

# CITATION REPORT

List of articles citing

## Dengue virus RNA structure specialization facilitates host adaptation

DOI: [10.1371/journal.ppat.1004604](https://doi.org/10.1371/journal.ppat.1004604)  
PLoS Pathogens, 2015, 11, e1004604.

**Source:** <https://exaly.com/paper-pdf/62008293/citation-report.pdf>

**Version:** 2024-04-28

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

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

#	Paper	IF	Citations
130	Analysis of Dengue Virus Genetic Diversity during Human and Mosquito Infection Reveals Genetic Constraints. <i>PLoS Neglected Tropical Diseases</i> , <b>2015</b> , 9, e0004044	4.8	42
129	New hypotheses derived from the structure of a flaviviral Xrn1-resistant RNA: Conservation, folding, and host adaptation. <b>2015</b> , 12, 1169-77		62
128	Dengue Non-coding RNA: TRIMmed for Transmission. <b>2015</b> , 18, 133-4		12
127	The HIV-1 Rev response element (RRE) adopts alternative conformations that promote different rates of virus replication. <b>2015</b> , 43, 4676-86		47
126	Viral RNA switch mediates the dynamic control of flavivirus replicase recruitment by genome cyclization. <b>2016</b> , 5,		47
125	Genomic characterization and phylogenetic analysis of Zika virus circulating in the Americas. <b>2016</b> , 43, 43-9		81
124	Noncoding Subgenomic Flavivirus RNA Is Processed by the Mosquito RNA Interference Machinery and Determines West Nile Virus Transmission by <i>Culex pipiens</i> Mosquitoes. <b>2016</b> , 90, 10145-10159		82
123	Targeted full-genome amplification and sequencing of dengue virus types 1-4 from South America. <b>2016</b> , 235, 158-167		21
122	Climate Change and the Arboviruses: Lessons from the Evolution of the Dengue and Yellow Fever Viruses. <b>2016</b> , 3, 125-145		35
121	Zika virus produces noncoding RNAs using a multi-pseudoknot structure that confounds a cellular exonuclease. <b>2016</b> , 354, 1148-1152		159
120	N6-Methyladenosine in Flaviviridae Viral RNA Genomes Regulates Infection. <b>2016</b> , 20, 654-665		244
119	Emerging Role of Zika Virus in Adverse Fetal and Neonatal Outcomes. <b>2016</b> , 29, 659-94		107
118	Structured RNAs that evade or confound exonucleases: function follows form. <b>2016</b> , 36, 40-7		19
117	Increasing Clinical Severity during a Dengue Virus Type 3 Cuban Epidemic: Deep Sequencing of Evolving Viral Populations. <b>2016</b> , 90, 4320-4333		25
116	Interaction of Virus Populations with Their Hosts. <b>2016</b> , 123-168		
115	RNA Structure Duplications and Flavivirus Host Adaptation. <b>2016</b> , 24, 270-283		112
114	Knotty Zika Virus Blocks Exonuclease to Produce Subgenomic Flaviviral RNAs. <b>2017</b> , 21, 1-2		17

