

Orbitrap Astral MS Literature List

Rethink what is possible



Peer Reviewed Articles

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, Jiaxi 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>

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>

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 & David Barford

Nat Struct Mol Biol. 2024 Apr 12

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

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>

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 Jun 28

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

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

Peer Reviewed Articles

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

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

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>

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 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

Nature Communications volume 15, Article number: 7016 (2024)

<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>

Plant Proteomics

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

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

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>

Plasma Proteomics

Evaluating the performance of the Astral mass analyzer

Peer Reviewed Articles

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.

<https://pubs.acs.org/doi/10.1021/acs.jproteome.4c003841>

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/S153594762400080X>

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

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 Discovery volume 10, Article number: 63 (2024)

Peer Reviewed Articles

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

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>

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 Kreutzmann, 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 Feb 5:e2300002

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

Ubiquitylation

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



Peer Reviewed Articles

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>

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 Ghaemmaghami

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

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

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, Tabiwan 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

Mol Cell Proteomics. 2024 Apr 3:100760

[https://www.mcponline.org/article/S1535-9476\(24\)00050-1/fulltext](https://www.mcponline.org/article/S1535-9476(24)00050-1/fulltext)

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, Tabiwan N. Arrey, Anna Pashkova, Santosh Renuse, Eduard Denisov, Johannes Petzoldt, Amelia C. Peterson, Florian

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

medRxiv 2024.08.01.2431136

<https://www.medrxiv.org/content/10.1101/2024.08.01.24311368v1>

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, QiuHong Jiang, Yu-Rong Mao, Shoupeng Wei, Ambrose Lo, and Dong-feng Huang

Research Square

<https://www.researchsquare.com/article/rs-3999543/v1>

Bacterial Proteomics

Structure and mechanism of Zorya anti-phage defense system

Haidai Hu, Thomas C.D. Hughes, Philipp F. Popp, Aritz Roa-Eguirara, 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

bioRxiv 2023.12.18.572097

<https://www.biorxiv.org/content/10.1101/2023.12.18.572097v1>

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, James L Keck

bioRxiv 2024.08.12.607615

<https://www.biorxiv.org/content/10.1101/2024.08.12.607615v1>

Breast Milk

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

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

bioRxiv 2024.05.22.595434

<https://www.biorxiv.org/content/10.1101/2024.05.22.595434v1.abstract>

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, Haizhen Wang

bioRxiv 2024.03.11.584401

<https://www.biorxiv.org/content/10.1101/2024.03.11.584401v1>

Cellular Stress Response

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

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

Preprints

Gustavo M. Silva

bioRxiv 2024.06.20.598218

<https://www.biorxiv.org/content/10.1101/2024.06.20.598218v1>

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, Yuezong 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

bioRxiv 2024.03.29.587381

<https://www.biorxiv.org/content/10.1101/2024.03.29.587381v1>

Data Analysis

Unifying the analysis of bottom-up proteomics data with CHIMERYS

Martin Frejno, Michelle T Berger, Johanna Tueshaus, Alexander Högbe, 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

bioRxiv 2024.05.27.596040

<https://www.biorxiv.org/content/10.1101/2024.05.27.596040v2>

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

bioRxiv 2024.06.03.597251

<https://www.biorxiv.org/content/10.1101/2024.06.03.597251v1>

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

bioRxiv 2024.06.01.596967

<https://www.biorxiv.org/content/10.1101/2024.06.01.596967v2>

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 MacLean, Alexey I. Nesvizhskii, and Mathias Wilhelm

bioRxiv 2024.06.01.596967

<https://www.biorxiv.org/content/10.1101/2024.06.01.596953v1>

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

bioRxiv 2024.05.13.593888

<https://www.biorxiv.org/content/10.1101/2024.05.13.593888v1>

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

Xiang Zheng, Andreas Mund, and Matthias Mann

bioRxiv 2024.05.22.595266

Preprints

<https://www.biorxiv.org/content/10.1101/2024.05.22.595266v1>

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

bioRxiv 2024.08.07.606985

<https://www.biorxiv.org/content/10.1101/2024.08.07.606985v1>

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

bioRxiv 2024.05.28.596134

<https://www.biorxiv.org/content/10.1101/2024.05.28.596134v1>

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

bioRxiv 2024.07.29.605591

<https://www.biorxiv.org/content/10.1101/2024.07.29.605591v1>

Gut Microbiota

Daytime-restricted feeding reshapes the gutmicrobiota to achieve intestinal radioprotectionthrough 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 Wang¹

Research Square

<https://www.researchsquare.com/article/rs-4817068/v1>

Inflammatory Bowel Disease

Paradigm shift in biomarker translation: a pipeline to generate clinical grade biomarker candidates from DIA-MS discovery

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

bioRxiv 2024.03.20.586018

<https://www.biorxiv.org/content/10.1101/2024.03.20.586018v1>

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-Remaileh, and Esther Sammler

bioRxiv 2024.05.17.594681

<https://www.biorxiv.org/content/10.1101/2024.05.17.594681v1>

Oxidative Response

Redox control of the deubiquitinating enzyme Ubp2 regulates translation during stress

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

bioRxiv 2024.04.30.591912

<https://www.biorxiv.org/content/10.1101/2024.04.30.591912v1>

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

medRxiv 2024.06.19.24308302

<https://www.medrxiv.org/>

[content/10.1101/2024.06.19.24308302v1](https://www.medrxiv.org/content/10.1101/2024.06.19.24308302v1)

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, Tabi Wang Arrey, Eugen Damoc, Simion Kreimer, Omid C. Farokhzad, Serafim Batzoglou, Asim Siddiqui, Jennifer E. Van Eyk, and Daniel Hornburg

bioRxiv 2023.08.28.555225

<https://www.biorxiv.org/content/10.1101/2023.08.28.555225v1>

Paradigm shift in biomarker translation: a pipeline to generate clinical grade biomarker candidates from DIA-MS discovery

Qin Fu, Manasa Vegesna, Niveda Sundararaman, Eugen Damoc, Tabi Wang N. Arrey, Anna Pashkova, Emebet Mengesha, Philip Debbas, Sandy Joung, Dalin Li, Susan Cheng, Jonathan Braun, Dermot P.B. McGovern, Christopher Murray, Yue Xuan, Jennifer E. Van Eyk

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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

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Preprints

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

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Single-Cell Proteomics

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

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

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

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Global analysis of protein turnover dynamics in single cells

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

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Single-Nucleus Proteomics

Filter-aided expansion proteomics

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Software Development

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

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Preprints

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Technology

A high dynamic range ion detector for the Astral™ analyzer

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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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