

Orbitrap Astral MS Literature List

Rethink what is possible



Peer Reviewed Articles

Activity-Based Protein Profiling

Achieving a 35-Plex tandem mass tag reagent set through deuterium incorporation

Nathan R. Zuniga, Dustin C. Frost, Karsten Kuhn, Myungsun Shin, Rebecca L. Whitehouse, Ting-Yu Wei, Yuchen He, Shane L. Dawson, Ian Pike, Ryan D. Bomgarden, Steven P. Gygi, and Joao A. Paulo

J Proteome Res. 2024 Nov 1;23(11):5153-5165

<https://pubs.acs.org/doi/10.1021/acs.jproteome.4c00668>

Aging

Single-cell m⁶A profiling in the mouse brain uncovers cell type-specific RNA methylomes and age-dependent differential methylation

Matthew Tegowski, Anna K. Prater, Christopher L. Holley, and Kate D. Meyer

Nat Neurosci. 2024 Sep 24.

<https://www.nature.com/articles/s41593-024-01768-3>

Bacterial Proteomics

Can Xenobiotics support the growth of Mn(II)-oxidizing bacteria (Mnob)? A case of phenol-utilizing Mnob *Pseudomonas Sp. An-1*

Aonan Qiao, Haixia Pan, Jiayi Zanga, Yiwen Zhang, Xianliang Yi, Yang Liu, Jingjing Zhan, Xiaojing Yang, Xu Zhaoa, Ang Li, and Hao Zhou

J Hazard Mater. 2024 May 5:469:134095

<https://www.sciencedirect.com/science/article/abs/pii/S0304389424006745>

Proteomic analysis of carbapenem-resistant *Klebsiella pneumoniae* outer membrane vesicles under the action of phages combined with tigecycline

Jing Mao, Xiaoyu Yang, Cheng Yan, Fan Wang, and Rui Zheng

Ann Clin Microbiol Antimicrob. 2024 Aug 20;23(1):73

<https://ann-clinmicrob.biomedcentral.com/articles/10.1186/s12941-024-00734-y>

TMT-based quantitative proteomics revealed the antibacterial mechanism of cinnamaldehyde against MRSA

Xiaohui Chen, Panpan Liu, Jingge Wang, Xiaoqiang He, Jianchong Wang, Haorong Chen, and Guiqin Wang

J Proteome Res. 2024 Oct 4;23(10):4637-4647

<https://pubs.acs.org/doi/10.1021/acs.jproteome.4c00520>

Beverage Proteomics

Interactions of *Saccharomyces cerevisiae* and *Lactiplantibacillus plantarum* Isolated from Light-Flavor Jiupeitai at Various Fermentation Temperatures

Pu Yang, Bo Xi, Ying Han, Jiayang Li, Lujun Luo, Chaofan Qu, Junfang Li, Shuai Liu, Le Kang, Baoqing Bai, Ben Zhang, Shaojie Zhao, Pan Zhen and Lizhen Zhang

Foods. 2024 Sep 12;13(18):2884

<https://www.mdpi.com/2304-8158/13/18/2884>

Transcriptomics and proteomics analyses reveal the molecular mechanisms of yeast cells regulated by Phe-Cys against ethanol-oxidation cross-stress

Caiyun Wu, Hexin Zhang, Nana Yang, Chengxin Wang, Mengmeng Zhang, Na Liu, and Hongjie Lei

Food Chem. 2024 Oct 18;464(Pt 2):141694

Peer Reviewed Articles

<https://www.sciencedirect.com/science/article/abs/pii/S0308814624033442>

Crosslinking-MS

Structure of the native γ -tubulin ring complex capping spindle microtubules

Tom Dendooven, Stanislau Yatskevich, Alister Burt, Zhuo A. Chen, Dom Bellini, Juri Rappsilber, John V. Kilmartin, and David Barford

Nat Struct Mol Biol. 2024 Apr 12

<https://www.nature.com/articles/s41594-024-01281-y>

Data Analysis

Reanalysis of DIA data demonstrates the capabilities of MS/MS-free proteomics to reveal new biological insights in disease-related samples

Mark V. Ivanov, Anna S. Kopeykina, and Mikhail V. Gorshkov

J Am Soc Mass Spectrom. 2024 Aug 7;35(8):1775-1785

<https://pubs.acs.org/doi/abs/10.1021/jasms.4c00134>

NovoLign: metaproteomics by sequence alignment

Hugo B.C. Kleikamp, Ramon van der Zwaan, Ramon van Valderen, Jitske M. van Ede, Mario Pronk, Pim Schaasberg, Maximilienne T. Allaart, Mark C.M. van Loosdrecht, and Martin Pabst

ISME Commun. 2024 Oct 12;4(1):ycae121

<https://academic.oup.com/ismecommun/advance-article/doi/10.1093/ismeco/ycae121/7819827>

Deep Visual Proteomics

Spatial proteomics identifies JAKi as treatment for a

lethal skin disease

Thierry M. Nordmann, Holly Anderton, Akito Hasegawa, Lisa Schweizer, Peng Zhang, Pia-Charlotte Stadler, Ankit Sinha, Andreas Metousis, Florian A. Rosenberger, Maximilian Zwiebel, Takashi K. Satoh, Florian Anzengruber, Maximilian T. Strauss, Maria C. Tanzer, Yuki Saito, Ting Gong, Marvin Thielert, Haruna Kimura, Natasha Silke, Edwin H. Rodriguez, Gaetana Restivo, Hong Ha Nguyen, Annette Gross, Laurence Feldmeyer, Lukas Joerg, Mitchell P. Levesque, Peter J. Murray, Saskia Ingen-Housz-Oro, Andreas Mund, Riichiro Abe, John Silke, Chao Ji, Lars E. French, and Matthias Mann

Nature. 2024 Oct 16

<https://www.nature.com/articles/s41586-024-08061-0>

Drug Resistance

Sterol 14- α demethylase (CYP51) activity in *Leishmania donovani* is likely dependent upon cytochrome P450 reductase 1

Lindsay B. Tulloch, Michele Tinti, Richard J. Wall, Stefan K. Weidt, Victoriano Corpas- Lopez, Gourav Dey, Terry K. Smith, Alan H. Fairlamb, Michael P. Barrett, and Susan Wyllie

PLoS Pathog. 2024 Jul 11;20(7):e1012382

<https://journals.plos.org/plospathogens/article?id=10.1371/journal.ppat.1012382>

Electroactive Biofilms

Linking proteomic function and structure to electroactive biofilms development across electrode orientations

