

Houssam Attoui

List of Publications by Citations

Source: <https://exaly.com/author-pdf/2222142/houssam-attoui-publications-by-citations.pdf>

Version: 2024-04-19

This document has been generated based on the publications and citations recorded by exaly.com. 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.

101
papers

5,343
citations

37
h-index

71
g-index

107
ext. papers

5,968
ext. citations

5.6
avg, IF

4.83
L-index

#	Paper	IF	Citations
101	Uniformity of rotavirus strain nomenclature proposed by the Rotavirus Classification Working Group (RCWG). <i>Archives of Virology</i> , 2011 , 156, 1397-413	2.6	699
100	Recommendations for the classification of group A rotaviruses using all 11 genomic RNA segments. <i>Archives of Virology</i> , 2008 , 153, 1621-9	2.6	523
99	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	4.9	224
98	Tick-borne virus diseases of human interest in Europe. <i>Clinical Microbiology and Infection</i> , 2004 , 10, 1040-55	4.5	210
97	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 Aquareovirus, family Reoviridae). <i>Journal of General Virology</i> , 2002 , 83, 1941-1951	4.9	179
96	Rapid cDNA synthesis and sequencing techniques for the genetic study of bluetongue and other dsRNA viruses. <i>Journal of Virological Methods</i> , 2007 , 143, 132-9	2.6	173
95	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	4.9	172
94	Strategies for the sequence determination of viral dsRNA genomes. <i>Journal of Virological Methods</i> , 2000 , 89, 147-58	2.6	155
93	Detection of a fourth orbivirus non-structural protein. <i>PLoS ONE</i> , 2011 , 6, e25697	3.7	155
92	Sequence analysis of bluetongue virus serotype 8 from the Netherlands 2006 and comparison to other European strains. <i>Virology</i> , 2008 , 377, 308-18	3.6	152
91	Complete genome characterisation of a novel 26th bluetongue virus serotype from Kuwait. <i>PLoS ONE</i> , 2011 , 6, e26147	3.7	136
90	Complete coding sequence of the Alkhurma virus, a tick-borne flavivirus causing severe hemorrhagic fever in humans in Saudi Arabia. <i>Biochemical and Biophysical Research Communications</i> , 2001 , 287, 455-61	3.4	111
89	Complete sequence determination and genetic analysis of Banna virus and Kadipiro virus: proposal for assignment to a new genus (Seadornavirus) within the family Reoviridae. <i>Journal of General Virology</i> , 2000 , 81, 1507-15	4.9	91
88	Complete characterisation of the American grass carp reovirus genome (genus Aquareovirus: family Reoviridae) reveals an evolutionary link between aquareoviruses and coltivirus. <i>Virology</i> , 2008 , 373, 310-21	3.6	82
87	Coltiviruses and seadornaviruses in North America, Europe, and Asia. <i>Emerging Infectious Diseases</i> , 2005 , 11, 1673-9	10.2	80
86	Sequence of genome segments 1, 2, and 3 of the grass carp reovirus (Genus Aquareovirus, family Reoviridae). <i>Biochemical and Biophysical Research Communications</i> , 2000 , 274, 762-6	3.4	73
85	Genus Coltivirus (family Reoviridae): genomic and morphologic characterization of Old World and New World viruses. <i>Archives of Virology</i> , 2002 , 147, 533-61	2.6	69

