Santiago F Elena

List of Publications by Year
in descending order

276 papers	16,385 citations	17440 63 h-index	23533 111 g-index
326 all docs	326 docs citations	326 times ranked	10683 citing authors

#	Article	IF	Citations
1	Evolution experiments with microorganisms: the dynamics and genetic bases of adaptation. Nature Reviews Genetics, 2003, 4, 457-469.	16.3	1,179
2	The distribution of fitness effects caused by single-nucleotide substitutions in an RNA virus. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 8396-8401.	7.1	513
3	PERSPECTIVE: EVOLUTION AND DETECTION OF GENETIC ROBUSTNESS. Evolution; International Journal of Organic Evolution, 2003, 57, 1959-1972.	2.3	504
4	PERSPECTIVE:EVOLUTION AND DETECTION OF GENETIC ROBUSTNESS. Evolution; International Journal of Organic Evolution, 2003, 57, 1959.	2.3	467
5	Basic concepts in RNA virus evolution. FASEB Journal, 1996, 10, 859-864.	0.5	416
6	Test of synergistic interactions among deleterious mutations in bacteria. Nature, 1997, 390, 395-398.	27.8	399
7	Punctuated Evolution Caused by Selection of Rare Beneficial Mutations. Science, 1996, 272, 1802-1804.	12.6	325
8	Exponential increases of RNA virus fitness during large population transmissions.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 5841-5844.	7.1	273
9	Adaptive Value of High Mutation Rates of RNA Viruses: Separating Causes from Consequences. Journal of Virology, 2005, 79, 11555-11558.	3.4	265
10	Clonal Interference and the Evolution of RNA Viruses. Science, 1999, 285, 1745-1747.	12.6	257
11	The evolution of sex: empirical insights into the roles of epistasis and drift. Nature Reviews Genetics, 2007, 8, 139-149.	16.3	244
12	Editorial: A home for virology, ecology, epidemiology, and evolutionary biology. Virus Evolution, 2015, 1, 1-3.	4.9	242
13	GroEL buffers against deleterious mutations. Nature, 2002, 417, 398-398.	27.8	241
14	The contribution of epistasis to the architecture of fitness in an RNA virus. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 15376-15379.	7.1	216
15	Extremely High Mutation Rate of a Hammerhead Viroid. Science, 2009, 323, 1308-1308.	12.6	215
16	Cost of Host Radiation in an RNA Virus. Genetics, 2000, 156, 1465-1470.	2.9	201
17	Distributions of epistasis in microbes fit predictions from a fitness landscape model. Nature Genetics, 2007, 39, 555-560.	21.4	195
18	Genetic bottlenecks and population passages cause profound fitness differences in RNA viruses. Journal of Virology, 1993, 67, 222-228.	3.4	181

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19	The causes of epistasis. Proceedings of the Royal Society B: Biological Sciences, 2011, 278, 3617-3624.	2.6	175
20	Distribution of Fitness and Virulence Effects Caused by Single-Nucleotide Substitutions in <i>Tobacco Etch Virus</i>. Journal of Virology, 2007, 81, 12979-12984.	3.4	172
21	The Fittest versus the Flattest: Experimental Confirmation of the Quasispecies Effect with Subviral Pathogens. PLoS Pathogens, 2006, 2, e136.	4.7	168
22	Evolution and Emergence of Plant Viruses. Advances in Virus Research, 2014, 88, 161-191.	2.1	167
23	Evolution and ecology of plant viruses. Nature Reviews Microbiology, 2019, 17, 632-644.	28.6	166
24	The red queen reigns in the kingdom of RNA viruses.. Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 4821-4824.	7.1	160
25	Size of genetic bottlenecks leading to virus fitness loss is determined by mean initial population fitness. Journal of Virology, 1995, 69, 2869-2872.	3.4	148
26	The evolution of RNA viruses: A population genetics view. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 6967-6973.	7.1	146
27	Epistasis correlates to genomic complexity. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14402-14405.	7.1	146
28	Viroids: Survivors from the RNA World?. Annual Review of Microbiology, 2014, 68, 395-414.	7.3	142
29	Matters of Size: Genetic Bottlenecks in Virus Infection and Their Potential Impact on Evolution. Annual Review of Virology, 2015, 2, 161-179.	6.7	139
30	Mechanisms of genetic robustness in RNA viruses. EMBO Reports, 2006, 7, 168-173.	4.5	136
31	Subclonal components of consensus fitness in an RNA virus clone. Journal of Virology, 1994, 68, 4295-4301.	3.4	136
32	Multihost Experimental Evolution of a Plant RNA Virus Reveals Local Adaptation and Host-Specific Mutations. Molecular Biology and Evolution, 2012, 29, 1481-1492.	8.9	129
33	Distribution of fitness effects caused by random insertion mutations in Escherichia coli. Genetica, 1998, 102/103, 349-358.	1.1	126
34	RNA virus quasispecies: significance for viral disease and epidemiology. Infectious Agents and Disease, 1994, 3, 201-14.	1.2	121
35	Phylogeny of viroids, viroidlike satellite RNAs, and the viroidlike domain of hepatitis delta virus RNA.. Proceedings of the National Academy of Sciences of the United States of America, 1991, 88, 5631-5634.	7.1	116
36	Extreme fitness differences in mammalian and insect hosts after continuous replication of vesicular stomatitis virus in sandfly cells. Journal of Virology, 1995, 69, 6805-6809.	3.4	112

