

Allen Gerard Rodrigo

List of Publications by Citations

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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.

112 papers	7,051 citations	35 h-index	83 g-index
122 ext. papers	7,888 ext. citations	5.7 avg, IF	5.49 L-index

#	Paper	IF	Citations
112	Likelihood-based tests of topologies in phylogenetics. <i>Systematic Biology</i> , 2000 , 49, 652-70	8.4	930
111	Consistent viral evolutionary changes associated with the progression of human immunodeficiency virus type 1 infection. <i>Journal of Virology</i> , 1999 , 73, 10489-502	6.6	790
110	Estimating mutation parameters, population history and genealogy simultaneously from temporally spaced sequence data. <i>Genetics</i> , 2002 , 161, 1307-20	4	744
109	Time-dependent rates of molecular evolution. <i>Molecular Ecology</i> , 2011 , 20, 3087-101	5.7	383
108	Assessing the complex sponge microbiota: core, variable and species-specific bacterial communities in marine sponges. <i>ISME Journal</i> , 2012 , 6, 564-76	11.9	368
107	Measurably evolving populations. <i>Trends in Ecology and Evolution</i> , 2003 , 18, 481-488	10.9	300
106	Description of <i>Caldicellulosiruptor saccharolyticus</i> gen. nov., sp. nov.: an obligately anaerobic, extremely thermophilic, cellulolytic bacterium. <i>FEMS Microbiology Letters</i> , 1994 , 120, 263-6	2.9	166
105	HIV quasispecies and resampling. <i>Science</i> , 1996 , 273, 415-6	33.3	148
104	Modeling the site-specific variation of selection patterns along lineages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 12957-62	11.5	132
103	Quantitation of target molecules from polymerase chain reaction-based limiting dilution assays. <i>AIDS Research and Human Retroviruses</i> , 1997 , 13, 737-42	1.6	126
102	Pervasive genomic recombination of HIV-1 in vivo. <i>Genetics</i> , 2004 , 167, 1573-83	4	125
101	Transition between stochastic evolution and deterministic evolution in the presence of selection: general theory and application to virology. <i>Microbiology and Molecular Biology Reviews</i> , 2001 , 65, 151-85 ^{13.2}	13.2	123
100	Evolution of envelope sequences from the genital tract and peripheral blood of women infected with clade A human immunodeficiency virus type 1. <i>Journal of Virology</i> , 1998 , 72, 8240-51	6.6	118
99	Consensus and ancestral state HIV vaccines. <i>Science</i> , 2003 , 299, 1515-8; author reply 1515-8	33.3	112
98	Genetic diversity of feline immunodeficiency virus: dual infection, recombination, and distinct evolutionary rates among envelope sequence clades. <i>Journal of Virology</i> , 1997 , 71, 4241-53	6.6	112
97	Viral quasi-species evolution during hepatitis Be antigen seroconversion. <i>Gastroenterology</i> , 2007 , 133, 951-8	13.3	104
96	Human immunodeficiency virus type 1 subtype B ancestral envelope protein is functional and elicits neutralizing antibodies in rabbits similar to those elicited by a circulating subtype B envelope. <i>Journal of Virology</i> , 2005 , 79, 11214-24	6.6	103

