tolic, Richard D. Smith, Tujin Shi, Joshua N. Adkins, Wei-Jun Qian, Ryan T. Kelly, Charles Ansong, and Ying Zhu

Anal Chem 2019, 91 (20), 13119-13127
https://pubs.acs.org/doi/abs/10.1021/acs.analchem.9b03349

Nanoliter-scale oil-air-droplet chip-based single cell proteomic analysis

Zi-Yi Li, Min Huang, Xiu-Kun Wang, Ying Zhu, Jin-Song Li, Catherine C. L. Wong, and Qun Fang u

Anal Chem 2018, 90 (8), 5430-5438
https://pubs.acs.org/doi/abs/10.1021/acs.analchem.8b00661

Automated coupling of nanodroplet sample preparation with liquid chromatography–mass spectrometry for high-throughput single-cell proteomics

Sarah M. Williams, Andrey V. Liyu, Chia-Feng Tsai, Ronald J. Moore, Daniel J. Orton, William B. Chrisler, Matthew J. Gaffrey, Tao Liu, Richard D. Smith, Ryan T. Kelly, Ljiljana Pasa-Tolic, and Ying Zhu

Anal Chem 2020, 92 (15), 10588-10596
https://pubs.acs.org/doi/10.1021/acs.analchem.0c01551

Proteomic analysis of single mammalian cells enabled by microfluidic nanodroplet sample preparation and ultrasensitive nanoLC-MS

Ying Zhu, Geremy Clair, William B. Chrisler, Yufeng Shen, Rui Zhao, Anil K. Shukla, Ronald J. Moore, Ravi S. Misra, Gloria S. Pryhuber, Richard D. Smith, Charles Ansong, and Ryan T. Kelly

Angew Chem Int Ed Engl 2018, 57 (38), 12370-12374
https://onlinelibrary.wiley.com/doi/abs/10.1002/anie.201802843

Surfactant-assisted one-pot sample preparation for label-free single-cell proteomics

Chia-Feng Tsai, Pengfei Zhang, David Scholten, Kendall Martin, Yi-Ting Wang, Rui Zhao, William B. Chrisler, Dhwani B. Patel, Maowei Dou, Yuzhi Jia, Carolina Reduzzi, Xia Liu, Ronald J. Moore, Kristin E. Burnum-Johnson, Miao-Hsia Lin, Chuan-Chih Hsu, Jon M. Jacobs, Jacob Kagan, Sudhir Srivastava, Karin D. Rodland, H. Steven Wiley, Wei-Jun Qian, Richard D. Smith, Ying Zhu, Massimo Cristofanilli, Tao Liu, Huiping Liu, and Tujin Shi

Commun Biol 2021, 4 (1), 265
https://www.nature.com/articles/s42003-021-01797-9

Digital microfluidic isolation of single cells for -Omics

Julian Lamanna, Erica Y. Scott, Harrison S. Edwards, M. Dean Chamberlain, Michael D. M. Dryden, Jiaxi Peng, Barbara Mair, Adam Lee, Calvin Chan, Alexandros A. Sklavounos, Austin Heffernan, Farhana Abbas, Charis Lam, Maxwell E. Olson, Jason Moffat, and Aaron R. Wheeler

Nat Commun 2020, 11 (1), 5632
https://www.nature.com/articles/s41467-020-19394-5

Fully automated sample processing and analysis workflow for low-input proteome profiling

Yiran Liang, Hayden Acor, Michaela A. McCown, Andikan J. Nwosu, Hannah Boekweg, Nathaniel B. Axtell, Thy Truong, Yongzheng Cong, Samuel H. Payne, and Ryan T. Kelly

Anal Chem 2021, 93 (3), 1658-1666
https://pubs.acs.org/doi/10.1021/acs.analchem.0c04240

High-throughput and high-efficiency sample preparation for single-cell proteomics using a nested nanowell chip