Yue Dong, Yiying Jiang, Mingrui Sui, Jimeng Yu, Jiaxin Wu, Ziyi Gu, and Xiangtong Zhou

Bioresour Technol. 2024 Aug 28:131375

Peer Reviewed Articles

<https://www.sciencedirect.com/science/article/abs/pii/S0960852424010794>

Food Proteomics

Astral-based DIA proteomics explored the flavor enhancement mechanism of Chinese traditional smoked bacon by staphylococcal co-fermentation

Li Yang, Hongjun Li, Han Wu, Xueling Sun, Shuyun Liu, Kaitong Lang, and Zhifei He

Food Chem. 2024 Oct 9;463(Pt 4):141563

<https://www.sciencedirect.com/science/article/abs/pii/S0308814624032138>

Fungal Infection

Integrated transcriptomics–proteomics analysis reveals the response mechanism of *Morchella sextelata* to *Pseudodiploëspora longispora* infection

Shurong Wang, Jingyi Wang, Tengyun Wang, Tonglou Li, Lijing Xu, Yanfen Cheng, Mingchang Chang, Junlong Meng, and Ludan Hou

J Fungi (Basel). 2024 Aug 26;10(9):604

<https://www.mdpi.com/2309-608X/10/9/604>

Inflammatory Bowel Disease

A proteomics pipeline for generating clinical grade biomarker candidates from data-independent acquisition mass spectrometry (DIA-MS) discovery

Qin Fu, Manasa Vegesna, Niveda Sundararaman, Eugen Damoc, Tabiwang N Arrey, Anna Pashkova, Emebet Mengesha, Philip Debbas, Sandy Joung, Dalin Li, Susan Cheng, Jonathan Braun, Dermot Govern, Christopher Murray, Yue Xuan, and Jennifer E Van Eyk

Angew Chem Int Ed Engl. 2024 Oct 21:e202409446

<https://onlinelibrary.wiley.com/doi/abs/10.1002/anie.202409446>

Intestinal Stem Cells

BMP suppresses Wnt signaling via the Bcl11b-regulated NuRD complex to maintain intestinal stem cells

Yehua Li, Xiaodan Wang, Meimei Huang, Xu Wang, Chunlin Li, Siqi Li, Yuhui Tang, Shicheng Yu, Yalong Wang, Wanglu Song, Wei Wu, Yuan Liu, and Ye-Guang Chen

EMBO J. 2024 Oct 21

<https://www.embopress.org/doi/full/10.1038/s44318-024-00276-1>

Metaproteomics

The astounding exhaustiveness and speed of the Astral mass analyzer for highly complex samples is a quantum leap in the functional analysis of microbiomes

Thibaut Dumas, Roxana Martinez Pinna, Clément Lozano, Sonja Radau, Olivier Pible, Lucia Grenga, and Jean Armengaud

Microbiome. 2024 Mar 7;12(1):46

<https://microbiomejournal.biomedcentral.com/articles/10.1186/s40168-024-01766-4>

Mamalian Development

A novel protein CYTB-187AA encoded by the mitochondrial gene CYTB modulates mammalian early development

Zhijuan Hu, Liang Yang, Maolei Zhang, Haite Tang, Yile Huang, Yujie Su, Yingzhe Ding, Chong Li, Mengfei Wang, Yunhao Zhou, Qing Zhang, Liman Guo, Yue Wu, Qianqian Wang, Ning Liu, Haoran Kang, Yi Wu, Deyang Yao, Yukun Li, Zifeng Ruan, Hao Wang, Feixiang Bao, Guopan Liu, Junwei Wang, Yaofeng Wang,

Peer Reviewed Articles

Wuming Wang, Gang Lu, Dajiang Qin, Duanqing Pei, Wai-Yee Chan, and Xingguo Liu

Cell Metab. 2024 Jul 2;36(7):1586-1597.e7

<https://www.sciencedirect.com/science/article/abs/pii/S1550413124001323>

Milk Proteomics

Size-dependent composition and in-situ structure analysis of the milk fat globule membrane in buffalo milk

Yi Wang, Mengyuan Guo, Peipei Wu, Chong Chen, Weibo Zhang, Fazheng Ren, Pengjie Wang, Shouyun Wu, Jianhuan Wei, Jie Luo, and Jinghua Yu

Food Chem. 2024 Oct 23;464(Pt 2):141766

<https://www.sciencedirect.com/science/article/abs/pii/S0308814624034162>

Oxidation

Methionine alkylation as an approach to quantify methionine oxidation using mass spectrometry

Margaret Hoare, Ruiyue Tan, Kevin A. Welle, Kyle Swovick, Jennifer R. Hryhorenko, and Sina Ghaemmaghani

J Am Soc Mass Spectrom. 2024 Mar 6;35(3):433-440

<https://pubs.acs.org/doi/full/10.1021/jasms.3c00337>

Oxidative Response

Redox control of the deubiquitinating enzyme Ubp2 regulates translation during stress

Clara M. Santos, Blanche K. Cizubu, Dinachi A. Okonkwo, Chia-Yu Chen, Natori Maske, Nathan A. Snyder, Vanessa Simoes, Erica J. Washington, and Gustavo M. Silva

J Biol Chem. 2024 Oct 7:107870

<https://www.sciencedirect.com/science/article/pii/S002192582402372X>

Parasite Proteomics

Cell cycle-regulated transcription factor AP2XII-9 is a key activator for asexual division and apicoplast inheritance in *Toxoplasma gondii* tachyzoite

Yuehong Shi, Xuan Li, Yingying Xue, Dandan Hu, and Xingju Song

mBio. 2024 Oct 16;15(10):e0133624

<https://journals.asm.org/doi/10.1128/mbio.01336-24>

Proteomics analysis reveals the differential protein expression of female and male adult *Toxocara canis* using Orbitrap Astral analyzer

Hui-Jie Qiu, Ya-Jia Zhou, Zhi-Yu Li, Yi-Han Lv, Xing-Quan Zhu, and Wen-Bin Zheng

Infect Dis Poverty. 2024 Oct 9;13(1):73

<https://link.springer.com/article/10.1186/s40249-024-01246-9>

Phosphoproteomics

Systematic optimization of automated phosphopeptide enrichment for high-sensitivity phosphoproteomics

Patricia Bortel, Ilaria Piga, Claire Koenig, Christopher Gerner, Ana Martinez del Val, and Jesper V Olsen

