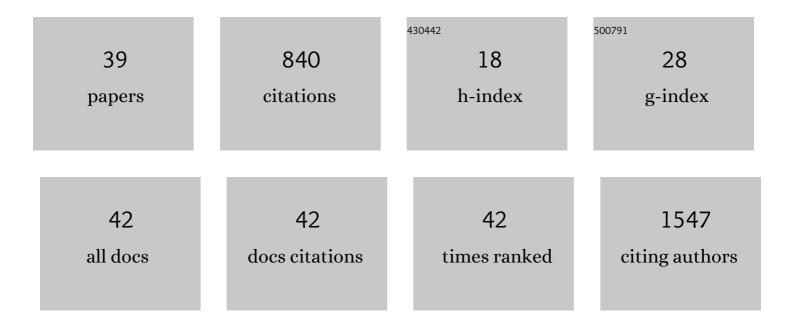
## **Oliver Ozohanics**

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Proteomic characterization of thymocyte-derived microvesicles and apoptotic bodies in BALB/c mice. Journal of Proteomics, 2011, 74, 2025-2033.	1.2	128
2	GlycoMiner: a new software tool to elucidate glycopeptide composition. Rapid Communications in Mass Spectrometry, 2008, 22, 3245-3254.	0.7	72
3	Stimulation of reactive oxygen species generation by disease-causing mutations of lipoamide dehydrogenase. Human Molecular Genetics, 2011, 20, 2984-2995.	1.4	47
4	High-performance liquid chromatography coupled to mass spectrometry methodology for analyzing site-specific N-glycosylation patterns. Journal of Chromatography A, 2012, 1259, 200-212.	1.8	45
5	Highly potent dUTPase inhibition by a bacterial repressor protein reveals a novel mechanism for gene expression control. Nucleic Acids Research, 2014, 42, 11912-11920.	6.5	36
6	Investigation of genetic variants of α-1 acid glycoprotein by ultra-performance liquid chromatography–mass spectrometry. Analytical and Bioanalytical Chemistry, 2009, 393, 991-998.	1.9	34
7	Structural Characterization of Arginine Fingers: Identification of an Arginine Finger for the Pyrophosphatase dUTPases. Journal of the American Chemical Society, 2016, 138, 15035-15045.	6.6	32
8	Distinguishing Core and Antenna Fucosylated Glycopeptides Based on Low-Energy Tandem Mass Spectra. Analytical Chemistry, 2018, 90, 12776-12782.	3.2	28
9	Fragmentation characteristics of glycopeptides. International Journal of Mass Spectrometry, 2013, 345-347, 71-79.	0.7	27
10	Digestion protocol for small protein amounts for nano-HPLC-MS(MS) analysis. Journal of Proteomics, 2011, 74, 942-947.	1.2	25
11	A multipronged approach unravels unprecedented protein–protein interactions in the human 2-oxoglutarate dehydrogenase multienzyme complex. Journal of Biological Chemistry, 2018, 293, 19213-19227.	1.6	25
12	Hydrogen-Deuterium Exchange Mass Spectrometry: A Novel Structural Biology Approach to Structure, Dynamics and Interactions of Proteins and Their Complexes. Life, 2020, 10, 286.	1.1	24
13	Quantitative Comparison of Tandem Mass Spectra Obtained on Various Instruments. Journal of the American Society for Mass Spectrometry, 2016, 27, 1357-1365.	1.2	23
14	Structure of the dihydrolipoamide succinyltransferase (E2) component of the human alpha-ketoglutarate dehydrogenase complex (hKGDHc) revealed by cryo-EM and cross-linking mass spectrometry: Implications for the overall hKGDHc structure. Biochimica Et Biophysica Acta - General Subjects, 2021, 1865, 129889.	1.1	23
15	Ferrocenyl pyrazolines: Preparation, structure, redox properties and DFT study on regioselective ring-closure. Journal of Organometallic Chemistry, 2009, 694, 4185-4195.	0.8	21
16	Structure and enzymatic mechanism of a moonlighting dUTPase. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2298-2308.	2.5	21
17	Sensitive method for glycosaminoglycan analysis of tissue sections. Journal of Chromatography A, 2018, 1544, 41-48.	1.8	21
18	Composite Aromatic Boxes for Enzymatic Transformations of Quaternary Ammonium Substrates. Angewandte Chemie - International Edition, 2014, 53, 13471-13476.	7.2	20