95	Immune-mediated positive selection drives human immunodeficiency virus type 1 molecular variation and predicts disease duration. <i>Journal of Virology</i> , 2002 , 76, 11715-20	6.6	100
94	Maximum likelihood supertrees. <i>Systematic Biology</i> , 2008 , 57, 243-50	8.4	96
93	Ultrafast evolution and loss of CRISPRs following a host shift in a novel wildlife pathogen, <i>Mycoplasma gallisepticum</i> . <i>PLoS Genetics</i> , 2012 , 8, e1002511	6	95
92	Coalescent estimates of HIV-1 generation time in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999 , 96, 2187-91	11.5	94
91	DNA surveillance: web-based molecular identification of whales, dolphins, and porpoises. <i>Journal of Heredity</i> , 2003 , 94, 111-4	2.4	82
90	Feline Lentivirus Evolution in Cross-Species Infection Reveals Extensive G-to-A Mutation and Selection on Key Residues in the Viral Polymerase. <i>Journal of Virology</i> , 2006 , 80, 8845-8845	6.6	78
89	A randomisation test of the null hypothesis that two cladograms are sample estimates of a parametric phylogenetic tree. <i>New Zealand Journal of Botany</i> , 1993 , 31, 257-268	1	78
88	Reconstructing genealogies of serial samples under the assumption of a molecular clock using serial-sample UPGMA. <i>Molecular Biology and Evolution</i> , 2000 , 17, 1807-15	8.3	76
87	Evolution of human immunodeficiency virus type 1 envelope sequences in infected individuals with differing disease progression profiles. <i>Virology</i> , 1998 , 241, 251-9	3.6	74
86	Epidemiology, genetic diversity, and evolution of endemic feline immunodeficiency virus in a population of wild cougars. <i>Journal of Virology</i> , 2003 , 77, 9578-89	6.6	68
85	The perils of plenty: what are we going to do with all these genes?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008 , 363, 3893-902	5.8	64
84	Selection for human immunodeficiency virus type 1 recombinants in a patient with rapid progression to AIDS. <i>Journal of Virology</i> , 2002 , 76, 10674-84	6.6	64
83	Testing the hypothesis of a recombinant origin of human immunodeficiency virus type 1 subtype E. <i>Journal of Virology</i> , 2000 , 74, 10752-65	6.6	57
82	Feline lentivirus evolution in cross-species infection reveals extensive G-to-A mutation and selection on key residues in the viral polymerase. <i>Journal of Virology</i> , 2006 , 80, 2728-37	6.6	48
81	The inference of stepwise changes in substitution rates using serial sequence samples. <i>Molecular Biology and Evolution</i> , 2001 , 18, 1365-71	8.3	45
80	Immunogen sequence: the fourth tier of AIDS vaccine design. <i>Expert Review of Vaccines</i> , 2004 , 3, S151-9	5.2	41
79	A comment on Baum's method for combining phylogenetic trees. <i>Taxon</i> , 1993 , 42, 631-636	0.8	38
78	Patterns of gut bacterial colonization in three primate species. <i>PLoS ONE</i> , 2015 , 10, e0124618	3.7	37

77	Neutral Models of Microbiome Evolution. <i>PLoS Computational Biology</i> , 2015 , 11, e1004365	5	35
76	Using temporally spaced sequences to simultaneously estimate migration rates, mutation rate and population sizes in measurably evolving populations. <i>Genetics</i> , 2004 , 168, 2407-20	4	35
75	Examination of Trichoderma phylogenies derived from ribosomal DNA sequence data. <i>Mycological Research</i> , 2000 , 104, 23-34		32
74	Covariability of V3 loop amino acids. <i>AIDS Research and Human Retroviruses</i> , 1996 , 12, 1401-11	1.6	32
73	Cumulative viral evolutionary changes in chronic hepatitis B virus infection precedes hepatitis B e antigen seroconversion. <i>Gut</i> , 2013 , 62, 1347-55	19.2	30
72	On combining cladograms. <i>Taxon</i> , 1996 , 45, 267-274	0.8	30
71	Synthesis Centers as Critical Research Infrastructure. <i>BioScience</i> , 2017 , 67, 750-759	5.7	29
70	Evolution of relative synonymous codon usage in Human Immunodeficiency Virus type-1. <i>Journal of Bioinformatics and Computational Biology</i> , 2005 , 3, 157-68	1	29
69	Genetic analysis of viral variants selected in transmission of human immunodeficiency viruses to newborns. <i>AIDS Research and Human Retroviruses</i> , 2000 , 16, 1223-33	1.6	29
68	Human immunodeficiency virus type 1 molecular evolution and the measure of selection. <i>AIDS Research and Human Retroviruses</i> , 1996 , 12, 1681-5	1.6	28
67	Calibrating the bootstrap test of monophyly. <i>International Journal for Parasitology</i> , 1993 , 23, 507-14	4.3	28
66	The Effects of Population Bottlenecks on Multilocus DNA Variation in Robins. <i>Journal of Heredity</i> , 1997 , 88, 179-186	2.4	27
65	Phylogenetic analysis of feline immunodeficiency virus in feral and companion domestic cats of New Zealand. <i>Journal of Virology</i> , 2007 , 81, 2999-3004	6.6	27
64	HIV-1 dynamics in children. <i>Journal of Acquired Immune Deficiency Syndromes</i> , 1999 , 20, 468-73		27
63	Increased viral quasispecies evolution in HBeAg seroconverter patients treated with oral nucleoside therapy. <i>Journal of Hepatology</i> , 2013 , 58, 217-24	13.4	26
62	An Assessment of Matrix Representation with Compatibility in Supertree Construction. <i>Computational Biology</i> , 2004 , 35-63	0.7	26
61	Molecular epidemiology of feline immunodeficiency virus in the domestic cat (<i>Felis catus</i>). <i>Veterinary Immunology and Immunopathology</i> , 2010 , 134, 68-74	2	24
60	Science incubators: synthesis centers and their role in the research ecosystem. <i>PLoS Biology</i> , 2013 , 11, e1001468	9.7	23