Mol Cell Proteomics. 2024 Mar 26:100754

<https://www.sciencedirect.com/science/article/pii/S1535947624000446>

Fast and deep phosphoproteome analysis with the Orbitrap Astral mass spectrometer

Noah M. Lancaster, Pavel Sinitcyn, Patrick Forny, Trenton M. Peters-Clarke, Caroline Fecher, Andrew J. Smith, Evgenia

Peer Reviewed Articles

Shishkova, Tabiwang N. Arrey, Anna Pashkova, Margaret Lea Robinson, Nicholas Arp, Jing Fan, Juli Hansen, Andrea Galmozzi, Lia R. Serrano, Julie Rojas, Audrey P. Gasch, Michael S. Westphall, Hamish Stewart, Christian Hock, Eugen Damoc, David J. Pagliarini, Vlad Zabrouskov, and Joshua J. Coon

Nat Commun. 2024 Aug 15;15(1):7016

<https://www.nature.com/articles/s41467-024-51274-0>

Presynaptic Rac1 in the hippocampus selectively regulates working memory

Jaebin Kim, Edwin Bustamante, Peter Sotonyi, Nicholas Maxwell, Pooja Parameswaran, Julie K Kent, William C Wetsel, Erik J. Soderblom, Bence Rácz, and Scott H. Soderling

Elife. 2024 Jul 24;13:RP97289

<https://elifesciences.org/articles/97289>

SIMKK4 is responsible for pollen development in tomato

Lifei Chen, Leiqing Chen, Hong Zhang, Chaoyue Xi, Yulin Fang, Yiru Lai, Changtian Pan, Gang Lu, and Yunkun Wu

Plant Physiol Biochem. 2024 Oct 15;216:109201

<https://www.sciencedirect.com/science/article/abs/pii/S0981942824008696>

Spatial proteomics identifies JAKi as treatment for a lethal skin disease

Thierry M. Nordmann, Holly Anderton, Akito Hasegawa, Lisa Schweizer, Peng Zhang, Pia-Charlotte Stadler, Ankit Sinha, Andreas Metousis, Florian A. Rosenberger, Maximilian Zwiebel, Takashi K. Satoh, Florian Anzengruber, Maximilian T. Strauss, Maria C. Tanzer, Yuki Saito, Ting Gong, Marvin Thielert, Haruna Kimura, Natasha Silke, Edwin H. Rodriguez, Gaetana Restivo, Hong Ha Nguyen, Annette Gross, Laurence Feldmeyer, Lukas Joerg, Mitchell P. Levesque, Peter J. Murray, Saskia Ingen-Housz-Oro, Andreas Mund, Riichiro Abe, John Silke, Chao Ji, Lars E. French, and Matthias Mann

Nature. 2024 Oct 16

<https://www.nature.com/articles/s41586-024-08061-0>

Quantitative comparison of deparaffinization, rehydration, and extraction methods for FFPE tissue proteomics and phosphoproteomics

Erin M. Humphries, Clare Loudon, George E. Craft, Peter G. Hains, and Phillip J. Robinson

Anal Chem. 2024 Aug 20;96(33):13358-13370

<https://pubs.acs.org/doi/10.1021/acs.analchem.3c04479>

Plant Proteomics

Soybean symbiotic-nodule zonation and cell differentiation are defined by NIN2 signaling and GH3-dependent auxin homeostasis

Tianli Tu, Zhen Gao, Linfang Li, Jiansheng Chen, Kangzhuo Ye, Tao Xu, Siyuan Mai, Qingqing Han, Chaofan Chen, Shengwei Wu, Yankun Dong, Jiaomei Chen, Laimei Huang, Yuefeng Guan, Fang Xie, and Xu Chen

Dev Cell. 2024 Jul 17:S1534-5807(24)00424-6

<https://www.sciencedirect.com/science/article/pii/S1534580724004246>

Glucose-induced glycation enhances the foaming properties of *Trichosanthes kirilowii* seed protein isolate: Insights into structure, interfacial behavior, and proteomics

Patricia Bortel, Ilaria Piga, Claire Koenig, Christopher Gerner, Ana Martinez del Val, and Jesper V Olsen

Food Hydrocolloids, Volume 157, 2024, 110444

<https://www.sciencedirect.com/science/article/abs/pii/S0268005X24007185>

Multi-omics analysis reveals the transcription factor AtuMYB306 improves drought tolerance by regulating flavonoid metabolism in Chinese chive (*Allium tuberosum* Rottler)

Peer Reviewed Articles

Taotao Li, Zhen Wang, Yanyan Chen, Pengqiang Yao, Zhongqiu Zhang, Shenao Cai, Yutao Zhu, Yingying Yu, Chunli Liao, Dongxiao Liu, Xiaofei Yang, Lianzhe Wang, and Xuan Ma

Dev Cell. 2024 Jul 17:S1534-5807(24)00424-6

<https://www.sciencedirect.com/science/article/pii/S2667064X24002446>

SIMKK4 is responsible for pollen development in tomato

Lifei Chen, Leiqing Chen, Hong Zhang, Chaoyue Xi, Yulin Fang, Yiru Lai, Changtian Pan, Gang Lu, and Yunkun Wu

Plant Physiol Biochem. 2024 Oct 15:216:109201

<https://www.sciencedirect.com/science/article/abs/pii/S0981942824008696>

Plasma Proteomics

Evaluating the performance of the Astral mass analyzer for quantitative proteomics using data-independent acquisition

Lilian R. Heil, Eugen Damoc, Tabiwang N. Arrey, Anna Pashkova, Eduard Denisov, Johannes Petzoldt, Amelia C. Peterson, Chris Hsu, Brian C. Searle, Nicholas Shulman, Michael Riffle, Brian Connolly, Brendan X. MacLean, Philip M. Remes, Michael W. Senko, Hamish I. Stewart, Christian Hock, Alexander A. Makarov, Daniel Hermanson, Vlad Zabrouskov, Christine C. Wu, and Michael J. MacCoss

J Proteome Res. 2023 Oct 6;22(10):3290-3300

<https://pubs.acs.org/doi/10.1021/acs.jproteome.3c00357>

An inflection point in high-throughput proteomics with Orbitrap Astral: analysis of biofluids, cells, and tissues

Nathan G. Hendricks, Santosh D. Bhosale, Angel J. Keoseyan, Josselin Ortiz, Aleksandr Stotland, Saeed Seyedmohammad, Chi D. L. Nguyen, Jonathan T. Bui, Annie

