

# Alexey L Chernobrovkin

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

20  
papers

252  
citations

10  
h-index

15  
g-index

25  
ext. papers

357  
ext. citations

7.1  
avg, IF

3.31  
L-index

#	Paper	IF	Citations
20	DeMix workflow for efficient identification of cofragmented peptides in high resolution data-dependent tandem mass spectrometry. <i>Molecular and Cellular Proteomics</i> , <b>2014</b> , 13, 3211-23	7.6	44
19	Functional Identification of Target by Expression Proteomics (FITeXP) reveals protein targets and highlights mechanisms of action of small molecule drugs. <i>Scientific Reports</i> , <b>2015</b> , 5, 11176	4.9	30
18	Cytotoxic and Proinflammatory Effects of Metal-Based Nanoparticles on THP-1 Monocytes Characterized by Combined Proteomics Approaches. <i>Journal of Proteome Research</i> , <b>2017</b> , 16, 689-697	5.6	28
17	Methionine to isothreonine conversion as a source of false discovery identifications of genetically encoded variants in proteogenomics. <i>Journal of Proteomics</i> , <b>2015</b> , 120, 169-78	3.9	19
16	Anticancer Effect of Deuterium Depleted Water - Redox Disbalance Leads to Oxidative Stress. <i>Molecular and Cellular Proteomics</i> , <b>2019</b> , 18, 2373-2387	7.6	18
15	Comparative Proteomics of Dying and Surviving Cancer Cells Improves the Identification of Drug Targets and Sheds Light on Cell Life/Death Decisions. <i>Molecular and Cellular Proteomics</i> , <b>2018</b> , 17, 1144-1155	7.6	16
14	ProTargetMiner as a proteome signature library of anticancer molecules for functional discovery. <i>Nature Communications</i> , <b>2019</b> , 10, 5715	17.4	16
13	System-wide identification and prioritization of enzyme substrates by thermal analysis. <i>Nature Communications</i> , <b>2021</b> , 12, 1296	17.4	16
12	DAF-16/FOXO requires Protein Phosphatase 4 to initiate transcription of stress resistance and longevity promoting genes. <i>Nature Communications</i> , <b>2020</b> , 11, 138	17.4	15
11	Expression proteomics study to determine metallodrug targets and optimal drug combinations. <i>Scientific Reports</i> , <b>2017</b> , 7, 1590	4.9	14
10	A Tale of Two Tails: Efficient Profiling of Protein Degradation by Specific Functional and Target Engagement Readouts. <i>SLAS Discovery</i> , <b>2021</b> , 26, 534-546	3.4	7
9	How well can morphology assess cell death modality? A proteomics study. <i>Cell Death Discovery</i> , <b>2016</b> , 2, 16068	6.9	6
8	CETSA MS Profiling for a Comparative Assessment of FDA-Approved Antivirals Repurposed for COVID-19 Therapy Identifies TRIP13 as a Remdesivir Off-Target. <i>SLAS Discovery</i> , <b>2021</b> , 26, 336-344	3.4	6
7	Proteomic Identification of Heat Shock-Induced Danger Signals in a Melanoma Cell Lysate Used in Dendritic Cell-Based Cancer Immunotherapy. <i>Journal of Immunology Research</i> , <b>2018</b> , 2018, 3982942	4.5	5
6	Detection of viral proteins in human cells lines by xeno-proteomics: elimination of the last valid excuse for not testing every cellular proteome dataset for viral proteins. <i>PLoS ONE</i> , <b>2014</b> , 9, e91433	3.7	3
5	In-depth characterization of Staurosporine induced proteome thermal stability changes		2
4	CETSA MS profiling for a comparative assessment of FDA approved antivirals repurposed for COVID-19 therapy identifies Trip13 as a Remdesivir off-target		1

3	Histone Purification Combined with High-Resolution Mass Spectrometry to Examine Histone Post-Translational Modifications and Histone Variants in <i>Caenorhabditis elegans</i> . <i>Current Protocols in Protein Science</i> , <b>2020</b> , 102, e114	3.1	1
2	Changes in the plasma microvesicle proteome during the ovarian hyperstimulation phase of assisted reproductive technology. <i>Scientific Reports</i> , <b>2020</b> , 10, 13645	4.9	1
1	A mass spectrometry-based non-radioactive differential radial capillary action of ligand assay (DRaCALA) to assess ligand binding to proteins.. <i>Journal of Mass Spectrometry</i> , <b>2022</b> , 57, e4822	2.2	0