

Vladislav A Petyuk

List of Publications by Citations

Source: <https://exaly.com/author-pdf/9132768/vladislav-a-petyuk-publications-by-citations.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.

87
papers

5,343
citations

36
h-index

72
g-index

93
ext. papers

7,203
ext. citations

11.2
avg, IF

4.94
L-index

#	Paper	IF	Citations
87	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016 , 166, 755-765	56.2	544
86	Comparative analysis of proteome and transcriptome variation in mouse. <i>PLoS Genetics</i> , 2011 , 7, e1001303		417
85	DAnTE: a statistical tool for quantitative analysis of -omics data. <i>Bioinformatics</i> , 2008 , 24, 1556-8	7.2	333
84	Ischemia in tumors induces early and sustained phosphorylation changes in stress kinase pathways but does not affect global protein levels. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 1690-704	7.6	239
83	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. <i>Cell</i> , 2019 , 177, 1035-1049.e19	56.2	237
82	Large-scale proteomic analysis of Alzheimer's disease brain and cerebrospinal fluid reveals early changes in energy metabolism associated with microglia and astrocyte activation. <i>Nature Medicine</i> , 2020 , 26, 769-780	50.5	226
81	A transcriptomic atlas of aged human microglia. <i>Nature Communications</i> , 2018 , 9, 539	17.4	223
80	Nanodroplet processing platform for deep and quantitative proteome profiling of 10-100 mammalian cells. <i>Nature Communications</i> , 2018 , 9, 882	17.4	213
79	Reproducible workflow for multiplexed deep-scale proteome and phosphoproteome analysis of tumor tissues by liquid chromatography-mass spectrometry. <i>Nature Protocols</i> , 2018 , 13, 1632-1661	18.8	176
78	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019 , 179, 964-983.e31	56.2	173
77	Liquid chromatography-mass spectrometry-based quantitative proteomics. <i>Journal of Biological Chemistry</i> , 2011 , 286, 25443-9	5.4	147
76	Robust algorithm for alignment of liquid chromatography-mass spectrometry analyses in an accurate mass and time tag data analysis pipeline. <i>Analytical Chemistry</i> , 2006 , 78, 7397-409	7.8	147
75	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020 , 180, 729-748.e26	56.2	122
74	Characterization of the mouse brain proteome using global proteomic analysis complemented with cysteinyl-peptide enrichment. <i>Journal of Proteome Research</i> , 2006 , 5, 361-9	5.6	122
73	Sources of technical variability in quantitative LC-MS proteomics: human brain tissue sample analysis. <i>Journal of Proteome Research</i> , 2013 , 12, 2128-37	5.6	118
72	Label-free quantitative LC-MS proteomics of Alzheimer's disease and normally aged human brains. <i>Journal of Proteome Research</i> , 2012 , 11, 3053-67	5.6	104
71	Prediction of cognition in Parkinson's disease with a clinical-genetic score: a longitudinal analysis of nine cohorts. <i>Lancet Neurology</i> , <i>The</i> , 2017 , 16, 620-629	24.1	98

