

# Darren P Martin

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

127 papers	10,305 citations	45 h-index	101 g-index
139 ext. papers	14,985 ext. citations	8.1 avg, IF	6.41 L-index

#	Paper	IF	Citations
127	Exploring the natural origins of SARS-CoV-2 in the light of recombination.. <i>Genome Biology and Evolution</i> , <b>2022</b> ,	3.9	14
126	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa.. <i>Nature</i> , <b>2022</b> ,	50.4	205
125	Altered TMPRSS2 usage by SARS-CoV-2 Omicron impacts tropism and fusogenicity.. <i>Nature</i> , <b>2022</b> ,	50.4	95
124	Neutralisation sensitivity of the SARS-CoV-2 omicron (B.1.1.529) variant: a cross-sectional study.. <i>Lancet Infectious Diseases</i> , <i>The</i> , <b>2022</b> ,	25.5	7
123	Selection analysis identifies clusters of unusual mutational changes in Omicron lineage BA.1 that likely impact Spike function.. <i>Molecular Biology and Evolution</i> , <b>2022</b> ,	8.3	10
122	Emergence and phenotypic characterization of the global SARS-CoV-2 C.1.2 lineage.. <i>Nature Communications</i> , <b>2022</b> , 13, 1976	17.4	3
121	HIV-1 Evolutionary Dynamics under Nonsuppressive Antiretroviral Therapy.. <i>MBio</i> , <b>2022</b> , e0026922	7.8	0
120	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> , <b>2022</b> , 14, 853	6.2	0
119	Omicron extensively but incompletely escapes Pfizer BNT162b2 neutralization.. <i>Nature</i> , <b>2021</b> ,	50.4	209
118	ICTV Virus Taxonomy Profile: 2021.. <i>Journal of General Virology</i> , <b>2021</b> , 102,	4.9	16
117	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , <b>2021</b> , 374, 423-431	33.3	35
116	Establishment of five new genera in the family Geminiviridae: Citlodavirus, Maldovirus, Mulcrilevirus, Opunvirus, and Topilevirus. <i>Archives of Virology</i> , <b>2021</b> , 1	2.6	7
115	Contribution of historical herbarium small RNAs to the reconstruction of a cassava mosaic geminivirus evolutionary history. <i>Scientific Reports</i> , <b>2021</b> , 11, 21280	4.9	0
114	RDP5: a computer program for analyzing recombination in, and removing signals of recombination from, nucleotide sequence datasets. <i>Virus Evolution</i> , <b>2021</b> , 7, veaa087	3.7	55
113	The emergence and ongoing convergent evolution of the N501Y lineages coincides with a major global shift in the SARS-CoV-2 selective landscape <b>2021</b> ,		46
112	Detection of a SARS-CoV-2 variant of concern in South Africa. <i>Nature</i> , <b>2021</b> , 592, 438-443	50.4	685
111	New World Cactaceae Plants Harbor Diverse Geminiviruses. <i>Viruses</i> , <b>2021</b> , 13,	6.2	2

