Ron Geller

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Severe Acute Respiratory Syndrome Coronavirus 2 Adaptive Immunity in Nursing Home Residents Following a Third Dose of the Comirnaty Coronavirus Disease 2019 Vaccine. Clinical Infectious Diseases, 2022, 75, e865-e868.	5.8	12
2	Neutralizing antibodies against SARS-CoV-2 variants of concern elicited by the comirnaty COVID-19 vaccine in nursing home residents. Scientific Reports, 2022, 12, 3788.	3.3	22
3	Identification of Cytoplasmic Chaperone Networks Relevant for Respiratory Syncytial Virus Replication. Frontiers in Microbiology, 2022, 13, .	3.5	3
4	The structural role of SARS-CoV-2 genetic background in the emergence and success of spike mutations: The case of the spike A222V mutation. PLoS Pathogens, 2022, 18, e1010631.	4.7	11
5	Potential Influence of Helminth Molecules on COVID-19 Pathology. Trends in Parasitology, 2021, 37, 11-14.	3.3	29
6	Suitability of two rapid lateral flow immunochromatographic assays for predicting SARSâ€CoVâ€⊋ neutralizing activity of sera. Journal of Medical Virology, 2021, 93, 2301-2306.	5.0	12
7	Globally defining the effects of mutations in a picornavirus capsid. ELife, 2021, 10, .	6.0	8
8	Inference of SARS-CoV-2 spike-binding neutralizing antibody titers in sera from hospitalized COVID-19 patients by using commercial enzyme and chemiluminescent immunoassays. European Journal of Clinical Microbiology and Infectious Diseases, 2021, 40, 485-494.	2.9	37
9	Adoptive transfer of ex vivo expanded SARSâ€CoVâ€2â€specific cytotoxic lymphocytes: A viable strategy for COVIDâ€19 immunosuppressed patients?. Transplant Infectious Disease, 2021, 23, e13602.	1.7	9
10	Increased RNA virus population diversity improves adaptability. Scientific Reports, 2021, 11, 6824.	3.3	14
11	Evolutionary and Phenotypic Characterization of Two Spike Mutations in European Lineage 20E of SARS-CoV-2. MBio, 2021, 12, e0231521.	4.1	6
12	Preservation of anti-SARS-CoV-2 neutralising antibodies in convalescent plasma after pathogen reduction with methylene blue and visible light. Blood Transfusion, 2021, , .	0.4	4
13	SARS-CoV-2 antibodies, serum inflammatory biomarkers and clinical severity of hospitalized COVID-19 patients. Journal of Clinical Virology, 2020, 131, 104611.	3.1	61
14	Globally Defining the Effects of Amino Acid Mutations across a Picornavirus Capsid. Proceedings (mdpi), 2020, 50, .	0.2	0
15	Coxsackieviruses Undergo Intercellular Transmission as Pools of Sibling Viral Genomes Associated to Membranes. Proceedings (mdpi), 2020, 50, 120.	0.2	0
16	Valosin-Containing Protein (VCP/p97) Is a Potential Antiviral Target against Mononegavirales. Proceedings (mdpi), 2020, 50, 108.	0.2	0
17	Membrane-Associated Enteroviruses Undergo Intercellular Transmission as Pools of Sibling Viral Genomes. Cell Reports, 2019, 29, 714-723.e4.	6.4	28
18	Hsp90 shapes protein and RNA evolution to balance trade-offs between protein stability and aggregation. Nature Communications, 2018, 9, 1781.	12.8	64

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19	Chaperoning the Mononegavirales: Current Knowledge and Future Directions. Viruses, 2018, 10, 699.	3.3	11
20	Highly heterogeneous mutation rates in the hepatitis C virus genome. Nature Microbiology, 2016, 1, 16045.	13.3	44
21	Extremely High Mutation Rate of HIV-1 In Vivo. PLoS Biology, 2015, 13, e1002251.	5.6	291
22	The external domains of the HIV-1 envelope are a mutational cold spot. Nature Communications, 2015, 6, 8571.	12.8	39
23	Single-Cell Analysis of RNA Virus Infection Identifies Multiple Genetically Diverse Viral Genomes within Single Infectious Units. Cell Host and Microbe, 2015, 18, 424-432.	11.0	75
24	Hsp90 Inhibitors Exhibit Resistance-Free Antiviral Activity against Respiratory Syncytial Virus. PLoS ONE, 2013, 8, e56762.	2.5	54
25	Discovery and validation of small-molecule heat-shock protein 90 inhibitors through multimodality molecular imaging in living subjects. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E2476-85.	7.1	23
26	Broad action of Hsp90 as a host chaperone required for viral replication. Biochimica Et Biophysica Acta - Molecular Cell Research, 2012, 1823, 698-706.	4.1	191
27	Evolutionary constraints on chaperone-mediated folding provide an antiviral approach refractory to development of drug resistance. Genes and Development, 2007, 21, 195-205.	5.9	246
28	The chaperonin TRiC controls polyglutamine aggregation and toxicity through subunit-specific interactions. Nature Cell Biology, 2006, 8, 1155-1162.	10.3	273
29	The D0 Domain of KIR3D Acts as a Major Histocompatibility Complex Class I Binding Enhancer. Journal of Experimental Medicine, 2002, 196, 911-921.	8.5	67
30	Linkage of Patr-AL to Patr-A and- B in the major histocompatibility complex of the common chimpanzee (Pan troglodytes). Immunogenetics, 2002, 54, 212-215.	2.4	10