

# Dã³ra TombÃ¡cz

## List of Publications by Year in descending order

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63  
papers

1,641  
citations

304743

22  
h-index

345221

36  
g-index

81  
all docs

81  
docs citations

81  
times ranked

1170  
citing authors

#	ARTICLE	IF	CITATIONS
1	Long-Read Isoform Sequencing Reveals a Hidden Complexity of the Transcriptional Landscape of Herpes Simplex Virus Type 1. <i>Frontiers in Microbiology</i> , 2017, 8, 1079.	3.5	97
2	Full-Length Isoform Sequencing Reveals Novel Transcripts and Substantial Transcriptional Overlaps in a Herpesvirus. <i>PLoS ONE</i> , 2016, 11, e0162868.	2.5	93
3	Genetically timed, activity-sensor and rainbow transsynaptic viral tools. <i>Nature Methods</i> , 2009, 6, 127-130.	19.0	85
4	Whole-genome analysis of pseudorabies virus gene expression by real-time quantitative RT-PCR assay. <i>BMC Genomics</i> , 2009, 10, 491.	2.8	80
5	Characterization of the Dynamic Transcriptome of a Herpesvirus with Long-read Single Molecule Real-Time Sequencing. <i>Scientific Reports</i> , 2017, 7, 43751.	3.3	76
6	Long-Read Sequencing – A Powerful Tool in Viral Transcriptome Research. <i>Trends in Microbiology</i> , 2019, 27, 578-592.	7.7	76
7	Long-Read Sequencing of Human Cytomegalovirus Transcriptome Reveals RNA Isoforms Carrying Distinct Coding Potentials. <i>Scientific Reports</i> , 2017, 7, 15989.	3.3	75
8	Long-read sequencing uncovers a complex transcriptome topology in varicella zoster virus. <i>BMC Genomics</i> , 2018, 19, 873.	2.8	66
9	Multi-Platform Sequencing Approach Reveals a Novel Transcriptome Profile in Pseudorabies Virus. <i>Frontiers in Microbiology</i> , 2018, 8, 2708.	3.5	64
10	Third-generation Sequencing Reveals Extensive Polycistronism and Transcriptional Overlapping in a Baculovirus. <i>Scientific Reports</i> , 2018, 8, 8604.	3.3	58
11	High-Coverage Whole-Exome Sequencing Identifies Candidate Genes for Suicide in Victims with Major Depressive Disorder. <i>Scientific Reports</i> , 2017, 7, 7106.	3.3	56
12	Single-nuclei isoform RNA sequencing unlocks barcoded exon connectivity in frozen brain tissue. <i>Nature Biotechnology</i> , 2022, 40, 1082-1092.	17.5	52
13	Multi-platform analysis reveals a complex transcriptome architecture of a circovirus. <i>Virus Research</i> , 2017, 237, 37-46.	2.2	49
14	Characterization of Novel Transcripts in Pseudorabies Virus. <i>Viruses</i> , 2015, 7, 2727-2744.	3.3	46
15	Long-read sequencing of the human cytomegalovirus transcriptome with the Pacific Biosciences RSII platform. <i>Scientific Data</i> , 2017, 4, 170194.	5.3	46
16	Characterization of pseudorabies virus transcriptome by Illumina sequencing. <i>BMC Microbiology</i> , 2015, 15, 130.	3.3	45
17	Multiple Long-Read Sequencing Survey of Herpes Simplex Virus Dynamic Transcriptome. <i>Frontiers in Genetics</i> , 2019, 10, 834.	2.3	44
18	Dynamic transcriptome profiling dataset of vaccinia virus obtained from long-read sequencing techniques. <i>GigaScience</i> , 2018, 7, .	6.4	38

