

Zhen Lin

List of Publications by Year in descending order

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42
papers

2,633
citations

201674

27
h-index

276875

41
g-index

43
all docs

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docs citations

43
times ranked

4381
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of natural compounds tubercidin and lycorine HCl against smallâ€cell lung cancer and BCAT1 as a therapeutic target. <i>Journal of Cellular and Molecular Medicine</i> , 2022, 26, 2557-2565.	3.6	6
2	A smartphone-read ultrasensitive and quantitative saliva test for COVID-19. <i>Science Advances</i> , 2021, 7, .	10.3	175
3	Role of Virally Encoded Circular RNAs in the Pathogenicity of Human Oncogenic Viruses. <i>Frontiers in Microbiology</i> , 2021, 12, 657036.	3.5	9
4	Pathogenic Role of Epsteinâ€Barr Virus in Lung Cancers. <i>Viruses</i> , 2021, 13, 877.	3.3	14
5	An Epidemiologic Study of COVID-19 Patients in a State Psychiatric Hospital: High Penetrance With Early CDC Guidelines. <i>Psychiatric Services</i> , 2020, 71, 1285-1287.	2.0	14
6	Ubiquitin Modification of the Epstein-Barr Virus Immediate Early Transactivator Zta. <i>Journal of Virology</i> , 2020, 94, .	3.4	7
7	Ultra-sensitive and high-throughput CRISPR-p owered COVID-19 diagnosis. <i>Biosensors and Bioelectronics</i> , 2020, 164, 112316.	10.1	265
8	Targeting Sphingosine Kinase by ABC294640 against Diffuse Intrinsic Pontine Glioma (DIPG). <i>Journal of Cancer</i> , 2020, 11, 4683-4690.	2.5	5
9	Identification of new therapeutic targets and natural compounds against diffuse intrinsic pontine glioma (DIPG). <i>Bioorganic Chemistry</i> , 2020, 99, 103847.	4.1	14
10	High-Throughput Sequence Analysis of Peripheral T-Cell Lymphomas Indicates Subtype-Specific Viral Gene Expression Patterns and Immune Cell Microenvironments. <i>MSphere</i> , 2019, 4, .	2.9	13
11	The Role of the miR-21/SPRY2 Axis in Modulating Proangiogenic Factors, Epithelial Phenotypes, and Wound Healing in Corneal Epithelial Cells. , 2019, 60, 3854.		28
12	Detection of Epstein-Barr Virus Infection in Non-Small Cell Lung Cancer. <i>Cancers</i> , 2019, 11, 759.	3.7	36
13	Extracellular Vesicles in Epstein-Barr Virusâ€™ Life Cycle and Pathogenesis. <i>Microorganisms</i> , 2019, 7, 48.	3.6	33
14	Interleukin-17A in the Pathogenesis of Lung Adenocarcinoma. <i>Annals of the American Thoracic Society</i> , 2018, 15, S125-S125.	3.2	0
15	Gas6 is dispensable for pubertal mammary gland development. <i>PLoS ONE</i> , 2018, 13, e0208550.	2.5	21
16	The Epstein Barr virus circRNAome. <i>PLoS Pathogens</i> , 2018, 14, e1007206.	4.7	112
17	KSHV co-infection, a new co-factor for HPV-related cervical carcinogenesis?. <i>American Journal of Cancer Research</i> , 2018, 8, 2176-2184.	1.4	1
18	Induction of a novel isoform of the lnc<sc>RNA HOTAIR</sc> in Claudinâ€low breast cancer cells attached to extracellular matrix. <i>Molecular Oncology</i> , 2017, 11, 1698-1710.	4.6	29

