

Darren P Martin

List of Publications by Year in descending order

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Version: 2024-02-01

129
papers

17,604
citations

38742

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h-index

17105

122
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139
all docs

139
docs citations

139
times ranked

18590
citing authors

#	ARTICLE	IF	CITATIONS
1	Establishment of five new genera in the family Geminiviridae: Citlodavirus, Maldovirus, Mulcrilevirus, Opunvirus, and Topilevirus. <i>Archives of Virology</i> , 2022, 167, 695-710.	2.1	43
2	In Silico Characterisation of Putative Prophages in Lactobacillaceae Used in Probiotics for Vaginal Health. <i>Microorganisms</i> , 2022, 10, 214.	3.6	5
3	Exploring the Natural Origins of SARS-CoV-2 in the Light of Recombination. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	93
4	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. <i>Nature</i> , 2022, 603, 679-686.	27.8	1,210
5	Altered TMPRSS2 usage by SARS-CoV-2 Omicron impacts infectivity and fusogenicity. <i>Nature</i> , 2022, 603, 706-714.	27.8	756
6	Omicron extensively but incompletely escapes Pfizer BNT162b2 neutralization. <i>Nature</i> , 2022, 602, 654-656.	27.8	928
7	Neutralisation sensitivity of the SARS-CoV-2 omicron (B.1.1.529) variant: a cross-sectional study. <i>Lancet Infectious Diseases</i> , The, 2022, 22, 813-820.	9.1	64
8	Selection Analysis Identifies Clusters of Unusual Mutational Changes in Omicron Lineage BA.1 That Likely Impact Spike Function. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	84
9	Emergence and phenotypic characterization of the global SARS-CoV-2 C.1.2 lineage. <i>Nature Communications</i> , 2022, 13, 1976.	12.8	27
10	HIV-1 Evolutionary Dynamics under Nonsuppressive Antiretroviral Therapy. <i>MBio</i> , 2022, 13, e0026922.	4.1	5
11	Recent Zoonotic Spillover and Tropism Shift of a Canine Coronavirus Is Associated with Relaxed Selection and Putative Loss of Function in NTD Subdomain of Spike Protein. <i>Viruses</i> , 2022, 14, 853.	3.3	11
12	Conserved recombination patterns across coronavirus subgenera. <i>Virus Evolution</i> , 2022, 8, .	4.9	14
13	Virion-Associated Nucleic Acid-Based Metagenomics: A Decade of Advances in Molecular Characterization of Plant Viruses. <i>Phytopathology</i> , 2022, 112, 2253-2272.	2.2	7
14	Detection of SARS-CoV-2 intra-host recombination during superinfection with Alpha and Epsilon variants in New York City. <i>Nature Communications</i> , 2022, 13, .	12.8	22
15	crAssphage genomes identified in fecal samples of an adult and infants with evidence of positive genomic selective pressure within tail protein genes. <i>Virus Research</i> , 2021, 292, 198219.	2.2	10
16	Transmission dynamics of SARS-CoV-2 within-host diversity in two major hospital outbreaks in South Africa. <i>Virus Evolution</i> , 2021, 7, veab041.	4.9	30
17	Sixteen novel lineages of SARS-CoV-2 in South Africa. <i>Nature Medicine</i> , 2021, 27, 440-446.	30.7	326
18	Detection of a SARS-CoV-2 variant of concern in South Africa. <i>Nature</i> , 2021, 592, 438-443.	27.8	1,381

