

# David H O'connor

## List of Publications by Year in descending order

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230  
papers

13,548  
citations

24978

57  
h-index

29081

104  
g-index

268  
all docs

268  
docs citations

268  
times ranked

13472  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Major Genetic Determinants of HIV-1 Control Affect HLA Class I Peptide Presentation. <i>Science</i> , 2010, 330, 1551-1557.	6.0	1,054
2	Tat-specific cytotoxic T lymphocytes select for SIV escape variants during resolution of primary viraemia. <i>Nature</i> , 2000, 407, 386-390.	13.7	657
3	Virus-specific cytotoxic T-lymphocyte responses select for amino-acid variation in simian immunodeficiency virus Env and Nef. <i>Nature Medicine</i> , 1999, 5, 1270-1276.	15.2	364
4	A rhesus macaque model of Asian-lineage Zika virus infection. <i>Nature Communications</i> , 2016, 7, 12204.	5.8	353
5	Acute phase cytotoxic T lymphocyte escape is a hallmark of simian immunodeficiency virus infection. <i>Nature Medicine</i> , 2002, 8, 493-499.	15.2	350
6	Reversion of CTL escape variant immunodeficiency viruses in vivo. <i>Nature Medicine</i> , 2004, 10, 275-281.	15.2	349
7	HIV-1 superinfection despite broad CD8+ T-cell responses containing replication of the primary virus. <i>Nature</i> , 2002, 420, 434-439.	13.7	321
8	Biological and Structural Characterization of a Host-Adapting Amino Acid in Influenza Virus. <i>PLoS Pathogens</i> , 2010, 6, e1001034.	2.1	299
9	The High-Frequency Major Histocompatibility Complex Class I Allele Mamu-B * 17 Is Associated with Control of Simian Immunodeficiency Virus SIVmac239 Replication. <i>Journal of Virology</i> , 2006, 80, 5074-5077.	1.5	266
10	Reorganization and expansion of the nidoviral family Arteriviridae. <i>Archives of Virology</i> , 2016, 161, 755-768.	0.9	254
11	Attenuation of Simian Immunodeficiency Virus SIVmac239 Infection by Prophylactic Immunization with DNA and Recombinant Adenoviral Vaccine Vectors Expressing Gag. <i>Journal of Virology</i> , 2005, 79, 15547-15555.	1.5	249
12	Vaccine-Induced Cellular Immune Responses Reduce Plasma Viral Concentrations after Repeated Low-Dose Challenge with Pathogenic Simian Immunodeficiency Virus SIVmac239. <i>Journal of Virology</i> , 2006, 80, 5875-5885.	1.5	237
13	Chloroquine, an Endocytosis Blocking Agent, Inhibits Zika Virus Infection in Different Cell Models. <i>Viruses</i> , 2016, 8, 322.	1.5	227
14	Cytotoxic T Lymphocyte-based Control of Simian Immunodeficiency Virus Replication in a Preclinical AIDS Vaccine Trial. <i>Journal of Experimental Medicine</i> , 2004, 199, 1709-1718.	4.2	208
15	Highly efficient maternal-fetal Zika virus transmission in pregnant rhesus macaques. <i>PLoS Pathogens</i> , 2017, 13, e1006378.	2.1	201
16	Mesenchymal Stem Cells Enhance Allogeneic Islet Engraftment in Nonhuman Primates. <i>Diabetes</i> , 2010, 59, 2558-2568.	0.3	192
17	Major Histocompatibility Complex Class I Alleles Associated with Slow Simian Immunodeficiency Virus Disease Progression Bind Epitopes Recognized by Dominant Acute-Phase Cytotoxic-T-Lymphocyte Responses. <i>Journal of Virology</i> , 2003, 77, 9029-9040.	1.5	170
18	Rapid Viral Escape at an Immunodominant Simian-Human Immunodeficiency Virus Cytotoxic T-Lymphocyte Epitope Exact a Dramatic Fitness Cost. <i>Journal of Virology</i> , 2005, 79, 5721-5731.	1.5	164

