

Alice Fusaro

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6325983/publications.pdf>

Version: 2024-02-01

96
papers

3,020
citations

172207

29
h-index

182168

51
g-index

96
all docs

96
docs citations

96
times ranked

2832
citing authors

#	ARTICLE	IF	CITATIONS
1	S1 gene-based phylogeny of infectious bronchitis virus: An attempt to harmonize virus classification. <i>Infection, Genetics and Evolution</i> , 2016, 39, 349-364.	1.0	296
2	Updated unified phylogenetic classification system and revised nomenclature for Newcastle disease virus. <i>Infection, Genetics and Evolution</i> , 2019, 74, 103917.	1.0	227
3	Phylogeography and Evolutionary History of Reassortant H9N2 Viruses with Potential Human Health Implications. <i>Journal of Virology</i> , 2011, 85, 8413-8421.	1.5	139
4	Evidence for differing evolutionary dynamics of A/H5N1 viruses among countries applying or not applying avian influenza vaccination in poultry. <i>Vaccine</i> , 2011, 29, 9368-9375.	1.7	135
5	Emergence of a Highly Pathogenic Avian Influenza Virus from a Low-Pathogenic Progenitor. <i>Journal of Virology</i> , 2014, 88, 4375-4388.	1.5	124
6	Molecular epidemiology and evolutionary dynamics of betanodavirus in southern Europe. <i>Infection, Genetics and Evolution</i> , 2012, 12, 63-70.	1.0	122
7	Evidence of Infection by H5N2 Highly Pathogenic Avian Influenza Viruses in Healthy Wild Waterfowl. <i>PLoS Pathogens</i> , 2008, 4, e1000127.	2.1	110
8	Highly Pathogenic Avian Influenza Virus Subtype H5N1 in Africa: A Comprehensive Phylogenetic Analysis and Molecular Characterization of Isolates. <i>PLoS ONE</i> , 2009, 4, e4842.	1.1	101
9	Emergence of a new genetic lineage of Newcastle disease virus in West and Central Africaâ€”Implications for diagnosis and control. <i>Veterinary Microbiology</i> , 2010, 142, 168-176.	0.8	91
10	H9N2 influenza A virus circulates in H5N1 endemically infected poultry population in Egypt. <i>Influenza and Other Respiratory Viruses</i> , 2013, 7, 240-243.	1.5	72
11	Genetic Diversity of Highly Pathogenic Avian Influenza A(H5N8/H5N5) Viruses in Italy, 2016â€“17. <i>Emerging Infectious Diseases</i> , 2017, 23, 1543-1547.	2.0	62
12	Disentangling the role of Africa in the global spread of H5 highly pathogenic avian influenza. <i>Nature Communications</i> , 2019, 10, 5310.	5.8	61
13	Comparison of 2016â€“17 and Previous Epizootics of Highly Pathogenic Avian Influenza H5 Guangdong Lineage in Europe. <i>Emerging Infectious Diseases</i> , 2018, 24, 2270-2283.	2.0	60
14	Highly Pathogenic Avian Influenza A(H5N1) Virus in Poultry, Nigeria, 2015. <i>Emerging Infectious Diseases</i> , 2015, 21, 1275-1277.	2.0	50
15	Poultry vaccination directed evolution of H9N2 low pathogenicity avian influenza viruses in Korea. <i>Virology</i> , 2016, 488, 225-231.	1.1	45
16	Avian influenza overview December 2021 â€“ March 2022. <i>EFSA Journal</i> , 2022, 20, e07289.	0.9	45
17	Reassortant Avian Influenza Virus (H5N1) in Poultry, Nigeria, 2007. <i>Emerging Infectious Diseases</i> , 2008, 14, 637-640.	2.0	44
18	A distinct CDV genotype causing a major epidemic in Alpine wildlife. <i>Veterinary Microbiology</i> , 2011, 150, 63-69.	0.8	44