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19	Determination of energy metabolites in cancer cells by porous graphitic carbon liquid chromatography electrospray ionization mass spectrometry for the assessment of energy metabolism. Analytica Chimica Acta, 2014, 819, 108-115.	2.6	18
20	High sensitivity proteomics of prostate cancer tissue microarrays to discriminate between healthy and cancerous tissue. Journal of Proteomics, 2019, 197, 82-91.	1.2	18
21	Widespread alterations in the synaptic proteome of the adolescent cerebral cortex following prenatal immune activation in rats. Brain, Behavior, and Immunity, 2016, 56, 289-309.	2.0	17
22	Synthesis of alkyl α- and β-d-glucopyranoside-based chiral crown ethers and their application as enantioselective phase-transfer catalysts. Research on Chemical Intermediates, 2018, 44, 1627-1645.	1.3	16
23	Changes of protein glycosylation in the course of radiotherapy. Journal of Pharmaceutical and Biomedical Analysis, 2016, 118, 380-386.	1.4	15
24	Rapamycin (mTORC1 inhibitor) reduces the production of lactate and 2-hydroxyglutarate oncometabolites in IDH1 mutant fibrosarcoma cells. Journal of Experimental and Clinical Cancer Research, 2017, 36, 74.	3.5	15
25	Structural model of human dUTPase in complex with a novel proteinaceous inhibitor. Scientific Reports, 2018, 8, 4326.	1.6	15
26	Molecular Mechanism for the Thermo-Sensitive Phenotype of CHO-MT58 Cell Line Harbouring a Mutant CTP:Phosphocholine Cytidylyltransferase. PLoS ONE, 2015, 10, e0129632.	1.1	10
27	HPLC enrichment/isolation of proteins for post-translational modification studies from complex mixtures. Journal of Pharmaceutical and Biomedical Analysis, 2014, 98, 393-400.	1.4	9
28	Comparison of glycopeptide/glycoprotein enrichment techniques. Rapid Communications in Mass Spectrometry, 2012, 26, 215-217.	0.7	8
29	The Stl repressor from <i>Staphylococcus aureus</i> is an efficient inhibitor of the eukaryotic fruitfly <scp>dUTP</scp> ase. FEBS Open Bio, 2018, 8, 158-167.	1.0	7
30	HDX and Native Mass Spectrometry Reveals the Different Structural Basis for Interaction of the Staphylococcal Pathogenicity Island Repressor Stl with Dimeric and Trimeric Phage dUTPases. Biomolecules, 2019, 9, 488.	1.8	7
31	Structure–function analyses of the G729R 2-oxoadipate dehydrogenase genetic variant associated with a disorder of I-lysine metabolism. Journal of Biological Chemistry, 2020, 295, 8078-8095.	1.6	7
32	Proteomic identification of membrane-associated placental protein 4 (MP4) as perlecan and characterization of its placental expression in normal and pathologic pregnancies. PeerJ, 2019, 7, e6982.	0.9	6
33	Analysis of Complex Oligosaccharides Using Graphitized Carbon Liquid Chromatography/Mass Spectrometry. European Journal of Mass Spectrometry, 2008, 14, 419-422.	0.5	5
34	Potential steps in the evolution of a fused trimeric allâ€Î² dUTPase involve a catalytically competent fused dimeric intermediate. FEBS Journal, 2016, 283, 3268-3286.	2.2	5
35	Mass spectrometryâ€based analysis of macromolecular complexes of Staphylococcus aureus uracilâ€DNA glycosylase and its inhibitor reveals specific variations due to naturally occurring mutations. FEBS Open Bio, 2019, 9, 420-427.	1.0	5
36	Syntheses and complexing ability of α-d-gluco- and α-d-xylofuranoside-based lariat ethers. Journal of Inclusion Phenomena and Macrocyclic Chemistry, 2016, 85, 19-32.	0.9	3

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37	Simple correction improving longâ€ŧerm reproducibility of HPLC–MS. Journal of Mass Spectrometry, 2015, 50, 1130-1135.	0.7	1
38	Structure of the Dihydrolipoamide Succinyltransferase (E2) Component of the Human α-ketoglutarate dehydrogenase complex (hKGDHc) revealed by cryo-EM and Cross-linking mass spectrometry: Implications for the overall hKGDHc structure. Free Radical Biology and Medicine, 2020, 159, S29-S30.	1.3	1
39	Redox status of cysteines does not alter functional properties of human dUTPase but the Y54C mutation involved in monogenic diabetes decreases protein stability. Scientific Reports, 2021, 11, 19197.	1.6	Ο