113	Host Range Restriction of Insect-Specific Flaviviruses Occurs at Several Levels of the Viral Life Cycle. <b>2017</b> , 2,		44
112	Zika virus: An emerging flavivirus. <b>2017</b> , 55, 204-219		63
111	Aedes-Borne Virus-Mosquito Interactions: Mass Spectrometry Strategies and Findings. <b>2017</b> , 17, 361-375		5
110	Mosquito-specific and mosquito-borne viruses: evolution, infection, and host defense. <b>2017</b> , 22, 16-27		43
109	Neurodevelopmental protein Musashi-1 interacts with the Zika genome and promotes viral replication. <b>2017</b> , 357, 83-88		101
108	Making the Mark: The Role of Adenosine Modifications in the Life Cycle of RNA Viruses. <b>2017</b> , 21, 661-669		50
107	Molecular evolution of Zika virus as it crossed the Pacific to the Americas. <b>2017</b> , 33, 1-20		17
106	Genome-Wide Mutagenesis of Dengue Virus Reveals Plasticity of the NS1 Protein and Enables Generation of Infectious Tagged Reporter Viruses. <b>2017</b> , 91,		17
105	Arbovirus Adaptation: Roles in Transmission and Emergence. <b>2017</b> , 4, 159-166		2
104	Characterization of $\omega$ -Acting RNA Elements of Zika Virus by Using a Self-Splicing Ribozyme-Dependent Infectious Clone. <b>2017</b> , 91,		29
103	The 5' and 3' Untranslated Regions of the Flaviviral Genome. <i>Viruses</i> , <b>2017</b> , 9,	6.2	84
102	Dengue virus genomic variation associated with mosquito adaptation defines the pattern of viral non-coding RNAs and fitness in human cells. <i>PLoS Pathogens</i> , <b>2017</b> , 13, e1006265	7.6	71
101	A Review of Flaviviruses that Have No Known Arthropod Vector. <i>Viruses</i> , <b>2017</b> , 9,	6.2	39
100	Biochemistry and Molecular Biology of Flaviviruses. <b>2018</b> , 118, 4448-4482		126
99	Flaviviruses Produce a Subgenomic Flaviviral RNA That Enhances Mosquito Transmission. <b>2018</b> , 37, 154-159		12
98	Mechanism and structural diversity of exoribonuclease-resistant RNA structures in flaviviral RNAs. <i>Nature Communications</i> , <b>2018</b> , 9, 119	17.4	59
97	Dengue Virus Selectively Annexes Endoplasmic Reticulum-Associated Translation Machinery as a Strategy for Co-opting Host Cell Protein Synthesis. <b>2018</b> , 92,		37
96	Identification and characterization of host proteins bound to dengue virus 3' UTR reveal an antiviral role for quaking proteins. <b>2018</b> , 24, 803-814		20

95	A systematic approach to the development of a safe live attenuated Zika vaccine. <i>Nature Communications</i> , <b>2018</b> , 9, 1031	17.4	25
94	Non-coding RNA: a key regulator of the pathogenicity and immunity of Flaviviridae viruses infection. <b>2018</b> , 15, 185-186		0
93	Functional RNA during Zika virus infection. <b>2018</b> , 254, 41-53		53
92	Highlights on the Application of Genomics and Bioinformatics in the Fight Against Infectious Diseases: Challenges and Opportunities in Africa. <b>2018</b> , 9, 575		12
91	The Multiples Fates of the Flavivirus RNA Genome During Pathogenesis. <b>2018</b> , 9, 595		43
90	Changes in temperature alter the potential outcomes of virus host shifts. <i>PLoS Pathogens</i> , <b>2018</b> , 14, e1007185	16	
89	Subgenomic flaviviral RNAs: What do we know after the first decade of research. <b>2018</b> , 159, 13-25		49
88	Homologous RNA secondary structure duplications in 3' untranslated region influence subgenomic RNA production and replication of dengue virus. <b>2018</b> , 524, 114-126		6
87	Flaviviral RNA Structures and Their Role in Replication and Immunity. <b>2018</b> , 1062, 45-62		6
86	Chikungunya virus evolution following a large 3'UTR deletion results in host-specific molecular changes in protein-coding regions. <b>2018</b> , 4, vey012		17
85	Mechanisms and Concepts in RNA Virus Population Dynamics and Evolution. <b>2018</b> , 5, 69-92		62
84	Know Your Enemy: Successful Bioinformatic Approaches to Predict Functional RNA Structures in Viral RNAs. <b>2017</b> , 8, 2582		15
83	Disruption of a stem-loop structure located upstream of pseudoknot domain in Tobacco mosaic virus enhanced its infectivity and viral RNA accumulation. <b>2018</b> , 519, 170-179		2
82	Genomic variations in the 3'-termini of Rice stripe virus in the rotation between vector insect and host plant. <b>2018</b> , 219, 1085-1096		14
81	Effects of Arbovirus Multi-Host Life Cycles on Dinucleotide and Codon Usage Patterns. <i>Viruses</i> , <b>2019</b> , 11,	6.2	8
80	Review of Emerging Japanese Encephalitis Virus: New Aspects and Concepts about Entry into the Brain and Inter-Cellular Spreading. <b>2019</b> , 8,		36
79	Dengue NS2A Protein Orchestrates Virus Assembly. <b>2019</b> , 26, 606-622.e8		39
78	Impact of genetic diversity on biological characteristics of Usutu virus strains in Africa. <b>2019</b> , 273, 197753		2

