

Houssam Attoui

List of Publications by Year in descending order

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102
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6,463
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107
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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. | 2.1 | 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. | 2.1 | 642 |
| 3 | Tick-borne virus diseases of human interest in Europe. <i>Clinical Microbiology and Infection</i> , 2004, 10, 1040-1055. | 6.0 | 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. | 2.9 | 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. | 2.9 | 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. | 2.1 | 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. | 2.9 | 197 |
| 8 | Detection of a Fourth Orbivirus Non-Structural Protein. <i>PLoS ONE</i> , 2011, 6, e25697. | 2.5 | 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. | 2.4 | 172 |
| 10 | Strategies for the sequence determination of viral dsRNA genomes. <i>Journal of Virological Methods</i> , 2000, 89, 147-158. | 2.1 | 168 |
| 11 | Complete Genome Characterisation of a Novel 26th Bluetongue Virus Serotype from Kuwait. <i>PLoS ONE</i> , 2011, 6, e26147. | 2.5 | 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. | 2.1 | 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. | 2.9 | 112 |
| 14 | Coltiviruses and Seadornaviruses in North America, Europe, and Asia. <i>Emerging Infectious Diseases</i> , 2005, 11, 1673-1679. | 4.3 | 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. | 2.9 | 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. | 2.4 | 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. | 2.2 | 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. | 3.1 | 83 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 19 | Sequence of Genome Segments 1, 2, and 3 of the Grass Carp Reovirus (Genus Aquareovirus, Family) Tj ETQq1 1 0.784314 rgBT /Over | 2.1 | 79 |
| 20 | Genus Coltivirus (family Reoviridae): genomic and morphologic characterization of Old World and New World viruses. Archives of Virology, 2002, 147, 533-561. | 2.1 | 78 |
| 21 | Implicating Culicoides Biting Midges as Vectors of Schmallenberg Virus Using Semi-Quantitative RT-PCR. PLoS ONE, 2013, 8, e57747. | 2.5 | 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. | 2.4 | 74 |
| 23 | Yunnan orbivirus, a new orbivirus species isolated from Culex tritaeniorhynchus mosquitoes in China. Journal of General Virology, 2005, 86, 3409-3417. | 2.9 | 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. | 2.9 | 68 |
| 25 | Peruvian horse sickness virus and Yunnan orbivirus, isolated from vertebrates and mosquitoes in Peru and Australia. Virology, 2009, 394, 298-310. | 2.4 | 65 |
| 26 | Bluetongue Virus: From BTV-1 to BTV-27. Advances in Virus Research, 2017, 99, 161-197. | 2.1 | 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. | 2.9 | 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. | 2.9 | 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. | 5.0 | 58 |
| 30 | Complete sequence characterization of isolates of Getah virus (genus Alphavirus, family Togaviridae) from China. Journal of General Virology, 2008, 89, 1446-1456. | 2.9 | 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. | 2.9 | 57 |
| 32 | Low Diversity of Alkhurma Hemorrhagic Fever Virus, Saudi Arabia, 1994-1999. Emerging Infectious Diseases, 2005, 11, 683-688. | 4.3 | 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. | 2.9 | 54 |
| 34 | ICTV virus taxonomy profile: Birnaviridae. Journal of General Virology, 2019, 100, 5-6. | 2.9 | 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. | 3.1 | 53 |
| 36 | Full-Genome Sequencing as a Basis for Molecular Epidemiology Studies of Bluetongue Virus in India. PLoS ONE, 2015, 10, e0131257. | 2.5 | 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. | 2.9 | 50 |
| 38 | Structural organization of an encephalitic human isolate of Banna virus (genus Seadornavirus, family Tj ETQq0 0 0,ggBT /Overlock 10 Tf | 2.9 | 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. | 2.2 | 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. | 2.9 | 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. | 3.9 | 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. | 2.6 | 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. | 1.4 | 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. | 2.1 | 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. | 2.2 | 39 |
