David A Matthews

List of Publications by Year
in descending order

63	6,310	159525 30	118793 62
papers	citations	h-index	g-index

80	80	80	12073
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Structural insights in cell-type specific evolution of intra-host diversity by SARS-CoV-2. Nature Communications, 2022, 13, 222.	5.8	23
2	Nanopore ReCappable sequencing maps SARS-CoV-2 5â€² capping sites and provides new insights into the structure of sgRNAs. Nucleic Acids Research, 2022, 50, 3475-3489.	6.5	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. GigaScience, 2022, 11, .	3.3	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. Genome Medicine, 2021, 13, 5.	3.6	9
5	Editorial: Host Innate Immune Responses to Infection by Avian- and Bat-Borne Viruses. Frontiers in Cellular and Infection Microbiology, 2021, 11, 651289.	1.8	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. Genome Medicine, 2021, 13, 43.	3.6	44
7	The furin cleavage site in the SARS-CoV-2 spike protein is required for transmission in ferrets. Nature Microbiology, 2021, 6, 899-909.	5.9	556
8	Amplicon and Metagenomic Analysis of Middle East Respiratory Syndrome (MERS) Coronavirus and the Microbiome in Patients with Severe MERS. MSphere, 2021, 6, e0021921.	1.3	12
9	TMPRSS2 promotes SARS-CoV-2 evasion from NCOA7-mediated restriction. PLoS Pathogens, 2021, 17, e1009820.	2.1	13
10	Neuropilin-1 is a host factor for SARS-CoV-2 infection. Science, 2020, 370, 861-865.	6.0	1,015
11	Variation around the dominant viral genome sequence contributes to viral load and outcome in patients with Ebola virus disease. Genome Biology, 2020, 21, 238.	3.8	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. Genome Medicine, 2020, 12, 68.	3.6	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. Viruses, 2020, 12, 1164.	1.5	51
14	Deep splicing plasticity of the human adenovirus type 5 transcriptome drives virus evolution. Communications Biology, 2020, 3, 124.	2.0	37
15	High Resolution Analysis of Respiratory Syncytial Virus Infection In Vivo. Viruses, 2019, 11, 926.	1.5	13
16	High throughput discovery of protein variants using proteomics informed by transcriptomics. Nucleic Acids Research, 2018, 46, 4893-4902.	6.5	5
17	Zika Virus Infection Preferentially Counterbalances Human Peripheral Monocyte and/or NK Cell Activity. MSphere, 2018, 3, .	1.3	32
18	PITDB: a database of translated genomic elements. Nucleic Acids Research, 2018, 46, D1223-D1228.	6.5	2

#	Article	IF	Citations
19	Transcriptomic signatures differentiate survival from fatal outcomes in humans infected with Ebola virus. Genome Biology, 2017, 18, 4.	3.8	115
20	A comparison of host gene expression signatures associated with infection in vitro by the Makona and Ecran (Mayinga) variants of Ebola virus. Scientific Reports, 2017, 7, 43144.	1.6	21
21	Virus genomes reveal factors that spread and sustained the Ebola epidemic. Nature, 2017, 544, 309-315.	13.7	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. MSphere, 2017, 2, .	1.3	30
23	Proteomics technique opens new frontiers in mobilome research. Mobile Genetic Elements, 2017, 7, 1-9.	1.8	4
24	Proteomics informed by transcriptomics for characterising active transposable elements and genome annotation in Aedes aegypti. BMC Genomics, 2017, 18, 101.	1.2	49
25	Proteomics informed by transcriptomics for characterising differential cellular susceptibility to Nelson Bay orthoreovirus infection. BMC Genomics, 2017, 18, 615.	1.2	6
26	Comparison of protein expression during wild-type, and E1B-55k-deletion, adenovirus infection using quantitative time-course proteomics. Journal of General Virology, 2017, 98, 1377-1388.	1.3	11
27	Investigating the Influence of Ribavirin on Human Respiratory Syncytial Virus RNA Synthesis by Using a High-Resolution Transcriptome Sequencing Approach. Journal of Virology, 2016, 90, 4876-4888.	1.5	32
28	Real-time, portable genome sequencing for Ebola surveillance. Nature, 2016, 530, 228-232.	13.7	1,179
29	Galaxy Integrated Omics: Web-based Standards-Compliant Workflows for Proteomics Informed by Transcriptomics*. Molecular and Cellular Proteomics, 2015, 14, 3087-3093.	2.5	30
30	Identification of Epstein-Barr Virus Replication Proteins in Burkittâ€™s Lymphoma Cells. Pathogens, 2015, 4, 739-751.	1.2	17
31	Temporal and spatial analysis of the 2014â€“2015 Ebola virus outbreak in West Africa. Nature, 2015, 524, 97-101.	13.7	272
32	Elucidating variations in the nucleotide sequence of Ebola virus associated with increasing pathogenicity. Genome Biology, 2014, 15, 540.	3.8	44
33	Analysis of purified Wild type and mutant adenovirus particles by SILAC based quantitative proteomics. Journal of General Virology, 2014, 95, 2504-2511.	1.3	13
34	Factors affecting de novo RNA synthesis and back-priming by the respiratory syncytial virus polymerase. Virology, 2014, 462-463, 318-327.	1.1	24
35	Elucidation of the Ebola Virus VP24 Cellular Interactome and Disruption of Virus Biology through Targeted Inhibition of Host-Cell Protein Function. Journal of Proteome Research, 2014, 13, 5120-5135.	1.8	79
36	High-Throughput Quantitative Proteomic Analysis of Dengue Virus Type 2 Infected A549 Cells. PLoS ONE, 2014, 9, e93305.	1.1	62

