

Edward Emmott

List of Publications by Year in descending order

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37
papers

2,068
citations

304743

22
h-index

330143

37
g-index

55
all docs

55
docs citations

55
times ranked

3149
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-cell proteomic and transcriptomic analysis of macrophage heterogeneity using SCoPE2. <i>Genome Biology</i> , 2021, 22, 50.	8.8	298
2	Nucleolar targeting: the hub of the matter. <i>EMBO Reports</i> , 2009, 10, 231-238.	4.5	249
3	On the value of preprints: An early career researcher perspective. <i>PLoS Biology</i> , 2019, 17, e3000151.	5.6	116
4	Multiplexed single-cell proteomics using SCoPE2. <i>Nature Protocols</i> , 2021, 16, 5398-5425.	12.0	108
5	Quantitative Proteomics Using Stable Isotope Labeling with Amino Acids in Cell Culture Reveals Changes in the Cytoplasmic, Nuclear, and Nucleolar Proteomes in Vero Cells Infected with the Coronavirus Infectious Bronchitis Virus. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1920-1936.	3.8	83
6	Quantitative Proteomic Analysis of A549 Cells Infected with Human Respiratory Syncytial Virus. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2438-2459.	3.8	82
7	The Cellular Interactome of the Coronavirus Infectious Bronchitis Virus Nucleocapsid Protein and Functional Implications for Virus Biology. <i>Journal of Virology</i> , 2013, 87, 9486-9500.	3.4	77
8	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
9	Characterising proteolysis during SARS-CoV-2 infection identifies viral cleavage sites and cellular targets with therapeutic potential. <i>Nature Communications</i> , 2021, 12, 5553.	12.8	76
10	IFIT3 and IFIT2/3 promote IFIT1-mediated translation inhibition by enhancing binding to non-self RNA. <i>Nucleic Acids Research</i> , 2018, 46, 5269-5285.	14.5	72
11	Ribosome Stoichiometry: From Form to Function. <i>Trends in Biochemical Sciences</i> , 2019, 44, 95-109.	7.5	71
12	Using SILAC and quantitative proteomics to investigate the interactions between viral and host proteomes. <i>Proteomics</i> , 2012, 12, 666-672.	2.2	57
13	The COVID-19 MS Coalition "accelerating diagnostics, prognostics, and treatment. <i>Lancet</i> , The, 2020, 395, 1761-1762.	13.7	51
14	Noroviruses subvert the core stress granule component G3BP1 to promote viral VPg-dependent translation. <i>ELife</i> , 2019, 8, .	6.0	48
15	Norovirus-Mediated Modification of the Translational Landscape via Virus and Host-Induced Cleavage of Translation Initiation Factors. <i>Molecular and Cellular Proteomics</i> , 2017, 16, S215-S229.	3.8	40
16	Progress towards the prevention and treatment of norovirus infections. <i>Future Microbiology</i> , 2013, 8, 1475-1487.	2.0	38
17	Adenovirus type 5 E4 Orf3 protein targets promyelocytic leukaemia (PML) protein nuclear domains for disruption via a sequence in PML isoform II that is predicted as a protein interaction site by bioinformatic analysis. <i>Journal of General Virology</i> , 2009, 90, 95-104.	2.9	37
18	Viral nucleolar localisation signals determine dynamic trafficking within the nucleolus. <i>Virology</i> , 2008, 380, 191-202.	2.4	34

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19	Evidence for Human Norovirus Infection of Dogs in the United Kingdom. <i>Journal of Clinical Microbiology</i> , 2015, 53, 1873-1883.	3.9	34
20	Elucidation of the avian nucleolar proteome by quantitative proteomics using SILAC and changes in cells infected with the coronavirus infectious bronchitis virus. <i>Proteomics</i> , 2010, 10, 3558-3562.	2.2	31
21	Temporal Proteomic Analysis of Herpes Simplex Virus 1 Infection Reveals Cell-Surface Remodeling via pUL56-Mediated GOPC Degradation. <i>Cell Reports</i> , 2020, 33, 108235.	6.4	29
22	A Cell-based Fluorescence Resonance Energy Transfer (FRET) Sensor Reveals Inter- and Intra-genogroup Variations in Norovirus Protease Activity and Polyprotein Cleavage. <i>Journal of Biological Chemistry</i> , 2015, 290, 27841-27853.	3.4	25
23	Serological Evidence for Multiple Strains of Canine Norovirus in the UK Dog Population. <i>PLoS ONE</i> , 2013, 8, e81596.	2.5	23
24	VPS18 recruits VPS41 to the human HOPS complex via a RING-RING interaction. <i>Biochemical Journal</i> , 2017, 474, 3615-3626.	3.7	23
25	Identification of Protein Interaction Partners in Mammalian Cells Using SILAC-immunoprecipitation Quantitative Proteomics. <i>Journal of Visualized Experiments</i> , 2014, , .	0.3	19
26	Selection and Characterization of Rupintrivir-Resistant Norwalk Virus Replicon Cells <i>In Vitro</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	18
27	Polyprotein processing and intermolecular interactions within the viral replication complex spatially and temporally control norovirus protease activity. <i>Journal of Biological Chemistry</i> , 2019, 294, 4259-4271.	3.4	18
28	Ifit1 regulates norovirus infection and enhances the interferon response in murine macrophage-like cells. <i>Wellcome Open Research</i> , 2019, 4, 82.	1.8	16
29	Phosphoproteomic Analysis Reveals the Importance of Kinase Regulation During Orbivirus Infection. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1990-2005.	3.8	12
30	Approaches for Studying Ribosome Specialization. <i>Trends in Biochemical Sciences</i> , 2019, 44, 478-479.	7.5	11
31	Vesivirus 2117 capsids more closely resemble sapovirus and lagovirus particles than other known vesivirus structures. <i>Journal of General Virology</i> , 2017, 98, 68-76.	2.9	9
32	Construction of <i>À la carte</i> QconCAT protein standards for multiplexed quantification of user-specified target proteins. <i>BMC Biology</i> , 2021, 19, 195.	3.8	8
33	In vitro sensitivity of human parainfluenza 3 clinical isolates to ribavirin, favipiravir and zanamivir. <i>Journal of Clinical Virology</i> , 2018, 102, 19-26.	3.1	7
34	UK circulating strains of human parainfluenza 3: an amplicon based next generation sequencing method and phylogenetic analysis. <i>Wellcome Open Research</i> , 2018, 3, 118.	1.8	6
35	Unrecognised Outbreak: Human parainfluenza virus infections in a pediatric oncology unit. A new diagnostic PCR and virus monitoring system may allow early detection of future outbreaks. <i>Wellcome Open Research</i> , 2018, 3, 119.	1.8	5
36	UK circulating strains of human parainfluenza 3: an amplicon based next generation sequencing method and phylogenetic analysis. <i>Wellcome Open Research</i> , 2018, 3, 118.	1.8	4

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37	The Cryo-EM Structure of Vesivirus 2117 Highlights Functional Variations in Entry Pathways for Viruses in Different Clades of the <i>Vesivirus</i> Genus. Journal of Virology, 2021, 95, e0028221.	3.4	1