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19	Template-switching artifacts resemble alternative polyadenylation. <i>BMC Genomics</i> , 2019, 20, 824.	2.8	32
20	Transcriptome-wide survey of pseudorabies virus using next- and third-generation sequencing platforms. <i>Scientific Data</i> , 2018, 5, 180119.	5.3	31
21	Strain Kaplan of Pseudorabies Virus Genome Sequenced by PacBio Single-Molecule Real-Time Sequencing Technology. <i>Genome Announcements</i> , 2014, 2, .	0.8	29
22	Transcriptomic study of Herpes simplex virus type-1 using full-length sequencing techniques. <i>Scientific Data</i> , 2018, 5, 180266.	5.3	27
23	Novel classes of replication-associated transcripts discovered in viruses. <i>RNA Biology</i> , 2019, 16, 166-175.	3.1	26
24	Long-Read Sequencing Revealed an Extensive Transcript Complexity in Herpesviruses. <i>Frontiers in Genetics</i> , 2018, 9, 259.	2.3	23
25	Multiplatform next-generation sequencing identifies novel RNA molecules and transcript isoforms of the endogenous retrovirus isolated from cultured cells. <i>FEMS Microbiology Letters</i> , 2018, 365, .	1.8	21
26	The ICP22 protein selectively modifies the transcription of different kinetic classes of pseudorabies virus genes. <i>BMC Molecular Biology</i> , 2013, 14, 2.	3.0	17
27	Long-read assays shed new light on the transcriptome complexity of a viral pathogen. <i>Scientific Reports</i> , 2020, 10, 13822.	3.3	17
28	Full Genome Sequence of the Western Reserve Strain of Vaccinia Virus Determined by Third-Generation Sequencing. <i>Genome Announcements</i> , 2018, 6, .	0.8	16
29	Interactions between the transcription and replication machineries regulate the RNA and DNA synthesis in the herpesviruses. <i>Virus Genes</i> , 2019, 55, 274-279.	1.6	16
30	Dual Platform Long-Read RNA-Sequencing Dataset of the Human Cytomegalovirus Lytic Transcriptome. <i>Frontiers in Genetics</i> , 2018, 9, 432.	2.3	14
31	Short and Long-Read Sequencing Survey of the Dynamic Transcriptomes of African Swine Fever Virus and the Host Cells. <i>Frontiers in Genetics</i> , 2020, 11, 758.	2.3	14
32	Location of parotid preganglionic neurons in the inferior salivatory nucleus and their relation to the superior salivatory nucleus of rat. <i>Neuroscience Letters</i> , 2008, 440, 265-269.	2.1	13
33	Herpesvirus-Mediated Delivery of a Genetically Encoded FluorescentCa2+Sensor to Canine Cardiomyocytes. <i>Journal of Biomedicine and Biotechnology</i> , 2009, 2009, 1-12.	3.0	13
34	Combined Short and Long-Read Sequencing Reveals a Complex Transcriptomic Architecture of African Swine Fever Virus. <i>Viruses</i> , 2021, 13, 579.	3.3	13
35	Effects of deletion of the early protein 0 gene of pseudorabies virus on the overall viral gene expression. <i>Gene</i> , 2012, 493, 235-242.	2.2	11
36	Evaluation of whole exome sequencing as an alternative to BeadChip and whole genome sequencing in human population genetic analysis. <i>BMC Genomics</i> , 2018, 19, 778.	2.8	11