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19	Simian Immunodeficiency Virus SIVmac239 Infection of Major Histocompatibility Complex-Identical Cynomolgus Macaques from Mauritius. <i>Journal of Virology</i> , 2007, 81, 349-361.	1.5	157
20	CD8+ Lymphocytes from Simian Immunodeficiency Virus-Infected Rhesus Macaques Recognize 14 Different Epitopes Bound by the Major Histocompatibility Complex Class I Molecule Mamu-A*01: Implications for Vaccine Design and Testing. <i>Journal of Virology</i> , 2001, 75, 738-749.	1.5	143
21	Major histocompatibility complex genotyping with massively parallel pyrosequencing. <i>Nature Medicine</i> , 2009, 15, 1322-1326.	15.2	136
22	Heterologous Protection against Asian Zika Virus Challenge in Rhesus Macaques. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0005168.	1.3	125
23	Comprehensive characterization of MHC class II haplotypes in Mauritian cynomolgus macaques. <i>Immunogenetics</i> , 2007, 59, 449-462.	1.2	122
24	The genome of the vervet ( <i>Chlorocebus aethiops sabaeus</i> ). <i>Genome Research</i> , 2015, 25, 1921-1933.	2.4	114
25	Characterization of Mauritian cynomolgus macaque major histocompatibility complex class I haplotypes by high-resolution pyrosequencing. <i>Immunogenetics</i> , 2010, 62, 773-780.	1.2	112
26	Tat-Vaccinated Macaques Do Not Control Simian Immunodeficiency Virus SIVmac239 Replication. <i>Journal of Virology</i> , 2002, 76, 4108-4112.	1.5	110
27	Unusually High Frequency MHC Class I Alleles in Mauritian Origin Cynomolgus Macaques. <i>Journal of Immunology</i> , 2005, 175, 5230-5239.	0.4	108
28	Measuring immunity to SARS-CoV-2 infection: comparing assays and animal models. <i>Nature Reviews Immunology</i> , 2020, 20, 727-738.	10.6	107
29	Sequence diversity analyses of an improved rhesus macaque genome enhance its biomedical utility. <i>Science</i> , 2020, 370, .	6.0	105
30	Zika in the Americas, year 2: What have we learned? What gaps remain? A report from the Global Virus Network. <i>Antiviral Research</i> , 2017, 144, 223-246.	1.9	104
31	Extraepitopic Compensatory Substitutions Partially Restore Fitness to Simian Immunodeficiency Virus Variants That Escape from an Immunodominant Cytotoxic-T-Lymphocyte Response. <i>Journal of Virology</i> , 2004, 78, 2581-2585.	1.5	99
32	Haplessly Hoping: Macaque Major Histocompatibility Complex Made Easy. <i>ILAR Journal</i> , 2013, 54, 196-210.	1.8	98
33	Maternal CD4 <sup>+</sup> T cells protect against severe congenital cytomegalovirus disease in a novel nonhuman primate model of placental cytomegalovirus transmission. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13645-13650.	3.3	90
34	A Dominant Role for CD8 <sup>+</sup> T-Lymphocyte Selection in Simian Immunodeficiency Virus Sequence Variation. <i>Journal of Virology</i> , 2004, 78, 14012-14022.	1.5	89
35	Ocular and uteroplacental pathology in a macaque pregnancy with congenital Zika virus infection. <i>PLoS ONE</i> , 2018, 13, e0190617.	1.1	89
36	A Novel Hepacivirus with an Unusually Long and Intrinsically Disordered NS5A Protein in a Wild Old World Primate. <i>Journal of Virology</i> , 2013, 87, 8971-8981.	1.5	88

