

Liang Chen

List of Publications by Year in descending order

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33
papers

2,487
citations

331670

21
h-index

414414

32
g-index

33
all docs

33
docs citations

33
times ranked

5057
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	Tissue Specificity of Gene Expression Evolves Across Mammal Species. <i>Journal of Computational Biology</i> , 2022, 29, 880-891.	1.6	5
4	Alternative splicing: Human disease and quantitative analysis from high-throughput sequencing. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 183-195.	4.1	57
5	Global Reprogramming of Apoptosis-Related Genes during Brain Development. <i>Cells</i> , 2021, 10, 2901.	4.1	10
6	Quantile regression for challenging cases of eQTL mapping. <i>Briefings in Bioinformatics</i> , 2020, 21, 1756-1765.	6.5	3
7	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
8	Developmental Attenuation of Neuronal Apoptosis by Neural-Specific Splicing of Bak1 Microexon. <i>Neuron</i> , 2020, 107, 1180-1196.e8.	8.1	38
9	Axonogenesis Is Coordinated by Neuron-Specific Alternative Splicing Programming and Splicing Regulator PTBP2. <i>Neuron</i> , 2019, 101, 690-706.e10.	8.1	58
10	BCseq: accurate single cell RNA-seq quantification with bias correction. <i>Nucleic Acids Research</i> , 2018, 46, e82-e82.	14.5	30
11	Functional interlayer of PVDF-HFP and carbon nanofiber for long-life lithium-sulfur batteries. <i>Nano Research</i> , 2018, 11, 3340-3352.	10.4	60
12	Synthesis, Characterization, and Device Application of Antimony-Substituted Violet Phosphorus: A Layered Material. <i>ACS Nano</i> , 2017, 11, 4105-4113.	14.6	41
13	Black Phosphorus Field-Effect Transistors with Work Function Tunable Contacts. <i>ACS Nano</i> , 2017, 11, 7126-7133.	14.6	54
14	PTBP1 and PTBP2 Serve Both Specific and Redundant Functions in Neuronal Pre-mRNA Splicing. <i>Cell Reports</i> , 2016, 17, 2766-2775.	6.4	97
15	High-Performance WSe ₂ Field-Effect Transistors <i>via</i> Controlled Formation of In-Plane Heterojunctions. <i>ACS Nano</i> , 2016, 10, 5153-5160.	14.6	135
16	Inference of kinship using spatial distributions of SNPs for genome-wide association studies. <i>BMC Genomics</i> , 2016, 17, 372.	2.8	4
17	Chemical Vapor Deposition Growth of Monolayer WSe ₂ with Tunable Device Characteristics and Growth Mechanism Study. <i>ACS Nano</i> , 2015, 9, 6119-6127.	14.6	340
18	Step-Edge-Guided Nucleation and Growth of Aligned WSe ₂ on Sapphire <i>via</i> a Layer-over-Layer Growth Mode. <i>ACS Nano</i> , 2015, 9, 8368-8375.	14.6	168

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19	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
20	Black Phosphorus Gas Sensors. ACS Nano, 2015, 9, 5618-5624.	14.6	599
21	WemIQ: an accurate and robust isoform quantification method for RNA-seq data. Bioinformatics, 2015, 31, 878-885.	4.1	23
22	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
23	Statistical and Computational Methods for High-Throughput Sequencing Data Analysis of Alternative Splicing. Statistics in Biosciences, 2013, 5, 138-155.	1.2	11
24	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
25	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
26	Statistical and Computational Studies on Alternative Splicing. , 2011, , 31-53.		4
27	A global comparison between nuclear and cytosolic transcriptomes reveals differential compartmentalization of alternative transcript isoforms. Nucleic Acids Research, 2010, 38, 1086-1097.	14.5	25
28	A link between H3K27me3 mark and exon length in the gene promoters of pluripotent and differentiated cells. Bioinformatics, 2010, 26, 855-859.	4.1	3
29	A two-parameter generalized Poisson model to improve the analysis of RNA-seq data. Nucleic Acids Research, 2010, 38, e170-e170.	14.5	131
30	A hierarchical Bayesian model for comparing transcriptomes at the individual transcript isoform level. Nucleic Acids Research, 2009, 37, e75-e75.	14.5	49
31	Studying alternative splicing regulatory networks through partial correlation analysis. Genome Biology, 2009, 10, R3.	9.6	49
32	Considering dependence among genes and markers for false discovery control in eQTL mapping. Bioinformatics, 2008, 24, 2015-2022.	4.1	12
33	Identify Alternative Splicing Events Based on Position-Specific Evolutionary Conservation. PLoS ONE, 2008, 3, e2806.	2.5	24