

Mass spectrometry

DIA Publications

Featuring Thermo Scientific Orbitrap Eclipse Tribrid Mass Spectrometers

Western diet induced remodelling of the tongue proteome

Mriga Dutt, Yaan-Kit Ng, Jeffrey Molendijk, Hamzeh Karimkhanloo, Luoping Liao, Ronnie Blazev, Magdalene K. Montgomery, Matthew J. Watt, Benjamin L. Parker

Proteomes 2021, 9(2), 22.

<https://www.mdpi.com/2227-7382/9/2/22/htm>

Altered glycosylation in the aging heart

Patricia Franzka, Lynn Krüger, Mona K. Schurig, Maja Olecka, Steve Hoffmann, Véronique Blanchard, Christian A. Hübner

Front Mol Biosci. 2021; 8: 673044.

<https://www.frontiersin.org/articles/10.3389/fmolb.2021.673044/full>

DIAMeter: matching peptides to data-independent acquisition mass spectrometry data

Yang Young Lu, Jeff Bilmes, Ricard A. Rodriguez-Mias, Judit Villén, William Stafford Noble

Bioinformatics, Volume 37, Issue Supplement_1, July 2021, Pages i434–i442.

https://academic.oup.com/bioinformatics/article/37/Supplement_1/i434/6319661?searchresul t=1

The autoimmune signature of hyperinflammatory multisystem inflammatory syndrome in children

Rebecca A. Porritt, Aleksandra Binek, Lisa Paschold, Magali Noval Rivas, Angela Mc Ardle, Lael M. Yonker, Galit Alter, Harsha Chandnani, Merrick Lopez, Alessio Fasano, Jennifer E. Van Eyk, Mascha Binder, Moshe Arditi

J Clin Invest. 2021.

<https://www.jci.org/articles/view/151520>

TDP-43 loss and ALS-risk SNPs drive mis-splicing and depletion of UNC13A

Anna-Leigh Brown, Oscar G. Wilkins, Matthew J. Keuss, Sarah E. Hill, Matteo Zanovello, Weaverly Colleen Lee, Alexander Bampton, Flora C. Y. Lee, Laura Masino, Yue A. Qi, Sam Bryce-Smith, Ariana Gatt, Martina Hallegger, Delphine Fagegaltier, Hemali Phatnani, NYGC ALS Consortium, Jia Newcombe, Emil K. Gustavsson, Sahba Seddighi, Joel F. Reyes, Steven L. Coon, Daniel Ramos, Giampietro Schiavo, Elizabeth M. C. Fisher, Towfique Raj, Maria Secrier, Tammarn Lashley, Jernej Ule, Emanuele Buratti, Jack Humphrey, Michael E. Ward, Pietro Fratta

Nature (2022).

<https://www.nature.com/articles/s41586-022-04436-3>

Streamlined single-cell proteomics by an integrated microfluidic chip and data-independent 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, Hsiung-Lin Tu

Nature Communications, Volume 13, Article number: 37 (2022).

<https://www.nature.com/articles/s41467-021-27778-4>

Sample size-comparable spectral library enhances data-independent acquisition-based proteome coverage of low-input cells

Asad Ali Siyal, Eric Sheng-Wen Chen, Hsin-Ju Chan, Reta Birhanu Kitata, Jhih-Ci Yang, Hsiung-Lin Tu, Yu-Ju Chen

Analytical Chemistry 2021, 93, 51, 17003-17011.

<https://pubs.acs.org/doi/10.1021/acs.analchem.1c03477>

Benchmarking of analysis strategies for data-independent acquisition proteomics using a large-scale dataset comprising inter-patient heterogeneity

Klemens Fröhlich, Eva Brombacher, Matthias Fahrner, Daniel Vogele, Lucas Kook, Niko Pinter, Peter Bronsert, Sylvia Timme-Bronsert, Alexander Schmidt, Katja Bärenfaller, Clemens Kreutz, Oliver Schilling

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S100A9-CXCL12 activation in BRCA1-mutant breast cancer promotes an immunosuppressive microenvironment associated with resistance to immunotherapy

Jianjie Li, Xiaodong Shu, Jun Xu, Sek Man Su, Un In Chan, Lihua Mo, Jianlin Liu, Xin Zhang, Ragini Adhav, Qiang Chen, Yuqing Wang, Tingting An, Xu Zhang, Xueying Lyu, Xiaoling Li, Josh Haipeng Lei, Kai Miao, Heng Sun, Fuqiang Xing, Aiping Zhang, Chuxia Deng, Xiaoling Xu

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Data-independent acquisition protease-multiplexing enables increased proteome sequence coverage across multiple fragmentation modes

Alicia L. Richards, Kuei-Ho Chen, Damien B. Willburn, Erica Stevenson, Benjamin J. Polacco, Brian C. Searle, Danielle L. Swaney

Journal of Proteome Research 2022, 21, 4, 1124-1136.