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37	Infection via mosquito bite alters Zika virus tissue tropism and replication kinetics in rhesus macaques. <i>Nature Communications</i> , 2017, 8, 2096.	5.8	87
38	Miscarriage and stillbirth following maternal Zika virus infection in nonhuman primates. <i>Nature Medicine</i> , 2018, 24, 1104-1107.	15.2	85
39	Transmission of SARS-CoV-2 in domestic cats imposes a narrow bottleneck. <i>PLoS Pathogens</i> , 2021, 17, e1009373.	2.1	84
40	Identification of Seventeen New Simian Immunodeficiency Virus-Derived CD8+ T Cell Epitopes Restricted by the High Frequency Molecule, Mamu-A*02, and Potential Escape from CTL Recognition. <i>Journal of Immunology</i> , 2004, 173, 5064-5076.	0.4	83
41	Nomenclature report on the major histocompatibility complex genes and alleles of Great Ape, Old and New World monkey species. <i>Immunogenetics</i> , 2012, 64, 615-631.	1.2	82
42	MHC Heterozygote Advantage in Simian Immunodeficiency Virus-Infected Mauritian Cynomolgus Macaques. <i>Science Translational Medicine</i> , 2010, 2, 22ra18.	5.8	80
43	Selection on haemagglutinin imposes a bottleneck during mammalian transmission of reassortant H5N1 influenza viruses. <i>Nature Communications</i> , 2013, 4, 2636.	5.8	80
44	Acute SARS-CoV-2 infections harbor limited within-host diversity and transmit via tight transmission bottlenecks. <i>PLoS Pathogens</i> , 2021, 17, e1009849.	2.1	80
45	Complete Characterization of Killer Ig-Like Receptor (KIR) Haplotypes in Mauritian Cynomolgus Macaques: Novel Insights into Nonhuman Primate KIR Gene Content and Organization. <i>Journal of Immunology</i> , 2008, 181, 6301-6308.	0.4	78
46	Escape in One of Two Cytotoxic T-Lymphocyte Epitopes Bound by a High-Frequency Major Histocompatibility Complex Class I Molecule, Mamu-A*02: a Paradigm for Virus Evolution and Persistence?. <i>Journal of Virology</i> , 2002, 76, 11623-11636.	1.5	77
47	Identification of MHC class I sequences in Chinese-origin rhesus macaques. <i>Immunogenetics</i> , 2008, 60, 37-46.	1.2	75
48	Low-Cost Ultra-Wide Genotyping Using Roche/454 Pyrosequencing for Surveillance of HIV Drug Resistance. <i>PLoS ONE</i> , 2012, 7, e36494.	1.1	75
49	Postnatal Zika virus infection is associated with persistent abnormalities in brain structure, function, and behavior in infant macaques. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	75
50	Definition of Five New Simian Immunodeficiency Virus Cytotoxic T-Lymphocyte Epitopes and Their Restricting Major Histocompatibility Complex Class I Molecules: Evidence for an Influence on Disease Progression. <i>Journal of Virology</i> , 2000, 74, 7400-7410.	1.5	72
51	Mauritian Cynomolgus Macaques Share Two Exceptionally Common Major Histocompatibility Complex Class I Alleles That Restrict Simian Immunodeficiency Virus-Specific CD8 <sup>+</sup> T Cells. <i>Journal of Virology</i> , 2009, 83, 6011-6019.	1.5	72
52	Analysis of Pigtail Macaque Major Histocompatibility Complex Class I Molecules Presenting Immunodominant Simian Immunodeficiency Virus Epitopes. <i>Journal of Virology</i> , 2005, 79, 684-695.	1.5	71
53	Comparative Characterization of Transfection- and Infection-Derived Simian Immunodeficiency Virus Challenge Stocks for <i>In Vivo</i> Nonhuman Primate Studies. <i>Journal of Virology</i> , 2013, 87, 4584-4595.	1.5	71
54	No assembly required: Full-length MHC class I allele discovery by PacBio circular consensus sequencing. <i>Human Immunology</i> , 2015, 76, 891-896.	1.2	68

