

David H O'connor

List of Publications by Year in descending order

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Version: 2024-02-01

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	Characterization of the SARS-CoV-2 B.1.621 (Mu) variant. <i>Science Translational Medicine</i> , 2022, 14, eabm4908.	5.8	21
2	Anti-membrane Antibodies Persist at Least One Year and Discriminate Between Past Coronavirus Disease 2019 Infection and Vaccination. <i>Journal of Infectious Diseases</i> , 2022, 226, 1897-1902.	1.9	9
3	Human immune globulin treatment controls Zika viremia in pregnant rhesus macaques. <i>PLoS ONE</i> , 2022, 17, e0266664.	1.1	4
4	Transmission of SARS-CoV-2 in domestic cats imposes a narrow bottleneck. <i>PLoS Pathogens</i> , 2021, 17, e1009373.	2.1	84
5	Consistent ultra-long DNA sequencing with automated slow pipetting. <i>BMC Genomics</i> , 2021, 22, 182.	1.2	9
6	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
7	Development and Characterization of a cDNA-Launch Recombinant Simian Hemorrhagic Fever Virus Expressing Enhanced Green Fluorescent Protein: ORF 2bâ€™™ Is Not Required for In Vitro Virus Replication. <i>Viruses</i> , 2021, 13, 632.	1.5	5
8	Early Embryonic Loss Following Intravaginal Zika Virus Challenge in Rhesus Macaques. <i>Frontiers in Immunology</i> , 2021, 12, 686437.	2.2	9
9	The landscape of antibody binding in SARS-CoV-2 infection. <i>PLoS Biology</i> , 2021, 19, e3001265.	2.6	58
10	Specific COVID-19 Symptoms Correlate with High Antibody Levels against SARS-CoV-2. <i>ImmunoHorizons</i> , 2021, 5, 466-476.	0.8	23
11	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
12	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
13	Previous exposure to dengue virus is associated with increased Zika virus burden at the maternal-fetal interface in rhesus macaques. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009641.	1.3	20
14	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
15	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
16	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
17	Mind the gap from research laboratory to clinic: Challenges and opportunities for next-generation assays in human diseases. <i>Vaccine</i> , 2021, 39, 5233-5239.	1.7	0
18	Neonatal Development in Prenatally Zika Virus-Exposed Infant Macaques with Dengue Immunity. <i>Viruses</i> , 2021, 13, 1878.	1.5	11

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19	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
20	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
21	Initial Evaluation of a Mobile SARS-CoV-2 RT-LAMP Testing Strategy. <i>Journal of Biomolecular Techniques</i> , 2021, 32, 137-147.	0.8	11
22	The First COVIDecade. <i>Wisconsin Medical Journal</i> , 2021, 120, 162-163.	0.3	0
23	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
24	Nomenclature report 2019: major histocompatibility complex genes and alleles of Great and Small Ape and Old and New World monkey species. <i>Immunogenetics</i> , 2020, 72, 25-36.	1.2	17
25	Nomenclature report for killer-cell immunoglobulin-like receptors (KIR) in macaque species: new genes/alleles, renaming recombinant entities and IPD-NHKIR updates. <i>Immunogenetics</i> , 2020, 72, 37-47.	1.2	14
26	Functional Interactions of Common Allotypes of Rhesus Macaque FcγR2A and FcγR3A with Human and Macaque IgG Subclasses. <i>Journal of Immunology</i> , 2020, 205, 3319-3332.	0.4	9
27	Revealing fine-scale spatiotemporal differences in SARS-CoV-2 introduction and spread. <i>Nature Communications</i> , 2020, 11, 5558.	5.8	39
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	Discovery of a Novel Simian Pegivirus in Common Marmosets (<i>Callithrix jacchus</i>) with Lymphocytic Enterocolitis. <i>Microorganisms</i> , 2020, 8, 1509.	1.6	3
30	Sequence diversity analyses of an improved rhesus macaque genome enhance its biomedical utility. <i>Science</i> , 2020, 370, .	6.0	105
31	Discovery of Lanama Virus, a Distinct Member of Species Kunsagivirus C (Picornavirales): Tj ETQq1 1 0.784314 rgBT 1.5 Overlock 10 Tf 5		
32	Long-Term Protection of Rhesus Macaques from Zika Virus Reinfection. <i>Journal of Virology</i> , 2020, 94, .	1.5	7
33	Spondweni virus causes fetal harm in <i>Ifnar1</i> mice and is transmitted by <i>Aedes aegypti</i> mosquitoes. <i>Virology</i> , 2020, 547, 35-46.	1.1	12
34	Characterization of 100 extended major histocompatibility complex haplotypes in Indonesian cynomolgus macaques. <i>Immunogenetics</i> , 2020, 72, 225-239.	1.2	16
35	High-Throughput Identification of MHC Class I Binding Peptides Using an Ultradense Peptide Array. <i>Journal of Immunology</i> , 2020, 204, 1689-1696.	0.4	13
36	Quantitative definition of neurobehavior, vision, hearing and brain volumes in macaques congenitally exposed to Zika virus. <i>PLoS ONE</i> , 2020, 15, e0235877.	1.1	16

