

# Allen Gerard Rodrigo

## 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.

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

| #   | Paper  | IF   | Citations |
|-----|--|------|-----------|
| 112 | An assembly-free method of phylogeny reconstruction using short-read sequences from pooled samples without barcodes. <i>PLoS Computational Biology</i> , <b>2021</b> , 17, e1008949  | 5    |           |
| 111 | Genetic Variants of and Are Associated With Risk of Non-Small Cell Lung Cancer. <i>Frontiers in Oncology</i> , <b>2021</b> , 11, 709829  | 5.3  | 1         |
| 110 | Effective machine-learning assembly for next-generation amplicon sequencing with very low coverage. <i>BMC Bioinformatics</i> , <b>2019</b> , 20, 654  | 3.6  | 1         |
| 109 | Complete mitochondrial genome of the green-lipped mussel, (Mollusca: Mytiloidea), from long nanopore sequencing reads. <i>Mitochondrial DNA Part B: Resources</i> , <b>2018</b> , 3, 175-176   | 0.5  | 9         |
| 108 | Neutral models of short-term microbiome dynamics with host subpopulation structure and migration limitation. <i>Microbiome</i> , <b>2018</b> , 6, 80   | 16.6 | 12        |
| 107 | Feeding strategy shapes gut metagenomic enrichment and functional specialization in captive lemurs. <i>Gut Microbes</i> , <b>2018</b> , 9, 202-217   | 8.8  | 11        |
| 106 | Bamboo Specialists from Two Mammalian Orders (Primates, Carnivora) Share a High Number of Low-Abundance Gut Microbes. <i>Microbial Ecology</i> , <b>2018</b> , 76, 272-284   | 4.4  | 20        |
| 105 | HaploJuice : accurate haplotype assembly from a pool of sequences with known relative concentrations. <i>BMC Bioinformatics</i> , <b>2018</b> , 19, 389  | 3.6  | 1         |
| 104 | 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> , <b>2018</b> , 13, e0195090 | 3.7  | 3         |
| 103 | The Evolutionary Value of Helpful Microbes: A Response to Shapira. <i>Trends in Ecology and Evolution</i> , <b>2017</b> , 32, 84-85  | 10.9 | 5         |
| 102 | Synthesis Centers as Critical Research Infrastructure. <i>BioScience</i> , <b>2017</b> , 67, 750-759   | 5.7  | 29        |
| 101 | Models of microbiome evolution incorporating host and microbial selection. <i>Microbiome</i> , <b>2017</b> , 5, 127  | 16.6 | 22        |
| 100 | Identifying predictors of time-inhomogeneous viral evolutionary processes. <i>Virus Evolution</i> , <b>2016</b> , 2, vey023  | 9.7  | 9         |
| 99  | Computational Evaluation of the Strict Master and Random Template Models of Endogenous Retrovirus Evolution. <i>PLoS ONE</i> , <b>2016</b> , 11, e0162454  | 3.7  | 1         |
| 98  | Linking Evolution, Ecology, and Health: TriCEM. <i>BioScience</i> , <b>2015</b> , 65, 748-749  | 5.7  |           |
| 97  | Estimation of evolutionary parameters using short, random and partial sequences from mixed samples of anonymous individuals. <i>BMC Bioinformatics</i> , <b>2015</b> , 16, 357   | 3.6  |           |
| 96  | Patterns of gut bacterial colonization in three primate species. <i>PLoS ONE</i> , <b>2015</b> , 10, e0124618  | 3.7  | 37        |