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37	The Interactome of the Human Respiratory Syncytial Virus NS1 Protein Highlights Multiple Effects on Host Cell Biology. Journal of Virology, 2012, 86, 7777-7789.	1.5	61
38	Adenoviral protein V promotes a process of viral assembly through nucleophosmin 1. Virology, 2012, 432, 283-295.	1.1	26
39	De novo derivation of proteomes from transcriptomes for transcript and protein identification. Nature Methods, 2012, 9, 1207-1211.	9.0	167
40	Nucleolar proteomics and viral infection. Proteomics, 2010, 10, 4077-4086.	1.3	59
41	Proteomics Analysis of the Nucleolus in Adenovirus-infected Cells. Molecular and Cellular Proteomics, 2010, 9, 117-130.	2.5	106
42	Quantitative Proteomics Using SILAC Coupled to LCâˆ'MS/MS Reveals Changes in the Nucleolar Proteome in Influenza A Virus-Infected Cells. Journal of Proteome Research, 2010, 9, 5335-5345.	1.8	76
43	In Vitro Dynamic Visualization Analysis of Fluorescently Labeled Minor Capsid Protein IX and Core Protein V by Simultaneous Detection. Journal of Molecular Biology, 2010, 395, 55-78.	2.0	16
44	Upstream-binding factor is sequestered into herpes simplex virus type 1 replication compartments. Journal of General Virology, 2009, 90, 69-73.	1.3	15
45	A Role for Transportin in the Nuclear Import of Adenovirus Core Proteins and DNA. Traffic, 2007, 8, 1313-1322.	1.3	57
46	Relationship between adenovirus DNA replication proteins and nucleolar proteins B23.1 and B23.2. Journal of General Virology, 2007, 88, 3244-3248.	1.3	26
47	Study of Nucleolar Localization of Adenovirus Core Proteins. Methods in Molecular Medicine, 2007, 131, 73-81.	0.8	0
48	Core labeling of adenovirus with EGFP. Virology, 2006, 351, 291-302.	1.1	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. Journal of Cell Science, 2006, 119, 2621-2631.	1.2	38
50	Novel molecular approaches to cystic fibrosis gene therapy. Biochemical Journal, 2005, 387, 1-15.	1.7	73
51	The herpesvirus saimiri ORF73 gene product interacts with host-cell mitotic chromosomes and self-associates via its C terminus. Journal of General Virology, 2004, 85, 147-153.	1.3	33
52	Precursor of human adenovirus core polypeptide Mu targets the nucleolus and modulates the expression of E2 proteins. Journal of General Virology, 2004, 85, 185-196.	1.3	29
53	Comparison between the interactions of adenovirus-derived peptides with plasmid DNA and their role in gene delivery mediated by liposomeâ€"peptideâ€"DNA virus-like nanoparticles. Organic and Biomolecular Chemistry, 2003, 1, 2430-2438.	1.5	21
54	Adenovirus core protein VII contains distinct sequences that mediate targeting to the nucleus and nucleolus, and colocalization with human chromosomes. Journal of General Virology, 2003, 84, 3423-3428.	1.3	47

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55	The Herpesvirus Saimiri Open Reading Frame 73 Gene Product Interacts with the Cellular Protein p32. Journal of Virology, 2002, 76, 11612-11622.	1.5	33
56	Mitochondrial Protein p32 Can Accumulate in the Nucleus. Biochemical and Biophysical Research Communications, 2001, 281, 1161-1169.	1.0	54
57	Adenovirus Protein V Induces Redistribution of Nucleolin and B23 from Nucleolus to Cytoplasm. Journal of Virology, 2001, 75, 1031-1038.	1.5	112
58	Enhanced cationic liposome-mediated transfection using the DNA-binding peptide Î¼ (mu) from the adenovirus core. Gene Therapy, 2001, 8, 453-460.	2.3	78
59	Interaction between Herpes Simplex Virus Type 1 IE63 Protein and Cellular Protein p32. Journal of Virology, 2000, 74, 11322-11328.	1.5	46
60	The splicing factor-associated protein, p32, regulates RNA splicing by inhibiting ASF/SF2 RNA binding and phosphorylation. EMBO Journal, 1999, 18, 1014-1024.	3.5	153
61	Identification of mutations contributing to the reduced virulence of a modified strain of respiratory syncytial virus. Vaccine, 1996, 14, 1637-1646.	1.7	43
62	Analysis of relatedness of subgroup A respiratory syncytial viruses isolated worldwide. Virus Research, 1992, 25, 15-22.	1.1	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. Virus Research, 1991, 18, 263-270.	1.1	23