84	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, 200-10	6.4	68
83	TT virus infection: prevalence of elevated viraemia and arguments for the immune control of viral load. <i>Journal of Clinical Virology</i> , 2001 , 21, 135-41	14.5	68
82	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, 2836-45	4.9	67
81	Implicating <i>Culicoides</i> biting midges as vectors of Schmallenberg virus using semi-quantitative RT-PCR. <i>PLoS ONE</i> , 2013 , 8, e57747	3.7	66
80	Expansion of family <i>Reoviridae</i> to include nine-segmented dsRNA viruses: isolation and characterization of a new virus designated <i>Aedes pseudoscutellaris</i> reovirus assigned to a proposed genus (<i>Dinovernavirus</i>). <i>Virology</i> , 2005 , 343, 212-23	3.6	65
79	Complete sequence characterization of the genome of the St Croix River virus, a new orbivirus isolated from cells of <i>Ixodes scapularis</i> . <i>Journal of General Virology</i> , 2001 , 82, 795-804	4.9	64
78	Yunnan orbivirus, a new orbivirus species isolated from <i>Culex tritaeniorhynchus</i> mosquitoes in China. <i>Journal of General Virology</i> , 2005 , 86, 3409-3417	4.9	62
77	Circular genomes related to anelloviruses identified in human and animal samples by using a combined rolling-circle amplification/sequence-independent single primer amplification approach. <i>Journal of General Virology</i> , 2007 , 88, 2696-2701	4.9	55
76	Peruvian horse sickness virus and Yunnan orbivirus, isolated from vertebrates and mosquitoes in Peru and Australia. <i>Virology</i> , 2009 , 394, 298-310	3.6	53
75	Genetic analysis of full-length genomes and subgenomic sequences of TT virus-like mini virus human isolates. <i>Journal of General Virology</i> , 2001 , 82, 379-383	4.9	53
74	Distribution and genetic analysis of TTV and TTMV major phylogenetic groups in French blood donors. <i>Journal of Medical Virology</i> , 2006 , 78, 298-304	19.7	51
73	Low diversity of Alkhurma hemorrhagic fever virus, Saudi Arabia, 1994-1999. <i>Emerging Infectious Diseases</i> , 2005 , 11, 683-8	10.2	50
72	<i>Micromonas pusilla</i> reovirus: a new member of the family <i>Reoviridae</i> assigned to a novel proposed genus (<i>Mimoreovirus</i>). <i>Journal of General Virology</i> , 2006 , 87, 1375-1383	4.9	49
71	Complete sequence of Great Island virus and comparison with the T2 and outer-capsid proteins of Kemerovo, Lipovnik and Tribec viruses (genus <i>Orbivirus</i> , family <i>Reoviridae</i>). <i>Journal of General Virology</i> , 2010 , 91, 2985-93	4.9	48
70	TT virus: a study of molecular epidemiology and transmission of genotypes 1, 2 and 3. <i>Journal of Clinical Virology</i> , 2000 , 17, 43-9	14.5	44
69	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	4.9	44
68	Full-Genome Sequencing as a Basis for Molecular Epidemiology Studies of Bluetongue Virus in India. <i>PLoS ONE</i> , 2015 , 10, e0131257	3.7	42
67	Complete sequence characterization of isolates of Getah virus (genus <i>Alphavirus</i> , family <i>Togaviridae</i>) from China. <i>Journal of General Virology</i> , 2008 , 89, 1446-1456	4.9	42

66	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	4.9	41
65	Structural organization of an encephalitic human isolate of Banna virus (genus Seadornavirus, family Reoviridae). <i>Journal of General Virology</i> , 2005 , 86, 1147-1157	4.9	40
64	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, 187-99	6.4	37
63	Genotype distribution and molecular epidemiology of hepatitis C virus in blood donors from southeast France. <i>Journal of Clinical Microbiology</i> , 2005 , 43, 3624-9	9.7	37
62	Bluetongue Virus: From BTV-1 to BTV-27. <i>Advances in Virus Research</i> , 2017 , 99, 161-197	10.7	35
61	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, 583-8	3.4	35
60	ICTV virus taxonomy profile: Birnaviridae. <i>Journal of General Virology</i> , 2019 , 100, 5-6	4.9	33
59	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	3.7	32
58	Complete sequences of two highly divergent european isolates of TT virus. <i>Biochemical and Biophysical Research Communications</i> , 2000 , 271, 837-41	3.4	30
57	Serologic and molecular diagnosis of Colorado tick fever viral infections. <i>American Journal of Tropical Medicine and Hygiene</i> , 1998 , 59, 763-8	3.2	29
56	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, 211-9	6.4	28
55	Bluetongue virus, other orbiviruses and other reoviruses: Their relationships and taxonomy 2009 , 23-52		28
54	The structure and function of the outer coat protein VP9 of Banna virus. <i>Structure</i> , 2005 , 13, 17-28	5.2	27
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	3.7	27
52	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	3.7	26
51	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, 1121-5	3.4	25
50	Genetic characterization of the tick-borne orbiviruses. <i>Viruses</i> , 2015 , 7, 2185-209	6.2	24
49	Endogenous tick viruses and modulation of tick-borne pathogen growth. <i>Frontiers in Cellular and Infection Microbiology</i> , 2013 , 3, 25	5.9	24

48	ICTV virus taxonomy profile: Picobirnaviridae. <i>Journal of General Virology</i> , 2019 , 100, 133-134	4.9	23
47	Molecular characterization of genotype 2 and 4 hepatitis C virus isolates in French blood donors. <i>Journal of Medical Virology</i> , 2008 , 80, 1732-9	19.7	22
46	Complete Genome Sequence of Bluetongue Virus Serotype 8, Which Reemerged in France in August 2015. <i>Genome Announcements</i> , 2016 , 4,		21
45	Immunisation with bacterial expressed VP2 and VP5 of bluetongue virus (BTV) protect \square interferon-receptor knock-out (IFNAR(-/-)) mice from homologous lethal challenge. <i>Vaccine</i> , 2014 , 32, 4059-67	4.1	21
44	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, 131-5	2.6	21
43	Prevalence of antibody against West Nile virus in volunteer blood donors living in southeastern France. <i>Transfusion</i> , 2001 , 41, 1320-1	2.9	21
42	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, 91-9	14.5	21
41	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,	4.6	21
40	Identification and functional analysis of VP3, the guanylyltransferase of Banna virus (genus Seadornavirus, family Reoviridae). <i>Journal of General Virology</i> , 2005 , 86, 1141-1146	4.9	19
39	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	4.9	18
38	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, 2102-5	9.7	18
37	Seroprevalence of Toscana virus in blood donors, France, 2007. <i>Emerging Infectious Diseases</i> , 2011 , 17, 941-3	10.2	17
36	High genetic diversity revealed by the study of TLMV infection in French hemodialysis patients. <i>Journal of Medical Virology</i> , 2002 , 67, 630-5	19.7	17
35	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	2.9	17
34	Analysis of hepatitis C virus strains circulating in Republic of the Congo. <i>Journal of Medical Virology</i> , 2010 , 82, 562-7	19.7	16
33	Identification of the Genome Segments of Bluetongue Virus Serotype 26 (Isolate KUV2010/02) that Restrict Replication in a <i>Culicoides sonorensis</i> Cell Line (KC Cells). <i>PLoS ONE</i> , 2016 , 11, e0149709	3.7	15
32	Acute Schmallenberg virus infections, France, 2012. <i>Emerging Infectious Diseases</i> , 2013 , 19, 321-2	10.2	14
31	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	4.9	14