Jongmin Woo, Sarah M. Williams, Lye Meng Markillie, Song Feng, Chia-Feng Tsai, Victor Aguilera-Vazquez, Ryan L. Sontag, Ronald J. Moore, Dehong Hu, Hardeep S. Mehta, Joshua Cantlon-Bruce, Tao Liu, Joshua N. Adkins, Richard D. Smith, Geremy C. Clair, Ljiljana Pasa-Tolic, and Ying Zhu

Nat Commun 2021, 12 (1), 6246
https://www.nature.com/articles/s41467-021-26514-2

Streamlined single-cell proteomics by an integrated microfluidic chip and dataindependent acquisition mass spectrometry

Sofani Tafesse Gebreyesus, Asad Ali Siyal, Reta Birhanu Kitata, Eric Sheng-Wen Chen, Bayarmaa Enkhbayar, Takashi Angata, Kuo-I Lin, Yu-Ju Chen, and Hsiung-Lin Tu

Nat Commun 2022, 13 (1), 37
https://www.nature.com/articles/s41467-021-27778-4

Integrated proteome analysis device for fast single-cell protein profiling

Xi Shao, Xuantang Wang, Sheng Guan, Haizhu Lin, Guoquan Yan, Mingxia Gao, Chunhui Deng, and Xiangmin Zhang

Anal Chem 2018, 90 (23), 14003-14010
https://pubs.acs.org/doi/10.1021/acs.analchem.8b03692

Redesigning the T-probe for mass spectrometry analysis of online lysis of non-adherent single cells

Yanlin Zhu, Renmeng Liu, and Zhibo Yang

Anal Chim Acta 2019, 1084, 53-59
https://www.sciencedirect.com/science/article/abs/pii/S0003267019308839

Development of a laser capture microscope-based single-cell-type proteomics tool for studying proteomes of individual cell layers of plant roots

Yingde Zhu, Hui Li, Sarabjit Bhatti, Suping Zhou, Yong Yang, Tara Fish, and Theodore W Thannhauser

Hortic Res 2016, 3, 16026
https://www.nature.com/articles/hortres201626

Water droplet-in-oil digestion method for single-cell proteomics

Takeshi Masuda, Yuma Inamori, Arisu Furukawa, Maki Yamahiro, Kazuki Momosaki, Chih-Hsiang Chang, Daiki Kobayashi, Hiroto Ohguchi, Yawara Kawano, Shingo Ito, Norie Araki, Shao-En Ong, and Sumio Ohtsuki

Anal Chem 2022, 94 (29), 10329-10336
https://pubs.acs.org/doi/10.1021/acs.analchem.1c05487

Exploring functional protein covariation across single cells using nPOP

Andrew Leduc, R. Gray Huffman, Joshua Cantlon, Saad Khan, and Nikolai Slavov

Genome Biol 2022, 23 (1), 261
https://genomebiology.biomedcentral.com/articles/10.1186/s13059-022-02817-5

Sample preparation methods for targeted single-cell proteomics

Azad Eshghi, Xiaofeng Xie, Darryl Hardie, Michael X. Chen, Fabiana Izaguirre, Rachael Newman, Ying Zhu, Ryan T. Kelly, and David R. Goodlett

J Proteome Res 2023
https://pubs.acs.org/doi/10.1021/acs.jproteome.2c00429

Robust and easy-to-use one-pot workflow for label-free single-cell proteomics

Manuel Matzinger, Elisabeth Müller, Gerhard Dürnberger, Peter Pichler, and Karl Mechtler

Anal Chem 2023, 95 (9), 4435-4445

https://pubs.acs.org/doi/10.1021/acs.analchem.2c05022

Xenopus Laevis Embryos

Single cell proteomics using frog (Xenopus laevis) blastomeres isolated from early stage embryos, which form a geometric progression in protein content

Liangliang Sun, Kyle M. Dubiak, Elizabeth H. Peuchen, Zhenbin Zhang, Guijie Zhu, Paul W. Huber, and Norman J. Dovichi

Anal Chem 2016, 88 (13), 6653-6657

https://pubs.acs.org/doi/10.1021/acs.analchem.6b01921

Single-cell mass spectrometry for discovery proteomics: quantifying translational cell heterogeneity in the 16-cell frog (Xenopus) embryo

