

David A Matthews

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

6,310
citations

159585

30
h-index

118850

62
g-index

80
all docs

80
docs citations

80
times ranked

12073
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural insights in cell-type specific evolution of intra-host diversity by SARS-CoV-2. <i>Nature Communications</i> , 2022, 13, 222.	12.8	23
2	Nanopore ReCappable sequencing maps SARS-CoV-2 5' capping sites and provides new insights into the structure of sgRNAs. <i>Nucleic Acids Research</i> , 2022, 50, 3475-3489.	14.5	12
3	Analysis of SARS-CoV-2 known and novel subgenomic mRNAs in cell culture, animal model, and clinical samples using LeTRS, a bioinformatic tool to identify unique sequence identifiers. <i>GigaScience</i> , 2022, 11, .	6.4	8
4	Analysis of an Ebola virus disease survivor whose host and viral markers were predictive of death indicates the effectiveness of medical countermeasures and supportive care. <i>Genome Medicine</i> , 2021, 13, 5.	8.2	9
5	Editorial: Host Innate Immune Responses to Infection by Avian- and Bat-Borne Viruses. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 651289.	3.9	1
6	SARS-CoV-2 vaccine ChAdOx1 nCoV-19 infection of human cell lines reveals low levels of viral backbone gene transcription alongside very high levels of SARS-CoV-2 S glycoprotein gene transcription. <i>Genome Medicine</i> , 2021, 13, 43.	8.2	44
7	The furin cleavage site in the SARS-CoV-2 spike protein is required for transmission in ferrets. <i>Nature Microbiology</i> , 2021, 6, 899-909.	13.3	556
8	Amplicon and Metagenomic Analysis of Middle East Respiratory Syndrome (MERS) Coronavirus and the Microbiome in Patients with Severe MERS. <i>MSphere</i> , 2021, 6, e0021921.	2.9	12
9	TMPRSS2 promotes SARS-CoV-2 evasion from NCOA7-mediated restriction. <i>PLoS Pathogens</i> , 2021, 17, e1009820.	4.7	13
10	Neuropilin-1 is a host factor for SARS-CoV-2 infection. <i>Science</i> , 2020, 370, 861-865.	12.6	1,015
11	Variation around the dominant viral genome sequence contributes to viral load and outcome in patients with Ebola virus disease. <i>Genome Biology</i> , 2020, 21, 238.	8.8	18
12	Characterisation of the transcriptome and proteome of SARS-CoV-2 reveals a cell passage induced in-frame deletion of the furin-like cleavage site from the spike glycoprotein. <i>Genome Medicine</i> , 2020, 12, 68.	8.2	386
13	Amplicon-Based Detection and Sequencing of SARS-CoV-2 in Nasopharyngeal Swabs from Patients With COVID-19 and Identification of Deletions in the Viral Genome That Encode Proteins Involved in Interferon Antagonism. <i>Viruses</i> , 2020, 12, 1164.	3.3	51
14	Deep splicing plasticity of the human adenovirus type 5 transcriptome drives virus evolution. <i>Communications Biology</i> , 2020, 3, 124.	4.4	37
15	High Resolution Analysis of Respiratory Syncytial Virus Infection In Vivo. <i>Viruses</i> , 2019, 11, 926.	3.3	13
16	High throughput discovery of protein variants using proteomics informed by transcriptomics. <i>Nucleic Acids Research</i> , 2018, 46, 4893-4902.	14.5	5
17	Zika Virus Infection Preferentially Counterbalances Human Peripheral Monocyte and/or NK Cell Activity. <i>MSphere</i> , 2018, 3, .	2.9	32
18	PITDB: a database of translated genomic elements. <i>Nucleic Acids Research</i> , 2018, 46, D1223-D1228.	14.5	2