#	Article	IF	Citations
37	The Evolutionary Genetics of Emerging Plant RNA Viruses. Molecular Plant-Microbe Interactions, 2011, 24, 287-293.	2.6	110
38	Mixed Infections of<i>Pepino Mosaic Virus</i>Strains Modulate the Evolutionary Dynamics of this Emergent Virus. Journal of Virology, 2009, 83, 12378-12387.	3.4	104
39	Virus Evolution: Insights from an Experimental Approach. Annual Review of Ecology, Evolution, and Systematics, 2007, 38, 27-52.	8.3	103
40	From Hypo- to Hypersuppression: Effect of Amino Acid Substitutions on the RNA-Silencing Suppressor Activity of the <i>Tobacco etch potyvirus</i> HC-Pro. Genetics, 2008, 180, 1039-1049.	2.9	101
41	The Evolution of Viruses in Multi-Host Fitness Landscapes. The Open Virology Journal, 2009, 3, 1-6.	1.8	99
42	Effect of Host Species on the Distribution of Mutational Fitness Effects for an RNA Virus. PLoS Genetics, 2011, 7, e1002378.	3.5	99
43	Viroids: an Ariadne's thread into the RNA labyrinth. EMBO Reports, 2006, 7, 593-598.	4.5	93
44	Epistasis and the Adaptability of an RNA Virus. Genetics, 2005, 170, 1001-1008.	2.9	86
45	Molecular Basis of Adaptive Convergence in Experimental Populations of RNA Viruses. Genetics, 2002, 162, 533-542.	2.9	86
46	One Is Enough: In Vivo Effective Population Size Is Dose-Dependent for a Plant RNA Virus. PLoS Pathogens, 2011, 7, e1002122.	4.7	85
47	Diminishing Returns of Population Size in the Rate of RNA Virus Adaptation. Journal of Virology, 2000, 74, 3566-3571.	3.4	84
48	Advances in Plant Virus Evolution: Translating Evolutionary Insights into Better Disease Management. Phytopathology, 2011, 101, 1136-1148.	2.2	83
49	A real-time RT-PCR assay for quantifying the fitness of tobacco etch virus in competition experiments. Journal of Virological Methods, 2007, 139, 181-188.	2.1	82
50	Molecular Evolution of a Viral Non-Coding Sequence under the Selective Pressure of amiRNA-Mediated Silencing. PLoS Pathogens, 2009, 5, e1000312.	4.7	82
51	Reverse-engineering the Arabidopsis thaliana transcriptional network under changing environmental conditions. Genome Biology, 2009, 10, R96.	9.6	81
52	Rate of deleterious mutation and the distribution of its effects on fitness in vesicular stomatitis virus. Journal of Evolutionary Biology, 1999, 12, 1078-1088.	1.7	80
53	Natural Selection Fails to Optimize Mutation Rates for Long-Term Adaptation on Rugged Fitness Landscapes. PLoS Computational Biology, 2008, 4, e1000187.	3.2	80
54	Fitness Declines in <i>Tobacco Etch Virus</i> upon Serial Bottleneck Transfers. Journal of Virology, 2007, 81, 4941-4947.	3.4	79

