

Darren P Martin

List of Publications by Year in descending order

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129
papers

17,604
citations

38742

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17105

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139
docs citations

139
times ranked

18590
citing authors

#	ARTICLE	IF	CITATIONS
1	RDP4: Detection and analysis of recombination patterns in virus genomes. <i>Virus Evolution</i> , 2015, 1, vev003.	4.9	2,621
2	RDP3: a flexible and fast computer program for analyzing recombination. <i>Bioinformatics</i> , 2010, 26, 2462-2463.	4.1	1,524
3	Detection of a SARS-CoV-2 variant of concern in South Africa. <i>Nature</i> , 2021, 592, 438-443.	27.8	1,381
4	RDP: detection of recombination amongst aligned sequences. <i>Bioinformatics</i> , 2000, 16, 562-563.	4.1	1,369
5	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. <i>Nature</i> , 2022, 603, 679-686.	27.8	1,210
6	Omicron extensively but incompletely escapes Pfizer BNT162b2 neutralization. <i>Nature</i> , 2022, 602, 654-656.	27.8	928
7	Altered TMPRSS2 usage by SARS-CoV-2 Omicron impacts infectivity and fusogenicity. <i>Nature</i> , 2022, 603, 706-714.	27.8	756
8	ICTV Virus Taxonomy Profile: Geminiviridae. <i>Journal of General Virology</i> , 2017, 98, 131-133.	2.9	676
9	Gene-Wide Identification of Episodic Selection. <i>Molecular Biology and Evolution</i> , 2015, 32, 1365-1371.	8.9	493
10	Plant Virus Metagenomics: Advances in Virus Discovery. <i>Phytopathology</i> , 2015, 105, 716-727.	2.2	340
11	Sixteen novel lineages of SARS-CoV-2 in South Africa. <i>Nature Medicine</i> , 2021, 27, 440-446.	30.7	326
12	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
13	Recombination Patterns in Aphthoviruses Mirror Those Found in Other Picornaviruses. <i>Journal of Virology</i> , 2006, 80, 11827-11832.	3.4	247
14	World Management of Geminiviruses. <i>Annual Review of Phytopathology</i> , 2018, 56, 637-677.	7.8	247
15	Capulavirus and Grablovirus: two new genera in the family Geminiviridae. <i>Archives of Virology</i> , 2017, 162, 1819-1831.	2.1	240
16	Recombination in Eukaryotic Single Stranded DNA Viruses. <i>Viruses</i> , 2011, 3, 1699-1738.	3.3	188
17	The emergence and ongoing convergent evolution of the SARS-CoV-2 N501Y lineages. <i>Cell</i> , 2021, 184, 5189-5200.e7.	28.9	186
18	Robust inference of positive selection from recombining coding sequences. <i>Bioinformatics</i> , 2006, 22, 2493-2499.	4.1	175

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19	Evolution and ecology of plant viruses. <i>Nature Reviews Microbiology</i> , 2019, 17, 632-644.	28.6	166
20	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
21	Alphasatellitidae: a new family with two subfamilies for the classification of geminivirus- and nanovirus-associated alphasatellites. <i>Archives of Virology</i> , 2018, 163, 2587-2600.	2.1	133
22	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
23	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
24	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
25	Maize streak virus: an old and complex "emerging" pathogen. <i>Molecular Plant Pathology</i> , 2010, 11, 1-12.	4.2	113
26	Detecting and Analyzing Genetic Recombination Using RDP4. <i>Methods in Molecular Biology</i> , 2017, 1525, 433-460.	0.9	113
27	Dragonfly cyclovirus, a novel single-stranded DNA virus discovered in dragonflies (Odonata: Tj ETQq1 1 0.784314 r/BT /Overlock 10	2.9	110
28	Analysing recombination in nucleotide sequences. <i>Molecular Ecology Resources</i> , 2011, 11, 943-955.	4.8	106
29	<i>Tomato leaf curl New Delhi virus</i>: a widespread bipartite begomovirus in the territory of monopartite begomoviruses. <i>Molecular Plant Pathology</i> , 2017, 18, 901-911.	4.2	106
30	The Evolutionary Value of Recombination Is Constrained by Genome Modularity. <i>PLoS Genetics</i> , 2005, 1, e51.	3.5	104
31	ICTV Virus Taxonomy Profile: Geminiviridae 2021. <i>Journal of General Virology</i> , 2021, 102, .	2.9	97
32	Exploring the Natural Origins of SARS-CoV-2 in the Light of Recombination. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	93
33	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
34	Rapid host adaptation by extensive recombination. <i>Journal of General Virology</i> , 2009, 90, 734-746.	2.9	88
35	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
36	Pervasive tertiary structure in the dengue virus RNA genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 11513-11518.	7.1	81