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37	Transcriptome-wide analysis of a baculovirus using nanopore sequencing. <i>Scientific Data</i> , 2018, 5, 180276.	5.3	10
38	An Integrated Sequencing Approach for Updating the Pseudorabies Virus Transcriptome. <i>Pathogens</i> , 2021, 10, 242.	2.8	9
39	Time-course profiling of bovine alphaherpesvirus 1.1 transcriptome using multiplatform sequencing. <i>Scientific Reports</i> , 2020, 10, 20496.	3.3	9
40	Deletion of the virion host shut-off gene of pseudorabies virus results in selective upregulation of the expression of early viral genes in the late stage of infection. <i>Genomics</i> , 2011, 98, 15-25.	2.9	8
41	Lytic Transcriptome Dataset of Varicella Zoster Virus Generated by Long-Read Sequencing. <i>Frontiers in Genetics</i> , 2018, 9, 460.	2.3	8
42	Combined nanopore and single-molecule real-time sequencing survey of human betaherpesvirus 5 transcriptome. <i>Scientific Reports</i> , 2021, 11, 14487.	3.3	8
43	Integrative profiling of Epstein-Barr virus transcriptome using a multiplatform approach. <i>Virology Journal</i> , 2022, 19, 7.	3.4	8
44	Analysis of the Complete Genome Sequence of a Novel, Pseudorabies Virus Strain Isolated in Southeast Europe. <i>Canadian Journal of Infectious Diseases and Medical Microbiology</i> , 2019, 2019, 1-12.	1.9	7
45	Meta-analytic approach for transcriptome profiling of herpes simplex virus type 1. <i>Scientific Data</i> , 2020, 7, 223.	5.3	7
46	The effects of viral load on pseudorabies virus gene expression. <i>BMC Microbiology</i> , 2010, 10, 311.	3.3	6
47	Visible Light-Generated Antiviral Effect on Plasmonic Ag-TiO <sub>2</sub> -Based Reactive Nanocomposite Thin Film. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 709462.	4.1	6
48	In-Depth Temporal Transcriptome Profiling of an Alphaherpesvirus Using Nanopore Sequencing. <i>Viruses</i> , 2022, 14, 1289.	3.3	6
49	Dynamic Transcriptome Sequencing of Bovine Alphaherpesvirus Type 1 and Host Cells Carried Out by a Multi-Technique Approach. <i>Frontiers in Genetics</i> , 2021, 12, 619056.	2.3	5
50	Time-course transcriptome analysis of host cell response to poxvirus infection using a dual long-read sequencing approach. <i>BMC Research Notes</i> , 2021, 14, 239.	1.4	5
51	Evaluation of the impact of ul54 gene-deletion on the global transcription and DNA replication of pseudorabies virus. <i>Archives of Virology</i> , 2017, 162, 2679-2694.	2.1	5
52	Whole-exome sequencing data of suicide victims who had suffered from major depressive disorder. <i>Scientific Data</i> , 2019, 6, 190010.	5.3	5
53	Deletion of the us7 and us8 genes of pseudorabies virus exerts a differential effect on the expression of early and late viral genes. <i>Virus Genes</i> , 2017, 53, 603-612.	1.6	4
54	Pinealocytes can not transport neurotropic viruses. Pinealo-to-retinal connection in prepubertal rats originates from pineal neurons: Light and electron microscopic immunohistochemical studies. <i>Neuroscience Letters</i> , 2021, 744, 135517.	2.1	4

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55	The Same Magnocellular Neurons Send Axon Collaterals to the Posterior Pituitary and Retina or to the Posterior Pituitary and Autonomic Preganglionic Centers of the Eye in Rats. <i>NeuroSci</i> , 2021, 2, 27-44.	1.2	4
56	Time course profiling of host cell response to herpesvirus infection using nanopore and synthetic long-read transcriptome sequencing. <i>Scientific Reports</i> , 2021, 11, 14219.	3.3	4
57	Time-Course Transcriptome Profiling of a Poxvirus Using Long-Read Full-Length Assay. <i>Pathogens</i> , 2021, 10, 919.	2.8	4
58	Long-Read Sequencing Reveals a GC Pressure during the Evolution of Porcine Endogenous Retrovirus. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
59	Dual isoform sequencing reveals complex transcriptomic and epitranscriptomic landscapes of a prototype baculovirus. <i>Scientific Reports</i> , 2022, 12, 1291.	3.3	3
60	Nanopore Assay Reveals Cell-Type-Dependent Gene Expression of Vesicular Stomatitis Indiana Virus and Differential Host Cell Response. <i>Pathogens</i> , 2021, 10, 1196.	2.8	2
61	Ex vivo infection of human embryonic spinal cord neurons prior to transplantation into adult mouse cord. <i>BMC Neuroscience</i> , 2010, 11, 65.	1.9	1
62	Genetic Adaptation of Porcine Circovirus Type 1 to Cultured Porcine Kidney Cells Revealed by Single-Molecule Long-Read Sequencing Technology. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
63	Transcriptome dataset of six human pathogen RNA viruses generated by nanopore sequencing. <i>Data in Brief</i> , 2022, 43, 108386.	1.0	1