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19	Hypoxia-inducible factor-1 β plays roles in Epstein-Barr virus's natural life cycle and tumorigenesis by inducing lytic infection through direct binding to the immediate-early BZLF1 gene promoter. <i>PLoS Pathogens</i> , 2017, 13, e1006404.	4.7	55
20	A comprehensive next generation sequencing-based virome assessment in brain tissue suggests no major virus - tumor association. <i>Acta Neuropathologica Communications</i> , 2016, 4, 71.	5.2	57
21	Secreted Oral Epithelial Cell Membrane Vesicles Induce Epstein-Barr Virus Reactivation in Latently Infected B Cells. <i>Journal of Virology</i> , 2016, 90, 3469-3479.	3.4	32
22	Latent Expression of the Epstein-Barr Virus (EBV)-Encoded Major Histocompatibility Complex Class I TAP Inhibitor, <i>BNLF2a</i> , in EBV-Positive Gastric Carcinomas. <i>Journal of Virology</i> , 2015, 89, 10110-10114.	3.4	30
23	New Noncoding Lytic Transcripts Derived from the Epstein-Barr Virus Latency Origin of Replication, <i>oriP</i> , Are Hyperedited, Bind the Paraspeckle Protein, NONO/p54nrb, and Support Viral Lytic Transcription. <i>Journal of Virology</i> , 2015, 89, 7120-7132.	3.4	46
24	High-Throughput RNA Sequencing-Based Virome Analysis of 50 Lymphoma Cell Lines from the Cancer Cell Line Encyclopedia Project. <i>Journal of Virology</i> , 2015, 89, 713-729.	3.4	61
25	Microbial Contamination in Next Generation Sequencing: Implications for Sequence-Based Analysis of Clinical Samples. <i>PLoS Pathogens</i> , 2014, 10, e1004437.	4.7	159
26	Expanding the Conversation on High-Throughput Virome Sequencing Standards To Include Consideration of Microbial Contamination Sources. <i>MBio</i> , 2014, 5, e01989.	4.1	2
27	Global Bidirectional Transcription of the Epstein-Barr Virus Genome during Reactivation. <i>Journal of Virology</i> , 2014, 88, 1604-1616.	3.4	57
28	Comprehensive High-Throughput RNA Sequencing Analysis Reveals Contamination of Multiple Nasopharyngeal Carcinoma Cell Lines with HeLa Cell Genomes. <i>Journal of Virology</i> , 2014, 88, 10696-10704.	3.4	87
29	Whole-Genome Sequencing of the Akata and Mutu Epstein-Barr Virus Strains. <i>Journal of Virology</i> , 2013, 87, 1172-1182.	3.4	98
30	Differences in Gastric Carcinoma Microenvironment Stratify According to EBV Infection Intensity: Implications for Possible Immune Adjuvant Therapy. <i>PLoS Pathogens</i> , 2013, 9, e1003341.	4.7	140
31	Epstein-Barr Virus and Human Herpesvirus 6 Detection in a Non-Hodgkin's Diffuse Large B-Cell Lymphoma Cohort by Using RNA Sequencing. <i>Journal of Virology</i> , 2013, 87, 13059-13062.	3.4	35
32	Detection of Murine Leukemia Virus in the Epstein-Barr Virus-Positive Human B-Cell Line JY, Using a Computational RNA-Seq-Based Exogenous Agent Detection Pipeline, PARSES. <i>Journal of Virology</i> , 2012, 86, 2970-2977.	3.4	27
33	Identification of New Viral Genes and Transcript Isoforms during Epstein-Barr Virus Reactivation using RNA-Seq. <i>Journal of Virology</i> , 2012, 86, 1458-1467.	3.4	54
34	The microRNA expression associated with morphogenesis of breast cancer cells in three-dimensional organotypic culture. <i>Oncology Reports</i> , 2012, 28, 117-126.	2.6	16
35	miRNAs in the pathogenesis of oncogenic human viruses. <i>Cancer Letters</i> , 2011, 305, 186-199.	7.2	55
36	Quantitative and Qualitative RNA-Seq-Based Evaluation of Epstein-Barr Virus Transcription in Type I Latency Burkitt's Lymphoma Cells. <i>Journal of Virology</i> , 2010, 84, 13053-13058.	3.4	43

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37	Differential Expression of the miR-200 Family MicroRNAs in Epithelial and B Cells and Regulation of Epstein-Barr Virus Reactivation by the miR-200 Family Member miR-429. <i>Journal of Virology</i> , 2010, 84, 7892-7897.	3.4	44
38	MicroRNA miR-155 Inhibits Bone Morphogenetic Protein (BMP) Signaling and BMP-Mediated Epstein-Barr Virus Reactivation. <i>Journal of Virology</i> , 2010, 84, 6318-6327.	3.4	89
39	Epstein-Barr virus growth/latency III program alters cellular microRNA expression. <i>Virology</i> , 2008, 382, 257-266.	2.4	140
40	MicroRNA-155 Is an Epstein-Barr Virus-Induced Gene That Modulates Epstein-Barr Virus-Regulated Gene Expression Pathways. <i>Journal of Virology</i> , 2008, 82, 5295-5306.	3.4	233
41	Epstein-Barr Virus Latent Membrane Protein 1 Induces Cellular MicroRNA miR-146a, a Modulator of Lymphocyte Signaling Pathways. <i>Journal of Virology</i> , 2008, 82, 1946-1958.	3.4	273
42	Identification of a Negative Regulatory Element in the Epstein-Barr Virus Zta Transactivation Domain That Is Regulated by the Cell Cycle Control Factors c-Myc and E2F1. <i>Journal of Virology</i> , 2004, 78, 11962-11971.	3.4	17