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37	Optimizing direct RT-LAMP to detect transmissible SARS-CoV-2 from primary nasopharyngeal swab samples. PLoS ONE, 2020, 15, e0244882.	1.1	35
38	Title is missing!. , 2020, 15, e0235877.		0
39	Title is missing!. , 2020, 15, e0235877.		0
40	Title is missing!. , 2020, 15, e0235877.		0
41	Title is missing!. , 2020, 15, e0235877.		0
42	Title is missing!. , 2020, 15, e0244882.		0
43	Title is missing!. , 2020, 15, e0244882.		0
44	Title is missing!. , 2020, 15, e0244882.		0
45	Title is missing!. , 2020, 15, e0244882.		0
46	Risk of Zika microcephaly correlates with features of maternal antibodies. Journal of Experimental Medicine, 2019, 216, 2302-2315.	4.2	41
47	Primary infection with dengue or Zika virus does not affect the severity of heterologous secondary infection in macaques. PLoS Pathogens, 2019, 15, e1007766.	2.1	46
48	MHC genotyping from rhesus macaque exome sequences. Immunogenetics, 2019, 71, 531-544.	1.2	16
49	Human, Nonhuman Primate, and Bat Cells Are Broadly Susceptible to Tibrovirus Particle Cell Entry. Frontiers in Microbiology, 2019, 10, 856.	1.5	8
50	Using Macaques to Address Critical Questions in Zika Virus Research. Annual Review of Virology, 2019, 6, 481-500.	3.0	27
51	Clinical Characterization of Host Response to Simian Hemorrhagic Fever Virus Infection in Permissive and Refractory Hosts: A Model for Determining Mechanisms of VHF Pathogenesis. Viruses, 2019, 11, 67.	1.5	3
52	Characterization of Mauritian Cynomolgus Macaque Fcγ3R Alleles Using Long-Read Sequencing. Journal of Immunology, 2019, 202, 151-159.	0.4	8
53	Restricted MHC class I A locus diversity in olive and hybrid olive/yellow baboons from the Southwest National Primate Research Center. Immunogenetics, 2018, 70, 449-458.	1.2	4
54	Postnatal Zika virus infection is associated with persistent abnormalities in brain structure, function, and behavior in infant macaques. Science Translational Medicine, 2018, 10, .	5.8	75