30	Virus Discovery Using Tick Cell Lines. <i>Evolutionary Bioinformatics</i> , 2016 , 12, 31-4	1.9	14
29	Isolates of Liao ning virus from wild-caught mosquitoes in the Xinjiang province of China in 2005. <i>PLoS ONE</i> , 2012 , 7, e37732	3.7	13
28	Detection and prevalence of the nonsyncytial American grass carp reovirus Aquareovirus G by quantitative reverse transcriptase polymerase chain reaction. <i>Journal of Aquatic Animal Health</i> , 2010 , 22, 8-13	2.6	13
27	Evolution of hepatitis C virus in blood donors and their respective recipients. <i>Journal of General Virology</i> , 2003 , 84, 441-446	4.9	13
26	Molecular diagnosis of group B coltivirus infections. <i>Journal of Virological Methods</i> , 1999 , 81, 39-45	2.6	13
25	Sequence analysis of a reovirus isolated from the winter moth <i>Operophtera brumata</i> (Lepidoptera: Geometridae) and its parasitoid wasp <i>Phobocampe tempestiva</i> (Hymenoptera: Ichneumonidae). <i>Virus Research</i> , 2008 , 135, 42-7	6.4	10
24	Human parvovirus 4 in kidney transplant patients, France. <i>Emerging Infectious Diseases</i> , 2008 , 14, 1811-210.2	10.2	10
23	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	2.6	10
22	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, 355-63	1.5	9
21	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, 248-53	14.5	9
20	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	2.3	8
19	The structure of bluetongue virus core and proteins 2009 , 101-133		6
18	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	3.7	6
17	Full genome characterization of the culicoides-borne marsupial orbiviruses: Wallal virus, Mudjinbarry virus and Warrego viruses. <i>PLoS ONE</i> , 2014 , 9, e108379	3.7	6
16	Strategies for Assessing Arbovirus Genetic Variability in Vectors and/or Mammals. <i>Pathogens</i> , 2020 , 9,	4.5	6
15	Bluetongue virus outer-capsid protein VP2 expressed in raises neutralising antibodies and a protective immune response in IFNAR mice. <i>Vaccine: X</i> , 2019 , 2, 100026	3.8	4
14	Continuous Cell Lines from the European Biting Midge (Meigen, 1830). <i>Microorganisms</i> , 2020 , 8,	4.9	3
13	Erroneous HCV genotype assignment by a hybridization typing assay in a case of posttransfusion HCV infection. <i>Transfusion</i> , 2001 , 41, 429-30	2.9	3

12	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,	6.2	3
11	Exploration of binary protein-protein interactions between tick-borne flaviviruses and <i>Ixodes ricinus</i> . <i>Parasites and Vectors</i> , 2021 , 14, 144	4	3
10	Inhibition of Orbivirus Replication by Fluvastatin and Identification of the Key Elements of the Mevalonate Pathway Involved. <i>Viruses</i> , 2021 , 13,	6.2	3
9	The complete coding sequence of a European isolate of GB-C/hepatitis G virus. <i>Biochemical and Biophysical Research Communications</i> , 1999 , 255, 432-7	3.4	2
8	How relevant are in vitro culture models for study of tick-pathogen interactions?. <i>Pathogens and Global Health</i> , 2021 , 115, 437-455	3.1	2
7	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	4.9	1
6	Coltiviruses and Seadornaviruses		1
5	Vector Transmission of Animal Viruses 2021 , 542-551		1
4	Orbiviruses. <i>Livestock Diseases and Management</i> , 2020 , 161-214	0.5	0
3	Orbiviruses and Bluetongue Virus 2015 , 1-18		
2	Coltiviruses and Seadornaviruses 2015 , 1-12		
1	Evaluation of Vector Competence of <i>Ixodes</i> Ticks for Kemerovo Virus. <i>Viruses</i> , 2022 , 14, 1102	6.2	