

Santiago F Elena

List of Publications by Year in descending order

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Version: 2024-02-01

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	Modelling temperature-dependent dynamics of single and mixed infections in a plant virus. <i>Applied Mathematical Modelling</i> , 2022, 102, 694-705.	4.2	4
2	Innate immune pathways act synergistically to constrain RNA virus evolution in <i>Drosophila melanogaster</i> . <i>Nature Ecology and Evolution</i> , 2022, 6, 565-578.	7.8	10
3	DVGfinder: A Metasearch Tool for Identifying Defective Viral Genomes in RNA-Seq Data. <i>Viruses</i> , 2022, 14, 1114.	3.3	8
4	The long and winding road to understanding organismal construction. <i>Physics of Life Reviews</i> , 2022, 42, 19-24.	2.8	0
5	Defects in plant immunity modulate the rates and patterns of RNA virus evolution. <i>Virus Evolution</i> , 2022, 8, .	4.9	14
6	Transmission of Diverse Variants of Strawberry Viruses Is Governed by a Vector Species. <i>Viruses</i> , 2022, 14, 1362.	3.3	3
7	Plant virus evolution under strong drought conditions results in a transition from parasitism to mutualism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	58
8	Genetic variability and evolutionary dynamics of tomato black ring virus population. <i>Plant Pathology</i> , 2021, 70, 1521-1531.	2.4	3
9	A genome-wide association study identifies <i>Arabidopsis thaliana</i> genes that contribute to differences in the outcome of infection with two <i>Turnip mosaic potyvirus</i> strains that differ in their evolutionary history and degree of host specialization. <i>Virus Evolution</i> , 2021, 7, veab063.	4.9	15
10	Why are viral genomes so fragile? The bottleneck hypothesis. <i>PLoS Computational Biology</i> , 2021, 17, e1009128.	3.2	8
11	Phase transitions in virology. <i>Reports on Progress in Physics</i> , 2021, 84, 115901.	20.1	4
12	From genotypes to organisms: State-of-the-art and perspectives of a cornerstone in evolutionary dynamics. <i>Physics of Life Reviews</i> , 2021, 38, 55-106.	2.8	49
13	Increasing temperature alters the within-host competition of viral strains and influences virus genetic variability. <i>Virus Evolution</i> , 2021, 7, veab017.	4.9	15
14	Revisiting Orthotospovirus phylogeny using full-genome data and testing the contribution of selection, recombination and segment reassortment in the origin of members of new species. <i>Archives of Virology</i> , 2021, 166, 491-499.	2.1	6
15	The Interplay between the Host Microbiome and Pathogenic Viral Infections. <i>MBio</i> , 2021, 12, e0249621.	4.1	11
16	Heterogeneity in the Response of Different Subtypes of <i>Drosophila melanogaster</i> Midgut Cells to Viral Infections. <i>Viruses</i> , 2021, 13, 2284.	3.3	1
17	An assessment of the transmission rate of Tomato black ring virus through tomato seeds. <i>Plant Protection Science</i> , 2020, 56, 9-12.	1.4	7
18	Identifying Early Warning Signals for the Sudden Transition from Mild to Severe Tobacco Etch Disease by Dynamical Network Biomarkers. <i>Viruses</i> , 2020, 12, 16.	3.3	9