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55	Virus Adaptation by Manipulation of Host's Gene Expression. PLoS ONE, 2008, 3, e2397.	2.5	79
56	Measuring Selection Coefficients Below 10âˆ’3: Method, Questions, and Prospects. Genetics, 2012, 190, 175-186.	2.9	75
57	Many-trillionfold amplification of single RNA virus particles fails to overcome the Muller's ratchet effect. Journal of Virology, 1993, 67, 3620-3623.	3.4	75
58	Contribution of recombination and selection to molecular evolution of Citrus tristeza virus. Journal of General Virology, 2009, 90, 1527-1538.	2.9	74
59	The pleiotropic cost of host-specialization in Tobacco etch potyvirus. Infection, Genetics and Evolution, 2008, 8, 806-814.	2.3	73
60	The Rate and Spectrum of Spontaneous Mutations in a Plant RNA Virus. Genetics, 2010, 185, 983-989.	2.9	73
61	Experimental evolution of plant RNA viruses. Heredity, 2008, 100, 478-483.	2.6	72
62	A Sliding Window-Based Method to Detect Selective Constraints in Protein-Coding Genes and Its Application to RNA Viruses. Journal of Molecular Evolution, 2002, 55, 509-521.	1.8	71
63	LONGâ€TERM EXPERIMENTAL EVOLUTION IN <i>ESCHERICHIA COLI.</i> VII. MECHANISMS MAINTAINING GENETIC VARIABILITY WITHIN POPULATIONS. Evolution; International Journal of Organic Evolution, 1997, 51, 1058-1067.	2.3	68
64	Distribution of fitness effects caused by random insertion mutations in Escherichia coli. Genetica, 1998, 102-103, 349-58.	1.1	68
65	Magnitude and sign epistasis among deleterious mutations in a positive-sense plant RNA virus. Heredity, 2012, 109, 71-77.	2.6	66
66	Evolution of plant virus movement proteins from the 30K superfamily and of their homologs integrated in plant genomes. Virology, 2015, 476, 304-315.	2.4	65
67	High genetic stability in natural populations of the plant RNA virus tobacco mild green mosaic virus. Journal of Molecular Evolution, 1991, 32, 328-332.	1.8	64
68	A Meta-Analysis Reveals the Commonalities and Differences in Arabidopsis thaliana Response to Different Viral Pathogens. PLoS ONE, 2012, 7, e40526.	2.5	64
69	Phylogeography and Molecular Evolution of Potato virus Y. PLoS ONE, 2012, 7, e37853.	2.5	60
70	Little Evidence for Synergism Among Deleterious Mutations in a Nonsegmented RNA Virus. Journal of Molecular Evolution, 1999, 49, 703-707.	1.8	59
71	EPISTASIS BETWEEN NEW MUTATIONS AND GENETIC BACKGROUND AND A TEST OF GENETIC CANALIZATION. Evolution; International Journal of Organic Evolution, 2001, 55, 1746-1752.	2.3	59
72	EFFECTS OF POPULATION SIZE AND MUTATION RATE ON THE EVOLUTION OF MUTATIONAL ROBUSTNESS. Evolution; International Journal of Organic Evolution, 2007, 61, 666-674.	2.3	58

