

Liang Chen

List of Publications by Year in descending order

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33
papers

2,487
citations

331670

21
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414414

32
g-index

33
all docs

33
docs citations

33
times ranked

5057
citing authors

#	ARTICLE	IF	CITATIONS
1	Black Phosphorus Gas Sensors. ACS Nano, 2015, 9, 5618-5624.	14.6	599
2	Chemical Vapor Deposition Growth of Monolayer WSe ₂ with Tunable Device Characteristics and Growth Mechanism Study. ACS Nano, 2015, 9, 6119-6127.	14.6	340
3	Step-Edge-Guided Nucleation and Growth of Aligned WSe ₂ on Sapphire <i>via</i> a Layer-over-Layer Growth Mode. ACS Nano, 2015, 9, 8368-8375.	14.6	168
4	Reversible Semiconducting-to-Metallic Phase Transition in Chemical Vapor Deposition Grown Monolayer WSe ₂ and Applications for Devices. ACS Nano, 2015, 9, 7383-7391.	14.6	164
5	Screw-Dislocation-Driven Growth of Two-Dimensional Few-Layer and Pyramid-like WSe ₂ by Sulfur-Assisted Chemical Vapor Deposition. ACS Nano, 2014, 8, 11543-11551.	14.6	146
6	High-Performance WSe ₂ Field-Effect Transistors <i>via</i> Controlled Formation of In-Plane Heterojunctions. ACS Nano, 2016, 10, 5153-5160.	14.6	135
7	A two-parameter generalized Poisson model to improve the analysis of RNA-seq data. Nucleic Acids Research, 2010, 38, e170-e170.	14.5	131
8	PTBP1 and PTBP2 Serve Both Specific and Redundant Functions in Neuronal Pre-mRNA Splicing. Cell Reports, 2016, 17, 2766-2775.	6.4	97
9	Characterization and comparison of human nuclear and cytosolic editomes. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2741-7.	7.1	63
10	Functional interlayer of PVDF-HFP and carbon nanofiber for long-life lithium-sulfur batteries. Nano Research, 2018, 11, 3340-3352.	10.4	60
11	Axonogenesis Is Coordinated by Neuron-Specific Alternative Splicing Programming and Splicing Regulator PTBP2. Neuron, 2019, 101, 690-706.e10.	8.1	58
12	Alternative splicing: Human disease and quantitative analysis from high-throughput sequencing. Computational and Structural Biotechnology Journal, 2021, 19, 183-195.	4.1	57
13	Black Phosphorus Field-Effect Transistors with Work Function Tunable Contacts. ACS Nano, 2017, 11, 7126-7133.	14.6	54
14	A hierarchical Bayesian model for comparing transcriptomes at the individual transcript isoform level. Nucleic Acids Research, 2009, 37, e75-e75.	14.5	49
15	Studying alternative splicing regulatory networks through partial correlation analysis. Genome Biology, 2009, 10, R3.	9.6	49
16	Synthesis, Characterization, and Device Application of Antimony-Substituted Violet Phosphorus: A Layered Material. ACS Nano, 2017, 11, 4105-4113.	14.6	41
17	A broadly applicable high-throughput screening strategy identifies new regulators of <i>Dlg4</i> (<i>Psd-95</i>) alternative splicing. Genome Research, 2013, 23, 998-1007.	5.5	40
18	Developmental Attenuation of Neuronal Apoptosis by Neural-Specific Splicing of Bak1 Microexon. Neuron, 2020, 107, 1180-1196.e8.	8.1	38

#	ARTICLE	IF	CITATIONS
19	BCseq: accurate single cell RNA-seq quantification with bias correction. <i>Nucleic Acids Research</i> , 2018, 46, e82-e82.	14.5	30
20	A global comparison between nuclear and cytosolic transcriptomes reveals differential compartmentalization of alternative transcript isoforms. <i>Nucleic Acids Research</i> , 2010, 38, 1086-1097.	14.5	25
21	Understand variability of COVID-19 through population and tissue variations in expression of SARS-CoV-2 host genes. <i>Informatics in Medicine Unlocked</i> , 2020, 21, 100443.	3.4	24
22	Identify Alternative Splicing Events Based on Position-Specific Evolutionary Conservation. <i>PLoS ONE</i> , 2008, 3, e2806.	2.5	24
23	WemlQ: an accurate and robust isoform quantification method for RNA-seq data. <i>Bioinformatics</i> , 2015, 31, 878-885.	4.1	23
24	Considering dependence among genes and markers for false discovery control in eQTL mapping. <i>Bioinformatics</i> , 2008, 24, 2015-2022.	4.1	12
25	Molecular profiling of individual FDA-approved clinical drugs identifies modulators of nonsense-mediated mRNA decay. <i>Molecular Therapy - Nucleic Acids</i> , 2022, 27, 304-318.	5.1	12
26	Statistical and Computational Methods for High-Throughput Sequencing Data Analysis of Alternative Splicing. <i>Statistics in Biosciences</i> , 2013, 5, 138-155.	1.2	11
27	Global Reprogramming of Apoptosis-Related Genes during Brain Development. <i>Cells</i> , 2021, 10, 2901.	4.1	10
28	Multilayered regulations of alternative splicing, NMD, and protein stability control temporal induction and tissue-specific expression of TRIM46 during axon formation. <i>Nature Communications</i> , 2022, 13, 2081.	12.8	8
29	Tissue Specificity of Gene Expression Evolves Across Mammal Species. <i>Journal of Computational Biology</i> , 2022, 29, 880-891.	1.6	5
30	Inference of kinship using spatial distributions of SNPs for genome-wide association studies. <i>BMC Genomics</i> , 2016, 17, 372.	2.8	4
31	Statistical and Computational Studies on Alternative Splicing., 2011, , 31-53.		4
32	A link between H3K27me3 mark and exon length in the gene promoters of pluripotent and differentiated cells. <i>Bioinformatics</i> , 2010, 26, 855-859.	4.1	3
33	Quantile regression for challenging cases of eQTL mapping. <i>Briefings in Bioinformatics</i> , 2020, 21, 1756-1765.	6.5	3