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| 95 | Neutral Models of Microbiome Evolution. <i>PLoS Computational Biology</i> , <b>2015</b> , 11, e1004365   | 5    | 35  |
| 94 | Frequency-dependent selection drives HBeAg seroconversion in chronic hepatitis B virus infection. <i>Evolution, Medicine and Public Health</i> , <b>2014</b> , 2014, 1-9                           | 3    | 3   |
| 93 | Reduced total genetic diversity following translocations? A metapopulation approach. <i>Conservation Genetics</i> , <b>2013</b> , 14, 1043-1055  | 2.6  | 8   |
| 92 | Increased viral quasispecies evolution in HBeAg seroconverter patients treated with oral nucleoside therapy. <i>Journal of Hepatology</i> , <b>2013</b> , 58, 217-24                               | 13.4 | 26  |
| 91 | Science incubators: synthesis centers and their role in the research ecosystem. <i>PLoS Biology</i> , <b>2013</b> , 11, e1001468   | 9.7  | 23  |
| 90 | Transient compartmentalization of simian immunodeficiency virus variants in the breast milk of african green monkeys. <i>Journal of Virology</i> , <b>2013</b> , 87, 11292-9                       | 6.6  | 6   |
| 89 | Coalescent entanglement and the conditional dependence of the times to common ancestry of mutually exclusive pairs of individuals. <i>Journal of Heredity</i> , <b>2013</b> , 104, 86-91           | 2.4  | 2   |
| 88 | Cumulative viral evolutionary changes in chronic hepatitis B virus infection precedes hepatitis B e antigen seroconversion. <i>Gut</i> , <b>2013</b> , 62, 1347-55                                 | 19.2 | 30  |
| 87 | HIV-1 transmission during early antiretroviral therapy: evaluation of two HIV-1 transmission events in the HPTN 052 prevention study. <i>PLoS ONE</i> , <b>2013</b> , 8, e71557                    | 3.7  | 17  |
| 86 | Assessing the complex sponge microbiota: core, variable and species-specific bacterial communities in marine sponges. <i>ISME Journal</i> , <b>2012</b> , 6, 564-76                                | 11.9 | 368 |
| 85 | A Bayesian model for classifying all differentially expressed proteins simultaneously in 2D PAGE gels. <i>BMC Bioinformatics</i> , <b>2012</b> , 13, 137   | 3.6  | 1   |
| 84 | Ultrafast evolution and loss of CRISPRs following a host shift in a novel wildlife pathogen, <i>Mycoplasma gallisepticum</i> . <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002511                    | 6    | 95  |
| 83 | Time-dependent rates of molecular evolution. <i>Molecular Ecology</i> , <b>2011</b> , 20, 3087-101   | 5.7  | 383 |
| 82 | 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> , <b>2011</b> , 92, 1800-1808 | 4.9  | 4   |
| 81 | 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> , <b>2010</b> , 84, 621-9             | 6.6  | 23  |
| 80 | Ecstatic display calls of the Adlie penguin honestly predict male condition and breeding success. <i>Behaviour</i> , <b>2010</b> , 147, 165-184  | 1.4  | 8   |
| 79 | Molecular epidemiology of feline immunodeficiency virus in the domestic cat ( <i>Felis catus</i> ). <i>Veterinary Immunology and Immunopathology</i> , <b>2010</b> , 134, 68-74                    | 2    | 24  |
| 78 | Using logistic regression models to predict breeding success in male Adlie penguins ( <i>Pygoscelis adeliae</i> ). <i>Polar Biology</i> , <b>2010</b> , 33, 1083-1094                              | 2    | 3   |