Camille Lombard-Banek, Sally A. Moody, and Peter Nemes

Angew Chem Int Ed Engl 2016, 55 (7), 2454-2458

https://onlinelibrary.wiley.com/doi/10.1002/anie.201510411

Single cell proteomics by data-independent acquisition to study embryonic asymmetry in Xenopus laevis

Anumita Saha-Shah, Melody Esmaeili, Simone Sidoli, Hyojeong Hwang, Jing Yang, Peter S. Klein, and Benjamin A. Garcia

Anal Chem 2019, 91 (14), 8891-8899

https://pubs.acs.org/doi/pdf/10.1021/acs.analchem.9b00327

Microsampling capillary electrophoresis mass spectrometry enables single-cell proteomics in complex tissues: Developing cell clones in live Xenopus laevis and zebrafish embryos

Camille Lombard-Banek, Sally A. Moody, M. Chiara Manzini, and Peter Nemes

Anal Chem 2019, 91 (7), 4797-4805

https://pubs.acs.org/doi/10.1021/acs.analchem.9b00345

Global absolute quantification reveals tight regulation of protein expression in single Xenopus eggs

Arne H. Smits, Rik G.H. Lindeboom, Matteo Perino, Simon J. van Heeringen, Gert Jan C. Veenstra, and Michiel Vermeulen

Nucleic Acids Res 2014, 42 (15), 9880-9891

https://academic.oup.com/nar/article/42/15/9880/2435191?login=true

Expression variation and covariation impair analog and enable binary signaling control

Kyle M Kovary, Brooks Taylor, Michael L Zhao, and Mary N Teruel

Molecular Systems Biology (2018)14:e7997

https://www.embopress.org/doi/full/10.15252/msb.20177997

Capillary electrophoresis mass spectrometry for scalable single-cell proteomics

Bowen Shen, Leena R. Pade, Sam B. Choi, Pablo Muñoz-LLancao, M. Chiara Manzini, and Peter Nemes

Front Chem 2022, 10, 863979

https://www.frontiersin.org/articles/10.3389/fchem.2022.863979/full

High-throughput, comprehensive single-cell proteomic analysis of Xenopus laevis embryos at the 50-Cell stage using a microplate-based MICROFASP system

Zhenbin Zhang, Kyle M. Dubiak, Evgenia Shishkova, Paul W. Huber, Joshua J. Coon, and Norman J. Dovichi

Anal Chem 2022, 94 (7), 3254-3259

https://pubs.acs.org/doi/abs/10.1021/acs.analchem.1c04987

Method Development

Three-dimensional feature matching improves coverage for single-cell proteomics based on ion mobility filtering

Jongmin Woo, Geremy C. Clair, Sarah M. Williams, Song Feng, Chia-Feng Tsai, Ronald J. Moore, William B. Chrisler, Richard D. Smith, Ryan T. Kelly, Ljiljana Pasa-Tolic, Charles Ansong, and Ying Zhu

Cell Syst 2022, 13 (5), 426-434.e424

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Real-time search-assisted acquisition on a tribrid mass spectrometer improves coverage in multiplexed single-cell proteomics

Benjamin Furtwängler, Nil Üresin, Khatereh Motamedchaboki, Romain Huguet, Daniel LopezFerrer, Vlad Zabrouskov, Bo T. Porse, and Erwin M. Schoof

Mol Cell Proteomics 2022, 21 (4), 100219
https://www.sciencedirect.com/science/article/pii/S1535947622000275

A simple, rapid, and practical method for single-cell proteomics based on mass-adaptive coating of synthetic peptides

Siqi Li, Kaichan Su, Zhenkun Zhuang, Qing Qin, Lei Gao, Yamei Deng, Xuyang Liu, Guixue Hou, Longtao Wang, Piliang Hao, Huanming Yang, Siqi Liu, Hongming Zhu, and Yan Ren

Sci Bull (Beijing) 2022, 67 (6), 581-584
https://www.sciencedirect.com/science/article/abs/pii/S209592732100788X?via%3Dihub

Label-free profiling of up to 200 single-cell proteomes per day using a dual-column nanoflow liquid chromatography platform