Moradian*, Susan M. Mockus, and Jennifer E. Van Eyk

J Proteome Res. 2024 Sep 6;23(9):4163-4169

<https://pubs.acs.org/doi/10.1021/acs.jproteome.4c00384>

A proteomics pipeline for generating clinical grade biomarker candidates from data-independent acquisition mass spectrometry (DIA-MS) discovery

Qin Fu, Manasa Vegesna, Niveda Sundararaman, Eugen Damoc, Tabiwang N Arrey, Anna Pashkova, Emebet Mengesha, Philip Debbas, Sandy Joung, Dalin Li, Susan Cheng, Jonathan Braun, Dermot Govern, Christopher Murray, Yue Xuan, and Jennifer E Van Eyk

Angew Chem Int Ed Engl. 2024 Oct 21:e202409446

<https://onlinelibrary.wiley.com/doi/abs/10.1002/anie.202409446>

Protein-Protein Interactions

hnRNP R promotes O-GlcNAcylation of eIF4G and facilitates axonal protein synthesis

Abdolhossein Zare, Saeede Salehi, Jakob Bader, Cornelius Schneider, Utz Fischer, Alexander Veh, Panagiota Arampatzi, Matthias Mann, Michael Briese, and Michael Sendtner

Nat Commun. 2024 Aug 28;15(1):7430

<https://www.nature.com/articles/s41467-024-51678-y>

Reproducibility

Fully automated workflow for integrated sample digestion and Evotip loading enabling high-throughput clinical proteomics

Anders H. Kverneland, Florian Harking, Joel Mario Vej-Nielsen, Magnus Huusfeldt, Dorte B. Bekker-Jensen, Inge Marie Svane, Nicolai Bache, and Jesper V. Olsen

Mol Cell Proteomics. 2024 Jul;23(7):100790

<https://www.sciencedirect.com/science/article/pii/>

Peer Reviewed Articles

[S153594762400080X](https://doi.org/10.1021/acs.jafc.4c01326)

Salivary Proteome

Umami altering salivary proteome: A study across a sensitivity spectrum on subjects

Yiwen Zhu, Xiaoxiao Feng, Ziyu Wang, Yin Zhang, Yuyu Zhang, Jianshe Chen, and Yuan Liu

J Agric Food Chem. 2024 Jun 12;72(23):13451-13464

<https://pubs.acs.org/doi/10.1021/acs.jafc.4c01326>

Single-Cell Proteomics

One-tip enables comprehensive proteome coverage in minimal cells and single zygotes

Zilu Ye, Pierre Sabatier, Javier Martin-Gonzalez, Akihiro Eguchi, Maico Lechner, Ole Østergaard, Jingsheng Xie, Yuan Guo, Lesley Schultz, Rafaela Truffer, Dorte B Bekker-Jensen, Nicolai Bache, and Jesper V Olsen

Nat Commun. 2024 Mar 20;15(1):2474

<https://www.nature.com/articles/s41467-024-46777-9>

AM-DMF-SCP: Integrated single-cell proteomics analysis on an active matrix digital microfluidic chip

Zhicheng Yang, Kai Jin, Yimin Chen, Qian Liu, Hongxu Chen, Siyi Hu, Yuqiu Wang, Zilu Pan, Fang Feng, Mude Shi, Hua Xie, Hanbin Ma, and Hu Zhou

JACS Au. 2024 Mar 26;4(5):1811-1823

<https://pubs.acs.org/doi/10.1021/jacsau.4c00027>

Spatial proteomics of single cells and organelles on tissue slides using filter-aided expansion proteomics

Zhen Dong, Wenhao Jiang, Chunlong Wu, Ting Chen, Jiayi Chen, Xuan Ding, Shu Zheng, Kiryl D. Piatkevich, Yi Zhu, and Tiannan Guo

Nat Commun. 2024 Oct 30;15(1):9378

<https://www.nature.com/articles/s41467-024-53683-7>

Single-Nucleus Proteomics

Spatial proteomics of single cells and organelles on tissue slides using filter-aided expansion proteomics

Zhen Dong, Wenhao Jiang, Chunlong Wu, Ting Chen, Jiayi Chen, Xuan Ding, Shu Zheng, Kiryl D. Piatkevich, Yi Zhu, and Tiannan Guo

Nat Commun. 2024 Oct 30;15(1):9378

<https://www.nature.com/articles/s41467-024-53683-7>

Spatial Proteomics

Single-cell sequencing depicts tumor architecture and empowers clinical decision in metastatic conjunctival melanoma

Hanhan Shi, Hao Tian, Tianyu Zhu, Qili Liao, Chang Liu, Peng Yuan, Yongyun Li, Jie Yang, Chunyan Zong, Shichong Jia, Jing Ruan, Shengfang Ge, Renbing Jia, Peiwei Chai, Shiqiong Xu, and Xianqun Fan

Cell Discov. 2024 Jun 11;10(1):63

<https://www.nature.com/articles/s41421-024-00683-y>

Technology

A conjoined rectilinear collision cell and pulsed extraction ion trap with auxiliary DC electrodes

Hamish Stewart, Dmitry Grinfeld, Alexander Wagner, Alexander Kholomeev, Matthias Biel, Anastassios Giannakopoulos, Alexander Makarov, and Christian Hock

J Am Soc Mass Spectrom. 2024 Jan 3;35(1):74-81

<https://pubs.acs.org/doi/10.1021/jasms.3c00311>

Peer Reviewed Articles

Parallelized acquisition of Orbitrap and Astral analyzers enables high-throughput quantitative analysis

Hamish I. Stewart, Dmitry Grinfeld, Anastassios Giannakopoulos, Johannes Petzoldt, Toby Shanley, Matthew Garland, Eduard Denisov, Amelia C. Peterson, Eugen Damoc, Martin Zeller, Tabiwang N. Arrey, Anna Pashkova, Santosh Renuse, Amirmansoor Hakimi, Andreas Kühn, Matthias Biel, Arne Kreuzmann, Bernd Hagedorn, Immo Colonius, Adrian Schütz, Arne Stefes, Ankit Dwivedi, Daniel Mourad, Max Hoek, Bastian Reitemeier, Philipp Cochems, Alexander Kholomeev, Robert Ostermann, Gregor Quiring, Maximilian Ochmann, Sascha Möhring, Alexander Wagner, André Petker, Sebastian Kanngiesser, Michael Wiedemeyer, Wilko Balschun, Daniel Hermanson, Vlad Zabrouskov, Alexander A. Makarov, and Christian Hock

Anal Chem. 2023 Oct 24;95(42):15656-15664

<https://pubs.acs.org/doi/10.1021/acs.analchem.3c02856>

Multi-reflection Astral mass spectrometer with isochronous drift in elongated on mirrors