59	Associations between HLA class I alleles and escape mutations in the hepatitis B virus core gene in New Zealand-resident Tongans. <i>Journal of Virology</i> , 2010 , 84, 621-9	6.6	23
58	Models of microbiome evolution incorporating host and microbial selection. <i>Microbiome</i> , 2017 , 5, 127	16.6	22
57	Bamboo Specialists from Two Mammalian Orders (Primates, Carnivora) Share a High Number of Low-Abundance Gut Microbes. <i>Microbial Ecology</i> , 2018 , 76, 272-284	4.4	20
56	HIV-1 transmission during early antiretroviral therapy: evaluation of two HIV-1 transmission events in the HPTN 052 prevention study. <i>PLoS ONE</i> , 2013 , 8, e71557	3.7	17
55	DNA barcoding of the endemic New Zealand leafroller moth genera, Ctenopseustis and Planotortrix. <i>Molecular Ecology Resources</i> , 2009 , 9, 691-8	8.4	17
54	Recombination in feline immunodeficiency virus from feral and companion domestic cats. <i>Virology Journal</i> , 2008 , 5, 76	6.1	17
53	Selecting taxa to save or sequence: desirable criteria and a greedy solution. <i>Systematic Biology</i> , 2008 , 57, 825-34	8.4	16
52	SQUINT: a multiple alignment program and editor. <i>Bioinformatics</i> , 2007 , 23, 1553-5	7.2	16
51	Inferring evolutionary rates using serially sampled sequences from several populations. <i>Molecular Biology and Evolution</i> , 2003 , 20, 2010-8	8.3	13
50	Neutral models of short-term microbiome dynamics with host subpopulation structure and migration limitation. <i>Microbiome</i> , 2018 , 6, 80	16.6	12
49	Substitution model of sequence evolution for the human immunodeficiency virus type 1 subtype B gp120 gene over the C2-V5 region. <i>Journal of Molecular Evolution</i> , 2001 , 53, 55-62	3.1	12
48	HIV evolutionary genetics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999 , 96, 10559-61	11.5	12
47	A statistical model to identify differentially expressed proteins in 2D PAGE gels. <i>PLoS Computational Biology</i> , 2009 , 5, e1000509	5	11
46	Dynamics of syncytium-inducing and non-syncytium-inducing type 1 human immunodeficiency viruses during primary infection. <i>AIDS Research and Human Retroviruses</i> , 1997 , 13, 1447-51	1.6	11
45	Feeding strategy shapes gut metagenomic enrichment and functional specialization in captive lemurs. <i>Gut Microbes</i> , 2018 , 9, 202-217	8.8	11
44	Complete mitochondrial genome of the green-lipped mussel, (Mollusca: Mytiloidea), from long nanopore sequencing reads. <i>Mitochondrial DNA Part B: Resources</i> , 2018 , 3, 175-176	0.5	9
43	Identifying predictors of time-inhomogeneous viral evolutionary processes. <i>Virus Evolution</i> , 2016 , 2, vey023	9.7	9
42	Reduced total genetic diversity following translocations? A metapopulation approach. <i>Conservation Genetics</i> , 2013 , 14, 1043-1055	2.6	8