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55	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
56	Novel full-length major histocompatibility complex class I allele discovery and haplotype definition in pig-tailed macaques. <i>Immunogenetics</i> , 2018, 70, 381-399.	1.2	9
57	Subclinical Infection of Macaques and Baboons with A Baboon Simarterivirus. <i>Viruses</i> , 2018, 10, 701.	1.5	3
58	Antibody responses to Zika virus proteins in pregnant and non-pregnant macaques. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006903.	1.3	15
59	Diversification of Bw4 Specificity and Recognition of a Nonclassical MHC Class I Molecule Implicated in Maternal Fetal Tolerance by Killer Cell Ig-like Receptors of the Rhesus Macaque. <i>Journal of Immunology</i> , 2018, 201, 2776-2786.	0.4	6
60	Miscarriage and stillbirth following maternal Zika virus infection in nonhuman primates. <i>Nature Medicine</i> , 2018, 24, 1104-1107.	15.2	85
61	Ocular and uteroplacental pathology in a macaque pregnancy with congenital Zika virus infection. <i>PLoS ONE</i> , 2018, 13, e0190617.	1.1	89
62	Molecularly barcoded Zika virus libraries to probe in vivo evolutionary dynamics. <i>PLoS Pathogens</i> , 2018, 14, e1006964.	2.1	38
63	Antibody Responses to Zika Virus Infections in Environments of Flavivirus Endemicity. <i>Vaccine Journal</i> , 2017, 24, .	3.2	48
64	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
65	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
66	Within-Host Evolution of Simian Arteriviruses in Crab-Eating Macaques. <i>Journal of Virology</i> , 2017, 91, .	1.5	4
67	Improved full-length killer cell immunoglobulin-like receptor transcript discovery in Mauritian cynomolgus macaques. <i>Immunogenetics</i> , 2017, 69, 325-339.	1.2	25
68	Seroprevalence of Zika Virus in Wild African Green Monkeys and Baboons. <i>MSphere</i> , 2017, 2, .	1.3	50
69	Macaque monkeys in Zika virus research: 1947 present. <i>Current Opinion in Virology</i> , 2017, 25, 34-40.	2.6	29
70	Oropharyngeal mucosal transmission of Zika virus in rhesus macaques. <i>Nature Communications</i> , 2017, 8, 169.	5.8	49
71	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
72	Genome Sequence of a Novel Kunsagivirus (<i>Picornaviridae</i> : <i>Kunsagivirus</i>) from a Wild Baboon (<i>Papio cynocephalus</i>). <i>Genome Announcements</i> , 2017, 5, .	0.8	2

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73	The orthologs of HLA-DQ and -DP genes display abundant levels of variability in macaque species. <i>Immunogenetics</i> , 2017, 69, 87-99.	1.2	15
74	Development of a Qualitative Quantitative Polymerase Chain Reaction Test to Identify Patients Failing First-Line Therapy to Non-Nucleotide Reverse Transcriptase Inhibitor. <i>AIDS Research and Human Retroviruses</i> , 2017, 33, 386-394.	0.5	0
75	Highly efficient maternal-fetal Zika virus transmission in pregnant rhesus macaques. <i>PLoS Pathogens</i> , 2017, 13, e1006378.	2.1	201
76	KIR3DL01 upregulation on gut natural killer cells in response to SIV infection of KIR- and MHC class I-defined rhesus macaques. <i>PLoS Pathogens</i> , 2017, 13, e1006506.	2.1	21
77	Pegivirus avoids immune recognition but does not attenuate acute-phase disease in a macaque model of HIV infection. <i>PLoS Pathogens</i> , 2017, 13, e1006692.	2.1	15
78	Divergent Simian Arteriviruses Cause Simian Hemorrhagic Fever of Differing Severities in Macaques. <i>MBio</i> , 2016, 7, e02009-15.	1.8	14
79	Chloroquine, an Endocytosis Blocking Agent, Inhibits Zika Virus Infection in Different Cell Models. <i>Viruses</i> , 2016, 8, 322.	1.5	227
80	Heterologous Protection against Asian Zika Virus Challenge in Rhesus Macaques. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0005168.	1.3	125
81	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
82	Forging Collaborative Relationships in Brazil: From AIDS to ZIKV. <i>Cell</i> , 2016, 166, 2-4.	13.5	3
83	Real-Time Sharing of Zika Virus Data in an Interconnected World. <i>JAMA Pediatrics</i> , 2016, 170, 633.	3.3	6
84	Arteriviruses, Pegiviruses, and Lentiviruses Are Common among Wild African Monkeys. <i>Journal of Virology</i> , 2016, 90, 6724-6737.	1.5	26
85	Tetherin Antagonism by HIV-1 Group M Nef Proteins. <i>Journal of Virology</i> , 2016, 90, 10701-10714.	1.5	16
86	A rhesus macaque model of Asian-lineage Zika virus infection. <i>Nature Communications</i> , 2016, 7, 12204.	5.8	353
87	Zoonotic Potential of Simian Arteriviruses. <i>Journal of Virology</i> , 2016, 90, 630-635.	1.5	48
88	Rapid identification of major histocompatibility complex class I haplotypes using deep sequencing in an endangered Old World monkey. <i>Conservation Genetics Resources</i> , 2016, 8, 23-26.	0.4	4
89	Reorganization and expansion of the nidoviral family Arteriviridae. <i>Archives of Virology</i> , 2016, 161, 755-768.	0.9	254
90	Specific Detection of Two Divergent Simian Arteriviruses Using RNAscope In Situ Hybridization. <i>PLoS ONE</i> , 2016, 11, e0151313.	1.1	7