Dmitry Grinfeld, Hamish Stewart, Wilko Balschun, Michael Skoblin, Christian Hock, and Alexander Makarov

Nuclear Instruments and Methods in Physics Research Section A: Accelerators, Spectrometers, Detectors and Associated Equipment Volume 1060, March 2024, 169017

<https://www.sciencedirect.com/science/article/abs/pii/S0168900223010173>

Proof of principle for enhanced resolution multi-pass methods for the Astral analyzer

Hamish Stewart, Dmitry Grinfeld, Bernd Hagedorn, Robert Ostermann, Alexander Makarov, and Christian Hock

International Journal of Mass Spectrometry Volume 498, April 2024, 117203

<https://www.sciencedirect.com/science/article/abs/pii/S1387380624000149>

Crowd control of ions in the Astral analyzer

Hamish Stewart, Dmitry Grinfeld, Johannes Petzoldt, Bernd Hagedorn, Michael Skoblin, Alexander Makarov, and Christian Hock

J Mass Spectrom. 2024 Apr;59(4):e5006

<https://analyticalsciencejournals.onlinelibrary.wiley.com/doi/10.1002/jms.5006>

Tissue Proteomics

Spindle apparatus coiled-coil Protein 1 (SPDL1) serves as a novel prognostic biomarker in triple-negative breast cancer

Xian-yan Yang, Xiao-xia Zheng, Xue-jia Zhai, Tao Tang, and Shi-cang Yu

Proteomics Clin Appl. 2024 Jul;18(4):e202300002

<https://onlinelibrary.wiley.com/doi/10.1002/prca.202300002>

Quantitative comparison of deparaffinization, rehydration, and extraction methods for FFPE tissue proteomics and phosphoproteomics

Erin M. Humphries, Clare Loudon, George E. Craft, Peter G. Hains, and Phillip J. Robinson

Anal Chem. 2024 Aug 20;96(33):13358-13370

<https://pubs.acs.org/doi/10.1021/acs.analchem.3c04479>

Ubiquitylation

Global, site-resolved analysis of ubiquitylation occupancy and turnover rate reveals systems properties

Gabriela Prus, Shankha Satpathy, Brian T. Weinert, Takeo Narita, and Chunaram Choudhary

Cell. 2024 Apr 8:S0092-8674(24)00315-5

<https://www.sciencedirect.com/science/article/pii/S0092867424003155>

Peer Reviewed Articles

Proteome birthdating reveals age-selectivity of protein ubiquitination

Michael E. Meadow, Sarah Broas, Margaret Hoare, Fatemeh Alimohammadi, Kevin A. Welle, Kyle Swovick, Jennifer R. Hryhorenko, John C. Martinez, Seyed Ali Biashad, Andrei Seluanov, Vera Gorbunova, Abigail Buchwalter, and Sina Ghaemmaghaniy

Mol Cell Proteomics. 2024 Jul;23(7):100791

<https://www.sciencedirect.com/science/article/pii/S1535947624000811>

Branched-chain amino acids alleviate NAFLD via inhibiting de novo lipogenesis and activating fatty acid β -oxidation in laying hens

Huafeng Jian, Ru Li, Xuan Huang, Jiankui Li, Yan Li, Jiangang Ma, Mingkun Zhu, Xinyang Dong, Hua Yang, and Xiaoting Zou

Redox Biol. 2024 Nov;77:103385

<https://www.sciencedirect.com/science/article/pii/S221323172400363X>

Mechanism of degrader-targeted protein ubiquitinability

Charlotte Crowe, Mark A. Nakasone, Sarah Chandler, Conner Craigon, Gajanan Sathe, Michael H. Tatham, Nikolai Makukhin, Ronald T. Hay, and Alessio Ciulli

Sci Adv. 2024 Oct 11;10(41):eado6492

<https://www.science.org/doi/10.1126/sciadv.ado6492>

Vaccine Research

Immunoactivity of a hybrid membrane biosurface on nanoparticles: enhancing interactions with dendritic cells to augment anti-tumor immune responses

Luying Yu, Ao Zhou, Jingyan Jia, Jieting Wang, Xueyang Ji, Yu Deng, Xinhua Lin, and Fang Wang

Biomater Sci. 2024 Feb 13;12(4):1016-1030

<https://pubs.rsc.org/en/content/articlelanding/2023/bm/>

[d3bm01628e/](#)

Whole Proteome

Ultra-fast label-free quantification and comprehensive proteome coverage with narrow-window data-independent acquisition

Ulises H. Guzman, Ana Martinez-Val, Zilu Ye, Eugen Damoc, Tabiwang N. Arrey, Anna Pashkova, Santosh Renuse, Eduard Denisov, Johannes Petzoldt, Amelia C. Peterson, Florian Harking, Ole Østergaard, Rasmus Rydbirk, Susana Aznar, Hamish Stewart, Yue Xuan, Daniel Hermanson, Stevan Horning, Christian Hock, Alexander Makarov, Vlad Zabrouskov, and Jesper V. Olsen

Nat Biotechnol. 2024 Feb 1

<https://www.nature.com/articles/s41587-023-02099-7>

The one hour human proteome

Lia R. Serrano, Trenton M. Peters-Clarke, Tabiwang N. Arrey, Nicolaie E. Damoc, Margaret Lea Robinson, Noah M. Lancaster, Evgenia Shishkova, Corinne Moss, Anna Pashkova, Pavel Sinitcyn, Dain R. Brademan, Scott T. Quarmby, Amelia C. Peterson, Martin Zeller, Daniel Hermanson, Hamish Stewart, Christian Hock, Alexander Makarov, Vlad Zabrouskov, and Joshua J. Coon

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Preprints

Aging

A plasma proteomic signature links secretome of senescent monocytes to aging- and obesity-related clinical outcomes in humans

Bradley Olinger, Reema Banarjee, Amit Dey, Dimitrios Tsitsipatis, Toshiko Tanaka, Anjana Ram, Thedoe Nyunt, Gulzar Daya, Zhongsheng Peng, Linna Cui, Julian Candia, Eleanor M Simonsick, Myriam Gorospe, Keenan A Walker, Luigi Ferrucci, and Nathan Basisty

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Alzheimer's Disease

Investigating the therapeutic potential of uric acid in Alzheimer's disease: Insights from the cGMP-PKG signaling pathway

Tara SR Chen, Lifang Li, Qihong Jiang, Yu-Rong Mao, Shoupeng Wei, Ambrose Lo, and Dong-feng Huang