<https://pubs.acs.org/doi/10.1021/acs.jproteome.1c00960>

Global post-translational modification profiling of HIV-1-infected cells reveals mechanisms of host cellular pathway remodeling

Jeffrey R. Johnson, David C. Crosby, Judd F. Hultquist, Andrew P. Kurland, Prithy Adhikary, Donna Li, John Marlett, Justine Swann, Ruth Hüttenhain, Erik Verschueren, Tasha L. Johnson, Billy W. Newton, Michael Shales, Viviana A. Simon, Pedro Beltrao, Alan D. Frankel, Alexander Marson, Jeffery S. Cox, Oliver I. Fregoso, John A.T. Young, Nevan J. Krogan

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Differential trafficking and expression of PIR proteins in acute and chronic plasmodium infections

Maria Giorgalli, Deirdre A. Cunningham, Malgorzata Broncel, Aaron Sait, Thomas E. Harrison, Caroline Hosking, Audrey Vandomme, Sarah I. Amis, Ana Antonello, Lauren Sullivan, Faith Uwadiae, Laura Torella, Matthew K. Higgins, Jean Langhorne

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Extracellular nicotinamide phosphoribosyltransferase is a component of the senescence-associated secretory phenotype

Chisaka Kuehnemann, Kang-Quan Hu, Kayla Butera, Sandip K. Patel, Joanna Bons, Birgit Schilling, Cristina Aguayo-Mazzucato, Christopher D. Wiley

Front Endocrinol (Lausanne). 2022; 13: 935106.

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Venomomics of the central European Myrmicine ants *Myrmica rubra* and *Myrmica ruginodis*

Hurka Sabine, Karina Brinkrolf, Rabia Özbek, Frank Förster, André Billion, John Heep, Thomas Timm, Günter Lochnit, Andreas Vilcinskas, Tim Lüddecke

Toxins 14, No. 5: 358, 2022.

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Premature ovarian insufficiency in CLPB deficiency: transcriptomic, proteomic and phenotypic insights

Elena J. Tucker, Megan J. Baker, Daniella H. Hock, Julia T. Warren, Sylvie Jaillard, Katrina M. Bell, Rajini Sreenivasan, Shabnam Bakhshalizadeh, Chloe A. Hanna, Nikeisha J. Caruana, Saskia B. Wortmann, Shamima Rahman, Robert D. S. Pitceathly, Jean Donadieu, Aurelia Alimi, Vincent Launay, Paul Coppo, Sophie Christin-Maitre, Gorjana Robevska, Jocelyn van den Bergen, Brianna L Kline, Katie L Ayers, Phoebe N Stewart, David A. Stroud, Diana Stojanovski, Andrew H. Sinclair

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High sensitivity limited material proteomics empowered by data-independent acquisition on linear ion traps

Teeradon Phlairaharn, Samuel Grégoire, Lukas R. Woltereck, Valdemaras Petrosius, Benjamin Furtwängler, Brian C. Searle, Erwin M. Schoof

Journal of Proteome Research 2022.

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Environmental signals act as a driving force for metabolic and defense responses in the Antarctic plant *Colobanthus quitensis*

Bertini, Laura, Silvia Proietti, Benedetta Fongaro, Aleš Holfeld, Paola Picotti, Gaia Salvatore Falconieri, Elisabetta Bizzarri, Gloria Capaldi, Patrizia Polverino de Laureto, Carla Caruso

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Deleterious variants in CRLS1 lead to cardiolipin deficiency and cause an autosomal recessive multi-system mitochondrial disease

Richard G. Lee, Shanti Balasubramaniam, Maike Stentenbach, Tom Kralj, Tim McCubbin, Benjamin Padman, Janine Smith, Lisa G. Riley, Archana Priyadarshi, Liuyu Peng, Madison R. Nuske, Richard Webster, Ken Peacock, Philip Roberts, Zornitza Stark, Gabrielle Lemire, Yoko A Ito, Care4Rare Canada Consortium, Kym M. Boycott, Michael T. Geraghty, Jan Bert van Klinken, Sacha Ferdinandusse, Ying Zhou, Rebecca Walsh, Esteban Marcellin, David R. Thorburn, Tony Roscioli, Janice Fletcher, Oliver Rackham, Frédéric M. Vaz, Gavin E. Reid, Aleksandra Filipovska

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Chemical proteomics reveals protein tyrosination extends beyond the alpha-tubulins in human cells

Dmytro Makarov, Pavel Kielkowski

Chembiochem, 2022, Oct 11: e202200414.

<https://chemistry-europe.onlinelibrary.wiley.com/doi/10.1002/cbic.202200414>