Katherine Smollett

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1418799/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Circulating SARS-CoV-2 spike N439K variants maintain fitness while evading antibody-mediated immunity. Cell, 2021, 184, 1171-1187.e20.	28.9	541
2	Changes in symptomatology, reinfection, and transmissibility associated with the SARS-CoV-2 variant B.1.1.7: an ecological study. Lancet Public Health, The, 2021, 6, e335-e345.	10.0	269
3	A plasmid DNA-launched SARS-CoV-2 reverse genetics system and coronavirus toolkit for COVID-19 research. PLoS Biology, 2021, 19, e3001091.	5.6	163
4	Formation and Abundance of 5â€Hydroxymethylcytosine in RNA. ChemBioChem, 2015, 16, 752-755.	2.6	148
5	Identification of a Novel <i>Citrobacter rodentium</i> Type III Secreted Protein, Espl, and Roles of This and Other Secreted Proteins in Infection. Infection and Immunity, 2004, 72, 2288-2302.	2.2	133
6	Genomic epidemiology reveals multiple introductions of SARS-CoV-2 from mainland Europe into Scotland. Nature Microbiology, 2021, 6, 112-122.	13.3	88
7	Global Analysis of the Regulon of the Transcriptional Repressor LexA, a Key Component of SOS Response in Mycobacterium tuberculosis. Journal of Biological Chemistry, 2012, 287, 22004-22014.	3.4	71
8	TFE and Spt4/5 open and close the RNA polymerase clamp during the transcription cycle. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E1816-25.	7.1	62
9	Enteropathogenic Escherichia coli Type III Effectors EspG and EspG2 Disrupt the Microtubule Network of Intestinal Epithelial Cells. Infection and Immunity, 2005, 73, 4385-4390.	2.2	61
10	Complete architecture of the archaeal RNA polymerase open complex from single-molecule FRET and NPS. Nature Communications, 2015, 6, 6161.	12.8	54
11	Archaeal TFE $\hat{1}$ is a hybrid of TFIIE and the RNA polymerase III subcomplex hRPC62/39. ELife, 2015, 4, e08378.	6.0	50
12	A global analysis of transcription reveals two modes of Spt4/5 recruitment to archaeal RNA polymerase. Nature Microbiology, 2017, 2, 17021.	13.3	47
13	The histone chaperone HIRA promotes the induction of host innate immune defences in response to HSV-1 infection. PLoS Pathogens, 2019, 15, e1007667.	4.7	47
14	Experimental determination of translational start sites resolves uncertainties in genomic open reading frame predictions – application to Mycobacterium tuberculosis. Microbiology (United) Tj ETQq0 0 0 rg	BT1/ @ verlc	ock400 Tf 50 2
15	EspG of enteropathogenic and enterohemorrhagic E. coli binds the Golgi matrix protein GM130 and disrupts the Golgi structure and function. Cellular Microbiology, 2011, 13, 1429-1439.	2.1	36
16	Molecular Mechanisms of Transcription Initiation—Structure, Function, and Evolution of TFE/TFIIE-Like Factors and Open Complex Formation. Journal of Molecular Biology, 2016, 428, 2592-2606.	4.2	35
17	Repression of RNA polymerase by the archaeo-viral regulator ORF145/RIP. Nature Communications, 2016, 7, 13595.	12.8	20
18	The antiviral state has shaped the CpG composition of the vertebrate interferome to avoid	5.6	18

self-targeting. PLoS Biology, 2021, 19, e3001352.

KATHERINE SMOLLETT

#	Article	IF	CITATIONS
19	Function and distribution of EspG2, a type III secretion system effector of enteropathogenic Escherichia coli. Microbes and Infection, 2006, 8, 2220-2227.	1.9	17
20	Convalescent plasma therapy for persistent hepatitis E virus infection. Journal of Hepatology, 2019, 71, 434-438.	3.7	17
21	Promoter-proximal elongation regulates transcription in archaea. Nature Communications, 2021, 12, 5524.	12.8	17
22	Characterisation of the Mycobacterium tuberculosis alternative sigma factor SigG: Its operon and regulon. Tuberculosis, 2013, 93, 482-491.	1.9	16
23	Archaeology of RNA polymerase: factor swapping during the transcription cycle. Biochemical Society Transactions, 2013, 41, 362-367.	3.4	15
24	SigG Does Not Control Gene Expression in Response to DNA Damage in <i>Mycobacterium tuberculosis</i> H37Rv. Journal of Bacteriology, 2011, 193, 1007-1011.	2.2	12
25	Genetic epidemiology of SARS-CoV-2 transmission in renal dialysis units – A high risk community-hospital interface. Journal of Infection, 2021, 83, 96-103.	3.3	12
26	Mycobacterium tuberculosis H37Rv sigC is expressed from two promoters but is not auto-regulatory. Tuberculosis, 2012, 92, 48-55.	1.9	11
27	Transcription in Archaea: Preparation of Methanocaldococcus jannaschii Transcription Machinery. Methods in Molecular Biology, 2015, 1276, 291-303.	0.9	7
28	Seoul Virus Associated with Pet Rats, Scotland, UK, 2019. Emerging Infectious Diseases, 2021, 27, 2677-2680.	4.3	5
29	Transcription in Archaea: In Vitro Transcription Assays for mjRNAP. Methods in Molecular Biology, 2015, 1276, 305-314.	0.9	4
30	Hepatitis E virus: Whole genome sequencing as a new tool for understanding HEV epidemiology and phenotypes. Journal of Clinical Virology, 2021, 139, 104738.	3.1	3
31	A Global Characterisation of the Archaeal Transcription Machinery. Nucleic Acids and Molecular Biology, 2017, , 1-26.	0.2	2