#	ARTICLE	IF	CITATIONS
19	Influenza A(H9N2) Virus, Burkina Faso. <i>Emerging Infectious Diseases</i> , 2017, 23, 2118-2119.	2.0	44
20	Avian influenza H9N2 subtype in Ghana: virus characterization and evidence of co-infection. <i>Avian Pathology</i> , 2019, 48, 470-476.	0.8	44
21	Viral encephalopathy and retinopathy outbreak in freshwater fish farmed in Italy. <i>Diseases of Aquatic Organisms</i> , 2011, 96, 45-54.	0.5	42
22	Introduction into Nigeria of a Distinct Genotype of Avian Influenza Virus (H5N1). <i>Emerging Infectious Diseases</i> , 2009, 15, 445-447.	2.0	41
23	Evolutionary Dynamics of Multiple Sublineages of H5N1 Influenza Viruses in Nigeria from 2006 to 2008. <i>Journal of Virology</i> , 2010, 84, 3239-3247.	1.5	35
24	Avian influenza overview December 2020 – February 2021. <i>EFSA Journal</i> , 2021, 19, e06497.	0.9	35
25	Avian influenza overview September – December 2021. <i>EFSA Journal</i> , 2021, 19, e07108.	0.9	34
26	Molecular Evolution and Phylogeography of Co-circulating IHN and VHSV in Italy. <i>Frontiers in Microbiology</i> , 2016, 7, 1306.	1.5	33
27	Next-Generation Sequencing in Veterinary Medicine: How Can the Massive Amount of Information Arising from High-Throughput Technologies Improve Diagnosis, Control, and Management of Infectious Diseases?. <i>Methods in Molecular Biology</i> , 2015, 1247, 415-436.	0.4	33
28	Co-circulation of two sublineages of HPAI H5N1 virus in the Kingdom of Saudi Arabia with unique molecular signatures suggesting separate introductions into the commercial poultry and falconry sectors. <i>Journal of General Virology</i> , 2008, 89, 2691-2697.	1.3	33
29	H5N1 Virus Evolution in Europe – An Updated Overview. <i>Viruses</i> , 2009, 1, 1351-1363.	1.5	30
30	Avian influenza overview August – December 2020. <i>EFSA Journal</i> , 2020, 18, e06379.	0.9	29
31	Concomitant Infection with <i>Leishmania donovani</i> and <i>L. major</i> in Single Ulcers of Cutaneous Leishmaniasis Patients from Sudan. <i>Journal of Tropical Medicine</i> , 2014, 2014, 1-8.	0.6	26
32	Molecular evolution of H9N2 avian influenza viruses in Israel. <i>Virus Genes</i> , 2014, 48, 457-463.	0.7	25
33	Detection of a New Genetic Cluster of Influenza D Virus in Italian Cattle. <i>Viruses</i> , 2019, 11, 1110.	1.5	25
34	First characterization of a Middle-East GI-23 lineage (Var2-like) of infectious bronchitis virus in Europe. <i>Virus Research</i> , 2017, 242, 43-48.	1.1	24
35	Intercontinental Spread of Eurasian Highly Pathogenic Avian Influenza A(H5N1) to Senegal. <i>Emerging Infectious Diseases</i> , 2022, 28, 234-237.	2.0	23
36	Avian influenza overview February – May 2021. <i>EFSA Journal</i> , 2021, 19, e06951.	0.9	22