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19	RNAs That Behave Like Prions. <i>MSphere</i> , 2020, 5, .	2.9	1
20	Effect of defective interfering RNAs on the vertical transmission of Tomato black ring virus. <i>Plant Protection Science</i> , 2020, 56, 261-267.	1.4	5
21	Natural variation in <i>Arabidopsis thaliana</i> rosette area unveils new genes involved in plant development. <i>Scientific Reports</i> , 2020, 10, 17600.	3.3	10
22	Molecular evolution of tomato black ring virus and de novo generation of a new type of defective RNAs during long-term passaging in different hosts. <i>Plant Pathology</i> , 2020, 69, 1767-1776.	2.4	6
23	Host-virus evolutionary dynamics with specialist and generalist infection strategies: Bifurcations, bistability, and chaos. <i>Chaos</i> , 2020, 30, 053128.	2.5	3
24	Modeling multipartite virus evolution: the genome formula facilitates rapid adaptation to heterogeneous environments. <i>Virus Evolution</i> , 2020, 6, veaa022.	4.9	22
25	Adaptation of turnip mosaic potyvirus to a specific niche reduces its genetic and environmental robustness. <i>Virus Evolution</i> , 2020, 6, veaa041.	4.9	14
26	Transmission modes affect the population structure of potato virus Y in potato. <i>PLoS Pathogens</i> , 2020, 16, e1008608.	4.7	31
27	From foes to friends: Viral infections expand the limits of host phenotypic plasticity. <i>Advances in Virus Research</i> , 2020, 106, 85-121.	2.1	24
28	Viral Fitness Determines the Magnitude of Transcriptomic and Epigenomic Reprogramming of Defense Responses in Plants. <i>Molecular Biology and Evolution</i> , 2020, 37, 1866-1881.	8.9	27
29	Evolution and ecology of plant viruses. <i>Nature Reviews Microbiology</i> , 2019, 17, 632-644.	28.6	166
30	Parsimonious Scenario for the Emergence of Viroid-Like Replicons De Novo. <i>Viruses</i> , 2019, 11, 425.	3.3	12
31	Mutagenesis Scanning Uncovers Evolutionary Constraints on Tobacco Etch Potyvirus Membrane-Associated 6K2 Protein. <i>Genome Biology and Evolution</i> , 2019, 11, 1207-1222.	2.5	8
32	Theoretical conditions for the coexistence of viral strains with differences in phenotypic traits: a bifurcation analysis. <i>Royal Society Open Science</i> , 2019, 6, 181179.	2.4	8
33	STABILITY OF A STOCHASTICALLY PERTURBED MODEL OF INTRACELLULAR SINGLE-STRANDED RNA VIRUS REPLICATION. <i>Journal of Biological Systems</i> , 2019, 27, 69-82.	1.4	1
34	Complete nucleotide sequence of a novel mycovirus from <i>Trichoderma harzianum</i> in China. <i>Archives of Virology</i> , 2019, 164, 1213-1216.	2.1	17
35	Role of host genetic diversity for susceptibility-to-infection in the evolution of virulence of a plant virus. <i>Virus Evolution</i> , 2019, 5, vez024.	4.9	39
36	Transmission rate of two Polish Tomato torrado virus isolates through tomato seeds. <i>Journal of General Plant Pathology</i> , 2019, 85, 109-115.	1.0	6

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37	Viral replication modes in single-peak fitness landscapes: A dynamical systems analysis. <i>Journal of Theoretical Biology</i> , 2019, 460, 170-183.	1.7	7
38	Exploring the role of cellular homologous of the 30K-superfamily of plant virus movement proteins. <i>Virus Research</i> , 2019, 262, 54-61.	2.2	5
39	Evolving by deleting: patterns of molecular evolution of Apple stem pitting virus isolates from Poland. <i>Journal of General Virology</i> , 2019, 100, 1442-1456.	2.9	9
40	Defective RNA particles derived from Tomato black ring virus genome interfere with the replication of parental virus. <i>Virus Research</i> , 2018, 250, 87-94.	2.2	20
41	Viral Fitness Correlates with the Magnitude and Direction of the Perturbation Induced in the Host's Transcriptome: The Tobacco Etch Potyvirus's Tobacco Case Study. <i>Molecular Biology and Evolution</i> , 2018, 35, 1599-1615.	8.9	21
42	The utility of fitness landscapes and big data for predicting evolution. <i>Heredity</i> , 2018, 121, 401-405.	2.6	39
43	Evolving Living Technologies—Insights from the EvoEvo Project. <i>Lecture Notes in Computer Science</i> , 2018, , 46-62.	1.3	1
44	Noise-induced bistability in the quasi-neutral coexistence of viral RNAs under different replication modes. <i>Journal of the Royal Society Interface</i> , 2018, 15, 20180129.	3.4	4
45	Engineered Functional Redundancy Relaxes Selective Constraints upon Endogenous Genes in Viral RNA Genomes. <i>Genome Biology and Evolution</i> , 2018, 10, 1823-1836.	2.5	17
46	Going, going, gone: predicting the fate of genomic insertions in plant RNA viruses. <i>Heredity</i> , 2018, 121, 499-509.	2.6	10
47	Alive or Dead?. , 2018, , 19-54.		0
48	Virus Dynamics and Arms Races. , 2018, , 91-119.		0
49	Computer Viruses and Beyond. , 2018, , 190-202.		0
50	Nonlinear trade-offs allow the cooperation game to evolve from Prisoner's Dilemma to Snowdrift. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20170228.	2.6	21
51	Time-Sampled Population Sequencing Reveals the Interplay of Selection and Genetic Drift in Experimental Evolution of <i>Potato Virus Y</i> . <i>Journal of Virology</i> , 2017, 91, .	3.4	24
52	Strain-dependent mutational effects for Pepino mosaic virus in a natural host. <i>BMC Evolutionary Biology</i> , 2017, 17, 67.	3.2	9
53	Virus-host interactome: Putting the accent on how it changes. <i>Journal of Proteomics</i> , 2017, 156, 1-4.	2.4	12
54	Within-host Evolution of Segments Ratio for the Tripartite Genome of Alfalfa Mosaic Virus. <i>Scientific Reports</i> , 2017, 7, 5004.	3.3	35