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19	Transcriptomic signatures differentiate survival from fatal outcomes in humans infected with Ebola virus. <i>Genome Biology</i> , 2017, 18, 4.	8.8	115
20	A comparison of host gene expression signatures associated with infection in vitro by the Makona and Ecran (Mayinga) variants of Ebola virus. <i>Scientific Reports</i> , 2017, 7, 43144.	3.3	21
21	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017, 544, 309-315.	27.8	346
22	Deep Sequencing of RNA from Blood and Oral Swab Samples Reveals the Presence of Nucleic Acid from a Number of Pathogens in Patients with Acute Ebola Virus Disease and Is Consistent with Bacterial Translocation across the Gut. <i>MSphere</i> , 2017, 2, .	2.9	30
23	Proteomics technique opens new frontiers in mobilome research. <i>Mobile Genetic Elements</i> , 2017, 7, 1-9.	1.8	4
24	Proteomics informed by transcriptomics for characterising active transposable elements and genome annotation in <i>Aedes aegypti</i> . <i>BMC Genomics</i> , 2017, 18, 101.	2.8	49
25	Proteomics informed by transcriptomics for characterising differential cellular susceptibility to Nelson Bay orthoreovirus infection. <i>BMC Genomics</i> , 2017, 18, 615.	2.8	6
26	Comparison of protein expression during wild-type, and E1B-55k-deletion, adenovirus infection using quantitative time-course proteomics. <i>Journal of General Virology</i> , 2017, 98, 1377-1388.	2.9	11
27	Investigating the Influence of Ribavirin on Human Respiratory Syncytial Virus RNA Synthesis by Using a High-Resolution Transcriptome Sequencing Approach. <i>Journal of Virology</i> , 2016, 90, 4876-4888.	3.4	32
28	Real-time, portable genome sequencing for Ebola surveillance. <i>Nature</i> , 2016, 530, 228-232.	27.8	1,179
29	Galaxy Integrated Omics: Web-based Standards-Compliant Workflows for Proteomics Informed by Transcriptomics*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 3087-3093.	3.8	30
30	Identification of Epstein-Barr Virus Replication Proteins in Burkitt's Lymphoma Cells. <i>Pathogens</i> , 2015, 4, 739-751.	2.8	17
31	Temporal and spatial analysis of the 2014-2015 Ebola virus outbreak in West Africa. <i>Nature</i> , 2015, 524, 97-101.	27.8	272
32	Elucidating variations in the nucleotide sequence of Ebola virus associated with increasing pathogenicity. <i>Genome Biology</i> , 2014, 15, 540.	8.8	44
33	Analysis of purified Wild type and mutant adenovirus particles by SILAC based quantitative proteomics. <i>Journal of General Virology</i> , 2014, 95, 2504-2511.	2.9	13
34	Factors affecting de novo RNA synthesis and back-priming by the respiratory syncytial virus polymerase. <i>Virology</i> , 2014, 462-463, 318-327.	2.4	24
35	Elucidation of the Ebola Virus VP24 Cellular Interactome and Disruption of Virus Biology through Targeted Inhibition of Host-Cell Protein Function. <i>Journal of Proteome Research</i> , 2014, 13, 5120-5135.	3.7	79
36	High-Throughput Quantitative Proteomic Analysis of Dengue Virus Type 2 Infected A549 Cells. <i>PLoS ONE</i> , 2014, 9, e93305.	2.5	62

