

Houssam Attoui

List of Publications by Year in descending order

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102
papers

6,463
citations

70961

41
h-index

66788

78
g-index

107
all docs

107
docs citations

107
times ranked

4922
citing authors

#	ARTICLE	IF	CITATIONS
1	Uniformity of rotavirus strain nomenclature proposed by the Rotavirus Classification Working Group (RCWG). <i>Archives of Virology</i> , 2011, 156, 1397-1413.	0.9	827
2	Recommendations for the classification of group A rotaviruses using all 11 genomic RNA segments. <i>Archives of Virology</i> , 2008, 153, 1621-1629.	0.9	642
3	Tick-borne virus diseases of human interest in Europe. <i>Clinical Microbiology and Infection</i> , 2004, 10, 1040-1055.	2.8	264
4	Sequences of flavivirus-related RNA viruses persist in DNA form integrated in the genome of <i>Aedes</i> spp. mosquitoes. <i>Journal of General Virology</i> , 2004, 85, 1971-1980.	1.3	250
5	Common evolutionary origin of aquareoviruses and orthoreoviruses revealed by genome characterization of Golden shiner reovirus, Grass carp reovirus, Striped bass reovirus and golden ide reovirus (genus <i>Aquareovirus</i> , family <i>Reoviridae</i>). <i>Journal of General Virology</i> , 2002, 83, 1941-1951.	1.3	200
6	Rapid cDNA synthesis and sequencing techniques for the genetic study of bluetongue and other dsRNA viruses. <i>Journal of Virological Methods</i> , 2007, 143, 132-139.	1.0	198
7	Analysis and phylogenetic comparisons of full-length VP2 genes of the 24 bluetongue virus serotypes. <i>Journal of General Virology</i> , 2007, 88, 621-630.	1.3	197
8	Detection of a Fourth Orbivirus Non-Structural Protein. <i>PLoS ONE</i> , 2011, 6, e25697.	1.1	174
9	Sequence analysis of bluetongue virus serotype 8 from the Netherlands 2006 and comparison to other European strains. <i>Virology</i> , 2008, 377, 308-318.	1.1	172
10	Strategies for the sequence determination of viral dsRNA genomes. <i>Journal of Virological Methods</i> , 2000, 89, 147-158.	1.0	168
11	Complete Genome Characterisation of a Novel 26th Bluetongue Virus Serotype from Kuwait. <i>PLoS ONE</i> , 2011, 6, e26147.	1.1	151
12	Complete Coding Sequence of the Alkharma Virus, a Tick-Borne Flavivirus Causing Severe Hemorrhagic Fever in Humans in Saudi Arabia. <i>Biochemical and Biophysical Research Communications</i> , 2001, 287, 455-461.	1.0	125
13	Complete sequence determination and genetic analysis of Banna virus and Kadapiro virus: proposal for assignment to a new genus (<i>Seadornavirus</i>) within the family <i>Reoviridae</i> . <i>Journal of General Virology</i> , 2000, 81, 1507-1515.	1.3	112
14	Coltiviruses and Seadornaviruses in North America, Europe, and Asia. <i>Emerging Infectious Diseases</i> , 2005, 11, 1673-1679.	2.0	99
15	Isolation and full-length sequence analysis of <i>Armigeres subalbatus</i> totivirus, the first totivirus isolate from mosquitoes representing a proposed novel genus (<i>Artivirus</i>) of the family <i>Totiviridae</i> . <i>Journal of General Virology</i> , 2010, 91, 2836-2845.	1.3	94
16	Complete characterisation of the American grass carp reovirus genome (genus <i>Aquareovirus</i> : family) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 310-321.	1.1	92
17	Genetic and phylogenetic analysis of the outer-coat proteins VP2 and VP5 of epizootic haemorrhagic disease virus (EHDV): Comparison of genetic and serological data to characterise the EHDV serogroup. <i>Virus Research</i> , 2009, 145, 200-210.	1.1	85
18	TT virus infection: prevalence of elevated viraemia and arguments for the immune control of viral load. <i>Journal of Clinical Virology</i> , 2001, 21, 135-141.	1.6	83