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19	Elucidation of Early Evolution of HIV-1 Group M in the Congo Basin Using Computational Methods. <i>Genes</i> , 2021, 12, 517.	2.4	0
20	New World Cactaceae Plants Harbor Diverse Geminiviruses. <i>Viruses</i> , 2021, 13, 694.	3.3	8
21	Identification of the Begomoviruses Squash Leaf Curl Virus and Watermelon Chlorotic Stunt Virus in Various Plant Samples in North America. <i>Viruses</i> , 2021, 13, 810.	3.3	6
22	The emergence and ongoing convergent evolution of the SARS-CoV-2 N501Y lineages. <i>Cell</i> , 2021, 184, 5189-5200.e7.	28.9	186
23	Ready-to-use public infrastructure for global SARS-CoV-2 monitoring. <i>Nature Biotechnology</i> , 2021, 39, 1178-1179.	17.5	21
24	Taxonomy update for the family Alphasatellitidae: new subfamily, genera, and species. <i>Archives of Virology</i> , 2021, 166, 3503-3511.	2.1	15
25	Complex evolutionary history of felid anelloviruses. <i>Virology</i> , 2021, 562, 176-189.	2.4	13
26	Circoviruses and cycloviruses identified in Weddell seal fecal samples from McMurdo Sound, Antarctica. <i>Infection, Genetics and Evolution</i> , 2021, 95, 105070.	2.3	7
27	A novel lineage of polyomaviruses identified in bark scorpions. <i>Virology</i> , 2021, 563, 58-63.	2.4	9
28	How virulent are emerging maize-infecting mastreviruses?. <i>Archives of Virology</i> , 2021, 166, 955-959.	2.1	3
29	RDP5: a computer program for analyzing recombination in, and removing signals of recombination from, nucleotide sequence datasets. <i>Virus Evolution</i> , 2021, 7, veaa087.	4.9	257
30	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021, 374, 423-431.	12.6	144
31	Contribution of historical herbarium small RNAs to the reconstruction of a cassava mosaic geminivirus evolutionary history. <i>Scientific Reports</i> , 2021, 11, 21280.	3.3	8
32	Novel circular DNA virus identified in <i>Opuntia discolor</i> (Cactaceae) that codes for proteins with similarity to those of geminiviruses. <i>Journal of General Virology</i> , 2021, 102, .	2.9	1
33	ICTV Virus Taxonomy Profile: Geminiviridae 2021. <i>Journal of General Virology</i> , 2021, 102, .	2.9	97
34	Evolutionary Analyses of Base-Pairing Interactions in DNA and RNA Secondary Structures. <i>Molecular Biology and Evolution</i> , 2020, 37, 576-592.	8.9	6
35	Large-scale survey reveals pervasiveness and potential function of endogenous geminiviral sequences in plants. <i>Virus Evolution</i> , 2020, 6, veaa071.	4.9	15
36	Diverse genomoviruses representing twenty-nine species identified associated with plants. <i>Archives of Virology</i> , 2020, 165, 2891-2901.	2.1	13

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37	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12522-12523.	7.1	68
38	Heterogeneity of the rice microbial community of the Chinese centuries-old Honghe Hani rice terraces system. <i>Environmental Microbiology</i> , 2020, 22, 3429-3445.	3.8	8
39	Sorghum mastrevirus-associated alphasatellites: new geminalphasatellites associated with an African streak mastrevirus infecting wild Poaceae plants on Reunion Island. <i>Archives of Virology</i> , 2020, 165, 1925-1928.	2.1	3
40	Machine Learning and Network Analyses Reveal Disease Subtypes of Pancreatic Cancer and their Molecular Characteristics. <i>Scientific Reports</i> , 2020, 10, 1212.	3.3	62
41	Compartmentalization and Clonal Amplification of HIV-1 in the Male Genital Tract Characterized Using Next-Generation Sequencing. <i>Journal of Virology</i> , 2020, 94, .	3.4	11
42	A Novel Divergent Geminivirus Identified in Asymptomatic New World Cactaceae Plants. <i>Viruses</i> , 2020, 12, 398.	3.3	10
43	Symptom evolution following the emergence of maize streak virus. <i>ELife</i> , 2020, 9, .	6.0	13
44	Evolution and ecology of plant viruses. <i>Nature Reviews Microbiology</i> , 2019, 17, 632-644.	28.6	166
45	Exploring the diversity of Poaceae-infecting mastreviruses on Reunion Island using a viral metagenomics-based approach. <i>Scientific Reports</i> , 2019, 9, 12716.	3.3	14
46	Evolutionary dynamics of ten novel Gamma-PVs: insights from phylogenetic incongruence, recombination and phylodynamic analyses. <i>BMC Genomics</i> , 2019, 20, 368.	2.8	5
47	Evidence for both Intermittent and Persistent Compartmentalization of HIV-1 in the Female Genital Tract. <i>Journal of Virology</i> , 2019, 93, .	3.4	9
48	Emergence of Southern Rice Black-Streaked Dwarf Virus in the Centuries-Old Chinese Yuanyang Agrosystem of Rice Landraces. <i>Viruses</i> , 2019, 11, 985.	3.3	7
49	Partner HIV Serostatus Impacts Viral Load, Genital HIV Shedding, and Immune Activation in HIV-Infected Individuals. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2019, 82, 51-60.	2.1	3
50	Novel circular DNA viruses associated with Apiaceae and Poaceae from South Africa and New Zealand. <i>Archives of Virology</i> , 2019, 164, 237-242.	2.1	12
51	Unravelling the complicated evolutionary and dissemination history of HIV-1M subtype A lineages. <i>Virus Evolution</i> , 2018, 4, vey003.	4.9	12
52	Geometagenomics illuminates the impact of agriculture on the distribution and prevalence of plant viruses at the ecosystem scale. <i>ISME Journal</i> , 2018, 12, 173-184.	9.8	132
53	New Isolates of <i>Sweet potato feathery mottle virus</i> and <i>Sweet potato virus C</i> : Biological and Molecular Properties, and Recombination Analysis Based on Complete Genomes. <i>Plant Disease</i> , 2018, 102, 1899-1914.	1.4	11
54	Nanovirus-phasatellite complex identified in <i>Vicia cracca</i> in the Rhône delta region of France. <i>Archives of Virology</i> , 2018, 163, 695-700.	2.1	25