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73	Tempo and Mode of Plant RNA Virus Escape from RNA Interference-Mediated Resistance. Journal of Virology, 2011, 85, 9686-9695.	3.4	58
74	Plant virus evolution under strong drought conditions results in a transition from parasitism to mutualism. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	58
75	Application of game theory to the interaction between plant viruses during mixed infections. Journal of General Virology, 2009, 90, 2815-2820.	2.9	57
76	Simple genomes, complex interactions: Epistasis in RNA virus. Chaos, 2010, 20, 026106.	2.5	57
77	Interaction network of tobacco etch potyvirus NIa protein with the host proteome during infection. BMC Genomics, 2016, 17, 87.	2.8	57
78	Insights into the Selective Pressures Restricting Pelargonium Flower Break Virus Genome Variability: Evidence for Host Adaptation. Journal of Virology, 2006, 80, 8124-8132.	3.4	56
79	Analysis of epistatic interactions and fitness landscapes using a new geometric approach. BMC Evolutionary Biology, 2007, 7, 60.	3.2	54
80	Changes in the gene expression profile of Arabidopsis thaliana after infection with Tobacco etch virus. Virology Journal, 2008, 5, 92.	3.4	54
81	Towards an integrated molecular model of plantâ€“virus interactions. Current Opinion in Virology, 2012, 2, 719-724.	5.4	54
82	Epistasis between mutations is host-dependent for an RNA virus. Biology Letters, 2013, 9, 20120396.	2.3	54
83	Within-Host Spatiotemporal Dynamics of Plant Virus Infection at the Cellular Level. PLoS Genetics, 2014, 10, e1004186.	3.5	54
84	A Viral Protein Mediates Superinfection Exclusion at the Whole-Organism Level but Is Not Required for Exclusion at the Cellular Level. Journal of Virology, 2014, 88, 11327-11338.	3.4	53
85	Evolution of Fitness in Experimental Populations of Vesicular Stomatitis Virus. Genetics, 1996, 142, 673-679.	2.9	53
86	The strands of both polarities of a small circular RNA from carnation self-cleavein vitrothrough alternative double- and single-hammerhead structures. Nucleic Acids Research, 1992, 20, 6323-6329.	14.5	52
87	Emerging viruses: why they are not jacks of all trades?. Current Opinion in Virology, 2015, 10, 1-6.	5.4	50
88	Distribution of fitness effects caused by random insertion mutations in Escherichia coli. Contemporary Issues in Genetics and Evolution, 1998, , 349-358.	0.9	50
89	EFFECT OF DELETERIOUS MUTATION-ACCUMULATION ON THE FITNESS OF RNA BACTERIOPHAGE MS2. Evolution; International Journal of Organic Evolution, 2000, 54, 686.	2.3	49
90	From genotypes to organisms: State-of-the-art and perspectives of a cornerstone in evolutionary dynamics. Physics of Life Reviews, 2021, 38, 55-106.	2.8	49

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91	Virus Satellites Drive Viral Evolution and Ecology. PLoS Genetics, 2015, 11, e1005609.	3.5	49
92	The promiscuous evolutionary history of the family Bromoviridae. Journal of General Virology, 2008, 89, 1739-1747.	2.9	48
93	EFFECT OF DELETERIOUS MUTATION-ACCUMULATION ON THE FITNESS OF RNA BACTERIOPHAGE MS2. Evolution; International Journal of Organic Evolution, 2000, 54, 686-691.	2.3	47
94	Evolution of RNA virus in spatially structured heterogeneous environments. Journal of Evolutionary Biology, 2003, 16, 456-466.	1.7	47
95	Dynamics of a Plant RNA Virus Intracellular Accumulation: Stamping Machine <i>vs.</i> Geometric Replication. Genetics, 2011, 188, 637-646.	2.9	47
96	EVOLUTION: Climb Every Mountain?. Science, 2003, 302, 2074-2075.	12.6	46
97	Phylogenetic Analysis of Viroid and Viroid-Like Satellite RNAs from Plants: A Reassessment. Journal of Molecular Evolution, 2001, 53, 155-159.	1.8	45
98	Transmission bottlenecks and the evolution of fitness in rapidly evolving RNA viruses. Infection, Genetics and Evolution, 2001, 1, 41-48.	2.3	45
99	Replication Mode and Landscape Topology Differentially Affect RNA Virus Mutational Load and Robustness. Journal of Virology, 2009, 83, 12579-12589.	3.4	44
100	Parasites and mutational load: an experimental test of a pluralistic theory for the evolution of sex. Proceedings of the Royal Society B: Biological Sciences, 2005, 272, 311-317.	2.6	43
101	In Silico Predicted Robustness of Viroids RNA Secondary Structures. I. The Effect of Single Mutations. Molecular Biology and Evolution, 2006, 23, 1427-1436.	8.9	43
102	The effect of genetic robustness on evolvability in digital organisms. BMC Evolutionary Biology, 2008, 8, 284.	3.2	43
103	EXPERIMENTAL EVOLUTION OF AN EMERGING PLANT VIRUS IN HOST GENOTYPES THAT DIFFER IN THEIR SUSCEPTIBILITY TO INFECTION. Evolution; International Journal of Organic Evolution, 2014, 68, 2467-2480.	2.3	43
104	Simple quasispecies models for the survival-of-the-flattest effect: The role of space. Journal of Theoretical Biology, 2008, 250, 560-568.	1.7	41
105	Pear Blister Canker Viroid is a Member of the Apple Scar Skin Subgroup (apscaviroids) and also has Sequence Homology with Viroids from other Subgroups. Journal of General Virology, 1992, 73, 2503-2507.	2.9	39
106	RNA virus genetic robustness: possible causes and some consequences. Current Opinion in Virology, 2012, 2, 525-530.	5.4	39
107	Experimental Evolution of Pseudogenization and Gene Loss in a Plant RNA Virus. Molecular Biology and Evolution, 2014, 31, 121-134.	8.9	39
108	The games plant viruses play. Current Opinion in Virology, 2014, 8, 62-67.	5.4	39