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55	Molecular and biological characterization of an isolate of Tomato mottle mosaic virus (ToMMV) infecting tomato and other experimental hosts in eastern Spain. <i>European Journal of Plant Pathology</i> , 2017, 149, 261-268.	1.7	23
56	High virulence does not necessarily impede viral adaptation to a new host: a case study using a plant RNA virus. <i>BMC Evolutionary Biology</i> , 2017, 17, 25.	3.2	5
57	Local adaptation of plant viruses: lessons from experimental evolution. <i>Molecular Ecology</i> , 2017, 26, 1711-1719.	3.9	33
58	Diminishing returns of inoculum size on the rate of a plant RNA virus evolution. <i>Europhysics Letters</i> , 2017, 120, 38001.	2.0	2
59	Spatially induced nestedness in a neutral model of phage-bacteria networks. <i>Virus Evolution</i> , 2017, 3, vex021.	4.9	10
60	or not : Experimental evolution of functional exogenous sequences in a plant RNA virus. <i>Genome Biology and Evolution</i> , 2017, 9, evw300.	2.5	12
61	A putative antiviral role of plant cytidine deaminases. <i>F1000Research</i> , 2017, 6, 622.	1.6	4
62	A putative antiviral role of plant cytidine deaminases. <i>F1000Research</i> , 2017, 6, 622.	1.6	4
63	The transcriptomics of an experimentally evolved plant-virus interaction. <i>Scientific Reports</i> , 2016, 6, 24901.	3.3	19
64	Predicting the Stability of Homologous Gene Duplications in a Plant RNA Virus. <i>Genome Biology and Evolution</i> , 2016, 8, 3065-3082.	2.5	20
65	Changes in the composition of the RNA virome mark evolutionary transitions in green plants. <i>BMC Biology</i> , 2016, 14, 68.	3.8	37
66	Effect of Host Species on Topography of the Fitness Landscape for a Plant RNA Virus. <i>Journal of Virology</i> , 2016, 90, 10160-10169.	3.4	20
67	Evolutionary transitions during RNA virus experimental evolution. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150441.	4.0	16
68	Efficient escape from local optima in a highly rugged fitness landscape by evolving RNA virus populations. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20160984.	2.6	15
69	Interaction network of tobacco etch potyvirus NIa protein with the host proteome during infection. <i>BMC Genomics</i> , 2016, 17, 87.	2.8	57
70	Genetic variation in fitness within a clonal population of a plant RNA virus. <i>Virus Evolution</i> , 2016, 2, vew006.	4.9	10
71	Assessing parallel gene histories in viral genomes. <i>BMC Evolutionary Biology</i> , 2016, 16, 32.	3.2	10
72	Multiple Barriers to the Evolution of Alternative Gene Orders in a Positive-Strand RNA Virus. <i>Genetics</i> , 2016, 202, 1503-1521.	2.9	31