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91	GB Virus C Coinfections in West African Ebola Patients. <i>Journal of Virology</i> , 2015, 89, 2425-2429.	1.5	65
92	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
93	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
94	Elite Control, Gut CD4 T Cell Sparing, and Enhanced Mucosal T Cell Responses in <i>Macaca nemestrina</i> Infected by a Simian Immunodeficiency Virus Lacking a gp41 Trafficking Motif. <i>Journal of Virology</i> , 2015, 89, 10156-10175.	1.5	19
95	LayerCake: a tool for the visual comparison of viral deep sequencing data. <i>Bioinformatics</i> , 2015, 31, 3522-3528.	1.8	5
96	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
97	Expansion of Simian Immunodeficiency Virus (SIV)-Specific CD8 T Cell Lines from SIV-Naive Mauritian <i>Cynomolgus</i> Macaques for Adoptive Transfer. <i>Journal of Virology</i> , 2015, 89, 9748-9757.	1.5	21
98	Genome Sequence of Bivens Arm Virus, a Tibrovirus Belonging to the Species <i>Tibrogargan virus</i> (<i>Tj ETQq0 0 0 rgBT</i>). <i>Overlook</i> 10 Tf 50 4	0.8	8
99	Maternal CD4 ⁺ 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
100	The TB-specific CD4 ⁺ T cell immune repertoire in both <i>cynomolgus</i> and rhesus macaques largely overlap with humans. <i>Tuberculosis</i> , 2015, 95, 722-735.	0.8	39
101	Novel MHC class I full-length allele and haplotype characterization in sooty mangabeys. <i>Immunogenetics</i> , 2015, 67, 437-445.	1.2	14
102	Historical Outbreaks of Simian Hemorrhagic Fever in Captive Macaques Were Caused by Distinct Arteriviruses. <i>Journal of Virology</i> , 2015, 89, 8082-8087.	1.5	21
103	The genome of the vervet (<i>Chlorocebus aethiops sabaeus</i>). <i>Genome Research</i> , 2015, 25, 1921-1933.	2.4	114
104	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
105	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
106	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
107	Genome Sequences of Simian Hemorrhagic Fever Virus Variant NIH LVR42-0/M6941 Isolates (Arteriviridae: Arterivirus). <i>Genome Announcements</i> , 2014, 2, .	0.8	9
108	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

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109	Candidate Loci Associated with AIDS Virus Replication Identified by Whole Genome Sequencing of SIV-Infected Macaques. <i>AIDS Research and Human Retroviruses</i> , 2014, 30, A41-A41.	0.5	0
110	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
111	Discovery and full genome characterization of a new SIV lineage infecting red-tailed guenons (<i>Cercopithecus ascanius schmidtii</i>) in Kibale National Park, Uganda. <i>Retrovirology</i> , 2014, 11, 55.	0.9	14
112	Tertiary Mutations Stabilize CD8 + T Lymphocyte Escape-Associated Compensatory Mutations following Transmission of Simian Immunodeficiency Virus. <i>Journal of Virology</i> , 2014, 88, 3598-3604.	1.5	2
113	Survey of major histocompatibility complex class II diversity in pig-tailed macaques. <i>Immunogenetics</i> , 2014, 66, 613-623.	1.2	29
114	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
115	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
116	Rapid, repeated, low-dose challenges with SIVmac239 infect animals in a condensed challenge window. <i>Retrovirology</i> , 2014, 11, 66.	0.9	6
117	Full-length novel MHC class I allele discovery by next-generation sequencing: two platforms are better than one. <i>Immunogenetics</i> , 2014, 66, 15-24.	1.2	13
118	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
119	Deep sequencing identifies two genotypes and high viral genetic diversity of human pegivirus (GB virus) Tj ETQq1 1,0,784314 rgBT /Ove	1.3	15
120	Selection on haemagglutinin imposes a bottleneck during mammalian transmission of reassortant H5N1 influenza viruses. <i>Nature Communications</i> , 2013, 4, 2636.	5.8	80
121	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
122	T cell response specificity and magnitude against SIVmac239 are not concordant in major histocompatibility complex-matched animals. <i>Retrovirology</i> , 2013, 10, 116.	0.9	7
123	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
124	Haplessly Hoping: Macaque Major Histocompatibility Complex Made Easy. <i>ILAR Journal</i> , 2013, 54, 196-210.	1.8	98
125	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
126	Adoptive Transfer of Lymphocytes Isolated from Simian Immunodeficiency Virus SIVmac239 ^Δ nef-Vaccinated Macaques Does Not Affect Acute-Phase Viral Loads but May Reduce Chronic-Phase Viral Loads in Major Histocompatibility Complex-Matched Recipients. <i>Journal of Virology</i> , 2013, 87, 7382-7392.	1.5	15