77	Flavors of Flaviviral RNA Structure: towards an Integrated View of RNA Function from Translation through Encapsidation. <b>2019</b> , 41, e1900003		3
76	Effects of Refolding on Large-Scale RNA Structure. <b>2019</b> , 58, 3069-3077		5
75	Evolution of Subgenomic RNA Shapes Dengue Virus Adaptation and Epidemiological Fitness. <b>2019</b> , 16, 94-105		13
74	RNA recombination at Chikungunya virus 3'UTR as an evolutionary mechanism that provides adaptability. <i>PLoS Pathogens</i> , <b>2019</b> , 15, e1007706	7.6	19
73	Vector-borne transmission and evolution of Zika virus. <b>2019</b> , 3, 561-569		56
72	Mosquito cells persistently infected with dengue virus produce viral particles with host-dependent replication. <b>2019</b> , 531, 1-18		10
71	Winning the Tug-of-War Between Effector Gene Design and Pathogen Evolution in Vector Population Replacement Strategies. <b>2019</b> , 10, 1072		24
70	Molecular epidemiology of dengue, yellow fever, Zika and Chikungunya arboviruses: An update. <b>2019</b> , 190, 99-111		30
69	RNA Structure Duplication in the Dengue Virus 3' UTR: Redundancy or Host Specificity?. <b>2019</b> , 10,		37
68	Interaction of virus populations with their hosts. <b>2020</b> , 123-166		4
67	Short Direct Repeats in the 3' Untranslated Region Are Involved in Subgenomic Flaviviral RNA Production. <b>2020</b> , 94,		9
66	Structure and function of cis-acting RNA elements of flavivirus. <i>Reviews in Medical Virology</i> , <b>2020</b> , 30, e2092	11.7	14
65	Viral genetics and structure. <b>2020</b> , 85-113		1
64	Using SHAPE-MaP To Model RNA Secondary Structure and Identify 3'UTR Variation in Chikungunya Virus. <b>2020</b> , 94,		7
63	Analytical ultracentrifuge: an ideal tool for characterization of non-coding RNAs. <b>2020</b> , 49, 809-818		2
62	The m6A epitranscriptome opens a new charter in immune system logic. <b>2021</b> , 16, 819-837		4
61	Dengue Immunopathogenesis: A Crosstalk between Host and Viral Factors Leading to Disease: Part I - Dengue Virus Tropism, Host Innate Immune Responses, and Subversion of Antiviral Responses. <b>2020</b> ,		1
60	Molecular mechanisms underlying the extreme mechanical anisotropy of the flaviviral exoribonuclease-resistant RNAs (xrRNAs). <i>Nature Communications</i> , <b>2020</b> , 11, 5496	17.4	5