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19	Sequence of Genome Segments 1, 2, and 3 of the Grass Carp Reovirus (Genus Aquareovirus, Family) Tj ETQq1 1 0.784314 rgBT /Over	1.0	79
20	Genus Coltivirus (family Reoviridae): genomic and morphologic characterization of Old World and New World viruses. Archives of Virology, 2002, 147, 533-561.	0.9	78
21	Implicating Culicoides Biting Midges as Vectors of Schmallenberg Virus Using Semi-Quantitative RT-PCR. PLoS ONE, 2013, 8, e57747.	1.1	75
22	Expansion of family Reoviridae to include nine-segmented dsRNA viruses: Isolation and characterization of a new virus designated aedes pseudoscutellaris reovirus assigned to a proposed genus (Dinovernavirus). Virology, 2005, 343, 212-223.	1.1	74
23	Yunnan orbivirus, a new orbivirus species isolated from Culex tritaeniorhynchus mosquitoes in China. Journal of General Virology, 2005, 86, 3409-3417.	1.3	71
24	Complete sequence characterization of the genome of the St Croix River virus, a new orbivirus isolated from cells of Ixodes scapularis. Journal of General Virology, 2001, 82, 795-804.	1.3	68
25	Peruvian horse sickness virus and Yunnan orbivirus, isolated from vertebrates and mosquitoes in Peru and Australia. Virology, 2009, 394, 298-310.	1.1	65
26	Bluetongue Virus: From BTV-1 to BTV-27. Advances in Virus Research, 2017, 99, 161-197.	0.9	65
27	Genetic analysis of full-length genomes and subgenomic sequences of TT virus-like mini virus human isolates. Journal of General Virology, 2001, 82, 379-383.	1.3	63
28	Circular genomes related to anelloviruses identified in human and animal samples by using a combined rolling-circle amplification/sequence-independent single primer amplification approach. Journal of General Virology, 2007, 88, 2696-2701.	1.3	62
29	Distribution and genetic analysis of TTV and TTMV major phylogenetic groups in French blood donors. Journal of Medical Virology, 2006, 78, 298-304.	2.5	58
30	Complete sequence characterization of isolates of Getah virus (genus Alphavirus, family Togaviridae) from China. Journal of General Virology, 2008, 89, 1446-1456.	1.3	58
31	Micromonas pusilla reovirus: a new member of the family Reoviridae assigned to a novel proposed genus (Mimoreovirus). Journal of General Virology, 2006, 87, 1375-1383.	1.3	57
32	Low Diversity of Alkhurma Hemorrhagic Fever Virus, Saudi Arabia, 1994-1999. Emerging Infectious Diseases, 2005, 11, 683-688.	2.0	55
33	Complete sequence of Great Island virus and comparison with the T2 and outer-capsid proteins of Kemerovo, Lipovnik and Tribec viruses (genus Orbivirus, family Reoviridae). Journal of General Virology, 2010, 91, 2985-2993.	1.3	54
34	ICTV virus taxonomy profile: Birnaviridae. Journal of General Virology, 2019, 100, 5-6.	1.3	54
35	TT virus: a study of molecular epidemiology and transmission of genotypes 1, 2 and 3. Journal of Clinical Virology, 2000, 17, 43-49.	1.6	53
36	Full-Genome Sequencing as a Basis for Molecular Epidemiology Studies of Bluetongue Virus in India. PLoS ONE, 2015, 10, e0131257.	1.1	52