70	Informed-Proteomics: open-source software package for top-down proteomics. <i>Nature Methods</i> , 2017 , 14, 909-914	21.6	83
69	Comprehensive identification of glycated peptides and their glycation motifs in plasma and erythrocytes of control and diabetic subjects. <i>Journal of Proteome Research</i> , 2011 , 10, 3076-88	5.6	81
68	Mitochondrial dysfunction, oxidative stress, and apoptosis revealed by proteomic and transcriptomic analyses of the striata in two mouse models of Parkinson's disease. <i>Journal of Proteome Research</i> , 2008 , 7, 666-77	5.6	79
67	Conservation of protein abundance patterns reveals the regulatory architecture of the EGFR-MAPK pathway. <i>Science Signaling</i> , 2016 , 9, rs6	8.8	78
66	Reduced insulin/insulin-like growth factor-1 signaling and dietary restriction inhibit translation but preserve muscle mass in <i>Caenorhabditis elegans</i> . <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 3624-39	7.6	63
65	The proteome and phosphoproteome of <i>Neurospora crassa</i> in response to cellulose, sucrose and carbon starvation. <i>Fungal Genetics and Biology</i> , 2014 , 72, 21-33	3.9	60
64	Neuropathological correlates and genetic architecture of microglial activation in elderly human brain. <i>Nature Communications</i> , 2019 , 10, 409	17.4	59
63	Targeted brain proteomics uncover multiple pathways to Alzheimer's dementia. <i>Annals of Neurology</i> , 2018 , 84, 78-88	9.4	56
62	The NINDS Parkinson's disease biomarkers program. <i>Movement Disorders</i> , 2016 , 31, 915-23	7	56
61	Region-specific protein abundance changes in the brain of MPTP-induced Parkinson's disease mouse model. <i>Journal of Proteome Research</i> , 2010 , 9, 1496-509	5.6	55
60	Spatial mapping of protein abundances in the mouse brain by voxelation integrated with high-throughput liquid chromatography-mass spectrometry. <i>Genome Research</i> , 2007 , 17, 328-36	9.7	53
59	Large-scale multiplexed quantitative discovery proteomics enabled by the use of an (18)O-labeled "universal" reference sample. <i>Journal of Proteome Research</i> , 2009 , 8, 290-9	5.6	52
58	Molecular Transducers of Physical Activity Consortium (MoTrPAC): Mapping the Dynamic Responses to Exercise. <i>Cell</i> , 2020 , 181, 1464-1474	56.2	51
57	Metabolic reprogramming during purine stress in the protozoan pathogen <i>Leishmania donovani</i> . <i>PLoS Pathogens</i> , 2014 , 10, e1003938	7.6	50
56	Distinguishing d- and l-aspartic and isoaspartic acids in amyloid β peptides with ultrahigh resolution ion mobility spectrometry. <i>Chemical Communications</i> , 2017 , 53, 7913-7916	5.8	45
55	LC-MS proteomics analysis of the insulin/IGF-1-deficient <i>Caenorhabditis elegans</i> daf-2(e1370) mutant reveals extensive restructuring of intermediary metabolism. <i>Journal of Proteome Research</i> , 2014 , 13, 1938-56	5.6	44
54	DtaRefinery, a software tool for elimination of systematic errors from parent ion mass measurements in tandem mass spectra data sets. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 486-96	7.6	44
53	Characterization of the mouse pancreatic islet proteome and comparative analysis with other mouse tissues. <i>Journal of Proteome Research</i> , 2008 , 7, 3114-26	5.6	41