59	Perspectives on Viral RNA Genomes and the RNA Folding Problem. <i>Viruses</i> , <b>2020</b> , 12,	6.2	5
58	Experimental adaptation of dengue virus 1 to <i>Aedes albopictus</i> mosquitoes by in vivo selection. <i>Scientific Reports</i> , <b>2020</b> , 10, 18404	4.9	4
57	Structures and Functions of the 3' Untranslated Regions of Positive-Sense Single-Stranded RNA Viruses Infecting Humans and Animals. <b>2020</b> , 10, 453		4
56	Understanding the Mechanisms Underlying Host Restriction of Insect-Specific Viruses. <i>Viruses</i> , <b>2020</b> , 12,	6.2	6
55	Disruption of Zika Virus xrRNA1-Dependent sfRNA1 Production Results in Tissue-Specific Attenuated Viral Replication. <i>Viruses</i> , <b>2020</b> , 12,	6.2	1
54	Host-virus evolutionary dynamics with specialist and generalist infection strategies: Bifurcations, bistability, and chaos. <b>2020</b> , 30, 053128		3
53	Zika virus noncoding RNA suppresses apoptosis and is required for virus transmission by mosquitoes. <i>Nature Communications</i> , <b>2020</b> , 11, 2205	17.4	24
52	Genome Analysis of a Novel Tembusu Virus in Taiwan. <i>Viruses</i> , <b>2020</b> , 12,	6.2	8
51	Zika Virus Subgenomic Flavivirus RNA Generation Requires Cooperativity between Duplicated RNA Structures That Are Essential for Productive Infection in Human Cells. <b>2020</b> , 94,		17
50	An RNA Thermometer Activity of the West Nile Virus Genomic 3'-Terminal Stem-Loop Element Modulates Viral Replication Efficiency during Host Switching. <i>Viruses</i> , <b>2020</b> , 12,	6.2	7
49	Different Degrees of 5'-to-3' DAR Interactions Modulate Zika Virus Genome Cyclization and Host-Specific Replication. <b>2020</b> , 94,		3
48	Universal RNA Structure Insight Into Mosquito-Borne (MBFV) Acting RNA Biology. <b>2020</b> , 11, 473		5
47	VIDHOP, viral host prediction with deep learning. <b>2021</b> , 37, 318-325		10
46	Impact of alphavirus 3'UTR plasticity on mosquito transmission. <b>2021</b> , 111, 148-155		2
45	Principles of dengue virus evolvability derived from genotype-fitness maps in human and mosquito cells. <b>2021</b> , 10,		8
44	Extracellular acidosis enhances Zika virus infection both in human cells and ex-vivo tissue cultures from female reproductive tract. <i>Emerging Microbes and Infections</i> , <b>2021</b> , 10, 1169-1179	18.9	1
43	Targeting structural features of viral genomes with a nano-sized supramolecular drug. <b>2021</b> , 12, 7174-7184		0
42	Guapiaū virus, a new insect-specific flavivirus isolated from two species of <i>Aedes</i> mosquitoes from Brazil. <i>Scientific Reports</i> , <b>2021</b> , 11, 4674	4.9	4

41	Coordination between terminal variation of the viral genome and insect microRNAs regulates rice stripe virus replication in insect vectors. <i>PLoS Pathogens</i> , <b>2021</b> , 17, e1009424	7.6	3
40	Genetic Variation in the Domain II, 3' Untranslated Region of Human and Mosquito Derived Dengue Virus Strains in Sri Lanka. <i>Viruses</i> , <b>2021</b> , 13,	6.2	1
39	The Pseudo-Circular Genomes of Flaviviruses: Structures, Mechanisms, and Functions of Circularization. <b>2021</b> , 10,		0
38	An African tick flavivirus forming an independent clade exhibits unique exoribonuclease-resistant RNA structures in the genomic 3'-untranslated region. <i>Scientific Reports</i> , <b>2021</b> , 11, 4883	4.9	2
37	Information Encoded by the Flavivirus Genomes beyond the Nucleotide Sequence. <b>2021</b> , 22,		6
36	Matrix metalloproteinases in the pathogenesis of dengue viral disease: Involvement of immune system and newer therapeutic strategies. <b>2021</b> , 93, 4629-4637		0
35	Mechanisms Underlying Host Range Variation in Flavivirus: From Empirical Knowledge to Predictive Models. <b>2021</b> , 89, 329-340		0
34	Mechanical strength of RNA knot in Zika virus protects against cellular defenses. <b>2021</b> , 17, 975-981		8
33	Generation and Application of a Luciferase Reporter Virus Based on Yellow Fever Virus 17D. <b>2021</b> , 1		0
32	Rational design of West Nile virus vaccine through large replacement of 3' UTR with internal poly(A). <b>2021</b> , 13, e14108		1
31	Analysis of Dengue Virus Serotype 2 Mutations Detected at the Intrahost Level in Patients with Different Clinical Outcomes. <b>2021</b> , 9, e0025621		0
30	Shared properties and singularities of exoribonuclease-resistant RNAs in viruses. <i>Computational and Structural Biotechnology Journal</i> , <b>2021</b> , 19, 4373-4380	6.8	0
29	Dengue Preventive Strategies Through Entomological Control, Vaccination and Biotechnology. <b>2021</b> , 57-69		
28	A Viral mRNA Motif at the 3'-Untranslated Region that Confers Translatability in a Cell-Specific Manner. Implications for Virus Evolution. <i>Scientific Reports</i> , <b>2016</b> , 6, 19217	4.9	17
27	VIDHOP, viral host prediction with Deep Learning.		2
26	Genome-wide Associations of Flavivirus Capsid Proteins.		2
25	Whole-Genome Sequencing Analysis from the Chikungunya Virus Caribbean Outbreak Reveals Novel Evolutionary Genomic Elements. <i>PLoS Neglected Tropical Diseases</i> , <b>2016</b> , 10, e0004402	4.8	79
24	Long non-coding subgenomic flavivirus RNAs have extended 3D structures and are flexible in solution. <i>EMBO Reports</i> , <b>2019</b> , 20, e47016	6.5	18