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127	Therapeutic Vaccination against the Rhesus Lymphocryptovirus EBNA-1 Homologue, rhEBNA-1, Elicits T Cell Responses to Novel Epitopes in Rhesus Macaques. <i>Journal of Virology</i> , 2013, 87, 13904-13910.	1.5	6
128	Major Histocompatibility Complex Class I Haplotype Diversity in Chinese Rhesus Macaques. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1195-1201.	0.8	44
129	Exceptional Simian Hemorrhagic Fever Virus Diversity in a Wild African Primate Community. <i>Journal of Virology</i> , 2013, 87, 688-691.	1.5	61
130	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
131	Acute Phase CD8+ T Lymphocytes against Alternate Reading Frame Epitopes Select for Rapid Viral Escape during SIV Infection. <i>PLoS ONE</i> , 2013, 8, e61383.	1.1	6
132	Inter- and Intra-Host Viral Diversity in a Large Seasonal DENV2 Outbreak. <i>PLoS ONE</i> , 2013, 8, e70318.	1.1	38
133	Specific CD8+ T Cell Responses Correlate with Control of Simian Immunodeficiency Virus Replication in Mauritian <i>Cynomolgus</i> Macaques. <i>Journal of Virology</i> , 2012, 86, 7596-7604.	1.5	56
134	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
135	Conditional CD8+ T Cell Escape during Acute Simian Immunodeficiency Virus Infection. <i>Journal of Virology</i> , 2012, 86, 605-609.	1.5	29
136	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
137	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
138	High-level, lasting antiviral immunity induced by a bimodal AIDS vaccine and boosted by live-virus exposure. <i>Aids</i> , 2012, 26, 149-155.	1.0	3
139	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
140	Ultra-high resolution HLA genotyping and allele discovery by highly multiplexed cDNA amplicon pyrosequencing. <i>BMC Genomics</i> , 2012, 13, 378.	1.2	38
141	Ex Vivo SIV-Specific CD8 T Cell Responses in Heterozygous Animals Are Primarily Directed against Peptides Presented by a Single MHC Haplotype. <i>PLoS ONE</i> , 2012, 7, e43690.	1.1	5
142	SIV Genome-Wide Pyrosequencing Provides a Comprehensive and Unbiased View of Variation within and outside CD8 T Lymphocyte Epitopes. <i>PLoS ONE</i> , 2012, 7, e47818.	1.1	9
143	Hepatitis C Virus NS3/NS4A DNA Vaccine Induces Multiepitope T Cell Responses in Rhesus Macaques Mimicking Human Immune Responses. <i>Molecular Therapy</i> , 2012, 20, 669-678.	3.7	36
144	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

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145	Visualizing virus population variability from next generation sequencing data. , 2011, , .		7
146	Direct identification of an HPV-16 tumor antigen from cervical cancer biopsy specimens. <i>Frontiers in Immunology</i> , 2011, 2, 75.	2.2	26
147	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
148	GagCM9-Specific CD8+ T Cells Expressing Limited Public TCR Clonotypes Do Not Suppress SIV Replication In Vivo. <i>PLoS ONE</i> , 2011, 6, e23515.	1.1	11
149	Screening and confirmatory testing of MHC class I alleles in pig-tailed macaques. <i>Immunogenetics</i> , 2011, 63, 511-521.	1.2	29
150	Characterization of full-length MHC class II sequences in Indonesian and Vietnamese cynomolgus macaques. <i>Immunogenetics</i> , 2011, 63, 611-618.	1.2	23
151	The role of MHC class I allele Mamu-A*07 during SIVmac239 infection. <i>Immunogenetics</i> , 2011, 63, 789-807.	1.2	19
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