41	Ecstatic display calls of the Adlie penguin honestly predict male condition and breeding success. <i>Behaviour</i> , 2010 , 147, 165-184	1.4	8
40	Integrating genealogy and epidemiology: the ancestral infection and selection graph as a model for reconstructing host virus histories. <i>Theoretical Population Biology</i> , 2005 , 68, 65-75	1.2	8
39	The effect of habitat on the helminth parasites of an island population of the Polynesian rat (<i>Rattus exulans</i>). <i>Journal of Zoology</i> , 1992 , 227, 109-125	2	8
38	A MODIFICATION TO WHEELER'S COMBINATORIAL WEIGHTS CALCULATIONS.. <i>Cladistics</i> , 1992 , 8, 165-170	3.5	8
37	Recombination in feline lentiviral genomes during experimental cross-species infection. <i>Virology</i> , 2007 , 359, 146-51	3.6	7
36	Estimating Population Parameters using the Structured Serial Coalescent with Bayesian MCMC Inference when some Demes are Hidden. <i>Evolutionary Bioinformatics</i> , 2006 , 2, 117693430600200	1.9	7
35	Estimating population parameters using the structured serial coalescent with Bayesian MCMC inference when some demes are hidden. <i>Evolutionary Bioinformatics</i> , 2007 , 2, 227-35	1.9	7
34	Transient compartmentalization of simian immunodeficiency virus variants in the breast milk of african green monkeys. <i>Journal of Virology</i> , 2013 , 87, 11292-9	6.6	6
33	Surficial sediment-heavy metal associations in the Avon-Heathcote Estuary, New Zealand. <i>New Zealand Journal of Marine and Freshwater Research</i> , 1989 , 23, 255-262	1.3	6
32	The Evolutionary Value of Helpful Microbes: A Response to Shapira. <i>Trends in Ecology and Evolution</i> , 2017 , 32, 84-85	10.9	5
31	The molecular biology and evolution of feline immunodeficiency viruses of cougars. <i>Veterinary Immunology and Immunopathology</i> , 2008 , 123, 154-8	2	5
30	Predicting demographic group structures based on DNA sequence data. <i>Molecular Biology and Evolution</i> , 2003 , 20, 1168-80	8.3	5
29	Sampling and Processing HIV Molecular Sequences: A Computational Evolutionary Biologist's Perspective 2002 , 1-17		5
28	Genealogies from Time-Stamped Sequence Data. <i>Lecture Notes in Statistics</i> , 2004 , 149-171	2.9	5
27	Combinability of phylogenies and bootstrap confidence envelopes. <i>Systematic Biology</i> , 1998 , 47, 727-33	8.4	5
26	Modelling the evolution of protein coding sequences sampled from Measurably Evolving Populations. <i>Genome Informatics</i> , 2008 , 21, 150-64		5
25	Evidence for reduced selection pressure on the hepatitis B virus core gene in hepatitis B e antigen-negative chronic hepatitis B. <i>Journal of General Virology</i> , 2011 , 92, 1800-1808	4.9	4
24	A heteroduplex method for detection of targeted sub-populations of bacterial communities. <i>FEMS Microbiology Letters</i> , 2002 , 208, 9-13	2.9	4