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55	Molecular characterization of faba bean necrotic yellows viruses in Tunisia. Archives of Virology, 2018, 163, 687-694.	2.1	16
56	Nanopore-based detection and characterization of yam viruses. Scientific Reports, 2018, 8, 17879.	3.3	57
57	The Westward Journey of Alfalfa Leaf Curl Virus. Viruses, 2018, 10, 542.	3.3	12
58	Pervasive tertiary structure in the dengue virus RNA genome. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 11513-11518.	7.1	81
59	Notes on recombination and reassortment in multipartite/segmented viruses. Current Opinion in Virology, 2018, 33, 156-166.	5.4	44
60	A19â€¢The impact of HIV-1 on the evolution of Mycobacterium tuberculosis. Virus Evolution, 2018, 4, .	4.9	0
61	Passion Fruit Chlorotic Mottle Virus: Molecular Characterization of a New Divergent Geminivirus in Brazil. Viruses, 2018, 10, 169.	3.3	42
62	Patterns of genomic site inheritance in HIV-1M inter-subtype recombinants delineate the most likely genomic sites of subtype-specific adaptation. Virus Evolution, 2018, 4, vey015.	4.9	3
63	Recombinant Goose Circoviruses Circulating in Domesticated and Wild Geese in Poland. Viruses, 2018, 10, 107.	3.3	14
64	Alphasatellitidae: a new family with two subfamilies for the classification of geminivirus- and nanovirus-associated alphasatellites. Archives of Virology, 2018, 163, 2587-2600.	2.1	133
65	World Management of Geminiviruses. Annual Review of Phytopathology, 2018, 56, 637-677.	7.8	247
66	From Spatial Metagenomics to Molecular Characterization of Plant Viruses: A Geminivirus Case Study. Advances in Virus Research, 2018, 101, 55-83.	2.1	34
67	Capulavirus and Grablovirus: two new genera in the family Geminiviridae. Archives of Virology, 2017, 162, 1819-1831.	2.1	240
68	Identification of a Nanovirus-Alphasatellite Complex in Sophora alopecuroides. Virus Research, 2017, 235, 24-32.	2.2	30
69	Genetic diversity and phylogenetic analysis of the ORF5 gene of PRRSV from central China. Research in Veterinary Science, 2017, 115, 226-234.	1.9	9
70	Genome sequences of a capulavirus infecting Plantago lanceolata in the Å..land archipelago of Finland. Archives of Virology, 2017, 162, 2041-2045.	2.1	39
71	Detecting and Analyzing Genetic Recombination Using RDP4. Methods in Molecular Biology, 2017, 1525, 433-460.	0.9	113
72	The Influence of HIV on the Evolution of Mycobacterium tuberculosis. Molecular Biology and Evolution, 2017, 34, 1654-1668.	8.9	27