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37	Liao ning virus, a new Chinese seadornavirus that replicates in transformed and embryonic mammalian cells. <i>Journal of General Virology</i> , 2006, 87, 199-208.	1.3	50
38	Structural organization of an encephalitic human isolate of Banna virus (genus Seadornavirus, family Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.3	48
39	Genetic and phylogenetic analysis of the core proteins VP1, VP3, VP4, VP6 and VP7 of epizootic haemorrhagic disease virus (EHDV). <i>Virus Research</i> , 2009, 145, 187-199.	1.1	48
40	Isolation and characterization of the full coding sequence of a novel densovirus from the mosquito <i>Culex pipiens pallens</i> . <i>Journal of General Virology</i> , 2008, 89, 195-199.	1.3	47
41	Genotype Distribution and Molecular Epidemiology of Hepatitis C Virus in Blood Donors from Southeast France. <i>Journal of Clinical Microbiology</i> , 2005, 43, 3624-3629.	1.8	45
42	Emerging Mosquito-Borne Threats and the Response from European and Eastern Mediterranean Countries. <i>International Journal of Environmental Research and Public Health</i> , 2018, 15, 2775.	1.2	45
43	Bluetongue virus, other orbiviruses and other reoviruses: Their relationships and taxonomy. , 2009, , 23-52.		44
44	Serologic and molecular diagnosis of Colorado tick fever viral infections.. <i>American Journal of Tropical Medicine and Hygiene</i> , 1998, 59, 763-768.	0.6	42
45	Sequence Characterization of Ndelle Virus Genome Segments 1, 5, 7, 8, and 10: Evidence for Reassignment to the Genus Orthoreovirus, Family Reoviridae. <i>Biochemical and Biophysical Research Communications</i> , 2001, 287, 583-588.	1.0	41
46	Genetic and phylogenetic analysis of the non-structural proteins NS1, NS2 and NS3 of epizootic haemorrhagic disease virus (EHDV). <i>Virus Research</i> , 2009, 145, 211-219.	1.1	39
47	ICTV virus taxonomy profile: Picobirnaviridae. <i>Journal of General Virology</i> , 2019, 100, 133-134.	1.3	39
48	Umatilla Virus Genome Sequencing and Phylogenetic Analysis: Identification of Stretch Lagoon Orbivirus as a New Member of the Umatilla virus Species. <i>PLoS ONE</i> , 2011, 6, e23605.	1.1	37
49	Genetic Characterization of the Tick-Borne Orbiviruses. <i>Viruses</i> , 2015, 7, 2185-2209.	1.5	36
50	Sequence Determination and Analysis of the Full-Length Genome of Colorado Tick Fever Virus, the Type Species of Genus Coltivirus (Family Reoviridae). <i>Biochemical and Biophysical Research Communications</i> , 2000, 273, 1121-1125.	1.0	35
51	The Structure and Function of the Outer Coat Protein VP9 of Banna Virus. <i>Structure</i> , 2005, 13, 17-28.	1.6	35
52	Complete Sequences of Two Highly Divergent European Isolates of TT Virus. <i>Biochemical and Biophysical Research Communications</i> , 2000, 271, 837-841.	1.0	34
53	Full-Genome Characterisation of Orungo, Lebombo and Changuinola Viruses Provides Evidence for Co-Evolution of Orbiviruses with Their Arthropod Vectors. <i>PLoS ONE</i> , 2014, 9, e86392.	1.1	33
54	Full Genome Sequencing and Genetic Characterization of Eubenangee Viruses Identify Pata Virus as a Distinct Species within the Genus Orbivirus. <i>PLoS ONE</i> , 2012, 7, e31911.	1.1	31