23	Frequency-dependent selection drives HBeAg seroconversion in chronic hepatitis B virus infection. <i>Evolution, Medicine and Public Health</i> , 2014 , 2014, 1-9	3	3
22	Using logistic regression models to predict breeding success in male Adlie penguins (<i>Pygoscelis adeliae</i>). <i>Polar Biology</i> , 2010 , 33, 1083-1094	2	3
21	The distribution of feline immunodeficiency virus in tissue compartments of feral domestic cats. <i>Archives of Virology</i> , 2010 , 155, 411-6	2.6	3
20	Covariation of branch lengths in phylogenies of functionally related genes. <i>PLoS ONE</i> , 2009 , 4, e8487	3.7	3
19	Reassembling haplotypes in a mixture of pooled amplicons when the relative concentrations are known: A proof-of-concept study on the efficient design of next-generation sequencing strategies. <i>PLoS ONE</i> , 2018 , 13, e0195090	3.7	3
18	Coalescent entanglement and the conditional dependence of the times to common ancestry of mutually exclusive pairs of individuals. <i>Journal of Heredity</i> , 2013 , 104, 86-91	2.4	2
17	On the use of bootstrapped topologies in coalescent-based Bayesian MCMC inference: a comparison of estimation and computational efficiencies. <i>Evolutionary Bioinformatics</i> , 2009 , 5, 97-105	1.9	2
16	Vector quantization of amino acids: Analysis of the HIV V3 loop region. <i>Journal of Statistical Planning and Inference</i> , 2005 , 130, 277-298	0.8	2
15	Sources of variation in ancestral sequence reconstruction for HIV-1 envelope genes. <i>Evolutionary Bioinformatics</i> , 2007 , 2, 53-76	1.9	2
14	Estimating the Ancestral States of a Continuous-Valued Character Using Squared-Change Parsimony: An Analytical Solution		2
13	A Bayesian model for classifying all differentially expressed proteins simultaneously in 2D PAGE gels. <i>BMC Bioinformatics</i> , 2012 , 13, 137	3.6	1
12	Sources of Variation in Ancestral Sequence Reconstruction for HIV-1 Envelope Genes. <i>Evolutionary Bioinformatics</i> , 2006 , 2, 117693430600200	1.9	1
11	Using PEBBLE for the evolutionary analysis of serially sampled molecular sequences. <i>Current Protocols in Bioinformatics</i> , 2004 , Chapter 6, Unit 6.8	24.2	1
10	HaploJuice: Accurate haplotype assembly from a pool of sequences with known relative concentrations		1
9	Computational Evaluation of the Strict Master and Random Template Models of Endogenous Retrovirus Evolution. <i>PLoS ONE</i> , 2016 , 11, e0162454	3.7	1
8	Effective machine-learning assembly for next-generation amplicon sequencing with very low coverage. <i>BMC Bioinformatics</i> , 2019 , 20, 654	3.6	1
7	HaploJuice : accurate haplotype assembly from a pool of sequences with known relative concentrations. <i>BMC Bioinformatics</i> , 2018 , 19, 389	3.6	1
6	Genetic Variants of and Are Associated With Risk of Non-Small Cell Lung Cancer. <i>Frontiers in Oncology</i> , 2021 , 11, 709829	5.3	1

- 5 Linking Evolution, Ecology, and Health: TriCEM. *BioScience*, **2015**, 65, 748-749 5.7
- 4 Estimation of evolutionary parameters using short, random and partial sequences from mixed samples of anonymous individuals. *BMC Bioinformatics*, **2015**, 16, 357 3.6
- 3 Two Optimality Criteria for Selecting Subsets of Most Parsimonious Trees. *Systematic Biology*, **1992**, 41, 33 8.4
- 2 Specific and general formulae for the number of band combinations for different colour-banding regimes. *New Zealand Journal of Zoology*, **1990**, 17, 285-288 0.8
- 1 An assembly-free method of phylogeny reconstruction using short-read sequences from pooled samples without barcodes. *PLoS Computational Biology*, **2021**, 17, e1008949 5