

Vladislav A Petyuk

List of Publications by Year in Descending Order

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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.

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	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
86	Inferring protein expression changes from mRNA in Alzheimer's dementia using deep neural networks.. <i>Nature Communications</i> , 2022 , 13, 655	17.4	3
85	Cortical Proteins and Individual Differences in Cognitive Resilience in Older Adults.. <i>Neurology</i> , 2022 ,	6.5	2
84	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
83	Mitochondrial respiratory chain protein co-regulation in the human brain. <i>Heliyon</i> , 2022 , 8, e09353	3.6	0
82	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
81	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
80	Enhancing Top-Down Proteomics of Brain Tissue with FAIMS. <i>Journal of Proteome Research</i> , 2021 , 20, 2780-2795	5.6	8
79	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
78	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
77	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
76	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
75	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
74	Molecular Transducers of Physical Activity Consortium (MoTrPAC): Mapping the Dynamic Responses to Exercise. <i>Cell</i> , 2020 , 181, 1464-1474	56.2	51
73	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020 , 180, 729-748.e26	56.2	122
72	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
71	CRNT4SBML: a Python package for the detection of bistability in biochemical reaction networks. <i>Bioinformatics</i> , 2020 , 36, 3922-3924	7.2	3

70	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
69	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
68	Proteomic assessment of serum biomarkers of longevity in older men. <i>Aging Cell</i> , 2020 , 19, e13253	9.9	3
67	Detecting differential protein abundance by combining peptide level P-values. <i>Molecular Omics</i> , 2020 , 16, 554-562	4.4	2
66	Proteogenomic Characterization of Ovarian HGSC Implicates Mitotic Kinases, Replication Stress in Observed Chromosomal Instability. <i>Cell Reports Medicine</i> , 2020 , 1,	18	24
65	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
64	Cognition may link cortical IGFBP5 levels with motor function in older adults. <i>PLoS ONE</i> , 2019 , 14, e0220968	9.68	6
63	Neuropathological correlates and genetic architecture of microglial activation in elderly human brain. <i>Nature Communications</i> , 2019 , 10, 409	17.4	59
62	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
61	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
60	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. <i>Cell</i> , 2019 , 177, 1035-1049.e19	56.2	237
59	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
58	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
57	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
56	Reproducibility and Transparency by Design. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, S202-S204	7.6	3
55	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019 , 179, 964-983.e31	58.1	173
54	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
53	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

52	Nanodroplet processing platform for deep and quantitative proteome profiling of 10-100 mammalian cells. <i>Nature Communications</i> , 2018 , 9, 882	17.4	213
51	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
50	A transcriptomic atlas of aged human microglia. <i>Nature Communications</i> , 2018 , 9, 539	17.4	223
49	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
48	The human brainome: network analysis identifies HSPA2 as a novel Alzheimer's disease target. <i>Brain</i> , 2018 , 141, 2721-2739	11.2	19
47	Residual tissue repositories as a resource for population-based cancer proteomic studies. <i>Clinical Proteomics</i> , 2018 , 15, 26	5	24
46	Targeted brain proteomics uncover multiple pathways to Alzheimer's dementia. <i>Annals of Neurology</i> , 2018 , 84, 78-88	9.4	56
45	Prediction of cognition in Parkinson's disease with a clinical-genetic score: a longitudinal analysis of nine cohorts. <i>Lancet Neurology</i> , 2017 , 16, 620-629	24.1	98
44	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
43	Informed-Proteomics: open-source software package for top-down proteomics. <i>Nature Methods</i> , 2017 , 14, 909-914	21.6	83
42	Changes of Protein Turnover in Aging. <i>Molecular and Cellular Proteomics</i> , 2017 , 16, 1621-1633	7.6	33
41	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
40	Position-dependent termination and widespread obligatory frameshifting in Euplotes translation. <i>Nature Structural and Molecular Biology</i> , 2017 , 24, 61-68	17.6	38
39	Conservation of protein abundance patterns reveals the regulatory architecture of the EGFR-MAPK pathway. <i>Science Signaling</i> , 2016 , 9, rs6	8.8	78
38	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016 , 166, 755-765	56.2	544
37	Reproducibility of Differential Proteomic Technologies in CPTAC Fractionated Xenografts. <i>Journal of Proteome Research</i> , 2016 , 15, 691-706	5.6	35
36	The NINDS Parkinson's disease biomarkers program. <i>Movement Disorders</i> , 2016 , 31, 915-23	7	56
35	Comprehensive quantitative analysis of ovarian and breast cancer tumor peptidomes. <i>Journal of Proteome Research</i> , 2015 , 14, 422-33	5.6	24

34	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
33	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
32	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
31	Metabolic reprogramming during purine stress in the protozoan pathogen <i>Leishmania donovani</i> . <i>PLoS Pathogens</i> , 2014 , 10, e1003938	7.6	50
30	Antibody-independent targeted quantification of TMPRSS2-ERG fusion protein products in prostate cancer. <i>Molecular Oncology</i> , 2014 , 8, 1169-80	7.9	20
29	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
28	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
27	Comparative phosphoproteomics reveals components of host cell invasion and post-transcriptional regulation during <i>Francisella</i> infection. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 3297-309	7.6	17
26	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
25	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
24	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
23	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
22	Liquid chromatography-mass spectrometry-based quantitative proteomics. <i>Journal of Biological Chemistry</i> , 2011 , 286, 25443-9	5.4	147
21	Comparative analysis of proteome and transcriptome variation in mouse. <i>PLoS Genetics</i> , 2011 , 7, e1001383		417
20	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
19	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
18	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
17	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

16	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
15	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
14	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
13	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
12	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
11	DANTE: a statistical tool for quantitative analysis of -omics data. <i>Bioinformatics</i> , 2008 , 24, 1556-8	7.2	333
10	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
9	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
8	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
7	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
6	Mass measurement accuracy in analyses of highly complex mixtures based upon multidimensional recalibration. <i>Analytical Chemistry</i> , 2006 , 78, 8374-85	7.8	31
5	Functional mapping of Cre recombinase by pentapeptide insertional mutagenesis. <i>Journal of Biological Chemistry</i> , 2004 , 279, 37040-8	5.4	12
4	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
3	Hybridization of antisense oligonucleotides with the 3' part of tRNA(Phe). <i>FEBS Letters</i> , 1999 , 444, 217-218	1.8	18
2	Multiplexed fractionated proteomics reveals synaptic factors associated with cognitive resilience in Alzheimer's Disease		2
1	BIN1 protein isoforms are differentially expressed in astrocytes, neurons, and microglia: neuronal and astrocyte BIN1 implicated in Tau pathology		1