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73	Fusion of genomic, proteomic and phenotypic data: the case of potyviruses. <i>Molecular BioSystems</i> , 2016, 12, 253-261.	2.9	2
74	Viral Strain-Specific Differential Alterations in Arabidopsis Developmental Patterns. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 1304-1315.	2.6	28
75	Distribution of mutational fitness effects and of epistasis in the 5'UTR untranslated region of a plant RNA virus. <i>BMC Evolutionary Biology</i> , 2015, 15, 274.	3.2	14
76	The impact of high-order epistasis in the within-host fitness of a positive-sense plant RNA virus. <i>Journal of Evolutionary Biology</i> , 2015, 28, 2236-2247.	1.7	23
77	Testing the Independent Action Hypothesis of Plant Pathogen Mode of Action: A Simple and Powerful New Approach. <i>Phytopathology</i> , 2015, 105, 18-25.	2.2	3
78	Molecular evolution of <i>Pepino mosaic virus</i> during long-term passaging in different hosts and its impact on virus virulence. <i>Annals of Applied Biology</i> , 2015, 166, 389-401.	2.5	16
79	Temporal Dynamics of Intra-host Molecular Evolution for a Plant RNA Virus. <i>Molecular Biology and Evolution</i> , 2015, 32, 1132-1147.	8.9	33
80	Evolution of plant virus movement proteins from the 30K superfamily and of their homologs integrated in plant genomes. <i>Virology</i> , 2015, 476, 304-315.	2.4	65
81	Brazilian <i>Potato virus Y</i> isolates identified as members of a new clade facilitate the reconstruction of evolutionary traits within this species. <i>Plant Pathology</i> , 2015, 64, 799-807.	2.4	9
82	Global-scale computational analysis of genomic sequences reveals the recombination pattern and coevolution dynamics of cereal-infecting geminiviruses. <i>Scientific Reports</i> , 2015, 5, 8153.	3.3	19
83	Editorial: A home for virology, ecology, epidemiology, and evolutionary biology. <i>Virus Evolution</i> , 2015, 1, 1-3.	4.9	242
84	Evaluating the within-host fitness effects of mutations fixed during virus adaptation to different ecotypes of a new host. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140292.	4.0	17
85	Matters of Size: Genetic Bottlenecks in Virus Infection and Their Potential Impact on Evolution. <i>Annual Review of Virology</i> , 2015, 2, 161-179.	6.7	139
86	Emerging viruses: why they are not jacks of all trades?. <i>Current Opinion in Virology</i> , 2015, 10, 1-6.	5.4	50
87	Virus Satellites Drive Viral Evolution and Ecology. <i>PLoS Genetics</i> , 2015, 11, e1005609.	3.5	49
88	Experimental Virus Evolution Reveals a Role of Plant Microtubule Dynamics and TORTIFOLIA1/SPIRAL2 in RNA Trafficking. <i>PLoS ONE</i> , 2014, 9, e105364.	2.5	15
89	Topology analysis and visualization of Potyvirus protein-protein interaction network. <i>BMC Systems Biology</i> , 2014, 8, 129.	3.0	31
90	Evolution and Emergence of Plant Viruses. <i>Advances in Virus Research</i> , 2014, 88, 161-191.	2.1	167