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| 77 | The distribution of feline immunodeficiency virus in tissue compartments of feral domestic cats. <i>Archives of Virology</i> , <b>2010</b> , 155, 411-6  | 2.6  | 3   |
| 76 | A statistical model to identify differentially expressed proteins in 2D PAGE gels. <i>PLoS Computational Biology</i> , <b>2009</b> , 5, e1000509   | 5    | 11  |
| 75 | DNA barcoding of the endemic New Zealand leafroller moth genera, <i>Ctenopseustis</i> and <i>Planotortrix</i> . <i>Molecular Ecology Resources</i> , <b>2009</b> , 9, 691-8                                | 8.4  | 17  |
| 74 | On the use of bootstrapped topologies in coalescent-based Bayesian MCMC inference: a comparison of estimation and computational efficiencies. <i>Evolutionary Bioinformatics</i> , <b>2009</b> , 5, 97-105 | 1.9  | 2   |
| 73 | Covariation of branch lengths in phylogenies of functionally related genes. <i>PLoS ONE</i> , <b>2009</b> , 4, e8487   | 3.7  | 3   |
| 72 | Recombination in feline immunodeficiency virus from feral and companion domestic cats. <i>Virology Journal</i> , <b>2008</b> , 5, 76   | 6.1  | 17  |
| 71 | The molecular biology and evolution of feline immunodeficiency viruses of cougars. <i>Veterinary Immunology and Immunopathology</i> , <b>2008</b> , 123, 154-8   | 2    | 5   |
| 70 | Maximum likelihood supertrees. <i>Systematic Biology</i> , <b>2008</b> , 57, 243-50  | 8.4  | 96  |
| 69 | Selecting taxa to save or sequence: desirable criteria and a greedy solution. <i>Systematic Biology</i> , <b>2008</b> , 57, 825-34   | 8.4  | 16  |
| 68 | 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> , <b>2008</b> , 363, 3893-902                           | 5.8  | 64  |
| 67 | Modelling the evolution of protein coding sequences sampled from Measurably Evolving Populations. <i>Genome Informatics</i> , <b>2008</b> , 21, 150-64   |      | 5   |
| 66 | Viral quasi-species evolution during hepatitis Be antigen seroconversion. <i>Gastroenterology</i> , <b>2007</b> , 133, 951-8   | 13.3 | 104 |
| 65 | Recombination in feline lentiviral genomes during experimental cross-species infection. <i>Virology</i> , <b>2007</b> , 359, 146-51  | 3.6  | 7   |
| 64 | SQUINT: a multiple alignment program and editor. <i>Bioinformatics</i> , <b>2007</b> , 23, 1553-5  | 7.2  | 16  |
| 63 | Phylogenetic analysis of feline immunodeficiency virus in feral and companion domestic cats of New Zealand. <i>Journal of Virology</i> , <b>2007</b> , 81, 2999-3004                                       | 6.6  | 27  |
| 62 | Sources of variation in ancestral sequence reconstruction for HIV-1 envelope genes. <i>Evolutionary Bioinformatics</i> , <b>2007</b> , 2, 53-76  | 1.9  | 2   |
| 61 | Estimating population parameters using the structured serial coalescent with Bayesian MCMC inference when some demes are hidden. <i>Evolutionary Bioinformatics</i> , <b>2007</b> , 2, 227-35              | 1.9  | 7   |
| 60 | 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> , <b>2006</b> , 80, 8845-8845   | 6.6  | 78  |

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| 59 | 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> , <b>2006</b> , 80, 2728-37   | 6.6  | 48  |
| 58 | Estimating Population Parameters using the Structured Serial Coalescent with Bayesian MCMC Inference when some Demes are Hidden. <i>Evolutionary Bioinformatics</i> , <b>2006</b> , 2, 117693430600200   | 1.9  | 7   |
| 57 | Sources of Variation in Ancestral Sequence Reconstruction for HIV-1 Envelope Genes. <i>Evolutionary Bioinformatics</i> , <b>2006</b> , 2, 117693430600200  | 1.9  | 1   |
| 56 | Integrating genealogy and epidemiology: the ancestral infection and selection graph as a model for reconstructing host virus histories. <i>Theoretical Population Biology</i> , <b>2005</b> , 68, 65-75  | 1.2  | 8   |
| 55 | Vector quantization of amino acids: Analysis of the HIV V3 loop region. <i>Journal of Statistical Planning and Inference</i> , <b>2005</b> , 130, 277-298  | 0.8  | 2   |
| 54 | Evolution of relative synonymous codon usage in Human Immunodeficiency Virus type-1. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2005</b> , 3, 157-68  | 1    | 29  |
| 53 | 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> , <b>2005</b> , 79, 11214-24 | 6.6  | 103 |
| 52 | Using temporally spaced sequences to simultaneously estimate migration rates, mutation rate and population sizes in measurably evolving populations. <i>Genetics</i> , <b>2004</b> , 168, 2407-20  | 4    | 35  |
| 51 | Pervasive genomic recombination of HIV-1 in vivo. <i>Genetics</i> , <b>2004</b> , 167, 1573-83   | 4    | 125 |
| 50 | 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> , <b>2004</b> , 101, 12957-62  | 11.5 | 132 |
| 49 | Immunogen sequence: the fourth tier of AIDS vaccine design. <i>Expert Review of Vaccines</i> , <b>2004</b> , 3, S151-9   | 5.2  | 41  |
| 48 | Genealogies from Time-Stamped Sequence Data. <i>Lecture Notes in Statistics</i> , <b>2004</b> , 149-171  | 2.9  | 5   |
| 47 | Using PEBBLE for the evolutionary analysis of serially sampled molecular sequences. <i>Current Protocols in Bioinformatics</i> , <b>2004</b> , Chapter 6, Unit 6.8   | 24.2 | 1   |
| 46 | An Assessment of Matrix Representation with Compatibility in Supertree Construction. <i>Computational Biology</i> , <b>2004</b> , 35-63  | 0.7  | 26  |
| 45 | Predicting demographic group structures based on DNA sequence data. <i>Molecular Biology and Evolution</i> , <b>2003</b> , 20, 1168-80   | 8.3  | 5   |
| 44 | Inferring evolutionary rates using serially sampled sequences from several populations. <i>Molecular Biology and Evolution</i> , <b>2003</b> , 20, 2010-8  | 8.3  | 13  |
| 43 | Consensus and ancestral state HIV vaccines. <i>Science</i> , <b>2003</b> , 299, 1515-8; author reply 1515-8  | 33.3 | 112 |
| 42 | DNA surveillance: web-based molecular identification of whales, dolphins, and porpoises. <i>Journal of Heredity</i> , <b>2003</b> , 94, 111-4  | 2.4  | 82  |