Research Square

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Bacterial Proteomics

Structure and mechanism of Zorya anti-phage defense system

Haidai Hu, Thomas C.D. Hughes, Philipp F. Popp, Aritz Roa-Eguiara, Freddie J.O. Martin, Nicole R. Rutbeek, Ivo Alexander Hendriks, Leighton J. Payne, Yumeng Yan, Victor Klein de Sousa, Yong Wang, Michael Lund Nielsen, Richard M. Berry, Marc Erhardt, Simon A. Jackson, and Nicholas M.I. Taylor

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Altering translation allows *E. coli* to overcome chemically stabilized G-quadruplexes

Rachel R Cueny, Andrew F Voter, Aidan M McKenzie, Marcel Morgenstern, Kevin S Myers, Michael M Place, Jason M Peters, Joshua J Coon, and James L Keck

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Breast Milk

Detection of nontoxic BoNT/A levels in post-facial botox injection breastmilk using a multi-technique approach

Helene Gu, Zhenyu Xu, Renata Koviagina, Pengcheng Tan, Changcheng Zheng, Ferdinand Kappes, Domna G. Kotsifaki, Fangrong Shen, and Anastasia Tsigkou

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Cardiac Diseases

Multimomics analysis reveals extensive remodeling of the extracellular matrix and cellular metabolism due to Plakophilin-2 knockdown in guinea pigs

Rui Song, Haiyan Wu, Lihui Yu, Jingning Yu, Wenhui yang, Wenjun Wu, Fei Sun, and Haizhen Wang

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Cellular Stress Response

Localized K63 ubiquitin signaling is regulated by VCP/p97 during oxidative stress

Austin O. Maduka, Sandhya Manohar, Matthew W. Foster, and

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Gustavo M. Silva

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Cerebrospinal Fluid

Enhanced proteome profiling of human cerebrospinal fluid using a commercial plasma enrichment strategy

Eva Borrás, Federica Anastasi, Olga Pastor, Marc Suarez-Calvet, and Eduard Sabido

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Colorectal Cancer

Recharacterization of RSL3 reveals that the selenoproteome is a druggable target in colorectal cancer

Stephen L. DeAngelo, Sofia Dziechciarz, Sumeet Solanki, Myungsun Shin, Liang Zhao, Andrii Balia, Marwa O El-Derany, Nupur K Das, Cristina Castillo, Hannah N Bell, Joao A. Paulo, Yuezhong Zhang, Nicholas J Rossiter, Elizabeth C. McCulla, Jianping He, Indrani Talukder, Zachary T. Schafer, Nouri Neamati, Joseph D. Mancias, Markos Koutmos, and Yatrik M. Shah

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Crohn's Disease

Targeting specific kinase substrates rescues increased colitis severity induced by the crohn's disease-linked LRRK2-N2081D variant

George R Heaton, Xianting Li, Xiaoting Zhou, Yuanxi Zhang, Duc Tung Vu, Marc Oeller, Ozge Karayel, Quyen Q Hoang, Meltem Ece Kars, Minghui Wang, Leonid Tarassishin, Matthias Mann, Inga

Peter, and Zhenyu Yue

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Data Analysis

Unifying the analysis of bottom-up proteomics data with CHIMERYs

Martin Frejno, Michelle T Berger, Johanna Tueshaus, Alexander Högrebe, Florian Seefried, Michael Graber, Patroklos Samaras, Samia Ben Fredj, Vishal Sukumar, Layla Eljagh, Igor Bronshtein, Lizi Mamisashvili, Markus Schneider, Siegfried Gessulat, Tobias Schmidt, Bernhard Kuster, Daniel P Zolg, and Mathias Wilhelm

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A transformer model for de novo sequencing of data-independent acquisition mass spectrometry data

Justin Sanders, Bo Wen, Paul Rudnick, Richard Johnson, Christine C. Wu, Sewoong Oh, Michael J. MacCoss, and William Stafford Noble

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Assessment of false discovery rate control in tandem mass spectrometry analysis using entrapment

Bo Wen, Jack Freestone, Michael Riffle, Michael J. MacCoss, William S. Noble, and Uri Keich

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Koina: Democratizing machine learning for proteomics research

Ludwig Lautenbacher, Kevin L. Yang, Tobias Kockmann, Christian Panse, Matthew Chambers, Elias Kahl, Fengchao Yu, Wassim Gabriel, Dulguun Bold, Tobias Schmidt, Kai Li, Brendan

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MacLean, Alexey I. Nesvizhskii, and Mathias Wilhelm

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Cloud-enabled scalable analysis of large proteomics cohorts

Harendra Guturu, Andrew Nichols, Lee S. Cantrell, Seth Just, Janos Kis, Theodore Platt, Iman Mohtashemi, Jian Wang, and Serafim Batzoglou

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Comet fragment-ion indexing for enhanced peptide sequencing

Christopher D. McGann, Erik J Bergstrom, Vagisha Sharma, Lilian R Heil, Qing Yu, Jimmy K Eng, and Devin K Schweppe

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Carafe enables high quality in silico spectral library generation for data-independent acquisition proteomics

Bo Wen, Chris Hsu, Wen-Feng Zeng, Michael Riffle, Alexis Chang, Miranda Mudge, Brook L. Nunn, Matthew D. Berg, Judit Villen, Michael J. MacCoss, and William S. Noble

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Evaluating signaling pathway inference from kinase-substrate interactions and phosphoproteomics data

Martin Garrido-Rodriguez, Clement Potel, Mira Lea Burtscher, Isabelle Becher, Pablo Rodriguez-Mier, Sophia Müller-Dott, Mikhail M Savitski, and Julio Saez-Rodriguez

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Deep Visual Proteomics

Deep Visual Proteomics advances human colon organoid models by revealing a switch to an in vivo-like phenotype upon xenotransplantation

Frederik Post, Annika Hausmann, Sonja Kabatnik, Sophia Steigerwald, Alexandra Brand, Ditte Lange Clement, Jonathan Skov, Theresa Louise Boye, Toshiro Sato, Casper Steenholdt, Andreas Mund, Ole Haagen Nielsen, Kim Bak Jensen, and Matthias Mann

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Deciphering functional tumor-immune crosstalk through highly multiplexed imaging and deep visual proteomics

Xiang Zheng, Andreas Mund, and Matthias Mann

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Deep Visual Proteomics reveals DNA replication stress as a hallmark of Signet Ring Cell Carcinoma