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109	The utility of fitness landscapes and big data for predicting evolution. Heredity, 2018, 121, 401-405.	2.6	39
110	Role of host genetic diversity for susceptibility-to-infection in the evolution of virulence of a plant virusâ€. Virus Evolution, 2019, 5, vez024.	4.9	39
111	Genetic Diversity and Potential Vectors and Reservoirs of <i>Cucurbit aphid-borne yellows virus</i> in Southeastern Spain. Phytopathology, 2013, 103, 1188-1197.	2.2	38
112	Ultradeep Sequencing Analysis of Population Dynamics of Virus Escape Mutants in RNAi-Mediated Resistant Plants. Molecular Biology and Evolution, 2012, 29, 3297-3307.	8.9	37
113	Estimation of the in vivo recombination rate for a plant RNA virus. Journal of General Virology, 2014, 95, 724-732.	2.9	37
114	Changes in the composition of the RNA virome mark evolutionary transitions in green plants. BMC Biology, 2016, 14, 68.	3.8	37
115	EVOLUTIONARY DYNAMICS OF FITNESS RECOVERY FROM THE DEBILITATING EFFECTS OF MULLER'S RATCHET. Evolution; International Journal of Organic Evolution, 1998, 52, 309-314.	2.3	37
116	Upper-limit mutation rate estimation for a plant RNA virus. Biology Letters, 2009, 5, 394-396.	2.3	36
117	Compensatory Molecular Evolution of HC-Pro, an RNA-Silencing Suppressor from a Plant RNA Virus. Molecular Biology and Evolution, 2010, 27, 543-551.	8.9	36
118	Dynamics of Molecular Evolution and Phylogeography of Barley yellow dwarf virus-PAV. PLoS ONE, 2011, 6, e16896.	2.5	36
119	Exon/intron structure of the human alpha 3(IV) gene encompassing the Goodpasture antigen (alpha) Tj ETQq1 1 0.784314 rgBT /Overlo Journal of Biological Chemistry, 1992, 267, 19780-4.	3.4	36
120	Within-host Evolution of Segments Ratio for the Tripartite Genome of Alfalfa Mosaic Virus. Scientific Reports, 2017, 7, 5004.	3.3	35
121	Temporal Dynamics of Intrahost Molecular Evolution for a Plant RNA Virus. Molecular Biology and Evolution, 2015, 32, 1132-1147.	8.9	33
122	Local adaptation of plant viruses: lessons from experimental evolution. Molecular Ecology, 2017, 26, 1711-1719.	3.9	33
123	Effect of citrus hosts on the generation, maintenance and evolutionary fate of genetic variability of citrus exocortis viroid. Journal of General Virology, 2009, 90, 2040-2049.	2.9	32
124	Improving the Effectiveness of Artificial MicroRNA (amiR)-Mediated Resistance against Turnip Mosaic Virus by Combining Two amiRs or by Targeting Highly Conserved Viral Genomic Regions. Journal of Virology, 2013, 87, 8254-8256.	3.4	32
125	Emergence and Phylodynamics of Citrus tristeza virus in Sicily, Italy. PLoS ONE, 2013, 8, e66700.	2.5	32
126	Error threshold in RNA quasispecies models with complementation. Journal of Theoretical Biology, 2010, 265, 278-286.	1.7	31