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73	Complete genome sequences of cowpea polerovirus 1 and cowpea polerovirus 2 infecting cowpea plants in Burkina Faso. <i>Archives of Virology</i> , 2017, 162, 2149-2152.	2.1	11
74	Molecular diversity, geographic distribution and host range of monocot-infecting mastreviruses in Africa and surrounding islands. <i>Virus Research</i> , 2017, 238, 171-178.	2.2	11
75	Novel mastreviruses identified in Australian wild rice. <i>Virus Research</i> , 2017, 238, 193-197.	2.2	13
76	Tomato leaf curl New Delhi virus: a widespread bipartite begomovirus in the territory of monopartite begomoviruses. <i>Molecular Plant Pathology</i> , 2017, 18, 901-911.	4.2	106
77	Occurrence of a novel mastrevirus in sugarcane germplasm collections in Florida, Guadeloupe and Réunion. <i>Virology Journal</i> , 2017, 14, 146.	3.4	20
78	ICTV Virus Taxonomy Profile: Geminiviridae. <i>Journal of General Virology</i> , 2017, 98, 131-133.	2.9	676
79	Molecular characterization and prevalence of two capulaviruses: Alfalfa leaf curl virus from France and Euphorbia caput-medusae latent virus from South Africa. <i>Virology</i> , 2016, 493, 142-153.	2.4	40
80	Divergent evolutionary and epidemiological dynamics of cassava mosaic geminiviruses in Madagascar. <i>BMC Evolutionary Biology</i> , 2016, 16, 182.	3.2	26
81	High Degree of HIV-1 Group M (HIV-1M) Genetic Diversity within Circulating Recombinant Forms: Insight into the Early Events of HIV-1M Evolution. <i>Journal of Virology</i> , 2016, 90, 2221-2229.	3.4	25
82	Metagenomic-Based Screening and Molecular Characterization of Cowpea-Infecting Viruses in Burkina Faso. <i>PLoS ONE</i> , 2016, 11, e0165188.	2.5	46
83	Near full-length HIV type 1M genomic sequences from Cameroon. <i>Evolution, Medicine and Public Health</i> , 2015, 2015, 254-265.	2.5	15
84	Complete Genome Sequences of Four African Horse Sickness Virus Strains from a Commercial Tetravalent Live Attenuated Vaccine. <i>Genome Announcements</i> , 2015, 3, .	0.8	7
85	Potent Sensitisation of Cancer Cells to Anticancer Drugs by a Quadruple Mutant of the Human Deoxycytidine Kinase. <i>PLoS ONE</i> , 2015, 10, e0140741.	2.5	2
86	Plant Virus Metagenomics: Advances in Virus Discovery. <i>Phytopathology</i> , 2015, 105, 716-727.	2.2	340
87	The genomes of many yam species contain transcriptionally active endogenous geminiviral sequences that may be functionally expressed. <i>Virus Evolution</i> , 2015, 1, vev002.	4.9	30
88	RDP4: Detection and analysis of recombination patterns in virus genomes. <i>Virus Evolution</i> , 2015, 1, vev003.	4.9	2,621
89	Complete Genome Sequences of the Three African Horse Sickness Virus Strains from a Commercial Trivalent Live Attenuated Vaccine. <i>Genome Announcements</i> , 2015, 3, .	0.8	8
90	Characterisation of a diverse range of circular replication-associated protein encoding DNA viruses recovered from a sewage treatment oxidation pond. <i>Infection, Genetics and Evolution</i> , 2015, 31, 73-86.	2.3	76

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91	Phylogenetics of HIV-1 subtype G env: Greater complexity and older origins than previously reported. <i>Infection, Genetics and Evolution</i> , 2015, 35, 9-18.	2.3	6
92	Functionally conserved architecture of hepatitis C virus RNA genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3692-3697.	7.1	117
93	Gene-Wide Identification of Episodic Selection. <i>Molecular Biology and Evolution</i> , 2015, 32, 1365-1371.	8.9	493
94	Molecular diversity of Chickpea chlorotic dwarf virus in Sudan: High rates of intra-species recombination â€” a driving force in the emergence of new strains. <i>Infection, Genetics and Evolution</i> , 2015, 29, 203-215.	2.3	20
95	Patterns of Recombination in HIV-1M Are Influenced by Selection Disfavouring the Survival of Recombinants with Disrupted Genomic RNA and Protein Structures. <i>PLoS ONE</i> , 2014, 9, e100400.	2.5	10
96	Inducible Resistance to Maize Streak Virus. <i>PLoS ONE</i> , 2014, 9, e105932.	2.5	12
97	Genome diversity and evidence of recombination and reassortment in nanoviruses from Europe. <i>Journal of General Virology</i> , 2014, 95, 1178-1191.	2.9	56
98	Extensive Recombination-Induced Disruption of Genetic Interactions Is Highly Deleterious but Can Be Partially Reversed by Small Numbers of Secondary Recombination Events. <i>Journal of Virology</i> , 2014, 88, 7843-7851.	3.4	18
99	Pigeon circoviruses display patterns of recombination, genomic secondary structure and selection similar to those of beak and feather disease viruses. <i>Journal of General Virology</i> , 2014, 95, 1338-1351.	2.9	36
100	Towards inferring the global movement of beak and feather disease virus. <i>Virology</i> , 2014, 450-451, 24-33.	2.4	53
101	Appearances Can Be Deceptive: Revealing a Hidden Viral Infection with Deep Sequencing in a Plant Quarantine Context. <i>PLoS ONE</i> , 2014, 9, e102945.	2.5	89
102	Characterization of HIV-1 gag and nef in Cameroon: further evidence of extreme diversity at the origin of the HIV-1 group M epidemic. <i>Virology Journal</i> , 2013, 10, 29.	3.4	20
103	Extensive recombination detected among beak and feather disease virus isolates from breeding facilities in Poland. <i>Journal of General Virology</i> , 2013, 94, 1086-1095.	2.9	56
104	Evidence of inter-component recombination, intra-component recombination and reassortment in banana bunchy top virus. <i>Journal of General Virology</i> , 2012, 93, 1103-1119.	2.9	44
105	Analysing recombination in nucleotide sequences. <i>Molecular Ecology Resources</i> , 2011, 11, 943-955.	4.8	106
106	Recombination in Eukaryotic Single Stranded DNA Viruses. <i>Viruses</i> , 2011, 3, 1699-1738.	3.3	188
107	Recombination patterns in dicot-infecting mastreviruses mirror those found in monocot-infecting mastreviruses. <i>Archives of Virology</i> , 2011, 156, 1463-1469.	2.1	11
108	Eragrostis minor streak virus: an Asian streak virus in Africa. <i>Archives of Virology</i> , 2011, 156, 1299-1303.	2.1	10