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91	Experimental Evolution of Pseudogenization and Gene Loss in a Plant RNA Virus. <i>Molecular Biology and Evolution</i> , 2014, 31, 121-134.	8.9	39
92	Within-Host Spatiotemporal Dynamics of Plant Virus Infection at the Cellular Level. <i>PLoS Genetics</i> , 2014, 10, e1004186.	3.5	54
93	A Viral Protein Mediates Superinfection Exclusion at the Whole-Organism Level but Is Not Required for Exclusion at the Cellular Level. <i>Journal of Virology</i> , 2014, 88, 11327-11338.	3.4	53
94	Molecular Evolution of Viral Multifunctional Proteins: The Case of Potyvirus HC-Pro. <i>Journal of Molecular Evolution</i> , 2014, 78, 75-86.	1.8	23
95	Estimation of the in vivo recombination rate for a plant RNA virus. <i>Journal of General Virology</i> , 2014, 95, 724-732.	2.9	37
96	Shrinkage of Genome Size in a Plant RNA Virus upon Transfer of an Essential Viral Gene into the Host Genome. <i>Genome Biology and Evolution</i> , 2014, 6, 538-550.	2.5	25
97	The games plant viruses play. <i>Current Opinion in Virology</i> , 2014, 8, 62-67.	5.4	39
98	Relocation of the NIb Gene in the Tobacco Etch Potyvirus Genome. <i>Journal of Virology</i> , 2014, 88, 4586-4590.	3.4	12
99	EXPERIMENTAL EVOLUTION OF AN EMERGING PLANT VIRUS IN HOST GENOTYPES THAT DIFFER IN THEIR SUSCEPTIBILITY TO INFECTION. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 2467-2480.	2.3	43
100	Viroids: Survivors from the RNA World?. <i>Annual Review of Microbiology</i> , 2014, 68, 395-414.	7.3	142
101	Onset of virus systemic infection in plants is determined by speed of cell-to-cell movement and number of primary infection foci. <i>Journal of the Royal Society Interface</i> , 2014, 11, 20140555.	3.4	29
102	Variability in mutational fitness effects prevents full lethal transitions in large quasispecies populations. <i>Scientific Reports</i> , 2014, 4, 4625.	3.3	11
103	Complex dynamics of defective interfering baculoviruses during serial passage in insect cells. <i>Journal of Biological Physics</i> , 2013, 39, 327-342.	1.5	15
104	Genotypic but not phenotypic historical contingency revealed by viral experimental evolution. <i>BMC Evolutionary Biology</i> , 2013, 13, 46.	3.2	30
105	Effects of the Number of Genome Segments on Primary and Systemic Infections with a multipartite Plant RNA Virus. <i>Journal of Virology</i> , 2013, 87, 10805-10815.	3.4	25
106	Intra-specific variability and biological relevance of P3N-PIPO protein length in potyviruses. <i>BMC Evolutionary Biology</i> , 2013, 13, 249.	3.2	14
107	Fate of Artificial MicroRNA-Mediated Resistance to Plant Viruses in Mixed Infections. <i>Phytopathology</i> , 2013, 103, 870-876.	2.2	25
108	Genetic Diversity and Potential Vectors and Reservoirs of Cucurbit aphid-borne yellows virus in Southeastern Spain. <i>Phytopathology</i> , 2013, 103, 1188-1197.	2.2	38