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127	Quasispecies Spatial Models for RNA Viruses with Different Replication Modes and Infection Strategies. PLoS ONE, 2011, 6, e24884.	2.5	31
128	A systems biology approach to the evolution of plantâ€"virus interactions. Current Opinion in Plant Biology, 2011, 14, 372-377.	7.1	31
129	Topology analysis and visualization of Potyvirus protein-protein interaction network. BMC Systems Biology, 2014, 8, 129.	3.0	31
130	Multiple Barriers to the Evolution of Alternative Gene Orders in a Positive-Strand RNA Virus. Genetics, 2016, 202, 1503-1521.	2.9	31
131	Transmission modes affect the population structure of potato virus Y in potato. PLoS Pathogens, 2020, 16, e1008608.	4.7	31
132	The Two Faces of Mutation: Extinction and Adaptation in RNA Viruses. IUBMB Life, 2000, 49, 5-9.	3.4	30
133	Environmental stress and the effects of mutation. Journal of Biology, 2003, 2, 12.	2.7	30
134	Genotypic but not phenotypic historical contingency revealed by viral experimental evolution. BMC Evolutionary Biology, 2013, 13, 46.	3.2	30
135	FREQUENCY-DEPENDENT SELECTION IN A MAMMALIAN RNA VIRUS. Evolution; International Journal of Organic Evolution, 1997, 51, 984-987.	2.3	29
136	NATURAL SELECTION AND THE ORGAN-SPECIFIC DIFFERENTIATION OF HIV-1 V3 HYPERVARIABLE REGION. Evolution; International Journal of Organic Evolution, 2004, 58, 1185-1194.	2.3	29
137	Onset of virus systemic infection in plants is determined by speed of cell-to-cell movement and number of primary infection foci. Journal of the Royal Society Interface, 2014, 11, 20140555.	3.4	29
138	Effect of population patchiness and migration rates on the adaptation and divergence of vesicular stomatitis virus quasispecies populations. Journal of General Virology, 1999, 80, 2051-2059.	2.9	29
139	Large-population passages of vesicular stomatitis virus in interferon-treated cells select variants of only limited resistance. Journal of Virology, 1996, 70, 6414-6417.	3.4	29
140	Long-Term Experimental Evolution in Escherichia coli. VII. Mechanisms Maintaining Genetic Variability Within Populations. Evolution; International Journal of Organic Evolution, 1997, 51, 1058.	2.3	28
141	Coinfection and superinfection in RNA virus populations: a selectionâ€"mutation model. Mathematical Biosciences, 2003, 183, 135-160.	1.9	28
142	In Silico Predicted Robustness of Viroid RNA Secondary Structures. II. Interaction between Mutation Pairs. Molecular Biology and Evolution, 2006, 23, 2123-2130.	8.9	28
143	Viral Strain-Specific Differential Alterations in Arabidopsis Developmental Patterns. Molecular Plant-Microbe Interactions, 2015, 28, 1304-1315.	2.6	28
144	Viral Fitness Determines the Magnitude of Transcriptomic and Epigenomic Reprograming of Defense Responses in Plants. Molecular Biology and Evolution, 2020, 37, 1866-1881.	8.9	27

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145	Multiple infection dynamics has pronounced effects on the fitness of RNA viruses. Journal of Evolutionary Biology, 2001, 14, 654-662.	1.7	26
146	Genetic diversity of the movement and coat protein genes of South American isolates of Prunus necrotic ringspot virus. Archives of Virology, 2008, 153, 909-919.	2.1	26
147	Adaptation of tobacco etch potyvirus to a susceptible ecotype of<i>Arabidopsis thaliana</i>capacitates it for systemic infection of resistant ecotypes. Philosophical Transactions of the Royal Society B: Biological Sciences, 2010, 365, 1997-2007.	4.0	26
148	Structural Discrimination of Robustness in Transcriptional Feedforward Loops for Pattern Formation. PLoS ONE, 2011, 6, e16904.	2.5	26
149	The Two Faces of Mutation: Extinction and Adaptation in RNA Viruses. IUBMB Life, 2000, 49, 5-9.	3.4	25
150	Phylodynamics of Pepino mosaic virus in Spain. European Journal of Plant Pathology, 2012, 134, 445-449.	1.7	25
151	Molecular evolution and phylogeography of potato virus Y based on the CP gene. Journal of General Virology, 2012, 93, 2496-2501.	2.9	25
152	Effects of the Number of Genome Segments on Primary and Systemic Infections with a Multipartite Plant RNA Virus. Journal of Virology, 2013, 87, 10805-10815.	3.4	25
153	Fate of Artificial MicroRNA-Mediated Resistance to Plant Viruses in Mixed Infections. Phytopathology, 2013, 103, 870-876.	2.2	25
154	Shrinkage of Genome Size in a Plant RNA Virus upon Transfer of an Essential Viral Gene into the Host Genome. Genome Biology and Evolution, 2014, 6, 538-550.	2.5	25
155	Genomic divergence of Escherichia coli strains: evidence for horizontal transfer and variation in mutation rates. International Microbiology, 2005, 8, 271-8.	2.4	25
156	Evolutionary Dynamics of Fitness Recovery from the Debilitating Effects of Muller's Ratchet. Evolution; International Journal of Organic Evolution, 1998, 52, 309.	2.3	24
157	Adaptive Covariation between the Coat and Movement Proteins of Prunus Necrotic Ringspot Virus. Journal of Virology, 2006, 80, 5833-5840.	3.4	24
158	Evolutionary Constraints to Viroid Evolution. Viruses, 2009, 1, 241-254.	3.3	24
159	Effects of Potyvirus Effective Population Size in Inoculated Leaves on Viral Accumulation and the Onset of Symptoms. Journal of Virology, 2012, 86, 9737-9747.	3.4	24
160	Transcript Profiling of Different Arabidopsis thaliana Ecotypes in Response to Tobacco etch potyvirus Infection. Frontiers in Microbiology, 2012, 3, 229.	3.5	24
161	Time-Sampled Population Sequencing Reveals the Interplay of Selection and Genetic Drift in Experimental Evolution of <i>Potato Virus Y</i>. Journal of Virology, 2017, 91, .	3.4	24
162	From foes to friends: Viral infections expand the limits of host phenotypic plasticity. Advances in Virus Research, 2020, 106, 85-121.	2.1	24