52	Position-dependent termination and widespread obligatory frameshifting in Euplotes translation. <i>Nature Structural and Molecular Biology</i> , 2017 , 24, 61-68	17.6	38
51	Reproducibility of Differential Proteomic Technologies in CPTAC Fractionated Xenografts. <i>Journal of Proteome Research</i> , 2016 , 15, 691-706	5.6	35
50	Changes of Protein Turnover in Aging. <i>Molecular and Cellular Proteomics</i> , 2017 , 16, 1621-1633	7.6	33
49	Elimination of systematic mass measurement errors in liquid chromatography-mass spectrometry based proteomics using regression models and a priori partial knowledge of the sample content. <i>Analytical Chemistry</i> , 2008 , 80, 693-706	7.8	32
48	Mass measurement accuracy in analyses of highly complex mixtures based upon multidimensional recalibration. <i>Analytical Chemistry</i> , 2006 , 78, 8374-85	7.8	31
47	Mapping protein abundance patterns in the brain using voxelation combined with liquid chromatography and mass spectrometry. <i>Methods</i> , 2010 , 50, 77-84	4.6	28
46	Brain expression of the vascular endothelial growth factor gene family in cognitive aging and alzheimer's disease. <i>Molecular Psychiatry</i> , 2021 , 26, 888-896	15.1	26
45	Comprehensive quantitative analysis of ovarian and breast cancer tumor peptidomes. <i>Journal of Proteome Research</i> , 2015 , 14, 422-33	5.6	24
44	Residual tissue repositories as a resource for population-based cancer proteomic studies. <i>Clinical Proteomics</i> , 2018 , 15, 26	5	24
43	Proteogenomic Characterization of Ovarian HGSC Implicates Mitotic Kinases, Replication Stress in Observed Chromosomal Instability. <i>Cell Reports Medicine</i> , 2020 , 1,	18	24
42	A genome-scale map of expression for a mouse brain section obtained using voxelation. <i>Physiological Genomics</i> , 2007 , 30, 313-21	3.6	23
41	Separation of β Amyloid Tryptic Peptide Species with Isomerized and Racemized l-Aspartic Residues with Ion Mobility in Structures for Lossless Ion Manipulations. <i>Analytical Chemistry</i> , 2019 , 91, 4374-4380	7.8	21
40	Antibody-independent targeted quantification of TMPRSS2-ERG fusion protein products in prostate cancer. <i>Molecular Oncology</i> , 2014 , 8, 1169-80	7.9	20
39	The human brainome: network analysis identifies HSPA2 as a novel Alzheimer's disease target. <i>Brain</i> , 2018 , 141, 2721-2739	11.2	19
38	Hybridization of antisense oligonucleotides with the 3' part of tRNA(Phe). <i>FEBS Letters</i> , 1999 , 444, 217-218	3.8	18
37	Association of Cortical β Amyloid Protein in the Absence of Insoluble Deposits With Alzheimer Disease. <i>JAMA Neurology</i> , 2019 , 76, 818-826	17.2	17
36	Comparative phosphoproteomics reveals components of host cell invasion and post-transcriptional regulation during Francisella infection. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 3297-309	7.6	17
35	Integrated post-experiment monoisotopic mass refinement: an integrated approach to accurately assign monoisotopic precursor masses to tandem mass spectrometric data. <i>Analytical Chemistry</i> , 2010 , 82, 8510-8	7.8	16

34	Identification of Hip BMD Loss and Fracture Risk Markers Through Population-Based Serum Proteomics. <i>Journal of Bone and Mineral Research</i> , 2017 , 32, 1559-1567	6.3	13
33	Phosphoproteome Analysis Reveals Estrogen-ER Pathway as a Modulator of mTOR Activity Via DEPTOR. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 1607-1618	7.6	13
32	High-throughput serum proteomics for the identification of protein biomarkers of mortality in older men. <i>Aging Cell</i> , 2018 , 17, e12717	9.9	13
31	STEPS: a grid search methodology for optimized peptide identification filtering of MS/MS database search results. <i>Proteomics</i> , 2013 , 13, 766-70	4.8	12
30	Functional mapping of Cre recombinase by pentapeptide insertional mutagenesis. <i>Journal of Biological Chemistry</i> , 2004 , 279, 37040-8	5.4	12
29	An Integrative Analysis of Tumor Proteomic and Phosphoproteomic Profiles to Examine the Relationships Between Kinase Activity and Phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, S26-S36	7.6	9
28	BIN1 protein isoforms are differentially expressed in astrocytes, neurons, and microglia: neuronal and astrocyte BIN1 are implicated in tau pathology. <i>Molecular Neurodegeneration</i> , 2020 , 15, 44	19	9
27	Enhancing Top-Down Proteomics of Brain Tissue with FAIMS. <i>Journal of Proteome Research</i> , 2021 , 20, 2780-2795	5.6	8
26	Block Design with Common Reference Samples Enables Robust Large-Scale Label-Free Quantitative Proteome Profiling. <i>Journal of Proteome Research</i> , 2020 , 19, 2863-2872	5.6	7
25	APOE ϵ -specific associations of VEGF gene family expression with cognitive aging and Alzheimer's disease. <i>Neurobiology of Aging</i> , 2020 , 87, 18-25	5.6	7
24	Cognition may link cortical IGFBP5 levels with motor function in older adults. <i>PLoS ONE</i> , 2019 , 14, e0220968	9.68	6
23	Dual spatial maps of transcript and protein abundance in the mouse brain. <i>Expert Review of Proteomics</i> , 2009 , 6, 243-9	4.2	6
22	Synaptic proteins associated with cognitive performance and neuropathology in older humans revealed by multiplexed fractionated proteomics. <i>Neurobiology of Aging</i> , 2021 , 105, 99-114	5.6	6
21	Detection of Head and Neck Cancer Based on Longitudinal Changes in Serum Protein Abundance. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020 , 29, 1665-1672	4	5
20	Hybridization of antisense oligonucleotides with alpha-sarcin loop region of Escherichia coli 23S rRNA. <i>Nucleosides, Nucleotides and Nucleic Acids</i> , 2004 , 23, 895-906	1.4	5
19	Brain IGFBP-5 modifies the relation of depressive symptoms to decline in cognition in older persons. <i>Journal of Affective Disorders</i> , 2019 , 250, 313-318	6.6	4
18	Microstructural changes in the brain mediate the association of AK4, IGFBP5, HSPB2, and ITPK1 with cognitive decline. <i>Neurobiology of Aging</i> , 2019 , 84, 17-25	5.6	4
17	Preconditioning in the Rhesus Macaque Induces a Proteomic Signature Following Cerebral Ischemia that Is Associated with Neuroprotection. <i>Translational Stroke Research</i> , 2019 , 10, 440-448	7.8	4