Sonja Kabatnik, Xiang Zheng, Georgios Pappas, Sophia Steigerwald, Matthew P Padula, and Matthias Mann

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The proteomic landscape of proteotoxic stress in a fibrogenic liver disease

Florian A Rosenberger, Sophia C Maedler, Katrine Holtz Thorhauge, Sophia Steigerwald, Malin Fromme, Mikhail Lebedev, Caroline A.M. Weiss, Marc Oeller, Maria Wahle, Maximilian Zwiebel, Niklas A Schmacke, Sonke Detlefsen, Peter Boor, Joseph Kaserman, Andrew A Wilson, Ondrej Fabian, Sona Frankova, Aleksander Krag, Pavel Strnad, and Matthias Mann

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Embryonic Development

The external microbiome communicates with the developing Zebrafish (*Danio rerio*) embryo through the protective chorion and influences developmental trajectory

Emily Green, Akila Harishchandra, Prabha Ranasinghe, Richard Di Giulio, and Nishad Jayasundara

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Glycoproteomics

Narrow window data-independent acquisition on the Orbitrap Astral Mass Spectrometer enables fast and deep coverage of the plasma glycoproteome

Shelley Jager, Martin Zeller, Anna Pashkova, Douwe Schulte, Eugen Damoc, Karli R. Reiding, Alexander A. Makarov, and Albert J.R. Heck

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Gut Microbiota

Daytime-restricted feeding reshapes the gut microbiota to achieve intestinal radioprotection through creatine-mediated ferroptosis inhibition

Cheng Wang, Yingjuan He, Gaomei Zhao, Xue Ouyang, Shaobo Wang, Yin Chen, Chenwenya Li, Yiyi Jiang, Tainong Xiong, Yongwu He, Jining Gao, Songling Han, Jinghong Zhao, and Junping Wang

Research Square

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Histones

Loss of KDM6A-mediated genomic instability and metabolic reprogramming differentially regulates responses to immune checkpoint therapy and chemotherapy in bladder cancer

Pratishtha Singh, Deblina Raychaudhuri, Bidisha Chakraborty, Swadhin Meher, Aminah J. Tannir, Anurag Majumdar, Jessalyn Hawkins, Yun Xiong, Philip Lorenzi, Padmanee Sharma, Patrick Pilie, and Sangeeta Goswami

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Lysosomal Profiling

Tagless LysolP method for molecular profiling of lysosomal content in clinical samples

Daniel Saarela, Pawel Lis, Sara Gomes, Raja S. Nirujogi, Wentao Dong, Eshaan Rawat, Sophie Glendinning, Karolina Zeneviciute, Enrico Bagnoli, Rotimi Fasimoye, Cindy Lin, Kwamina Nyame, Fanni A. Boros, Friederike Zunke, Frederic Lamoliatte, Sadik Elshani, Matthew Jaconnelli, Judith J. M. Jans, Margriet A. Huisman, Christian Posern, Lena M. Westermann, Angela Schulz, Peter M. van Hasselt, Dario R. Alessi, Monther Abu-Remaih, and Esther Sammler

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Lysosomal Storage Diseases

Global cellular proteo-lipidomic profiling of diverse lysosomal storage disease mutants using nMOST

Felix Kraus, Yuchen He, Sharan Swarup, Katherine A Overmyer, Johann Brenner, Cristina Capitanio, Anna Bieber, Annie Jen, Nicole M Nightingale, Benton J Anderson, Chan Lee, Joao A Paulo, Ian R Smith, Jurgen M Plitzko, Steven P Gygi, Brenda A Schulman, Florian Wilfling, Joshua J Coon, and J Wade Harper

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Metabolomics

Denoising search doubles the number of metabolite and exposome annotations in human plasma using an Orbitrap Astral mass spectrometer

Fanzhou Kong, Tong Shen, Yuanyue Li, Amer Bashar, and Susan S. Bird, and Oliver Fiehn

Research Square 2024

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Parkinson's Disease

PSMF1 variants cause a phenotypic spectrum from early-onset Parkinson's disease to perinatal lethality by disrupting mitochondrial pathways

Francesca Magrinelli, Christelle Tesson, Plamena R. Angelova, Ainara Salazar-Villacorta, Jose A. Rodriguez, Annarita Scardamaglia, Brian Hon-Yin Chung, Matthew Jaconelli, Barbara Vona, Noemi Esteras, Anna Ka-Yee Kwong, Thomas Courtin, Reza Maroofian, Shahryar Alavi, Raja Nirujogi, Mariasavina Severino, Patrick A. Lewis, Stephanie Efthymiou, Benjamin O'Callaghan, Rebecca Buchert, Linda Sofan, Pawel Lis, Chloé Pinon, Guido J. Breedveld, Martin Man-Chun Chui, David Murphy, Vanessa Pitz, Mary B. Makarios, Marlene Cassar, Bassem A. Hassan, Sana Iftikhar, Clarissa Rocca, Peter Bauer, Michele Tinazzi, Marina Svetel, Bedia Samanci, Haşmet A. Hanağası, Basar Bilgiç, José A. Obeso, Monica M. Kurtis, Guillaume Cogan, Ayşe Nazlı Başak, Güneş Kiziltan, Tuğçe Gül, Gül Yalçın, Bülent Elibol, Nina Barišić, Earny Wei-Sen Ng, Sze-Shing Fan, Tova Hershkovitz, Karin Weiss, Javeria Raza Alvi, Tipu Sultan, Issam Azmi Alkhawaja, Tawfiq Froukh, Hadeel Abdollah E Alrukban, Christine Fauth, Ulrich A. Schatz, Thomas Zöggeler, Michael Zech, Karen Stals, Vinod Varghese, Sonia Gandhi, Cornelis Blauwendraat, John A. Hardy, Suzanne Lesage, Vincenzo Bonifati, Tobias B. Haack, Aida M. Bertoli-Avella,

Robert Steinfeld, Dario R. Alessi, Hermann Steller, Alexis Brice, Andrey Y. Abramov, Kailash P. Bhatia, and Henry Houlden

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Plasma Proteomics

Protein coronas on functionalized nanoparticles enable quantitative and precise large-scale deep plasma proteomics

Ting Huang, Jian Wang, Alexey Stukalov, Margaret K. R. Donovan, Shadi Ferdosi, Lucy Williamson, Seth Just, Gabriel Castro, Lee S. Cantrell, Eltaher Elgierari, Ryan W. Benz, Yingxiang Huang, Khatereh Motamedchaboki, Amirmansoor Hakimi, Tabiwang Arrey, Eugen Damoc, Simion Kreimer, Omid C. Farokhzad, Serafim Batzoglou, Asim Siddiqui, Jennifer E. Van Eyk, and Daniel Hornburg