Kei G. I. Webber, Thy Truong, S. Madisyn Johnston, Sebastian E. Zapata, Yiran Liang, Jacob M. Davis, Alexander D. Buttars, Fletcher B. Smith, Hailey E. Jones, Arianna C. Mahoney, Richard H. Carson, Andikan J. Nwosu, Jacob L. Heninger, Andrey V. Liyu, Gregory P. Nordin, Ying Zhu, and Ryan T. Kelly

Anal Chem 2022, 94 (15), 6017-6025
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DART-ID increases single-cell proteome coverage

Albert Tian Chen, Alexander Franks, Nikolai Slavov

PLoS Comput Biol 2019, 15 (7), e1007082
https://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1007082

An improved boosting to amplify signal with Isobaric labeling (iBASIL) strategy for precise quantitative single-cell proteomics

C.-F. Tsai, R. Zhao, S.M. Williams, R.J. Moore, K. Schultz, W. Chrisler, L. Pasa-Tolic, K. Rodland, R.D. Smith, T. Shi, Y. Zhu, and T. Liu

Mol Cell Proteomics 2020, 19 (5), 828-838
https://www.sciencedirect.com/science/article/pii/S1535947620350064

Single-cell proteomic and transcriptomic analysis of macrophage heterogeneity using SCoPE2

Harrison Specht, Edward Emmott, Aleksandra A. Petelski, R. Gray Huffman, David H. Perlman, Marco Serra, Peter Kharchenko, Antonius Koller, and Nikolai Slavov

Genome Biol 2021, 22 (1), 50
https://genomebiology.biomedcentral.com/articles/10.1186/s13059-021-02267-5

Multiplexed single-cell proteomics using SCoPE2

Aleksandra A. Petelski, Edward Emmott, Andrew Leduc, R. Gray Huffman, Harrison Specht, David H. Perlman, and Nikolai Slavov

Nat Protoc 2021, 16 (12), 5398-5425
https://www.nature.com/articles/s41596-021-00616-z

Single cell proteomics using multiplexed isobaric labeling for mass spectrometric analysis

Akos Vegvari, Jimmy E. Rodriguez, and Roman A. Zubarev

Methods Mol Biol 2022, 2386, 113-127
https://link.springer.com/protocol/10.1007/978-1-0716-1771-7_8

Ultrasensitive single-cell proteomics workflow identifies >1000 protein groups per mammalian cell

Yongzheng Cong, Khatereh Motamedchaboki, Santosh A. Misal, Yiran Liang, Amanda J. Guise, Thy Truong, Romain Huguet, Edward D. Plowey, Ying Zhu, Daniel Lopez-Ferrer, and Ryan T. Kelly

Chem Sci 2020, 12 (3), 1001-1006
https://pubs.rsc.org/en/content/articlelanding/2021/sc/d0sc03636f#!divAbstract

Ultrasensitive nanoLC-MS of subnanogram protein samples using second generation micropillar array LC technology with Orbitrap Exploris 480 and FAIMS PRO

Karel Stejskal, Jeff Op de Beeck, Gerhard Dürnberger, Paul Jacobs, and Karl Mechtler

Anal Chem 2021, 93 (25), 8704-8710
https://pubs.acs.org/doi/10.1021/acs.analchem.1c00990

Improved single-cell proteome coverage using narrow-bore packed nanoLC columns and ultrasensitive mass spectrometry

Yongzheng Cong, Yiran Liang, Khatereh Motamedchaboki, Romain Huguet, Thy Truong, Rui Zhao, Yufeng Shen, Daniel Lopez-Ferrer, Ying Zhu, and Ryan T. Kelly

Anal Chem 2020, 92 (3), 2665-2671
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Quantitative accuracy and precision in multiplexed single-cell proteomics

Claudia Ctortecka, Karel Stejskal, Gabriela Krššáková, Sasha Mendjan, and Karl Mechtler

Anal Chem 2022, 94 (5), 2434-2443
https://pubs.acs.org/doi/10.1021/acs.analchem.1c04174