| 47 | ICTV virus taxonomy profile: Picobirnaviridae. <i>Journal of General Virology</i> , 2019, 100, 133-134. | 2.9 | 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. | 2.5 | 37 |
| 49 | Genetic Characterization of the Tick-Borne Orbiviruses. <i>Viruses</i> , 2015, 7, 2185-2209. | 3.3 | 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. | 2.1 | 35 |
| 51 | The Structure and Function of the Outer Coat Protein VP9 of Banna Virus. <i>Structure</i> , 2005, 13, 17-28. | 3.3 | 35 |
| 52 | Complete Sequences of Two Highly Divergent European Isolates of TT Virus. <i>Biochemical and Biophysical Research Communications</i> , 2000, 271, 837-841. | 2.1 | 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. | 2.5 | 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. | 2.5 | 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. | 1.6 | 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. | 3.9 | 29 |
| 57 | Endogenous tick viruses and modulation of tick-borne pathogen growth. <i>Frontiers in Cellular and Infection Microbiology</i> , 2013, 3, 25. | 3.9 | 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. | 3.8 | 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. | 2.1 | 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. | 5.0 | 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. | 3.1 | 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. | 1.6 | 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 | 2.9 | 22 |
| 65 | Seroprevalence of Toscana Virus in Blood Donors, France, 2007. <i>Emerging Infectious Diseases</i> , 2011, 17, 941-943. | 4.3 | 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. | 2.5 | 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. | 2.9 | 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. | 5.0 | 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. | 2.9 | 18 |
| 70 | Evolution of hepatitis C virus in blood donors and their respective recipients. <i>Journal of General Virology</i> , 2003, 84, 441-446. | 2.9 | 17 |
| 71 | Analysis of hepatitis C virus strains circulating in Republic of the Congo. <i>Journal of Medical Virology</i> , 2010, 82, 562-567. | 5.0 | 17 |
| 72 | Molecular diagnosis of group B coltivirus infections. <i>Journal of Virological Methods</i> , 1999, 81, 39-45. | 2.1 | 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. | 3.1 | 16 |
| 74 | Article Commentary: Virus Discovery Using Tick Cell Lines. <i>Evolutionary Bioinformatics</i> , 2016, 12s2, EBO.S39675. | 1.2 | 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. | 2.1 | 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. | 1.0 | 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. | 2.5 | 14 |
| 78 | Acute Schmallenberg Virus Infections, France, 2012. <i>Emerging Infectious Diseases</i> , 2013, 19, 321-322. | 4.3 | 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. | 2.2 | 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. | 1.4 | 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. | 2.5 | 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. | 3.3 | 12 |
| 83 | Human Parvovirus 4 in Kidney Transplant Patients, France. <i>Emerging Infectious Diseases</i> , 2008, 14, 1811-1812. | 4.3 | 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. | 2.1 | 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. | 2.5 | 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. | 1.6 | 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. | 2.5 | 9 |
| 88 | Strategies for Assessing Arbovirus Genetic Variability in Vectors and/or Mammals. <i>Pathogens</i> , 2020, 9, 915. | 2.8 | 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. | 3.3 | 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. | 3.3 | 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. | 3.6 | 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. | 2.3 | 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. | 1.6 | 5 |
| 95 | Tick Importin- β Is Implicated in the Interactome and Regulome of the Cofactor Subolesin. <i>Pathogens</i> , 2021, 10, 457. | 2.8 | 5 |
| 96 | Serological Cross-Reactions between Expressed VP2 Proteins from Different Bluetongue Virus Serotypes. <i>Viruses</i> , 2021, 13, 1455. | 3.3 | 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. | 2.1 | 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. | 3.3 | 1 |
| 101 | Seadornavirus. , 2011, , 1645-1652. | | 0 |
| 102 | Coltivirus. , 2011, , 1573-1577. | | 0 |