## Ron Geller

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6038344/publications.pdf

Version: 2024-02-01

30 papers

1,657 citations

16 h-index 27 g-index

42 all docs 42 docs citations

42 times ranked 2853 citing authors

#	Article	IF	CITATIONS
1	Extremely High Mutation Rate of HIV-1 In Vivo. PLoS Biology, 2015, 13, e1002251.	5.6	291
2	The chaperonin TRiC controls polyglutamine aggregation and toxicity through subunit-specific interactions. Nature Cell Biology, 2006, $8,1155-1162$ .	10.3	273
3	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
4	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
5	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
6	The DO Domain of KIR3D Acts as a Major Histocompatibility Complex Class I Binding Enhancer. Journal of Experimental Medicine, 2002, 196, 911-921.	8.5	67
7	Hsp90 shapes protein and RNA evolution to balance trade-offs between protein stability and aggregation. Nature Communications, 2018, 9, 1781.	12.8	64
8	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
9	Hsp90 Inhibitors Exhibit Resistance-Free Antiviral Activity against Respiratory Syncytial Virus. PLoS ONE, 2013, 8, e56762.	2.5	54
10	Highly heterogeneous mutation rates in the hepatitis C virus genome. Nature Microbiology, 2016, 1, $16045$ .	13.3	44
11	The external domains of the HIV-1 envelope are a mutational cold spot. Nature Communications, 2015, 6, 8571.	12.8	39
12	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
13	Potential Influence of Helminth Molecules on COVID-19 Pathology. Trends in Parasitology, 2021, 37, 11-14.	3.3	29
14	Membrane-Associated Enteroviruses Undergo Intercellular Transmission as Pools of Sibling Viral Genomes. Cell Reports, 2019, 29, 714-723.e4.	6.4	28
15	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
16	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
17	Increased RNA virus population diversity improves adaptability. Scientific Reports, 2021, 11, 6824.	3.3	14
18	Suitability of two rapid lateral flow immunochromatographic assays for predicting SARS oVâ€2 neutralizing activity of sera. Journal of Medical Virology, 2021, 93, 2301-2306.	5.0	12

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19	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
20	Chaperoning the Mononegavirales: Current Knowledge and Future Directions. Viruses, 2018, 10, 699.	3.3	11
21	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
22	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
23	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
24	Globally defining the effects of mutations in a picornavirus capsid. ELife, 2021, 10, .	6.0	8
25	Evolutionary and Phenotypic Characterization of Two Spike Mutations in European Lineage 20E of SARS-CoV-2. MBio, 2021, 12, e0231521.	4.1	6
26	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
27	Identification of Cytoplasmic Chaperone Networks Relevant for Respiratory Syncytial Virus Replication. Frontiers in Microbiology, 2022, 13, .	3.5	3
28	Globally Defining the Effects of Amino Acid Mutations across a Picornavirus Capsid. Proceedings (mdpi), 2020, 50, .	0.2	0
29	Coxsackieviruses Undergo Intercellular Transmission as Pools of Sibling Viral Genomes Associated to Membranes. Proceedings (mdpi), 2020, 50, 120.	0.2	0
30	Valosin-Containing Protein (VCP/p97) Is a Potential Antiviral Target against Mononegavirales. Proceedings (mdpi), 2020, 50, 108.	0.2	0