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55	GB Virus C Coinfections in West African Ebola Patients. <i>Journal of Virology</i> , 2015, 89, 2425-2429.	1.5	65
56	Simultaneous Positive and Purifying Selection on Overlapping Reading Frames of the tat and vpr Genes of Simian Immunodeficiency Virus. <i>Journal of Virology</i> , 2001, 75, 7966-7972.	1.5	63
57	Whole-Genome Characterization of Human and Simian Immunodeficiency Virus Intra-host Diversity by Ultradeep Pyrosequencing. <i>Journal of Virology</i> , 2010, 84, 12087-12092.	1.5	63
58	Novel, Divergent Simian Hemorrhagic Fever Viruses in a Wild Ugandan Red Colobus Monkey Discovered Using Direct Pyrosequencing. <i>PLoS ONE</i> , 2011, 6, e19056.	1.1	63
59	Characterization of a new SARS-CoV-2 variant that emerged in Brazil. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	63
60	Ultradeep Pyrosequencing Detects Complex Patterns of CD8 <sup>+</sup> T-Lymphocyte Escape in Simian Immunodeficiency Virus-Infected Macaques. <i>Journal of Virology</i> , 2009, 83, 8247-8253.	1.5	61
61	Exceptional Simian Hemorrhagic Fever Virus Diversity in a Wild African Primate Community. <i>Journal of Virology</i> , 2013, 87, 688-691.	1.5	61
62	KIR Polymorphisms Modulate Peptide-Dependent Binding to an MHC Class I Ligand with a Bw6 Motif. <i>PLoS Pathogens</i> , 2011, 7, e1001316.	2.1	60
63	The landscape of antibody binding in SARS-CoV-2 infection. <i>PLoS Biology</i> , 2021, 19, e3001265.	2.6	58
64	Specific CD8 <sup>+</sup> T Cell Responses Correlate with Control of Simian Immunodeficiency Virus Replication in Mauritian Cynomolgus Macaques. <i>Journal of Virology</i> , 2012, 86, 7596-7604.	1.5	56
65	The Role of MHC-E in T Cell Immunity Is Conserved among Humans, Rhesus Macaques, and Cynomolgus Macaques. <i>Journal of Immunology</i> , 2018, 200, 49-60.	0.4	54
66	Cytotoxic T-Lymphocyte Escape Does Not Always Explain the Transient Control of Simian Immunodeficiency Virus SIVmac239 Viremia in Adenovirus-Boosted and DNA-Primed Mamu-A*01-Positive Rhesus Macaques. <i>Journal of Virology</i> , 2005, 79, 15556-15566.	1.5	53
67	Infection with Escaped Virus Variants Impairs Control of Simian Immunodeficiency Virus SIVmac239 Replication in Mamu-B*08-Positive Macaques. <i>Journal of Virology</i> , 2009, 83, 11514-11527.	1.5	53
68	Effects of Cytotoxic T Lymphocytes (CTL) Directed against a Single Simian Immunodeficiency Virus (SIV) Gag CTL Epitope on the Course of SIVmac239 Infection. <i>Journal of Virology</i> , 2002, 76, 10507-10511.	1.5	52
69	MHC class I characterization of Indonesian cynomolgus macaques. <i>Immunogenetics</i> , 2008, 60, 339-51.	1.2	52
70	A novel single cDNA amplicon pyrosequencing method for high-throughput, cost-effective sequence-based HLA class I genotyping. <i>Human Immunology</i> , 2010, 71, 1011-1017.	1.2	50
71	Seroprevalence of Zika Virus in Wild African Green Monkeys and Baboons. <i>MSphere</i> , 2017, 2, .	1.3	50
72	Oropharyngeal mucosal transmission of Zika virus in rhesus macaques. <i>Nature Communications</i> , 2017, 8, 169.	5.8	49