Spectral library-based single-cell proteomics resolves cellular heterogeneity

Lakmini Senavirathna, Cheng Ma, Ru Chen, and Sheng Pan

Cells 2022, 11 (15)
https://www.mdpi.com/2073-4409/11/15/2450

DeepSCP: utilizing deep learning to boost single-cell proteome coverage

Bing Wang, Yue Wang, Yu Chen, Mengmeng Gao, Jie Ren, Yueshuai Guo, Chenghao Situ, Yaling Qi, Hui Zhu, Yan Li, and Xuejiang Guo

Brief Bioinform 2022, 23 (4)
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Evaluating linear ion trap for MS3-based multiplexed single-cell proteomics

Junho Park, Fengchao Yu, James M. Fulcher, Sarah M. Williams, Kristin Engbrecht, Ronald J. Moore, Geremy C. Clair, Vladislav Petyuk, Alexey I. Nesvizhskii, and Ying Zhu

Anal Chem 2023, 95 (3), 1888-1898
https://pubs.acs.org/doi/abs/10.1021/acs.analchem.2c03739

Maximizing hydrophobic peptide recovery in proteomics and antibody development using a mass spectrometry compatible surfactant

Song Nie, Reid O'Brien Johnson, Yuliya Livson, Tyler Greer, Xiaojing Zheng, and Ning Li

Anal Biochem 2022, 658, 114924
https://www.sciencedirect.com/science/article/pii/S0003269722003840

Prioritized mass spectrometry increases the depth, sensitivity and data completeness of single-cell proteomics

R. Gray Huffman, Andrew Leduc, Christoph Wichmann, Marco Di Gioia, Francesco Borriello, Harrison Specht, Jason Derks, Saad Khan, Luke Khoury, Edward Emmott, Aleksandra A. Petelski, David H. Perlman, Jürgen Cox, Ivan Zanoni, and Nikolai Slavov

Nat Methods 2023, 20 (5), 714-722
https://www.nature.com/articles/s41592-023-01830-1

A rapid and sensitive single-cell proteomic method based on fast liquid-chromatography separation, retention time prediction and MS1-only acquisition

Wei Fang, Zhuokun Du, Linlin Kong, Bin Fu, Guibin Wang, Yangjun Zhang, and Weijie Qin

Anal Chim Acta 2023, 1251, 341038
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HyperSCP: Combining Isotopic and Isobaric Labeling for Higher Throughput Single-Cell Proteomics

Yiran Liang, Thy Truong, Aubrianna J. Saxton, Hannah Boekweg, Samuel H. Payne, Pam M. Van Ry, and Ryan T. Kelly

Anal Chem 2023
https://pubs.acs.org/doi/10.1021/acs.analchem.3c00906

Cancer

Single-cell chemical proteomics (SCCP) interrogates the timing and heterogeneity of cancer cell commitment to death

Ákos Végvári, Jimmy E. Rodriguez, and Roman A. Zubarev

Anal Chem 2022, 94 (26), 9261-9269
https://pubs.acs.org/doi/full/10.1021/acs.analchem.2c00413

Quantitative single-cell proteomics as a tool to characterize cellular hierarchies

Erwin M. Schoof, Benjamin Furtwängler, Nil Üresin, Nicolas Rapin, Simonas Savickas, Coline Gentil, Eric Lechman, Ulrich auf dem Keller, John E. Dick, and Bo T. Porse

Nat Commun 2021, 12 (1), 3341
https://www.nature.com/articles/s41467-021-23667-y

SCoPE-MS: mass spectrometry of single mammalian cells quantifies proteome heterogeneity during cell differentiation

Bogdan Budnik, Ezra Levy, Guillaume Harmange, and Nikolai Slavov

Genome Biol 2018, 19 (1), 161
https://genomebiology.biomedcentral.com/articles/10.1186/s13059-018-1547-5?optIn=false

Proteome profiling of 1 to 5 spiked circulating tumor cells isolated from whole blood using immunodensity enrichment, laser capture microdissection, nanodroplet sample processing, and ultrasensitive nanoLC–MS

