

Xusheng Wang

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

2,463
citations

331670

21
h-index

414414

32
g-index

35
all docs

35
docs citations

35
times ranked

4478
citing authors

#	ARTICLE	IF	CITATIONS
1	Deep Multilayer Brain Proteomics Identifies Molecular Networks in Alzheimer's Disease Progression. <i>Neuron</i> , 2020, 105, 975-991.e7.	8.1	287
2	U1 small nuclear ribonucleoprotein complex and RNA splicing alterations in Alzheimer's disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 16562-16567.	7.1	268
3	Integrative Proteomics and Phosphoproteomics Profiling Reveals Dynamic Signaling Networks and Bioenergetics Pathways Underlying T Cell Activation. <i>Immunity</i> , 2017, 46, 488-503.	14.3	265
4	Joint mouse-human phenome-wide association to test gene function and disease risk. <i>Nature Communications</i> , 2016, 7, 10464.	12.8	190
5	Partial loss of psychiatric risk gene Mir137 in mice causes repetitive behavior and impairs sociability and learning via increased Pde10a. <i>Nature Neuroscience</i> , 2018, 21, 1689-1703.	14.8	127
6	JUMP: A Tag-based Database Search Tool for Peptide Identification with High Sensitivity and Accuracy. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3663-3673.	3.8	117
7	Identification of Therapeutic Targets in Rhabdomyosarcoma through Integrated Genomic, Epigenomic, and Proteomic Analyses. <i>Cancer Cell</i> , 2018, 34, 411-426.e19.	16.8	106
8	Integrated analysis of ultra-deep proteomes in cortex, cerebrospinal fluid and serum reveals a mitochondrial signature in Alzheimer's disease. <i>Molecular Neurodegeneration</i> , 2020, 15, 43.	10.8	104
9	Proteomic landscape of Alzheimer's Disease: novel insights into pathogenesis and biomarker discovery. <i>Molecular Neurodegeneration</i> , 2021, 16, 55.	10.8	95
10	Deep undepleted human serum proteome profiling toward biomarker discovery for Alzheimer's disease. <i>Clinical Proteomics</i> , 2019, 16, 16.	2.1	93
11	Extensive Peptide Fractionation and ^{15}N Ion-Based Interference Detection Method for Enabling Accurate Quantification by Isobaric Labeling and Mass Spectrometry. <i>Analytical Chemistry</i> , 2017, 89, 2956-2963.	6.5	91
12	Combinatorial expression of GPCR isoforms affects signalling and drug responses. <i>Nature</i> , 2020, 587, 650-656.	27.8	87
13	Blocking an N-terminal acetylation-dependent protein interaction inhibits an E3 ligase. <i>Nature Chemical Biology</i> , 2017, 13, 850-857.	8.0	80
14	Functionally Enigmatic Genes: A Case Study of the Brain Ignorome. <i>PLoS ONE</i> , 2014, 9, e88889.	2.5	77
15	JUMPg: An Integrative Proteogenomics Pipeline Identifying Unannotated Proteins in Human Brain and Cancer Cells. <i>Journal of Proteome Research</i> , 2016, 15, 2309-2320.	3.7	76
16	Systematic Optimization of Long Gradient Chromatography Mass Spectrometry for Deep Analysis of Brain Proteome. <i>Journal of Proteome Research</i> , 2015, 14, 829-838.	3.7	71
17	Detection, Validation, and Downstream Analysis of Allelic Variation in Gene Expression. <i>Genetics</i> , 2010, 184, 119-128.	2.9	60
18	Identification of a Functional Non-coding Variant in the GABAA Receptor $\alpha 2$ Subunit of the C57BL/6J Mouse Reference Genome: Major Implications for Neuroscience Research. <i>Frontiers in Genetics</i> , 2019, 10, 188.	2.3	56

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19	Refined phosphopeptide enrichment by phosphate additive and the analysis of human brain phosphoproteome. <i>Proteomics</i> , 2015, 15, 500-507.	2.2	42
20	Deep multiomics profiling of brain tumors identifies signaling networks downstream of cancer driver genes. <i>Nature Communications</i> , 2019, 10, 3718.	12.8	42
21	Quantitative Protein Analysis by Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2015, 1278, 281-305.	0.9	40
22	Integrating transcriptome and metabolome reveals molecular networks involved in genetic and environmental variation in tobacco. <i>DNA Research</i> , 2020, 27, .	3.4	21
23	Insights into the changes in the proteome of Alzheimer disease elucidated by a meta-analysis. <i>Scientific Data</i> , 2021, 8, 312.	5.3	12
24	Asymmetrical Macromolecular Complex Formation of Lysophosphatidic Acid Receptor 2 (LPA2) Mediates Gradient Sensing in Fibroblasts. <i>Journal of Biological Chemistry</i> , 2014, 289, 35757-35769.	3.4	11
25	Deep Proteome Profiling by Isobaric Labeling, Extensive Liquid Chromatography, Mass Spectrometry, and Software-assisted Quantification. <i>Journal of Visualized Experiments</i> , 2017, , .	0.3	10
26	JUMPm: A Tool for Large-Scale Identification of Metabolites in Untargeted Metabolomics. <i>Metabolites</i> , 2020, 10, 190.	2.9	8
27	Altered cGMP Dynamics at the Plasma Membrane Contribute to Diarrhea in Ulcerative Colitis. <i>American Journal of Pathology</i> , 2015, 185, 2790-2804.	3.8	7
28	Deep multilayer brain proteomics identifies molecular networks and Netrin-1 accumulation in Alzheimer's disease progression. <i>Alzheimer's and Dementia</i> , 2020, 16, e037231.	0.8	3
29	Genetic architecture of protein expression and its regulation in the mouse brain. <i>BMC Genomics</i> , 2021, 22, 875.	2.8	3
30	SMAP is a pipeline for sample matching in proteogenomics. <i>Nature Communications</i> , 2022, 13, 744.	12.8	3