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| 41 | Measurably evolving populations. <i>Trends in Ecology and Evolution</i> , <b>2003</b> , 18, 481-488  | 10.9 | 300 |
| 40 | Epidemiology, genetic diversity, and evolution of endemic feline immunodeficiency virus in a population of wild cougars. <i>Journal of Virology</i> , <b>2003</b> , 77, 9578-89  | 6.6  | 68  |
| 39 | Sampling and Processing HIV Molecular Sequences: A Computational Evolutionary Biologist's Perspective <b>2002</b> , 1-17   |      | 5   |
| 38 | A heteroduplex method for detection of targeted sub-populations of bacterial communities. <i>FEMS Microbiology Letters</i> , <b>2002</b> , 208, 9-13   | 2.9  | 4   |
| 37 | Immune-mediated positive selection drives human immunodeficiency virus type 1 molecular variation and predicts disease duration. <i>Journal of Virology</i> , <b>2002</b> , 76, 11715-20   | 6.6  | 100 |
| 36 | Selection for human immunodeficiency virus type 1 recombinants in a patient with rapid progression to AIDS. <i>Journal of Virology</i> , <b>2002</b> , 76, 10674-84  | 6.6  | 64  |
| 35 | Estimating mutation parameters, population history and genealogy simultaneously from temporally spaced sequence data. <i>Genetics</i> , <b>2002</b> , 161, 1307-20   | 4    | 744 |
| 34 | The inference of stepwise changes in substitution rates using serial sequence samples. <i>Molecular Biology and Evolution</i> , <b>2001</b> , 18, 1365-71  | 8.3  | 45  |
| 33 | 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> , <b>2001</b> , 65, 151-85 <sup>13.2</sup> |      | 123 |
| 32 | 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> , <b>2001</b> , 53, 55-62   | 3.1  | 12  |
| 31 | Genetic analysis of viral variants selected in transmission of human immunodeficiency viruses to newborns. <i>AIDS Research and Human Retroviruses</i> , <b>2000</b> , 16, 1223-33   | 1.6  | 29  |
| 30 | Reconstructing genealogies of serial samples under the assumption of a molecular clock using serial-sample UPGMA. <i>Molecular Biology and Evolution</i> , <b>2000</b> , 17, 1807-15   | 8.3  | 76  |
| 29 | Testing the hypothesis of a recombinant origin of human immunodeficiency virus type 1 subtype E. <i>Journal of Virology</i> , <b>2000</b> , 74, 10752-65   | 6.6  | 57  |
| 28 | Likelihood-based tests of topologies in phylogenetics. <i>Systematic Biology</i> , <b>2000</b> , 49, 652-70  | 8.4  | 930 |
| 27 | Examination of Trichoderma phylogenies derived from ribosomal DNA sequence data. <i>Mycological Research</i> , <b>2000</b> , 104, 23-34  |      | 32  |
| 26 | Consistent viral evolutionary changes associated with the progression of human immunodeficiency virus type 1 infection. <i>Journal of Virology</i> , <b>1999</b> , 73, 10489-502   | 6.6  | 790 |
| 25 | HIV-1 dynamics in children. <i>Journal of Acquired Immune Deficiency Syndromes</i> , <b>1999</b> , 20, 468-73  |      | 27  |
| 24 | HIV evolutionary genetics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1999</b> , 96, 10559-61   | 11.5 | 12  |