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37	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
38	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
39	Recombination Detection and Analysis Using RDP3. <i>Methods in Molecular Biology</i> , 2009, 537, 185-205.	0.9	72
40	Molecular Mechanisms of Recombination Restriction in the Envelope Gene of the Human Immunodeficiency Virus. <i>PLoS Pathogens</i> , 2009, 5, e1000418.	4.7	70
41	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
42	The epidemiology, economic impact and control of maize streak disease. <i>Food Security</i> , 2009, 1, 305-315.	5.3	65
43	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
44	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
45	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
46	Evidence of ancient papillomavirus recombination. <i>Journal of General Virology</i> , 2006, 87, 2527-2531.	2.9	59
47	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
48	Nanopore-based detection and characterization of yam viruses. <i>Scientific Reports</i> , 2018, 8, 17879.	3.3	57
49	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
50	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
51	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
52	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 pRBR-Rep binding. <i>Journal of General Virology</i> , 2005, 86, 803-813.	2.9	53
53	Towards inferring the global movement of beak and feather disease virus. <i>Virology</i> , 2014, 450-451, 24-33.	2.4	53
54	RNA Structures Facilitate Recombination-Mediated Gene Swapping in HIV-1. <i>Journal of Virology</i> , 2010, 84, 12675-12682.	3.4	51

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55	Metagenomic-Based Screening and Molecular Characterization of Cowpea-Infecting Viruses in Burkina Faso. <i>PLoS ONE</i> , 2016, 11, e0165188.	2.5	46
56	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
57	Notes on recombination and reassortment in multipartite/segmented viruses. <i>Current Opinion in Virology</i> , 2018, 33, 156-166.	5.4	44
58	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
59	Passion Fruit Chlorotic Mottle Virus: Molecular Characterization of a New Divergent Geminivirus in Brazil. <i>Viruses</i> , 2018, 10, 169.	3.3	42
60	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
61	Genome sequences of a capulavirus infecting <i>Plantago lanceolata</i> in the Åland archipelago of Finland. <i>Archives of Virology</i> , 2017, 162, 2041-2045.	2.1	39
62	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
63	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
64	From Spatial Metagenomics to Molecular Characterization of Plant Viruses: A Geminivirus Case Study. <i>Advances in Virus Research</i> , 2018, 101, 55-83.	2.1	34
65	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
66	Identification of a Nanovirus-AlphaSatellite Complex in <i>Sophora alopecuroides</i> . <i>Virus Research</i> , 2017, 235, 24-32.	2.2	30
67	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
68	Extensive purifying selection acting on synonymous sites in HIV-1 Group M sequences. <i>Virology Journal</i> , 2008, 5, 160.	3.4	27
69	The Influence of HIV on the Evolution of <i>Mycobacterium tuberculosis</i> . <i>Molecular Biology and Evolution</i> , 2017, 34, 1654-1668.	8.9	27
70	Emergence and phenotypic characterization of the global SARS-CoV-2 C.1.2 lineage. <i>Nature Communications</i> , 2022, 13, 1976.	12.8	27
71	Divergent evolutionary and epidemiological dynamics of cassava mosaic geminiviruses in Madagascar. <i>BMC Evolutionary Biology</i> , 2016, 16, 182.	3.2	26
72	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

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73	Nanovirus-alphasatellite 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
74	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
75	Ready-to-use public infrastructure for global SARS-CoV-2 monitoring. <i>Nature Biotechnology</i> , 2021, 39, 1178-1179.	17.5	21
76	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
77	Molecular diversity of Chickpea chlorotic dwarf virus in Sudan: High rates of intra-species recombination "a driving force in the emergence of new strains. <i>Infection, Genetics and Evolution</i> , 2015, 29, 203-215.	2.3	20
78	Occurrence of a novel mastrevirus in sugarcane germplasm collections in Florida, Guadeloupe and Réunion. <i>Virology Journal</i> , 2017, 14, 146.	3.4	20
79	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
80	Molecular characterization of faba bean necrotic yellows viruses in Tunisia. <i>Archives of Virology</i> , 2018, 163, 687-694.	2.1	16
81	Near full-length HIV type 1M genomic sequences from Cameroon. <i>Evolution, Medicine and Public Health</i> , 2015, 2015, 254-265.	2.5	15
82	Large-scale survey reveals pervasiveness and potential function of endogenous geminiviral sequences in plants. <i>Virus Evolution</i> , 2020, 6, veaa071.	4.9	15
83	Taxonomy update for the family Alphasatellitidae: new subfamily, genera, and species. <i>Archives of Virology</i> , 2021, 166, 3503-3511.	2.1	15
84	Recombinant Goose Circoviruses Circulating in Domesticated and Wild Geese in Poland. <i>Viruses</i> , 2018, 10, 107.	3.3	14
85	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
86	Conserved recombination patterns across coronavirus subgenera. <i>Virus Evolution</i> , 2022, 8, .	4.9	14
87	Novel mastreviruses identified in Australian wild rice. <i>Virus Research</i> , 2017, 238, 193-197.	2.2	13
88	Diverse genomoviruses representing twenty-nine species identified associated with plants. <i>Archives of Virology</i> , 2020, 165, 2891-2901.	2.1	13
89	Complex evolutionary history of felid anelloviruses. <i>Virology</i> , 2021, 562, 176-189.	2.4	13
90	Symptom evolution following the emergence of maize streak virus. <i>ELife</i> , 2020, 9, .	6.0	13