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55	Prevalence of antibody against West Nile virus in volunteer blood donors living in southeastern France. <i>Transfusion</i> , 2001, 41, 1320-1321.	0.8	29
56	Recombinant VP7-Based Enzyme-Linked Immunosorbent Assay for Detection of Immunoglobulin G Antibodies to Colorado Tick Fever Virus. <i>Journal of Clinical Microbiology</i> , 2003, 41, 2102-2105.	1.8	29
57	Endogenous tick viruses and modulation of tick-borne pathogen growth. <i>Frontiers in Cellular and Infection Microbiology</i> , 2013, 3, 25.	1.8	29
58	Immunisation with bacterial expressed VP2 and VP5 of bluetongue virus (BTV) protect $\hat{\pm}/\hat{\pm}^2$ interferon-receptor knock-out (IFNAR $\hat{\sim}/\hat{\sim}$) mice from homologous lethal challenge. <i>Vaccine</i> , 2014, 32, 4059-4067.	1.7	26
59	Evaluation of four PCR systems amplifying different genomic regions for molecular diagnosis of GB virus C infections. <i>Journal of Virological Methods</i> , 1997, 64, 131-135.	1.0	25
60	Molecular characterization of genotype 2 and 4 hepatitis C virus isolates in French blood donors. <i>Journal of Medical Virology</i> , 2008, 80, 1732-1739.	2.5	25
61	Comparison of systems performance for TT virus detection using PCR primer sets located in non-coding and coding regions of the viral genome. <i>Journal of Clinical Virology</i> , 2001, 22, 91-99.	1.6	24
62	Complete Genome Sequence of Bluetongue Virus Serotype 8, Which Reemerged in France in August 2015. <i>Genome Announcements</i> , 2016, 4, .	0.8	23
63	Prevalence of GB virus type C/hepatitis G virus RNA and anti-E2 among blood donors in Southeastern France. <i>Transfusion</i> , 1999, 39, 95-102.	0.8	22
64	Identification and functional analysis of VP3, the guanylyltransferase of Banna virus (genus) Tj ETQq0 0 0 rGBT /Overlock 10 Tf, 50 382 T	1.3	22
65	Seroprevalence of Toscana Virus in Blood Donors, France, 2007. <i>Emerging Infectious Diseases</i> , 2011, 17, 941-943.	2.0	22
66	Identification of the Genome Segments of Bluetongue Virus Serotype 26 (Isolate KUW2010/02) that Restrict Replication in a <i>Culicoides sonorensis</i> Cell Line (KC Cells). <i>PLoS ONE</i> , 2016, 11, e0149709.	1.1	22
67	Complete nucleotide sequence of Middelburg virus, isolated from the spleen of a horse with severe clinical disease in Zimbabwe. <i>Journal of General Virology</i> , 2007, 88, 3078-3088.	1.3	21
68	High genetic diversity revealed by the study of TLMV infection in French hemodialysis patients. <i>Journal of Medical Virology</i> , 2002, 67, 630-635.	2.5	19
69	Termination and read-through proteins encoded by genome segment 9 of Colorado tick fever virus. <i>Journal of General Virology</i> , 2004, 85, 2237-2244.	1.3	18
70	Evolution of hepatitis C virus in blood donors and their respective recipients. <i>Journal of General Virology</i> , 2003, 84, 441-446.	1.3	17
71	Analysis of hepatitis C virus strains circulating in Republic of the Congo. <i>Journal of Medical Virology</i> , 2010, 82, 562-567.	2.5	17
72	Molecular diagnosis of group B coltivirus infections. <i>Journal of Virological Methods</i> , 1999, 81, 39-45.	1.0	16