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73	Zoonotic Potential of Simian Arteriviruses. <i>Journal of Virology</i> , 2016, 90, 630-635.	1.5	48
74	Antibody Responses to Zika Virus Infections in Environments of Flavivirus Endemicity. <i>Vaccine Journal</i> , 2017, 24, .	3.2	48
75	MHC haplotype frequencies in a UK breeding colony of Mauritian cynomolgus macaques mirror those found in a distinct population from the same geographic origin. <i>Journal of Medical Primatology</i> , 2009, 38, 1-14.	0.3	47
76	Transcriptionally Abundant Major Histocompatibility Complex Class I Alleles Are Fundamental to Nonhuman Primate Simian Immunodeficiency Virus-Specific CD8 <sup>+</sup> T Cell Responses. <i>Journal of Virology</i> , 2011, 85, 3250-3261.	1.5	47
77	Primary infection with dengue or Zika virus does not affect the severity of heterologous secondary infection in macaques. <i>PLoS Pathogens</i> , 2019, 15, e1007766.	2.1	46
78	The pigtail macaque MHC class I allele Mane-A*10 presents an immunodominant SIV Gag epitope: identification, tetramer development and implications of immune escape and reversion. <i>Journal of Medical Primatology</i> , 2005, 34, 282-293.	0.3	45
79	Characterization of killer immunoglobulin-like receptor genetics and comprehensive genotyping by pyrosequencing in rhesus macaques. <i>BMC Genomics</i> , 2011, 12, 295.	1.2	45
80	Discovery and Characterization of Distinct Simian Pegiviruses in Three Wild African Old World Monkey Species. <i>PLoS ONE</i> , 2014, 9, e98569.	1.1	45
81	Major Histocompatibility Complex Class I Haplotype Diversity in Chinese Rhesus Macaques. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1195-1201.	0.8	44
82	Viral Sequencing to Investigate Sources of SARS-CoV-2 Infection in US Healthcare Personnel. <i>Clinical Infectious Diseases</i> , 2021, 73, e1329-e1336.	2.9	43
83	Analysis of Hepatitis C Virus Intra-host Diversity across the Coding Region by Ultradeep Pyrosequencing. <i>Journal of Virology</i> , 2012, 86, 3952-3960.	1.5	42
84	Understanding cytotoxic T-lymphocyte escape during simian immunodeficiency virus infection. <i>Immunological Reviews</i> , 2001, 183, 115-126.	2.8	41
85	Characterization of 47 MHC class I sequences in Filipino cynomolgus macaques. <i>Immunogenetics</i> , 2009, 61, 177-187.	1.2	41
86	Risk of Zika microcephaly correlates with features of maternal antibodies. <i>Journal of Experimental Medicine</i> , 2019, 216, 2302-2315.	4.2	41
87	Control of Simian Immunodeficiency Virus SIV <sub>mac239</sub> Is Not Predicted by Inheritance of Mamu-B * 17-Containing Haplotypes. <i>Journal of Virology</i> , 2007, 81, 406-410.	1.5	40
88	Comparative study of Tat vaccine regimens in Mauritian cynomolgus and Indian rhesus macaques: Influence of Mauritian MHC haplotypes on susceptibility/resistance to SHIV89.6P infection. <i>Vaccine</i> , 2008, 26, 3312-3321.	1.7	40
89	Major histocompatibility complex haplotyping and long-amplicon allele discovery in cynomolgus macaques from Chinese breeding facilities. <i>Immunogenetics</i> , 2017, 69, 211-229.	1.2	40
90	The TB-specific CD4 <sup>+</sup> T cell immune repertoire in both cynomolgus and rhesus macaques largely overlap with humans. <i>Tuberculosis</i> , 2015, 95, 722-735.	0.8	39

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91	Revealing fine-scale spatiotemporal differences in SARS-CoV-2 introduction and spread. <i>Nature Communications</i> , 2020, 11, 5558.	5.8	39
92	Variable Prevalence and Functional Diversity of the Antiretroviral Restriction Factor TRIMCyp in <i>Macaca fascicularis</i> . <i>Journal of Virology</i> , 2011, 85, 9956-9963.	1.5	38
93	Ultra-high resolution HLA genotyping and allele discovery by highly multiplexed cDNA amplicon pyrosequencing. <i>BMC Genomics</i> , 2012, 13, 378.	1.2	38
94	Inter- and Intra-Host Viral Diversity in a Large Seasonal DENV2 Outbreak. <i>PLoS ONE</i> , 2013, 8, e70318.	1.1	38
95	Simian Hemorrhagic Fever Virus Cell Entry Is Dependent on CD163 and Uses a Clathrin-Mediated Endocytosis-Like Pathway. <i>Journal of Virology</i> , 2015, 89, 844-856.	1.5	38
96	Microbial Translocation and Inflammation Occur in Hyperacute Immunodeficiency Virus Infection and Compromise Host Control of Virus Replication. <i>PLoS Pathogens</i> , 2016, 12, e1006048.	2.1	38
97	Molecularly barcoded Zika virus libraries to probe in vivo evolutionary dynamics. <i>PLoS Pathogens</i> , 2018, 14, e1006964.	2.1	38
98	MHC class I allele frequencies in pigtail macaques of diverse origin. <i>Immunogenetics</i> , 2006, 58, 995-1001.	1.2	37
99	Discovery and full genome characterization of two highly divergent simian immunodeficiency viruses infecting black-and-white colobus monkeys ( <i>Colobus guereza</i> ) in Kibale National Park, Uganda. <i>Retrovirology</i> , 2013, 10, 107.	0.9	37
100	Differential MHC class I expression in distinct leukocyte subsets. <i>BMC Immunology</i> , 2011, 12, 39.	0.9	36
101	Hepatitis C Virus NS3/NS4A DNA Vaccine Induces Multi-epitope T Cell Responses in Rhesus Macaques Mimicking Human Immune Responses. <i>Molecular Therapy</i> , 2012, 20, 669-678.	3.7	36
102	High Genetic Diversity and Adaptive Potential of Two Simian Hemorrhagic Fever Viruses in a Wild Primate Population. <i>PLoS ONE</i> , 2014, 9, e90714.	1.1	36
103	Consequences of Cytotoxic T-Lymphocyte Escape: Common Escape Mutations in Simian Immunodeficiency Virus Are Poorly Recognized in Naïve Hosts. <i>Journal of Virology</i> , 2004, 78, 10064-10073.	1.5	35
104	Optimizing direct RT-LAMP to detect transmissible SARS-CoV-2 from primary nasopharyngeal swab samples. <i>PLoS ONE</i> , 2020, 15, e0244882.	1.1	35
105	Identification of novel MHC class I sequences in pig-tailed macaques by amplicon pyrosequencing and full-length cDNA cloning and sequencing. <i>Immunogenetics</i> , 2009, 61, 689-701.	1.2	34
106	Trafficking, Persistence, and Activation State of Adoptively Transferred Allogeneic and Autologous Simian Immunodeficiency Virus-Specific CD8+T Cell Clones during Acute and Chronic Infection of Rhesus Macaques. <i>Journal of Immunology</i> , 2010, 184, 303-314.	0.4	34
107	Co-infection and cross-species transmission of divergent <i>Hepatozoon</i> lineages in a wild African primate community. <i>International Journal for Parasitology</i> , 2013, 43, 613-619.	1.3	32
108	Cross-clade simultaneous HIV drug resistance genotyping for reverse transcriptase, protease, and integrase inhibitor mutations by Illumina MiSeq. <i>Retrovirology</i> , 2014, 11, 122.	0.9	32