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109	Epistasis between mutations is host-dependent for an RNA virus. <i>Biology Letters</i> , 2013, 9, 20120396.	2.3	54
110	MicroRNA Precursors Are Not Structurally Robust but Plastic. <i>Genome Biology and Evolution</i> , 2013, 5, 181-186.	2.5	2
111	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. <i>Journal of Virology</i> , 2013, 87, 8254-8256.	3.4	32
112	Plant <scp>RNA</scp> virus fitness predictability: contribution of genetic and environmental factors. <i>Plant Pathology</i> , 2013, 62, 10-18.	2.4	14
113	Model-Selection-Based Approach for Calculating Cellular Multiplicity of Infection during Virus Colonization of Multi-Cellular Hosts. <i>PLoS ONE</i> , 2013, 8, e64657.	2.5	16
114	Emergence and Phylodynamics of Citrus tristeza virus in Sicily, Italy. <i>PLoS ONE</i> , 2013, 8, e66700.	2.5	32
115	Measuring Selection Coefficients Below 10^{-3} : Method, Questions, and Prospects. <i>Genetics</i> , 2012, 190, 175-186.	2.9	75
116	Fine-Tuning Tomato Agronomic Properties by Computational Genome Redesign. <i>PLoS Computational Biology</i> , 2012, 8, e1002528.	3.2	7
117	Dynamics of alternative modes of RNA replication for positive-sense RNA viruses. <i>Journal of the Royal Society Interface</i> , 2012, 9, 768-776.	3.4	21
118	Luria-Delbrück Estimation of Turnip Mosaic Virus Mutation Rate <i>In Vivo</i> . <i>Journal of Virology</i> , 2012, 86, 3386-3388.	3.4	16
119	Effects of Potyvirus Effective Population Size in Inoculated Leaves on Viral Accumulation and the Onset of Symptoms. <i>Journal of Virology</i> , 2012, 86, 9737-9747.	3.4	24
120	Ultra-deep Sequencing Analysis of Population Dynamics of Virus Escape Mutants in RNAi-Mediated Resistant Plants. <i>Molecular Biology and Evolution</i> , 2012, 29, 3297-3307.	8.9	37
121	Computational design of host transcription-factors sets whose misregulation mimics the transcriptomic effect of viral infections. <i>Scientific Reports</i> , 2012, 2, 1006.	3.3	4
122	Multihost Experimental Evolution of a Plant RNA Virus Reveals Local Adaptation and Host-Specific Mutations. <i>Molecular Biology and Evolution</i> , 2012, 29, 1481-1492.	8.9	129
123	Dynamics of the Establishment of Systemic Potyvirus Infection: Independent yet Cumulative Action of Primary Infection Sites. <i>Journal of Virology</i> , 2012, 86, 12912-12922.	3.4	23
124	Towards an integrated molecular model of plant-virus interactions. <i>Current Opinion in Virology</i> , 2012, 2, 719-724.	5.4	54
125	RNA virus genetic robustness: possible causes and some consequences. <i>Current Opinion in Virology</i> , 2012, 2, 525-530.	5.4	39
126	Phylodynamics of Pepino mosaic virus in Spain. <i>European Journal of Plant Pathology</i> , 2012, 134, 445-449.	1.7	25

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127	Computational design of genomic transcriptional networks with adaptation to varying environments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15277-15282.	7.1	14
128	Magnitude and sign epistasis among deleterious mutations in a positive-sense plant RNA virus. <i>Heredity</i> , 2012, 109, 71-77.	2.6	66
129	Molecular evolution and phylogeography of potato virus Y based on the CP gene. <i>Journal of General Virology</i> , 2012, 93, 2496-2501.	2.9	25
130	A Meta-Analysis Reveals the Commonalities and Differences in <i>Arabidopsis thaliana</i> Response to Different Viral Pathogens. <i>PLoS ONE</i> , 2012, 7, e40526.	2.5	64
131	Transcript Profiling of Different <i>Arabidopsis thaliana</i> Ecotypes in Response to Tobacco etch potyvirus Infection. <i>Frontiers in Microbiology</i> , 2012, 3, 229.	3.5	24
132	THE CAUSES OF EPISTASIS IN GENETIC NETWORKS. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 586-596.	2.3	20
133	Phylogeography and Molecular Evolution of Potato virus Y. <i>PLoS ONE</i> , 2012, 7, e37853.	2.5	60
134	Advances in Plant Virus Evolution: Translating Evolutionary Insights into Better Disease Management. <i>Phytopathology</i> , 2011, 101, 1136-1148.	2.2	83
135	The Core/E1 domain of hepatitis C virus genotype 4a in Egypt does not contain viral mutations or strains specific for hepatocellular carcinoma. <i>Journal of Clinical Virology</i> , 2011, 52, 333-338.	3.1	4
136	Population differentiation and selective constraints in Pelargonium line pattern virus. <i>Virus Research</i> , 2011, 155, 274-282.	2.2	6
137	The Evolutionary Genetics of Emerging Plant RNA Viruses. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 287-293.	2.6	110
138	Quasispecies Spatial Models for RNA Viruses with Different Replication Modes and Infection Strategies. <i>PLoS ONE</i> , 2011, 6, e24884.	2.5	31
139	Structural Discrimination of Robustness in Transcriptional Feedforward Loops for Pattern Formation. <i>PLoS ONE</i> , 2011, 6, e16904.	2.5	26
140	Virus Infection Suppresses <i>Nicotiana benthamiana</i> Adaptive Phenotypic Plasticity. <i>PLoS ONE</i> , 2011, 6, e17275.	2.5	2
141	Differences in Accumulation and Virulence Determine the Outcome of Competition during Tobacco etch virus Coinfection. <i>PLoS ONE</i> , 2011, 6, e17917.	2.5	19
142	A systems biology approach to the evolution of plant-virus interactions. <i>Current Opinion in Plant Biology</i> , 2011, 14, 372-377.	7.1	31
143	Tridimensional model structure and patterns of molecular evolution of Pepino mosaic virus TGBp3 protein. <i>Virology Journal</i> , 2011, 8, 318.	3.4	4
144	The causes of epistasis. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2011, 278, 3617-3624.	2.6	175