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73	Recombinant VP6-based enzyme-linked immunosorbent assay for detection of immunoglobulin G antibodies to Eyach virus (genus Coltivirus). <i>Journal of Clinical Virology</i> , 2004, 30, 248-253.	1.6	16
74	Article Commentary: Virus Discovery Using Tick Cell Lines. <i>Evolutionary Bioinformatics</i> , 2016, 12s2, EBO.S39675.	0.6	16
75	Recombinant VP9-based enzyme-linked immunosorbent assay for detection of immunoglobulin G antibodies to Banna virus (genus Seadornavirus). <i>Journal of Virological Methods</i> , 2004, 116, 55-61.	1.0	15
76	Association of vectors and environmental conditions during the emergence of Peruvian horse sickness orbivirus and Yunnan orbivirus in northern Peru. <i>Journal of Vector Ecology</i> , 2015, 40, 355-363.	0.5	15
77	Isolates of Liao Ning Virus from Wild-Caught Mosquitoes in the Xinjiang Province of China in 2005. <i>PLoS ONE</i> , 2012, 7, e37732.	1.1	14
78	Acute Schmallenberg Virus Infections, France, 2012. <i>Emerging Infectious Diseases</i> , 2013, 19, 321-322.	2.0	14
79	Sequence analysis of a reovirus isolated from the winter moth <i>Operophtera brumata</i> (Lepidoptera: Tj ETQq1 1 0.784314 rgBT /Overlock Research, 2008, 135, 42-47.	1.1	13
80	Detection and Prevalence of the Nonsyncytial American Grass Carp Reovirus <i>Aquareovirus G</i> by Quantitative Reverse Transcriptase Polymerase Chain Reaction. <i>Journal of Aquatic Animal Health</i> , 2010, 22, 8-13.	0.6	13
81	Full Genome Sequencing of Corriparta Virus, Identifies California Mosquito Pool Virus as a Member of the Corriparta virus Species. <i>PLoS ONE</i> , 2013, 8, e70779.	1.1	12
82	Evaluation of two artificial infection methods of live ticks as tools for studying interactions between tick-borne viruses and their tick vectors. <i>Scientific Reports</i> , 2022, 12, 491.	1.6	12
83	Human Parvovirus 4 in Kidney Transplant Patients, France. <i>Emerging Infectious Diseases</i> , 2008, 14, 1811-1812.	2.0	11
84	Bluetongue virus outer-capsid protein VP2 expressed in <i>Nicotiana benthamiana</i> raises neutralising antibodies and a protective immune response in IFNAR ^{-/-} mice. <i>Vaccine: X</i> , 2019, 2, 100026.	0.9	11
85	Exploration of binary protein-protein interactions between tick-borne flaviviruses and <i>Ixodes ricinus</i> . <i>Parasites and Vectors</i> , 2021, 14, 144.	1.0	11
86	The evolution of two homologues of the core protein VP6 of epizootic haemorrhagic disease virus (EHDV), which correspond to the geographical origin of the virus. <i>Virus Genes</i> , 2010, 40, 67-75.	0.7	9
87	Full Genome Characterization of the Culicoides-Borne Marsupial Orbiviruses: Wallal Virus, Mudjinbarry Virus and Warrego Viruses. <i>PLoS ONE</i> , 2014, 9, e108379.	1.1	9
88	Strategies for Assessing Arbovirus Genetic Variability in Vectors and/or Mammals. <i>Pathogens</i> , 2020, 9, 915.	1.2	8
89	Inhibition of Orbivirus Replication by Fluvastatin and Identification of the Key Elements of the Mevalonate Pathway Involved. <i>Viruses</i> , 2021, 13, 1437.	1.5	7
90	Identification of the Genome Segments of Bluetongue Virus Type 26/Type 1 Reassortants Influencing Horizontal Transmission in a Mouse Model. <i>Viruses</i> , 2021, 13, 2208.	1.5	7

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91	The structure of bluetongue virus core and proteins. , 2009, , 101-133.		6
92	Continuous Cell Lines from the European Biting Midge <i>Culicoides nubeculosus</i> (Meigen, 1830). <i>Microorganisms</i> , 2020, 8, 825.	1.6	6
93	How relevant are in vitro culture models for study of tick-pathogen interactions?. <i>Pathogens and Global Health</i> , 2021, 115, 437-455.	1.0	6
94	Erroneous HCV genotype assignment by a hybridization typing assay in a case of posttransfusion HCV infection. <i>Transfusion</i> , 2001, 41, 429-430.	0.8	5
95	Tick Importin- β Is Implicated in the Interactome and Regulome of the Cofactor Subolesin. <i>Pathogens</i> , 2021, 10, 457.	1.2	5
96	Serological Cross-Reactions between Expressed VP2 Proteins from Different Bluetongue Virus Serotypes. <i>Viruses</i> , 2021, 13, 1455.	1.5	5
97	The Complete Coding Sequence of a European Isolate of GB-C/Hepatitis G Virus. <i>Biochemical and Biophysical Research Communications</i> , 1999, 255, 432-437.	1.0	3
98	Vector Transmission of Animal Viruses. , 2021, , 542-551.		1
99	Orbiviruses. <i>Livestock Diseases and Management</i> , 2020, , 161-214.	0.5	1
100	Evaluation of Vector Competence of Ixodes Ticks for Kemerovo Virus. <i>Viruses</i> , 2022, 14, 1102.	1.5	1
101	Seadornavirus. , 2011, , 1645-1652.		0
102	Coltivirus. , 2011, , 1573-1577.		0