110	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> , <b>2021</b> , 292, 198219	6.4	2
109	Transmission dynamics of SARS-CoV-2 within-host diversity in two major hospital outbreaks in South Africa. <i>Virus Evolution</i> , <b>2021</b> , 7, veab041	3.7	8
108	Sixteen novel lineages of SARS-CoV-2 in South Africa. <i>Nature Medicine</i> , <b>2021</b> , 27, 440-446	50.5	206
107	The emergence and ongoing convergent evolution of the SARS-CoV-2 N501Y lineages. <i>Cell</i> , <b>2021</b> , 184, 5189-5200.e7	56.2	61
106	Ready-to-use public infrastructure for global SARS-CoV-2 monitoring. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 1178-1179	44.5	7
105	Taxonomy update for the family Alphasatellitidae: new subfamily, genera, and species. <i>Archives of Virology</i> , <b>2021</b> , 166, 3503-3511	2.6	4
104	Complex evolutionary history of felid anelloviruses. <i>Virology</i> , <b>2021</b> , 562, 176-189	3.6	0
103	Circoviruses and cycloviruses identified in Weddell seal fecal samples from McMurdo Sound, Antarctica. <i>Infection, Genetics and Evolution</i> , <b>2021</b> , 95, 105070	4.5	0
102	A novel lineage of polyomaviruses identified in bark scorpions. <i>Virology</i> , <b>2021</b> , 563, 58-63	3.6	2
101	How virulent are emerging maize-infecting mastreviruses?. <i>Archives of Virology</i> , <b>2021</b> , 166, 955-959	2.6	1
100	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> , <b>2020</b> , 117, 12522-12523	11.5	46
99	Heterogeneity of the rice microbial community of the Chinese centuries-old Honghe Hani rice terraces system. <i>Environmental Microbiology</i> , <b>2020</b> , 22, 3429-3445	5.2	2
98	Sorghum mastrevirus-associated alphasatellites: new geminialphasatellites associated with an African streak mastrevirus infecting wild Poaceae plants on Reunion Island. <i>Archives of Virology</i> , <b>2020</b> , 165, 1925-1928	2.6	2
97	Machine Learning and Network Analyses Reveal Disease Subtypes of Pancreatic Cancer and their Molecular Characteristics. <i>Scientific Reports</i> , <b>2020</b> , 10, 1212	4.9	28
96	Compartmentalization and Clonal Amplification of HIV-1 in the Male Genital Tract Characterized Using Next-Generation Sequencing. <i>Journal of Virology</i> , <b>2020</b> , 94,	6.6	4
95	Symptom evolution following the emergence of maize streak virus. <i>ELife</i> , <b>2020</b> , 9,	8.9	9
94	Evolutionary Analyses of Base-Pairing Interactions in DNA and RNA Secondary Structures. <i>Molecular Biology and Evolution</i> , <b>2020</b> , 37, 576-592	8.3	4
93	Large-scale survey reveals pervasiveness and potential function of endogenous geminiviral sequences in plants. <i>Virus Evolution</i> , <b>2020</b> , 6, veaa071	3.7	8

92	Diverse genomoviruses representing twenty-nine species identified associated with plants. <i>Archives of Virology</i> , <b>2020</b> , 165, 2891-2901	2.6	5
91	A Novel Divergent Geminivirus Identified in Asymptomatic New World Cactaceae Plants. <i>Viruses</i> , <b>2020</b> , 12,	6.2	5
90	Exploring the diversity of Poaceae-infecting mastreviruses on Reunion Island using a viral metagenomics-based approach. <i>Scientific Reports</i> , <b>2019</b> , 9, 12716	4.9	5
89	Evolutionary dynamics of ten novel Gamma-PVs: insights from phylogenetic incongruence, recombination and phylodynamic analyses. <i>BMC Genomics</i> , <b>2019</b> , 20, 368	4.5	5
88	Evidence for both Intermittent and Persistent Compartmentalization of HIV-1 in the Female Genital Tract. <i>Journal of Virology</i> , <b>2019</b> , 93,	6.6	3
87	Evolution and ecology of plant viruses. <i>Nature Reviews Microbiology</i> , <b>2019</b> , 17, 632-644	22.2	72
86	Emergence of Southern Rice Black-Streaked Dwarf Virus in the Centuries-Old Chinese Yuanyang Agrosystem of Rice Landraces. <i>Viruses</i> , <b>2019</b> , 11,	6.2	4
85	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> , <b>2019</b> , 82, 51-60	3.1	2
84	Novel circular DNA viruses associated with Apiaceae and Poaceae from South Africa and New Zealand. <i>Archives of Virology</i> , <b>2019</b> , 164, 237-242	2.6	5
83	Unravelling the complicated evolutionary and dissemination history of HIV-1M subtype A lineages. <i>Virus Evolution</i> , <b>2018</b> , 4, vey003	3.7	9
82	Geometagenomics illuminates the impact of agriculture on the distribution and prevalence of plant viruses at the ecosystem scale. <i>ISME Journal</i> , <b>2018</b> , 12, 173-184	11.9	72
81	New Isolates of Sweet potato feathery mottle virus and Sweet potato virus C: Biological and Molecular Properties, and Recombination Analysis Based on Complete Genomes. <i>Plant Disease</i> , <b>2018</b> , 102, 1899-1914	1.5	7
80	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> , <b>2018</b> , 4, vey015	3.7	2
79	Recombinant Goose Circoviruses Circulating in Domesticated and Wild Geese in Poland. <i>Viruses</i> , <b>2018</b> , 10,	6.2	6
78	Alphasatellitidae: a new family with two subfamilies for the classification of geminivirus- and nanovirus-associated alphasatellites. <i>Archives of Virology</i> , <b>2018</b> , 163, 2587-2600	2.6	78
77	World Management of Geminiviruses. <i>Annual Review of Phytopathology</i> , <b>2018</b> , 56, 637-677	10.8	133
76	From Spatial Metagenomics to Molecular Characterization of Plant Viruses: A Geminivirus Case Study. <i>Advances in Virus Research</i> , <b>2018</b> , 101, 55-83	10.7	20
75	Nanovirus-alphasatellite complex identified in <i>Vicia cracca</i> in the Rhône delta region of France. <i>Archives of Virology</i> , <b>2018</b> , 163, 695-700	2.6	14

