

Akshay Dhingra

List of Publications by Year in descending order

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11
papers

449
citations

1040056

9
h-index

1281871

11
g-index

12
all docs

12
docs citations

12
times ranked

708
citing authors

#	ARTICLE	IF	CITATIONS
1	Herpes Simplex Virus 2 Counteracts Neurite Outgrowth Repulsion during Infection in a Nerve Growth Factor-Dependent Manner. <i>Journal of Virology</i> , 2020, 94, .	3.4	9
2	Whole-Genome Approach to Assessing Human Cytomegalovirus Dynamics in Transplant Patients Undergoing Antiviral Therapy. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 267.	3.9	17
3	Targeting Kaposi's Sarcoma-Associated Herpesvirus ORF21 Tyrosine Kinase and Viral Lytic Reactivation by Tyrosine Kinase Inhibitors Approved for Clinical Use. <i>Journal of Virology</i> , 2020, 94, .	3.4	12
4	Molecular Evolution of Human Adenovirus (HAdV) Species C. <i>Scientific Reports</i> , 2019, 9, 1039.	3.3	101
5	Human Cytomegalovirus Genomes Sequenced Directly From Clinical Material: Variation, Multiple-Strain Infection, Recombination, and Gene Loss. <i>Journal of Infectious Diseases</i> , 2019, 220, 781-791.	4.0	84
6	Kaposi's sarcoma-associated herpesvirus vIRF2 protein utilizes an IFN-dependent pathway to regulate viral early gene expression. <i>PLoS Pathogens</i> , 2019, 15, e1007743.	4.7	12
7	A Novel CARMIL2 Mutation Resulting in Combined Immunodeficiency Manifesting with Dermatitis, Fungal, and Viral Skin Infections As Well as Selective Antibody Deficiency. <i>Journal of Clinical Immunology</i> , 2019, 39, 274-276.	3.8	27
8	A Fosmid-Based System for the Generation of Recombinant Cercopithecine Alphaherpesvirus 2 Encoding Reporter Genes. <i>Viruses</i> , 2019, 11, 1026.	3.3	5
9	Primary immunodeficiency disorder caused by phosphoinositide 3-kinase γ deficiency. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 142, 1650-1653.e2.	2.9	58
10	Human β T Cell Receptor Repertoires in Peripheral Blood Remain Stable Despite Clearance of Persistent Hepatitis C Virus Infection by Direct-Acting Antiviral Drug Therapy. <i>Frontiers in Immunology</i> , 2018, 9, 510.	4.8	31
11	Characterization of Human Cytomegalovirus Genome Diversity in Immunocompromised Hosts by Whole-Genome Sequencing Directly From Clinical Specimens. <i>Journal of Infectious Diseases</i> , 2017, 215, 1673-1683.	4.0	88