## Alexey L Chernobrovkin

## List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/1297152/alexey-l-chernobrovkin-publications-by-year.pdf

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

20	252	10	15
papers	citations	h-index	g-index
25	357 ext. citations	7.1	3.31
ext. papers		avg, IF	L-index

#	Paper	IF	Citations
20	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	O
19	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
18	A Tale of Two Tails: Efficient Profiling of Protein Degraders by Specific Functional and Target Engagement Readouts. <i>SLAS Discovery</i> , <b>2021</b> , 26, 534-546	3.4	7
17	System-wide identification and prioritization of enzyme substrates by thermal analysis. <i>Nature Communications</i> , <b>2021</b> , 12, 1296	17.4	16
16	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
15	Histone Purification Combined with High-Resolution Mass Spectrometry to Examine Histone Post-Translational Modifications and Histone Variants in Caenorhabditis elegans. <i>Current Protocols in Protein Science</i> , <b>2020</b> , 102, e114	3.1	1
14	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
13	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
12	ProTargetMiner as a proteome signature library of anticancer molecules for functional discovery. <i>Nature Communications</i> , <b>2019</b> , 10, 5715	17.4	16
11	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	-7155	16
10	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
9	Expression proteomics study to determine metallodrug targets and optimal drug combinations. <i>Scientific Reports</i> , <b>2017</b> , 7, 1590	4.9	14
8	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
7	How well can morphology assess cell death modality? A proteomics study. <i>Cell Death Discovery</i> , <b>2016</b> , 2, 16068	6.9	6
6	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
5	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
4	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

## LIST OF PUBLICATIONS

<i>)</i>	excuse for not testing every cellular proteome dataset for viral proteins. <i>PLoS ONE</i> , <b>2014</b> , 9, e91433	3.7	<i></i>	
2	In-depth characterization of Staurosporine induced proteome thermal stability changes		2	
	CETSAIL MS profiling for a comparative assessment of EDA approved antivirals repurposed for			

Detection of viral proteins in human cells lines by xeno-proteomics: elimination of the last valid

COVID-19 therapy identifies Trip13 as a Remdesivir off-target