74	Molecular characterization of faba bean necrotic yellows viruses in Tunisia. <i>Archives of Virology</i> , <b>2018</b> , 163, 687-694	2.6	11
73	Nanopore-based detection and characterization of yam viruses. <i>Scientific Reports</i> , <b>2018</b> , 8, 17879	4.9	27
72	The Westward Journey of Alfalfa Leaf Curl Virus. <i>Viruses</i> , <b>2018</b> , 10,	6.2	6
71	Pervasive tertiary structure in the dengue virus RNA genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, 11513-11518	11.5	50
70	Notes on recombination and reassortment in multipartite/segmented viruses. <i>Current Opinion in Virology</i> , <b>2018</b> , 33, 156-166	7.5	26
69	A19 The impact of HIV-1 on the evolution of Mycobacterium tuberculosis. <i>Virus Evolution</i> , <b>2018</b> , 4,	3.7	78
68	Passion Fruit Chlorotic Mottle Virus: Molecular Characterization of a New Divergent Geminivirus in Brazil. <i>Viruses</i> , <b>2018</b> , 10,	6.2	26
67	Capulavirus and Grablovirus: two new genera in the family Geminiviridae. <i>Archives of Virology</i> , <b>2017</b> , 162, 1819-1831	2.6	166
66	Identification of a Nanovirus-Alphasatellite Complex in Sophora alopecuroides. <i>Virus Research</i> , <b>2017</b> , 235, 24-32	6.4	19
65	Genetic diversity and phylogenetic analysis of the ORF5 gene of PRRSV from central China. <i>Research in Veterinary Science</i> , <b>2017</b> , 115, 226-234	2.5	5
64	Genome sequences of a capulavirus infecting Plantago lanceolata in the Åland archipelago of Finland. <i>Archives of Virology</i> , <b>2017</b> , 162, 2041-2045	2.6	29
63	Detecting and Analyzing Genetic Recombination Using RDP4. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1525, 433-460	1.4	70
62	The Influence of HIV on the Evolution of Mycobacterium tuberculosis. <i>Molecular Biology and Evolution</i> , <b>2017</b> , 34, 1654-1668	8.3	17
61	Complete genome sequences of cowpea polerovirus 1 and cowpea polerovirus 2 infecting cowpea plants in Burkina Faso. <i>Archives of Virology</i> , <b>2017</b> , 162, 2149-2152	2.6	5
60	Occurrence of a novel mastrevirus in sugarcane germplasm collections in Florida, Guadeloupe and Réunion. <i>Virology Journal</i> , <b>2017</b> , 14, 146	6.1	13
59	ICTV Virus Taxonomy Profile: Geminiviridae. <i>Journal of General Virology</i> , <b>2017</b> , 98, 131-133	4.9	400
58	Molecular diversity, geographic distribution and host range of monocot-infecting mastreviruses in Africa and surrounding islands. <i>Virus Research</i> , <b>2017</b> , 238, 171-178	6.4	9
57	Novel mastreviruses identified in Australian wild rice. <i>Virus Research</i> , <b>2017</b> , 238, 193-197	6.4	10