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|----|---|------|-----|
| 23 | Coalescent estimates of HIV-1 generation time in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1999</b> , 96, 2187-91   | 11.5 | 94  |
| 22 | Evolution of human immunodeficiency virus type 1 envelope sequences in infected individuals with differing disease progression profiles. <i>Virology</i> , <b>1998</b> , 241, 251-9                                 | 3.6  | 74  |
| 21 | Combinability of phylogenies and bootstrap confidence envelopes. <i>Systematic Biology</i> , <b>1998</b> , 47, 727-33   | 8.4  | 5   |
| 20 | 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> , <b>1998</b> , 72, 8240-51              | 6.6  | 118 |
| 19 | The Effects of Population Bottlenecks on Multilocus DNA Variation in Robins. <i>Journal of Heredity</i> , <b>1997</b> , 88, 179-186   | 2.4  | 27  |
| 18 | Dynamics of syncytium-inducing and non-syncytium-inducing type 1 human immunodeficiency viruses during primary infection. <i>AIDS Research and Human Retroviruses</i> , <b>1997</b> , 13, 1447-51                   | 1.6  | 11  |
| 17 | Quantitation of target molecules from polymerase chain reaction-based limiting dilution assays. <i>AIDS Research and Human Retroviruses</i> , <b>1997</b> , 13, 737-42  | 1.6  | 126 |
| 16 | Genetic diversity of feline immunodeficiency virus: dual infection, recombination, and distinct evolutionary rates among envelope sequence clades. <i>Journal of Virology</i> , <b>1997</b> , 71, 4241-53           | 6.6  | 112 |
| 15 | On combining cladograms. <i>Taxon</i> , <b>1996</b> , 45, 267-274   | 0.8  | 30  |
| 14 | HIV quasispecies and resampling. <i>Science</i> , <b>1996</b> , 273, 415-6  | 33.3 | 148 |
| 13 | Human immunodeficiency virus type 1 molecular evolution and the measure of selection. <i>AIDS Research and Human Retroviruses</i> , <b>1996</b> , 12, 1681-5  | 1.6  | 28  |
| 12 | Covariability of V3 loop amino acids. <i>AIDS Research and Human Retroviruses</i> , <b>1996</b> , 12, 1401-11   | 1.6  | 32  |
| 11 | Description of <i>Caldicellulosiruptor saccharolyticus</i> gen. nov., sp. nov: an obligately anaerobic, extremely thermophilic, cellulolytic bacterium. <i>FEMS Microbiology Letters</i> , <b>1994</b> , 120, 263-6 | 2.9  | 166 |
| 10 | 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> , <b>1993</b> , 31, 257-268                            | 1    | 78  |
| 9  | A comment on Baum's method for combining phylogenetic trees. <i>Taxon</i> , <b>1993</b> , 42, 631-636   | 0.8  | 38  |
| 8  | Calibrating the bootstrap test of monophyly. <i>International Journal for Parasitology</i> , <b>1993</b> , 23, 507-14   | 4.3  | 28  |
| 7  | Two Optimality Criteria for Selecting Subsets of Most Parsimonious Trees. <i>Systematic Biology</i> , <b>1992</b> , 41, 33  | 8.4  |     |
| 6  | 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> , <b>1992</b> , 227, 109-125                                     | 2    | 8   |

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| 5 | A MODIFICATION TO WHEELER'S COMBINATORIAL WEIGHTS CALCULATIONS.. <i>Cladistics</i> , <b>1992</b> , 8, 165-170  | 8     |
| 4 | Specific and general formulae for the number of band combinations for different colour-banding regimes. <i>New Zealand Journal of Zoology</i> , <b>1990</b> , 17, 285-288        | 0.8   |
| 3 | Surficial sediment-heavy metal associations in the Avon-Heathcote Estuary, New Zealand. <i>New Zealand Journal of Marine and Freshwater Research</i> , <b>1989</b> , 23, 255-262 | 1.3 6 |
| 2 | Estimating the Ancestral States of a Continuous-Valued Character Using Squared-Change Parsimony: An Analytical Solution  | 2     |
| 1 | HaploJuice: Accurate haplotype assembly from a pool of sequences with known relative concentrations  | 1     |