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145	Optimal viral strategies for bypassing RNA silencing. <i>Journal of the Royal Society Interface</i> , 2011, 8, 257-268.	3.4	21
146	Dynamics of a Plant RNA Virus Intracellular Accumulation: Stamping Machine <i>vs.</i> Geometric Replication. <i>Genetics</i> , 2011, 188, 637-646.	2.9	47
147	Tempo and Mode of Plant RNA Virus Escape from RNA Interference-Mediated Resistance. <i>Journal of Virology</i> , 2011, 85, 9686-9695.	3.4	58
148	Dynamics of Molecular Evolution and Phylogeography of Barley yellow dwarf virus-PAV. <i>PLoS ONE</i> , 2011, 6, e16896.	2.5	36
149	One Is Enough: In Vivo Effective Population Size Is Dose-Dependent for a Plant RNA Virus. <i>PLoS Pathogens</i> , 2011, 7, e1002122.	4.7	85
150	Effect of Host Species on the Distribution of Mutational Fitness Effects for an RNA Virus. <i>PLoS Genetics</i> , 2011, 7, e1002378.	3.5	99
151	Simple genomes, complex interactions: Epistasis in RNA virus. <i>Chaos</i> , 2010, 20, 026106.	2.5	57
152	HC-Pro hypo- and hypersuppressor mutants: differences in viral siRNA accumulation in vivo and siRNA binding activity in vitro. <i>Archives of Virology</i> , 2010, 155, 251-254.	2.1	13
153	Robust dynamical pattern formation from a multifunctional minimal genetic circuit. <i>BMC Systems Biology</i> , 2010, 4, 48.	3.0	8
154	Error threshold in RNA quasispecies models with complementation. <i>Journal of Theoretical Biology</i> , 2010, 265, 278-286.	1.7	31
155	The Rate and Spectrum of Spontaneous Mutations in a Plant RNA Virus. <i>Genetics</i> , 2010, 185, 983-989.	2.9	73
156	New experimental and theoretical approaches towards the understanding of the emergence of viral infections. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010, 365, 1867-1869.	4.0	7
157	Adaptation of tobacco etch potyvirus to a susceptible ecotype of <i>Arabidopsis thaliana</i> capacitates it for systemic infection of resistant ecotypes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010, 365, 1997-2007.	4.0	26
158	Compensatory Molecular Evolution of HC-Pro, an RNA-Silencing Suppressor from a Plant RNA Virus. <i>Molecular Biology and Evolution</i> , 2010, 27, 543-551.	8.9	36
159	Network design meets in silico evolutionary biology. <i>Biochimie</i> , 2010, 92, 746-752.	2.6	10
160	The Evolution of Viruses in Multi-Host Fitness Landscapes. <i>The Open Virology Journal</i> , 2009, 3, 1-6.	1.8	99
161	Extremely High Mutation Rate of a Hammerhead Viroid. <i>Science</i> , 2009, 323, 1308-1308.	12.6	215
162	Mixed Infections of <i>Pepino Mosaic Virus</i> Strains Modulate the Evolutionary Dynamics of this Emergent Virus. <i>Journal of Virology</i> , 2009, 83, 12378-12387.	3.4	104

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