Ying Zhu, Jennifer Podolak, Rui Zhao, Anil K. Shukla, Ronald J. Moore, George V. Thomas, and Ryan T. Kelly

Anal Chem 2018, 90(20), 11756–11759
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Optimized data-independent acquisition approach for proteomic analysis at single-cell level

Yuefan Wang, Tung-Shing Mamie Lih, Lijun Chen, Yuanwei Xu, Morgan D. Kuczler, Liwei Cao, Kenneth J. Pienta, Sarah R. Amend, and Hui Zhang

Clin Proteomics 2022, 19 (1), 24
https://link.springer.com/article/10.1186/s12014-022-09359-9

DNA Damage Response

Microscopy-based single-cell proteomic profiling reveals heterogeneity in DNA damage response dynamics

Pin-Rui Su, Li You, Cecile Beerens, Karel Bezstarosti, Jeroen Demmers, Martin Pabst, Roland Kanaar, Cheng-Chih Hsu, and Miao-Ping Chien

Cell Rep Methods 2022, 2 (6), 100237
https://www.sciencedirect.com/science/article/pii/S2667237522001060

Human Oocytes

Identification of maturation-specific proteins by single-cell proteomics of human oocytes

Irma Virant-Klun, Stefan Leicht, Christopher Hughes, and Jeroen Krijgsveld

Mol Cell Proteomics 2016, 15 (8), 2616-2627
https://www.sciencedirect.com/science/article/pii/S1535947620334927

Single-cell quantitative proteomic analysis of human oocyte maturation revealed high heterogeneity in in vitro matured oocytes

Yueshuai Guo, Lingbo Cai, Xiaofei Liu, Long Ma, Hao Zhang, Bing Wang, Yaling Qi, Jiayin Liu, Feiyang Diao, Jiahao Sha, and Xuejiang Guo

Mol Cell Proteomics 2022, 21 (8), 100267
https://www.sciencedirect.com/science/article/pii/S1535947622000755

Discovery of oogenesis biomarkers from mouse oocytes using a single-cell proteomics approach

Qian Li, Lu Mu, Xuebing Yang, Ge Wang, Jing Liang, Shaolin Wang, Hua Zhang, and Zhen Li

J Proteome Res 2023
https://pubs.acs.org/doi/10.1021/acs.jproteome.3c00157

Hair-Cell Development

Single-cell proteomics reveals changes in expression during hair-cell development

Ying Zhu, Mirko Scheibinger, Daniel Christian Ellwanger, Jocelyn F Krey, Dongseok Choi, Ryan T Kelly, Stefan Heller, and Peter G Barr-Gillespie

Elife 2019, 8
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Diet

Single-cell RNA sequencing combined with single-cell proteomics identifies the metabolic adaptation of islet cell subpopulations to high-fat diet in mice

Qi Fu, Hemin Jiang, Yu Qian, Hui Lv, Hao Dai, Yuncai Zhou, Yang Chen, Yunqiang He, Rui Gao, Shuai Zheng, Yucheng Liang, Siqi Li, Xinyu Xu, Kuanfeng Xu, and Tao Yang

Neurons

Single-cell proteome profiling of neuronal cells

A. Misal and Ryan T. Kelly

Other

Defining the carrier proteome limit for single-cell proteomics

Tommy K. Cheung, Chien-Yun Lee, Florian P. Bayer, Atticus McCoy, Bernhard Kuster, and Christopher M. Rose

Features of peptide fragmentation spectra in single-cell proteomics

Hannah Boekweg, Daisha Van Der Watt, Thy Truong, S. Madisyn Johnston, Amanda J. Guise, Edward D. Plowey, Ryan T. Kelly, and Samuel H. Payne

A deeper look at carrier proteome effects for single-cell proteomics

Zilu Ye, Tanveer S. Batth, Patrick Rüther, and Jesper V. Olsen

Software

Comparison of database searching programs for the analysis of single-cell proteomics data

Jiaxi Peng, Calvin Chan, Fei Meng, Yechen Hu, Lingfan Chen, Ge Lin, Shen Zhang, and Aaron R. Wheeler

Learn more at **thermofisher.com/singlecellproteomics**