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91	Inducible Resistance to Maize Streak Virus. PLoS ONE, 2014, 9, e105932.	2.5	12
92	Unravelling the complicated evolutionary and dissemination history of HIV-1M subtype A lineages. Virus Evolution, 2018, 4, vey003.	4.9	12
93	The Westward Journey of Alfalfa Leaf Curl Virus. Viruses, 2018, 10, 542.	3.3	12
94	Novel circular DNA viruses associated with Apiaceae and Poaceae from South Africa and New Zealand. Archives of Virology, 2019, 164, 237-242.	2.1	12
95	Recombination patterns in dicot-infecting mastreviruses mirror those found in monocot-infecting mastreviruses. Archives of Virology, 2011, 156, 1463-1469.	2.1	11
96	Complete genome sequences of cowpea polerovirus 1 and cowpea polerovirus 2 infecting cowpea plants in Burkina Faso. Archives of Virology, 2017, 162, 2149-2152.	2.1	11
97	Molecular diversity, geographic distribution and host range of monocot-infecting mastreviruses in Africa and surrounding islands. Virus Research, 2017, 238, 171-178.	2.2	11
98	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. Plant Disease, 2018, 102, 1899-1914.	1.4	11
99	Compartmentalization and Clonal Amplification of HIV-1 in the Male Genital Tract Characterized Using Next-Generation Sequencing. Journal of Virology, 2020, 94, .	3.4	11
100	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. Viruses, 2022, 14, 853.	3.3	11
101	Eragrostis minor streak virus: an Asian streak virus in Africa. Archives of Virology, 2011, 156, 1299-1303.	2.1	10
102	Patterns of Recombination in HIV-1M Are Influenced by Selection Disfavouring the Survival of Recombinants with Disrupted Genomic RNA and Protein Structures. PLoS ONE, 2014, 9, e100400.	2.5	10
103	A Novel Divergent Geminivirus Identified in Asymptomatic New World Cactaceae Plants. Viruses, 2020, 12, 398.	3.3	10
104	crAssphage genomes identified in fecal samples of an adult and infants with evidence of positive genomic selective pressure within tail protein genes. Virus Research, 2021, 292, 198219.	2.2	10
105	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
106	Evidence for both Intermittent and Persistent Compartmentalization of HIV-1 in the Female Genital Tract. Journal of Virology, 2019, 93, .	3.4	9
107	A novel lineage of polyomaviruses identified in bark scorpions. Virology, 2021, 563, 58-63.	2.4	9
108	Complete Genome Sequences of the Three African Horse Sickness Virus Strains from a Commercial Trivalent Live Attenuated Vaccine. Genome Announcements, 2015, 3, .	0.8	8

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109	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
110	New World Cactaceae Plants Harbor Diverse Geminiviruses. <i>Viruses</i> , 2021, 13, 694.	3.3	8
111	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
112	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
113	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
114	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
115	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
116	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
117	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
118	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
119	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
120	In Silico Characterisation of Putative Prophages in Lactobacillaceae Used in Probiotics for Vaginal Health. <i>Microorganisms</i> , 2022, 10, 214.	3.6	5
121	HIV-1 Evolutionary Dynamics under Nonsuppressive Antiretroviral Therapy. <i>MBio</i> , 2022, 13, e0026922.	4.1	5
122	Patterns of genomic site inheritance in HIV-1M inter-subtype recombinants delineate the most likely genomic sites of subtype-specific adaptation. <i>Virus Evolution</i> , 2018, 4, vey015.	4.9	3
123	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
124	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
125	How virulent are emerging maize-infecting mastreviruses?. <i>Archives of Virology</i> , 2021, 166, 955-959.	2.1	3
126	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

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127	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
128	A19â€The impact of HIV-1 on the evolution of <i>Mycobacterium tuberculosis</i> . <i>Virus Evolution</i> , 2018, 4, .	4.9	0
129	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