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109	Escape from CD8+ T Cell Responses in Mamu-B*00801+ Macaques Differentiates Progressors from Elite Controllers. <i>Journal of Immunology</i> , 2012, 188, 3364-3370.	0.4	31
110	Impact of Viral Dose and Major Histocompatibility Complex Class IB Haplotype on Viral Outcome in Mauritian Cynomolgus Monkeys Vaccinated with Tat upon Challenge with Simian/Human Immunodeficiency Virus SHIV89.6P. <i>Journal of Virology</i> , 2010, 84, 8953-8958.	1.5	30
111	Whole genome sequencing of SIV-infected macaques identifies candidate loci that may contribute to host control of virus replication. <i>Genome Biology</i> , 2014, 15, 478.	3.8	30
112	KIR3DL01 Recognition of Bw4 Ligands in the Rhesus Macaque: Maintenance of Bw4 Specificity since the Divergence of Apes and Old World Monkeys. <i>Journal of Immunology</i> , 2014, 192, 1907-1917.	0.4	30
113	Efficacy of Multivalent Adenovirus-Based Vaccine against Simian Immunodeficiency Virus Challenge. <i>Journal of Virology</i> , 2010, 84, 2996-3003.	1.5	29
114	Extralymphoid CD8 <sup>+</sup> T Cells Resident in Tissue from Simian Immunodeficiency Virus SIVmac239 <sup>nef</sup> -Vaccinated Macaques Suppress SIVmac239 Replication <i>Ex Vivo</i> . <i>Journal of Virology</i> , 2010, 84, 3362-3372.	1.5	29
115	Screening and confirmatory testing of MHC class I alleles in pig-tailed macaques. <i>Immunogenetics</i> , 2011, 63, 511-521.	1.2	29
116	Loss of Effector and Anti-Inflammatory Natural Killer T Lymphocyte Function in Pathogenic Simian Immunodeficiency Virus Infection. <i>PLoS Pathogens</i> , 2012, 8, e1002928.	2.1	29
117	Conditional CD8 <sup>+</sup> T Cell Escape during Acute Simian Immunodeficiency Virus Infection. <i>Journal of Virology</i> , 2012, 86, 605-609.	1.5	29
118	Survey of major histocompatibility complex class II diversity in pig-tailed macaques. <i>Immunogenetics</i> , 2014, 66, 613-623.	1.2	29
119	Macaque monkeys in Zika virus research: 1947â€‘present. <i>Current Opinion in Virology</i> , 2017, 25, 34-40.	2.6	29
120	Two Novel Simian Arteriviruses in Captive and Wild Baboons ( <i>Papio</i> spp.). <i>Journal of Virology</i> , 2014, 88, 13231-13239.	1.5	28
121	Oil immersed lossless total analysis system for integrated RNA extraction and detection of SARS-CoV-2. <i>Nature Communications</i> , 2021, 12, 4317.	5.8	28
122	Loop-Mediated Isothermal Amplification Detection of SARS-CoV-2 and Myriad Other Applications. <i>Journal of Biomolecular Techniques</i> , 2021, 32, 228-275.	0.8	28
123	Using Macaques to Address Critical Questions in Zika Virus Research. <i>Annual Review of Virology</i> , 2019, 6, 481-500.	3.0	27
124	Direct identification of an HPV-16 tumor antigen from cervical cancer biopsy specimens. <i>Frontiers in Immunology</i> , 2011, 2, 75.	2.2	26
125	Arteriviruses, Pegiviruses, and Lentiviruses Are Common among Wild African Monkeys. <i>Journal of Virology</i> , 2016, 90, 6724-6737.	1.5	26
126	African-Lineage Zika Virus Replication Dynamics and Maternal-Fetal Interface Infection in Pregnant Rhesus Macaques. <i>Journal of Virology</i> , 2021, 95, e0222020.	1.5	26