56	Tomato leaf curl New Delhi virus: a widespread bipartite begomovirus in the territory of monopartite begomoviruses. <i>Molecular Plant Pathology</i> , <b>2017</b> , 18, 901-911	5.7	61
55	Metagenomic-Based Screening and Molecular Characterization of Cowpea-Infecting Viruses in Burkina Faso. <i>PLoS ONE</i> , <b>2016</b> , 11, e0165188	3.7	32
54	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> , <b>2016</b> , 493, 142-53	3.6	33
53	Divergent evolutionary and epidemiological dynamics of cassava mosaic geminiviruses in Madagascar. <i>BMC Evolutionary Biology</i> , <b>2016</b> , 16, 182	3	15
52	Phylogenetics of HIV-1 subtype G env: Greater complexity and older origins than previously reported. <i>Infection, Genetics and Evolution</i> , <b>2015</b> , 35, 9-18	4.5	5
51	Functionally conserved architecture of hepatitis C virus RNA genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 3692-7	11.5	89
50	Gene-wide identification of episodic selection. <i>Molecular Biology and Evolution</i> , <b>2015</b> , 32, 1365-71	8.3	227
49	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> , <b>2015</b> , 29, 203-15	4.5	15
48	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> , <b>2015</b> , 90, 2221-9	6.6	21
47	Near full-length HIV type 1M genomic sequences from Cameroon : Evidence of early diverging under-sampled lineages in the country. <i>Evolution, Medicine and Public Health</i> , <b>2015</b> , 2015, 254-65	3	10
46	Complete Genome Sequences of Four African Horse Sickness Virus Strains from a Commercial Tetravalent Live Attenuated Vaccine. <i>Genome Announcements</i> , <b>2015</b> , 3,		4
45	Potent Sensitisation of Cancer Cells to Anticancer Drugs by a Quadruple Mutant of the Human Deoxycytidine Kinase. <i>PLoS ONE</i> , <b>2015</b> , 10, e0140741	3.7	2
44	Plant Virus Metagenomics: Advances in Virus Discovery. <i>Phytopathology</i> , <b>2015</b> , 105, 716-27	3.8	214
43	The genomes of many yam species contain transcriptionally active endogenous geminiviral sequences that may be functionally expressed. <i>Virus Evolution</i> , <b>2015</b> , 1, vev002	3.7	19
42	RDP4: Detection and analysis of recombination patterns in virus genomes. <i>Virus Evolution</i> , <b>2015</b> , 1, vev003	3.7	1740
41	Complete Genome Sequences of the Three African Horse Sickness Virus Strains from a Commercial Trivalent Live Attenuated Vaccine. <i>Genome Announcements</i> , <b>2015</b> , 3,		7
40	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> , <b>2015</b> , 31, 73-86	4.5	62
39	Genome diversity and evidence of recombination and reassortment in nanoviruses from Europe. <i>Journal of General Virology</i> , <b>2014</b> , 95, 1178-1191	4.9	31