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163	Restrictions to RNA virus adaptation: an experimental approach. Antonie Van Leeuwenhoek, 2002, 81, 135-142.	1.7	23
164	Dynamics of the Establishment of Systemic Potyvirus Infection: Independent yet Cumulative Action of Primary Infection Sites. Journal of Virology, 2012, 86, 12912-12922.	3.4	23
165	Molecular Evolution of Viral Multifunctional Proteins: The Case of Potyvirus HC-Pro. Journal of Molecular Evolution, 2014, 78, 75-86.	1.8	23
166	The impact of highâ€order epistasis in the withinâ€host fitness of a positiveâ€sense plant RNA virus. Journal of Evolutionary Biology, 2015, 28, 2236-2247.	1.7	23
167	Molecular and biological characterization of an isolate of Tomato mottle mosaic virus (ToMMV) infecting tomato and other experimental hosts in eastern Spain. European Journal of Plant Pathology, 2017, 149, 261-268.	1.7	23
168	Is group selection a factor modulating the virulence of RNA viruses?. Genetical Research, 1997, 69, 165-172.	0.9	22
169	Modeling multipartite virus evolution: the genome formula facilitates rapid adaptation to heterogeneous environmentsâ€. Virus Evolution, 2020, 6, veaa022.	4.9	22
170	Molecular Evolution of the Plant Virus Family Bromoviridae Based on RNA3-Encoded Proteins. Journal of Molecular Evolution, 2005, 61, 697-705.	1.8	21
171	Low genetic variability in the coat and movement proteins of American plum line pattern virus isolates from different geographic origins. Archives of Virology, 2008, 153, 367-373.	2.1	21
172	Optimal viral strategies for bypassing RNA silencing. Journal of the Royal Society Interface, 2011, 8, 257-268.	3.4	21
173	Dynamics of alternative modes of RNA replication for positive-sense RNA viruses. Journal of the Royal Society Interface, 2012, 9, 768-776.	3.4	21
174	Nonlinear trade-offs allow the cooperation game to evolve from Prisoner's Dilemma to Snowdrift. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20170228.	2.6	21
175	Viral Fitness Correlates with the Magnitude and Direction of the Perturbation Induced in the Hostâ€™s Transcriptome: The Tobacco Etch Potyvirusâ€"Tobacco Case Study. Molecular Biology and Evolution, 2018, 35, 1599-1615.	8.9	21
176	THE CAUSES OF EPISTASIS IN GENETIC NETWORKS. Evolution; International Journal of Organic Evolution, 2012, 66, 586-596.	2.3	20
177	Predicting the Stability of Homologous Gene Duplications in a Plant RNA Virus. Genome Biology and Evolution, 2016, 8, 3065-3082.	2.5	20
178	Effect of Host Species on Topography of the Fitness Landscape for a Plant RNA Virus. Journal of Virology, 2016, 90, 10160-10169.	3.4	20
179	Defective RNA particles derived from Tomato black ring virus genome interfere with the replication of parental virus. Virus Research, 2018, 250, 87-94.	2.2	20
180	RNA viruses as complex adaptive systems. BioSystems, 2005, 81, 31-41.	2.0	19

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