23	Genetic and biological characterisation of Zika virus isolates from different Brazilian regions. <i>Memorias Do Instituto Oswaldo Cruz</i> , <b>2019</b> , 114, e190150	2.6	7
22	Comparative analysis of protein evolution and RNA structural changes in the genome of pre-epidemic and epidemic Zika virus.		
21	Evolution of subgenomic RNA shapes dengue virus adaptation and epidemiological fitness.		
20	Molecular mechanisms underlying the extreme mechanical anisotropy of the flaviviral exoribonuclease-resistant RNAs (xrRNAs).		
19	Disruption of Zika virus xrRNA1-dependent sfRNA1 production results in tissue-specific attenuated viral replication.		0
18	Principles of dengue virus evolvability derived from genotype-fitness maps in human and mosquito cells.		
17	Pseudoknot length modulates the folding, conformational dynamics, and robustness of Xrn1 resistance of flaviviral xrRNAs. <i>Nature Communications</i> , <b>2021</b> , 12, 6417	17.4	2
16	Experimental adaptation of dengue virus 1 to <i>Aedes albopictus</i> mosquitoes by in vivo selection.		
15	Structural analysis of 3'UTRs in insect flaviviruses reveals novel determinants of sfRNA biogenesis and provides new insights into flavivirus evolution.. <i>Nature Communications</i> , <b>2022</b> , 13, 1279	17.4	1
14	Sequence Duplication in 3' UTR Modulates Virus Replication and Virulence of Japanese encephalitis virus. <i>Emerging Microbes and Infections</i> , <b>2021</b> , 1-31	18.9	1
13	Image_1.JPEG. <b>2020</b> ,		
12	Image_2.JPEG. <b>2020</b> ,		
11	Image_3.JPEG. <b>2020</b> ,		
10	Image_4.JPEG. <b>2020</b> ,		
9	Image_5.JPEG. <b>2020</b> ,		
8	Image_6.JPEG. <b>2020</b> ,		
7	Host and viral non-coding RNAs in dengue pathogenesis.. <i>Reviews in Medical Virology</i> , <b>2022</b> , e2360	11.7	0
6	N6-methyladenosine modification of the <i>Aedes aegypti</i> transcriptome and its alteration upon dengue virus infection in Aag2 cell line. <i>Communications Biology</i> , <b>2022</b> , 5,	6.7	0



- 5 Phylogenetic Characterisation of the Full Genome of a Bagaza Virus Isolate from Bird Fatalities in South Africa. *Viruses*, **2022**, 14, 1476 6.2
- 4 Pan-flavivirus analysis reveals that the insect-specific Kamiti River virus produces a new subgenomic RNA and high amounts of 3'UTR-derived siRNAs.
- 3 Evidence that untranslated genomic sequences are key determinants of insect-specific flavivirus host restriction. **2022**, 574, 102-114
- 2 Interactions of host miRNAs in the flavivirus 3'UTR genome: From bioinformatics predictions to practical approaches. 12, ○
- 1 Stem-Loop I of the Tembusu Virus 3'-Untranslated Region Is Responsible for Viral Host-Specific Adaptation and the Pathogenicity of the Virus in Mice. **2022**, 10, ○