16	Exploratory study reveals far reaching systemic and cellular effects of verapamil treatment in subjects with type 1 diabetes.. <i>Nature Communications</i> , 2022 , 13, 1159	17.4	4
15	CRNT4SBML: a Python package for the detection of bistability in biochemical reaction networks. <i>Bioinformatics</i> , 2020 , 36, 3922-3924	7.2	3
14	Reproducibility and Transparency by Design. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, S202-S204	7.6	3
13	Multi-omic data integration links deleted in breast cancer 1 (DBC1) degradation to chromatin remodeling in inflammatory response. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 2136-47	7.6	3
12	A numerical approach for detecting switch-like bistability in mass action chemical reaction networks with conservation laws.. <i>BMC Bioinformatics</i> , 2022 , 23, 1	3.6	3
11	Inferring protein expression changes from mRNA in Alzheimer's dementia using deep neural networks.. <i>Nature Communications</i> , 2022 , 13, 655	17.4	3
10	Proteomic assessment of serum biomarkers of longevity in older men. <i>Aging Cell</i> , 2020 , 19, e13253	9.9	3
9	Proteomic identification of select protein variants of the SNARE interactome associated with cognitive reserve in a large community sample. <i>Acta Neuropathologica</i> , 2021 , 141, 755-770	14.3	3
8	Genetic risk for Alzheimer's dementia predicts motor deficits through multi-omic systems in older adults. <i>Translational Psychiatry</i> , 2019 , 9, 241	8.6	2
7	Multiplexed fractionated proteomics reveals synaptic factors associated with cognitive resilience in Alzheimer's Disease		2
6	Detecting differential protein abundance by combining peptide level P-values. <i>Molecular Omics</i> , 2020 , 16, 554-562	4.4	2
5	Proteomic Profiling of the Substantia Nigra to Identify Determinants of Lewy Body Pathology and Dopaminergic Neuronal Loss. <i>Journal of Proteome Research</i> , 2021 , 20, 2266-2282	5.6	2
4	Cortical Proteins and Individual Differences in Cognitive Resilience in Older Adults.. <i>Neurology</i> , 2022 ,	6.5	2
3	The genetics of circulating BDNF: towards understanding the role of BDNF in brain structure and function in middle and old ages. <i>Brain Communications</i> , 2020 , 2, fcaa176	4.5	1
2	BIN1 protein isoforms are differentially expressed in astrocytes, neurons, and microglia: neuronal and astrocyte BIN1 implicated in Tau pathology		1
1	Mitochondrial respiratory chain protein co-regulation in the human brain. <i>Heliyon</i> , 2022 , 8, e09353	3.6	0