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37	The Interactome of the Human Respiratory Syncytial Virus NS1 Protein Highlights Multiple Effects on Host Cell Biology. <i>Journal of Virology</i> , 2012, 86, 7777-7789.	3.4	61
38	Adenoviral protein V promotes a process of viral assembly through nucleophosmin 1. <i>Virology</i> , 2012, 432, 283-295.	2.4	26
39	De novo derivation of proteomes from transcriptomes for transcript and protein identification. <i>Nature Methods</i> , 2012, 9, 1207-1211.	19.0	167
40	Nucleolar proteomics and viral infection. <i>Proteomics</i> , 2010, 10, 4077-4086.	2.2	59
41	Proteomics Analysis of the Nucleolus in Adenovirus-infected Cells. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 117-130.	3.8	106
42	Quantitative Proteomics Using SILAC Coupled to LC-MS/MS Reveals Changes in the Nucleolar Proteome in Influenza A Virus-Infected Cells. <i>Journal of Proteome Research</i> , 2010, 9, 5335-5345.	3.7	76
43	In Vitro Dynamic Visualization Analysis of Fluorescently Labeled Minor Capsid Protein IX and Core Protein V by Simultaneous Detection. <i>Journal of Molecular Biology</i> , 2010, 395, 55-78.	4.2	16
44	Upstream-binding factor is sequestered into herpes simplex virus type 1 replication compartments. <i>Journal of General Virology</i> , 2009, 90, 69-73.	2.9	15
45	A Role for Transportin in the Nuclear Import of Adenovirus Core Proteins and DNA. <i>Traffic</i> , 2007, 8, 1313-1322.	2.7	57
46	Relationship between adenovirus DNA replication proteins and nucleolar proteins B23.1 and B23.2. <i>Journal of General Virology</i> , 2007, 88, 3244-3248.	2.9	26
47	Study of Nucleolar Localization of Adenovirus Core Proteins. <i>Methods in Molecular Medicine</i> , 2007, 131, 73-81.	0.8	0
48	Core labeling of adenovirus with EGFP. <i>Virology</i> , 2006, 351, 291-302.	2.4	25
49	Nucleolar protein upstream binding factor is sequestered into adenovirus DNA replication centres during infection without affecting RNA polymerase I location or ablating rRNA synthesis. <i>Journal of Cell Science</i> , 2006, 119, 2621-2631.	2.0	38
50	Novel molecular approaches to cystic fibrosis gene therapy. <i>Biochemical Journal</i> , 2005, 387, 1-15.	3.7	73
51	The herpesvirus saimiri ORF73 gene product interacts with host-cell mitotic chromosomes and self-associates via its C terminus. <i>Journal of General Virology</i> , 2004, 85, 147-153.	2.9	33
52	Precursor of human adenovirus core polypeptide Mu targets the nucleolus and modulates the expression of E2 proteins. <i>Journal of General Virology</i> , 2004, 85, 185-196.	2.9	29
53	Comparison between the interactions of adenovirus-derived peptides with plasmid DNA and their role in gene delivery mediated by liposome-peptide-DNA virus-like nanoparticles. <i>Organic and Biomolecular Chemistry</i> , 2003, 1, 2430-2438.	2.8	21
54	Adenovirus core protein VII contains distinct sequences that mediate targeting to the nucleus and nucleolus, and colocalization with human chromosomes. <i>Journal of General Virology</i> , 2003, 84, 3423-3428.	2.9	47

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55	The Herpesvirus Saimiri Open Reading Frame 73 Gene Product Interacts with the Cellular Protein p32. <i>Journal of Virology</i> , 2002, 76, 11612-11622.	3.4	33
56	Mitochondrial Protein p32 Can Accumulate in the Nucleus. <i>Biochemical and Biophysical Research Communications</i> , 2001, 281, 1161-1169.	2.1	54
57	Adenovirus Protein V Induces Redistribution of Nucleolin and B23 from Nucleolus to Cytoplasm. <i>Journal of Virology</i> , 2001, 75, 1031-1038.	3.4	112
58	Enhanced cationic liposome-mediated transfection using the DNA-binding peptide $\hat{1}/4$ (μ) from the adenovirus core. <i>Gene Therapy</i> , 2001, 8, 453-460.	4.5	78
59	Interaction between Herpes Simplex Virus Type 1 IE63 Protein and Cellular Protein p32. <i>Journal of Virology</i> , 2000, 74, 11322-11328.	3.4	46
60	The splicing factor-associated protein, p32, regulates RNA splicing by inhibiting ASF/SF2 RNA binding and phosphorylation. <i>EMBO Journal</i> , 1999, 18, 1014-1024.	7.8	153
61	Identification of mutations contributing to the reduced virulence of a modified strain of respiratory syncytial virus. <i>Vaccine</i> , 1996, 14, 1637-1646.	3.8	43
62	Analysis of relatedness of subgroup A respiratory syncytial viruses isolated worldwide. <i>Virus Research</i> , 1992, 25, 15-22.	2.2	70
63	The nucleotide sequences of intergenic regions between nine genes of pneumonia virus of mice establish the physical order of these genes in the viral genome. <i>Virus Research</i> , 1991, 18, 263-270.	2.2	23