

# Eugen Damoc

## List of Publications by Year in descending order

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31  
papers

3,854  
citations

218677

26  
h-index

414414

32  
g-index

32  
all docs

32  
docs citations

32  
times ranked

5630  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mass Spectrometry-based Proteomics Using Q Exactive, a High-performance Benchtop Quadrupole Orbitrap Mass Spectrometer. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.011015.	3.8	701
2	A Dual Pressure Linear Ion Trap Orbitrap Instrument with Very High Sequencing Speed. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2759-2769.	3.8	398
3	High-sensitivity Orbitrap mass analysis of intact macromolecular assemblies. <i>Nature Methods</i> , 2012, 9, 1084-1086.	19.0	347
4	Ultra High Resolution Linear Ion Trap Orbitrap Mass Spectrometer (Orbitrap Elite) Facilitates Top Down LC MS/MS and Versatile Peptide Fragmentation Modes. <i>Molecular and Cellular Proteomics</i> , 2012, 11, O111.013698.	3.8	303
5	The Q Exactive HF, a Benchtop Mass Spectrometer with a Pre-filter, High-performance Quadrupole and an Ultra-high-field Orbitrap Analyzer. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3698-3708.	3.8	285
6	High-resolution mass spectrometry of small molecules bound to membrane proteins. <i>Nature Methods</i> , 2016, 13, 333-336.	19.0	205
7	From Protein Complexes to Subunit Backbone Fragments: A Multi-stage Approach to Native Mass Spectrometry. <i>Analytical Chemistry</i> , 2013, 85, 11163-11173.	6.5	148
8	Analysis of Intact Monoclonal Antibody IgG1 by Electron Transfer Dissociation Orbitrap FTMS. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1758-1767.	3.8	137
9	Defining the Stoichiometry and Cargo Load of Viral and Bacterial Nanoparticles by Orbitrap Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 2014, 136, 7295-7299.	13.7	134
10	Exploring an Orbitrap Analyzer for the Characterization of Intact Antibodies by Native Mass Spectrometry. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 12992-12996.	13.8	130
11	Structural Characterization of the Human Eukaryotic Initiation Factor 3 Protein Complex by Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1135-1146.	3.8	116
12	Orbitrap mass spectrometry with resolving powers above 1,000,000. <i>International Journal of Mass Spectrometry</i> , 2012, 325-327, 80-85.	1.5	116
13	Native mass spectrometry combined with enzymatic dissection unravels glycoform heterogeneity of biopharmaceuticals. <i>Nature Communications</i> , 2018, 9, 1713.	12.8	87
14	Structural identification and quantification of protein phosphorylations after gel electrophoretic separation using Fourier transform ion cyclotron resonance mass spectrometry and laser ablation inductively coupled plasma mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2003, 228, 985-997.	1.5	80
15	Determination of Phosphorus-, Copper-, and Zinc-Containing Human Brain Proteins by LA-ICPMS and MALDI-FTICR-MS. <i>Analytical Chemistry</i> , 2005, 77, 5851-5860.	6.5	78
16	Enhanced Fourier transform for Orbitrap mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2014, 369, 16-22.	1.5	66
17	Discrimination of Leucine and Isoleucine in Peptides Sequencing with Orbitrap Fusion Mass Spectrometer. <i>Analytical Chemistry</i> , 2014, 86, 7017-7022.	6.5	61
18	Thin-Chip Microspray System for High-Performance Fourier-Transform Ion-Cyclotron Resonance Mass Spectrometry of Biopolymers. <i>Angewandte Chemie - International Edition</i> , 2003, 42, 53-58.	13.8	58

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19	Petroteomics via Orbitrap mass spectrometry with resolving power above 100,000 at $m/z$ 200. RSC Advances, 2018, 8, 6183-6191.	3.6	58
20	Top-down analysis of immunoglobulin G isotypes 1 and 2 with electron transfer dissociation on a high-field Orbitrap mass spectrometer. Journal of Proteomics, 2017, 159, 67-76.	2.4	47
21	High resolution proteome analysis of cryoglobulins using Fourier transform-ion cyclotron resonance mass spectrometry. Proteomics, 2003, 3, 1425-1433.	2.2	43
22	High resolution mass spectrometric alveolar proteomics: Identification of surfactant protein SP-A and SP-D modifications in proteinosis and cystic fibrosis patients. Proteomics, 2004, 4, 2300-2309.	2.2	43
23	Phase-Constrained Spectrum Deconvolution for Fourier Transform Mass Spectrometry. Analytical Chemistry, 2017, 89, 1202-1211.	6.5	38
24	"Affinity-proteomics": direct protein identification from biological material using mass spectrometric epitope mapping. Analytical and Bioanalytical Chemistry, 2004, 378, 1102-1111.	3.7	34
25	N-Glycan structures and N-glycosylation sites of mouse soluble intercellular adhesion molecule-1 revealed by MALDI-TOF and FTICR mass spectrometry. Glycobiology, 2006, 16, 1033-1044.	2.5	33
26	Exploring frontiers of orbitrap performance for long transients. International Journal of Mass Spectrometry, 2021, 466, 116607.	1.5	29
27	Identification of N-glycosylation sites of the murine neural cell adhesion molecule NCAM by MALDI-TOF and MALDI-FTICR mass spectrometry. Analytical and Bioanalytical Chemistry, 2004, 378, 1129-1135.	3.7	28
28	High resolution top-down experimental strategies on the Orbitrap platform. Journal of Proteomics, 2018, 175, 42-55.	2.4	17
29	Lung alveolar proteomics of bronchoalveolar lavage from a pulmonary alveolar proteinosis patient using high-resolution FTICR mass spectrometry. Analytical and Bioanalytical Chemistry, 2007, 389, 1075-1085.	3.7	14
30	Ein Chip-Mikrospraysystem für die hochauflösende Fourier-Transformations-Ionenzyklotronresonanz-Massenspektrometrie von Biopolymeren. Angewandte Chemie, 2003, 115, 55-60.	2.0	13
31	Reprint of "Enhanced Fourier transform for Orbitrap mass spectrometry". International Journal of Mass Spectrometry, 2015, 377, 338-344.	1.5	5