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109	Complex Recombination Patterns Arising during Geminivirus Coinfections Preserve and Demarcate Biologically Important Intra-Genome Interaction Networks. <i>PLoS Pathogens</i> , 2011, 7, e1002203.	4.7	78
110	Dragonfly cyclovirus, a novel single-stranded DNA virus discovered in dragonflies (Odonata: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 702 T	2.9	110
111	Maize streak virus: an old and complex "emerging" pathogen. <i>Molecular Plant Pathology</i> , 2010, 11, 1-12.	4.2	113
112	RNA Structures Facilitate Recombination-Mediated Gene Swapping in HIV-1. <i>Journal of Virology</i> , 2010, 84, 12675-12682.	3.4	51
113	RDP3: a flexible and fast computer program for analyzing recombination. <i>Bioinformatics</i> , 2010, 26, 2462-2463.	4.1	1,524
114	Molecular Mechanisms of Recombination Restriction in the Envelope Gene of the Human Immunodeficiency Virus. <i>PLoS Pathogens</i> , 2009, 5, e1000418.	4.7	70
115	Rapid host adaptation by extensive recombination. <i>Journal of General Virology</i> , 2009, 90, 734-746.	2.9	88
116	Dating the origins of the maize-adapted strain of maize streak virus, MSV-A. <i>Journal of General Virology</i> , 2009, 90, 3066-3074.	2.9	57
117	The epidemiology, economic impact and control of maize streak disease. <i>Food Security</i> , 2009, 1, 305-315.	5.3	65
118	Recombination Detection and Analysis Using RDP3. <i>Methods in Molecular Biology</i> , 2009, 537, 185-205.	0.9	72
119	Extensive purifying selection acting on synonymous sites in HIV-1 Group M sequences. <i>Virology Journal</i> , 2008, 5, 160.	3.4	27
120	Recombination, decreased host specificity and increased mobility may have driven the emergence of maize streak virus as an agricultural pathogen. <i>Journal of General Virology</i> , 2008, 89, 2063-2074.	2.9	121
121	Genetic analysis of maize streak virus isolates from Uganda reveals widespread distribution of a recombinant variant. <i>Journal of General Virology</i> , 2007, 88, 3154-3165.	2.9	55
122	Inhibition of maize streak virus (MSV) replication by transient and transgenic expression of MSV replication-associated protein mutants. <i>Journal of General Virology</i> , 2007, 88, 325-336.	2.9	34
123	Recombination Patterns in Aphthoviruses Mirror Those Found in Other Picornaviruses. <i>Journal of Virology</i> , 2006, 80, 11827-11832.	3.4	247
124	Robust inference of positive selection from recombining coding sequences. <i>Bioinformatics</i> , 2006, 22, 2493-2499.	4.1	175
125	Evidence of ancient papillomavirus recombination. <i>Journal of General Virology</i> , 2006, 87, 2527-2531.	2.9	59
126	The Evolutionary Value of Recombination Is Constrained by Genome Modularity. <i>PLoS Genetics</i> , 2005, 1, e51.	3.5	104

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127	A three-nucleotide mutation altering the Maize streak virus Rep pRBR-interaction motif reduces symptom severity in maize and partially reverts at high frequency without restoring pRBRâ€™Rep binding. <i>Journal of General Virology</i> , 2005, 86, 803-813.	2.9	53
128	South West Indian Ocean islands tomato begomovirus populations represent a new major monopartite begomovirus group. <i>Journal of General Virology</i> , 2005, 86, 1533-1542.	2.9	60
129	RDP: detection of recombination amongst aligned sequences. <i>Bioinformatics</i> , 2000, 16, 562-563.	4.1	1,369