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A novel hybrid high speed mass spectrometer allows rapid translation from biomarker candidates to targeted clinical tests using ¹⁵N labeled proteins

Maria Wahle, Philip Remes, Vincent Albrecht, Johannes Bruno Mueller-Reif, Sophia Steigerwald, Lili Niu, Philip Loessl, Stevan Horning, Cristina Jacob, and Matthias Mann

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Technical assessment on Proteonano: A robust platform for deep plasma proteomics study

Yi Wang, Yonghao Zhang, Xiehua Ouyang, and Hao Wu

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An ultra-deep quantitative plasma proteomics strategy

Jialin Li, Chuanping Zhao, Yuanyuan Liu, Wanjun Zhang, and Weijie Qin

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Single-Cell Proteomics

Evaluating the capabilities of the Astral mass analyzer for single-cell proteomics

Valdemaras Petrosius, Pedro Aragon-Fernandez, Tabiwang N. Arrey, Nil Üresin, Benjamin Furtwängler, Hamish Stewart, Eduard Denisov, Johannes Petzoldt, Amelia C. Peterson, Christian Hock, Eugen Damoc, Alexander Makarov, Vlad Zabrouskov, Bo T. Porse, Erwin M. Schoof Porse, and Erwin M. Schoof

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High-throughput and scalable single cell proteomics identifies over 5000 proteins per cell

Zilu Ye, Pierre Sabatier, Leander Hoeven, Teeradon Phlairaharn, David Hartlmayr, Fabiana Izaguirre, Anjali Seth, Hiren Joshi, Dorte Bekker-Jensen, Nicolai Bache, and Jesper V Olsen

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Challenging the Astral™ mass analyzer — Going beyond 5200 proteins per single-cell at unseen quantitative accuracy to study cellular heterogeneity

Julia A. Bubis, Tabiwang N. Arrey, Eugen Damoc, Bernard Delanghe, Jana Slovakova, Theresa M. Sommer, Harunobu Kagawa, Peter Pichler, Nicolas Rivron, Karl Mechtler, and Manuel Matzinger

bioRxiv 2024.02.01.578358

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Global analysis of protein turnover dynamics in single cells

Pierre Sabatier, Zilu Ye, Maico Lechner, Ulises H Guzman, Christian M Beusch, Fabiana Izaguirre, Anjali Seth, Olga Gritsenko, Sergey Rodin, Karl-Henrik Grinnemo, and Jesper V Olsen

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Quantitative label-free single-cell proteomics on the Orbitrap Astral MS

Valdemaras Petrosius, Pedro Aragon-Fernandez, Tabiwang N. Arrey, Jakob Woessman, Nil Üresin, Bauke de Boer, Jinyu Su, Benjamin Furtwängler, Hamish Stewart, Eduard Denisov, Johannes Petzoldt, Amelia C. Peterson, Christian Hock, Eugen Damoc, Alexander Makarov, Vlad Zabrouskov, Bo T. Porse, and Erwin M. Schoof

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Single-Nucleus Proteomics

Filter-aided expansion proteomics

Zhen Dong, Yi Zhu, Fangfei Zhang, Chunlong Wu, Ting Chen, Jiayi Chen, Wenhao Jiang, Qi Xiao, Shu Zheng, Kiryl D. Piatkevich, and Tiannan Guo

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Sheep Proteomics

Proteomic analysis reveals the sperm protein difference among low, high quality and frozen semen of Sewa sheep in Tibet

Kui-yuan Su, Han-yu Fu, Ye-fen Xu, Zhan-kun Tan, Yi-long Yao, Guang-yin Xi, Zhen-da Shang, Yang Liu, Sangzhu baima, Bo-

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Research Square 2024

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Semyon Shofman, Ben-David Moti, Amit Weingarten, Sascha Kadyshkevitch, and Christian Hock

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Short Linear Motifs (SLiMs)

A proteome-wide dependency map of protein interaction motifs

Sara Ambjoern, Bob Meeusen, Johanna Kliche, Juanjuan Wang, Dimitriya Garvanska, Thomas Kruse, Blanca Lopez-Mendez, Matthias Mann, Niels Mailand, Emil Hertz, Norman E Davey, and Jakob Nilsson

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Software Development

AlphaDIA enables end-to-end transfer learning for feature-free proteomics

Georg Wallmann, Patricia Skowronek, Vincenth Brennstainer, Mikhail Lebedev, Marvin Thielert, Sophia Steigerwald, Mohamed Kotb, Tim Heymann, Xie-Xuan Zhou, Magnus Schwoerer, Maximilian T. Strauss, Constantin Ammar, Sander Willems, Wen-Feng Zeng, and Matthias Mann

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Technology

A high dynamic range ion detector for the Astral™ analyzer

Hamish Stewart, Johannes Petzoldt, Toby Shanley, Dmitry Grinfeld, Eduard Denisov, Bernd Hagedorn, Ankit Dwivedi, Daniel Mourad, Robert Ostermann, Maximilian Ochmann, Philipp Cochems, Alexander Wagner, Wilko Balchun, Alexander Makarov,

Learn more at thermofisher.com/OrbitrapAstral

Tissue Proteomics

Evolocumab as an immunomodulator in glioma: A window of opportunity trial evaluating PCSK9 inhibition to enhance surface MHC-I on tumor

Kirit Singh, Matthew W. Foster, Marlene J. Violette, Kelly M. Hotchkiss, Chelsea O. Railton, Emily E. Blandford, Kathryn E. Blethen, Elizabeth L. Thomas, David M. Ashley, Annick Desjardins, Henry S. Friedman, Margaret O. Johnson, Allan Friedman, Stephen Keir, Evan D. Buckley, James E. Herndon, Roger E. McLendon, John H. Sampson, Evan Calabrese, Giselle Y. Lopez, Gerald A. Grant, Anoop P. Patel, Chuan-Yuan Li, Peter E. Fecci, and Mustafa Khasraw

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Ultra-fast multi-organ proteomics unveils tissue-specific mechanisms of drug efficacy and toxicity

Yun Xiong, Lin Tan, Wai-kin Chan, Eric Yin, Sri Ramya Donepudi, Jibin Ding, Bo Wei, Bao Tran, Sara Martinez, Iqbal Mahmud, Hamish Stewart, Daniel Hermanson, John N. Weinstein, and Philip L. Lorenzi

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