

Norbert MoldovĂin

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

790
citations

759233

12
h-index

580821

25
g-index

40
all docs

40
docs citations

40
times ranked

472
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrative profiling of Epstein-Barr virus transcriptome using a multiplatform approach. <i>Virology Journal</i> , 2022, 19, 7.	3.4	8
2	Dual isoform sequencing reveals complex transcriptomic and epitranscriptomic landscapes of a prototype baculovirus. <i>Scientific Reports</i> , 2022, 12, 1291.	3.3	3
3	The Effect of Preanalytical and Physiological Variables on Cell-Free DNA Fragmentation. <i>Clinical Chemistry</i> , 2022, 68, 803-813.	3.2	16
4	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
5	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
6	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
7	Combined nanopore and single-molecule real-time sequencing survey of human betaherpesvirus 5 transcriptome. <i>Scientific Reports</i> , 2021, 11, 14487.	3.3	8
8	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
9	Time-Course Transcriptome Profiling of a Poxvirus Using Long-Read Full-Length Assay. <i>Pathogens</i> , 2021, 10, 919.	2.8	4
10	Meta-analytic approach for transcriptome profiling of herpes simplex virus type 1. <i>Scientific Data</i> , 2020, 7, 223.	5.3	7
11	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
12	Long-read assays shed new light on the transcriptome complexity of a viral pathogen. <i>Scientific Reports</i> , 2020, 10, 13822.	3.3	17
13	Time-course profiling of bovine alphaherpesvirus 1.1 transcriptome using multiplatform sequencing. <i>Scientific Reports</i> , 2020, 10, 20496.	3.3	9
14	Multiple Long-Read Sequencing Survey of Herpes Simplex Virus Dynamic Transcriptome. <i>Frontiers in Genetics</i> , 2019, 10, 834.	2.3	44
15	Template-switching artifacts resemble alternative polyadenylation. <i>BMC Genomics</i> , 2019, 20, 824.	2.8	32
16	Long-Read Sequencing – A Powerful Tool in Viral Transcriptome Research. <i>Trends in Microbiology</i> , 2019, 27, 578-592.	7.7	76
17	Novel classes of replication-associated transcripts discovered in viruses. <i>RNA Biology</i> , 2019, 16, 166-175.	3.1	26
18	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

#	ARTICLE	IF	CITATIONS
19	Long-read sequencing uncovers a complex transcriptome topology in varicella zoster virus. BMC Genomics, 2018, 19, 873.	2.8	66
20	Lytic Transcriptome Dataset of Varicella Zoster Virus Generated by Long-Read Sequencing. Frontiers in Genetics, 2018, 9, 460.	2.3	8
21	Multi-Platform Sequencing Approach Reveals a Novel Transcriptome Profile in Pseudorabies Virus. Frontiers in Microbiology, 2018, 8, 2708.	3.5	64
22	Third-generation Sequencing Reveals Extensive Polycistronism and Transcriptional Overlapping in a Baculovirus. Scientific Reports, 2018, 8, 8604.	3.3	58
23	Transcriptome-wide survey of pseudorabies virus using next- and third-generation sequencing platforms. Scientific Data, 2018, 5, 180119.	5.3	31
24	Transcriptome-wide analysis of a baculovirus using nanopore sequencing. Scientific Data, 2018, 5, 180276.	5.3	10
25	Genetic Adaptation of Porcine Circovirus Type 1 to Cultured Porcine Kidney Cells Revealed by Single-Molecule Long-Read Sequencing Technology. Genome Announcements, 2017, 5, .	0.8	1
26	Multi-platform analysis reveals a complex transcriptome architecture of a circovirus. Virus Research, 2017, 237, 37-46.	2.2	49
27	Characterization of the Dynamic Transcriptome of a Herpesvirus with Long-read Single Molecule Real-Time Sequencing. Scientific Reports, 2017, 7, 43751.	3.3	76
28	Long-Read Isoform Sequencing Reveals a Hidden Complexity of the Transcriptional Landscape of Herpes Simplex Virus Type 1. Frontiers in Microbiology, 2017, 8, 1079.	3.5	97
29	Long-Read Sequencing Reveals a GC Pressure during the Evolution of Porcine Endogenous Retrovirus. Genome Announcements, 2017, 5, .	0.8	4