38	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> , <b>2014</b> , 88, 7843-51	6.6	15
37	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> , <b>2014</b> , 95, 1338-1351	4.9	28
36	Towards inferring the global movement of beak and feather disease virus. <i>Virology</i> , <b>2014</b> , 450-451, 24-33.6	4.3	
35	Patterns of recombination in HIV-1M are influenced by selection disfavours the survival of recombinants with disrupted genomic RNA and protein structures. <i>PLoS ONE</i> , <b>2014</b> , 9, e100400	3.7	9
34	Inducible resistance to maize streak virus. <i>PLoS ONE</i> , <b>2014</b> , 9, e105932	3.7	11
33	Appearances can be deceptive: revealing a hidden viral infection with deep sequencing in a plant quarantine context. <i>PLoS ONE</i> , <b>2014</b> , 9, e102945	3.7	65
32	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> , <b>2013</b> , 10, 29	6.1	18
31	Extensive recombination detected among beak and feather disease virus isolates from breeding facilities in Poland. <i>Journal of General Virology</i> , <b>2013</b> , 94, 1086-1095	4.9	44
30	Evidence of inter-component recombination, intra-component recombination and reassortment in banana bunchy top virus. <i>Journal of General Virology</i> , <b>2012</b> , 93, 1103-1119	4.9	33
29	Analysing recombination in nucleotide sequences. <i>Molecular Ecology Resources</i> , <b>2011</b> , 11, 943-55	8.4	85
28	Recombination in eukaryotic single stranded DNA viruses. <i>Viruses</i> , <b>2011</b> , 3, 1699-738	6.2	141
27	Recombination patterns in dicot-infecting mastreviruses mirror those found in monocot-infecting mastreviruses. <i>Archives of Virology</i> , <b>2011</b> , 156, 1463-9	2.6	11
26	Eragrostis minor streak virus: an Asian streak virus in Africa. <i>Archives of Virology</i> , <b>2011</b> , 156, 1299-303	2.6	8
25	Complex recombination patterns arising during geminivirus coinfections preserve and demarcate biologically important intra-genome interaction networks. <i>PLoS Pathogens</i> , <b>2011</b> , 7, e1002203	7.6	65
24	Dragonfly cyclovirus, a novel single-stranded DNA virus discovered in dragonflies (Odonata: Anisoptera). <i>Journal of General Virology</i> , <b>2011</b> , 92, 1302-1308	4.9	88
23	Maize streak virus: an old and complex emerging pathogen. <i>Molecular Plant Pathology</i> , <b>2010</b> , 11, 1-12	5.7	89
22	RNA structures facilitate recombination-mediated gene swapping in HIV-1. <i>Journal of Virology</i> , <b>2010</b> , 84, 12675-82	6.6	45
21	Genetic Recombination and Bacterial Population Structure <b>2010</b> , 61-85		4



20	RDP3: a flexible and fast computer program for analyzing recombination. <i>Bioinformatics</i> , <b>2010</b> , 26, 2462-32	7.2	1392
19	Molecular mechanisms of recombination restriction in the envelope gene of the human immunodeficiency virus. <i>PLoS Pathogens</i> , <b>2009</b> , 5, e1000418	7.6	63
18	Rapid host adaptation by extensive recombination. <i>Journal of General Virology</i> , <b>2009</b> , 90, 734-746	4.9	78
17	Dating the origins of the maize-adapted strain of maize streak virus, MSV-A. <i>Journal of General Virology</i> , <b>2009</b> , 90, 3066-3074	4.9	46
16	The epidemiology, economic impact and control of maize streak disease. <i>Food Security</i> , <b>2009</b> , 1, 305-315	6.7	53
15	Recombination detection and analysis using RDP3. <i>Methods in Molecular Biology</i> , <b>2009</b> , 537, 185-205	1.4	67
14	Extensive purifying selection acting on synonymous sites in HIV-1 Group M sequences. <i>Virology Journal</i> , <b>2008</b> , 5, 160	6.1	21
13	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> , <b>2008</b> , 89, 2063-2074	4.9	107
12	Genetic analysis of maize streak virus isolates from Uganda reveals widespread distribution of a recombinant variant. <i>Journal of General Virology</i> , <b>2007</b> , 88, 3154-3165	4.9	50
11	Inhibition of maize streak virus (MSV) replication by transient and transgenic expression of MSV replication-associated protein mutants. <i>Journal of General Virology</i> , <b>2007</b> , 88, 325-336	4.9	31
10	Robust inference of positive selection from recombining coding sequences. <i>Bioinformatics</i> , <b>2006</b> , 22, 2493-9	7.2	159
9	Evidence of ancient papillomavirus recombination. <i>Journal of General Virology</i> , <b>2006</b> , 87, 2527-2531	4.9	56
8	Recombination patterns in aphthoviruses mirror those found in other picornaviruses. <i>Journal of Virology</i> , <b>2006</b> , 80, 11827-32	6.6	234
7	The evolutionary value of recombination is constrained by genome modularity. <i>PLoS Genetics</i> , <b>2005</b> , 1, e51	6	95
6	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> , <b>2005</b> , 86, 803-813	4.9	46
5	South West Indian Ocean islands tomato begomovirus populations represent a new major monopartite begomovirus group. <i>Journal of General Virology</i> , <b>2005</b> , 86, 1533-1542	4.9	56
4	RDP: detection of recombination amongst aligned sequences. <i>Bioinformatics</i> , <b>2000</b> , 16, 562-3	7.2	1145
3	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa		12



2	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	1
1	Conserved recombination patterns across coronavirus subgenera	2