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127	Improved full-length killer cell immunoglobulin-like receptor transcript discovery in Mauritian cynomolgus macaques. <i>Immunogenetics</i> , 2017, 69, 325-339.	1.2	25
128	Allogeneic Lymphocytes Persist and Traffic in Feral MHC-Matched Mauritian Cynomolgus Macaques. <i>PLoS ONE</i> , 2008, 3, e2384.	1.1	25
129	Long-Term Programming of Antigen-Specific Immunity from Gene Expression Signatures in the PBMC of Rhesus Macaques Immunized with an SIV DNA Vaccine. <i>PLoS ONE</i> , 2011, 6, e19681.	1.1	25
130	Interventions to Disrupt Coronavirus Disease Transmission at a University, Wisconsin, USA, August–October 2020. <i>Emerging Infectious Diseases</i> , 2021, 27, 2776-2785.	2.0	24
131	Characterization of full-length MHC class II sequences in Indonesian and Vietnamese cynomolgus macaques. <i>Immunogenetics</i> , 2011, 63, 611-618.	1.2	23
132	Specific COVID-19 Symptoms Correlate with High Antibody Levels against SARS-CoV-2. <i>ImmunoHorizons</i> , 2021, 5, 466-476.	0.8	23
133	Durable sequence stability and bone marrow tropism in a macaque model of human pegivirus infection. <i>Science Translational Medicine</i> , 2015, 7, 305ra144.	5.8	22
134	Severe Acute Respiratory Syndrome Coronavirus 2 Transmission in Intercollegiate Athletics Not Fully Mitigated With Daily Antigen Testing. <i>Clinical Infectious Diseases</i> , 2021, 73, S45-S53.	2.9	22
135	SARS-CoV-2 Genomic Surveillance Reveals Little Spread From a Large University Campus to the Surrounding Community. <i>Open Forum Infectious Diseases</i> , 2021, 8, ofab518.	0.4	22
136	Fatal Metacestode Infection in Bornean Orangutan Caused by Unknown <i>Versteria</i> Species. <i>Emerging Infectious Diseases</i> , 2014, 20, 109-113.	2.0	21
137	Linking Pig-Tailed Macaque Major Histocompatibility Complex Class I Haplotypes and Cytotoxic T Lymphocyte Escape Mutations in Simian Immunodeficiency Virus Infection. <i>Journal of Virology</i> , 2014, 88, 14310-14325.	1.5	21
138	Expansion of Simian Immunodeficiency Virus (SIV)-Specific CD8 T Cell Lines from SIV-Naive Mauritian Cynomolgus Macaques for Adoptive Transfer. <i>Journal of Virology</i> , 2015, 89, 9748-9757.	1.5	21
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