#	ARTICLE	IF	CITATIONS
37	Antigenic characterization of recent H5N1 highly pathogenic avian influenza viruses circulating in Egyptian poultry. <i>Virology</i> , 2013, 435, 350-356.	1.1	21
38	Highly Pathogenic Avian Influenza A(H5N8) Virus, Cameroon, 2017. <i>Emerging Infectious Diseases</i> , 2018, 24, 1367-1370.	2.0	21
39	Isolation and identification of highly pathogenic avian influenza H5N1 virus from Houbara bustards (<i>Chlamydotis undulata macqueenii</i>) and contact falcons. <i>Avian Pathology</i> , 2009, 38, 35-39.	0.8	20
40	Charged Residues in Hepatitis C Virus NS4B Are Critical for Multiple NS4B Functions in RNA Replication. <i>Journal of Virology</i> , 2011, 85, 8158-8171.	1.5	20
41	Genetically Different Highly Pathogenic Avian Influenza A(H5N1) Viruses in West Africa, 2015. <i>Emerging Infectious Diseases</i> , 2016, 22, 2132-2136.	2.0	20
42	Characterization of Newcastle disease virus isolates obtained from outbreak cases in commercial chickens and wild pigeons in Ethiopia. <i>SpringerPlus</i> , 2016, 5, 476.	1.2	20
43	Sub-Saharan Africa and Eurasia Ancestry of Reassortant Highly Pathogenic Avian Influenza A(H5N8) Virus, Europe, December 2019. <i>Emerging Infectious Diseases</i> , 2020, 26, 1557-1561.	2.0	20
44	Integration of genetic and epidemiological data to infer H5N8 HPAI virus transmission dynamics during the 2016-2017 epidemic in Italy. <i>Scientific Reports</i> , 2018, 8, 18037.	1.6	19
45	Avian influenza overview November 2019–February 2020. <i>EFSA Journal</i> , 2020, 18, e06096.	0.9	19
46	Avian influenza overview May – September 2021. <i>EFSA Journal</i> , 2022, 20, e07122.	0.9	18
47	Highly pathogenic avian influenza H5N8 Clade 2.3.4.4B virus in Uganda, 2017. <i>Infection, Genetics and Evolution</i> , 2018, 66, 269-271.	1.0	17
48	The introduction of fox rabies into Italy (2008–2011) was due to two viral genetic groups with distinct phylogeographic patterns. <i>Infection, Genetics and Evolution</i> , 2013, 17, 202-209.	1.0	16
49	Lethal nephrotropism of an H10N1 avian influenza virus stands out as an atypical pathotype. <i>Veterinary Microbiology</i> , 2014, 173, 189-200.	0.8	16
50	Evolutionary trajectories of two distinct avian influenza epidemics: Parallelisms and divergences. <i>Infection, Genetics and Evolution</i> , 2015, 34, 457-466.	1.0	16
51	Avian influenza overview May – August 2020. <i>EFSA Journal</i> , 2020, 18, e06270.	0.9	16
52	Two waves of canine distemper virus showing different spatio-temporal dynamics in Alpine wildlife (2006–2018). <i>Infection, Genetics and Evolution</i> , 2020, 84, 104359.	1.0	15
53	Replication of Influenza D Viruses of Bovine and Swine Origin in Ovine Respiratory Explants and Their Attachment to the Respiratory Tract of Bovine, Sheep, Goat, Horse, and Swine. <i>Frontiers in Microbiology</i> , 2020, 11, 1136.	1.5	15
54	Phylogenetic Analysis of Rabies Viruses from Burkina Faso, 2007. <i>Zoonoses and Public Health</i> , 2010, 57, e42-6.	0.9	14

#	ARTICLE	IF	CITATIONS
55	Unexpected Interfarm Transmission Dynamics during a Highly Pathogenic Avian Influenza Epidemic. <i>Journal of Virology</i> , 2016, 90, 6401-6411.	1.5	14
56	Modelling the impact of co-circulating low pathogenic avian influenza viruses on epidemics of highly pathogenic avian influenza in poultry. <i>Epidemics</i> , 2016, 17, 27-34.	1.5	13
57	Avian influenza overview February – May 2020. <i>EFSA Journal</i> , 2020, 18, e06194.	0.9	13
58	Fatal multiple outbreaks of equine influenza H3N8 in Nigeria, 2019: The first introduction of Florida clade 1 to West Africa. <i>Veterinary Microbiology</i> , 2020, 248, 108820.	0.8	12
59	Avian influenza overview – update on 19 November 2020, EU/EEA and the UK. <i>EFSA Journal</i> , 2020, 18, e06341.	0.9	12
60	Full-Length Genome Sequencing of the Polish HPAI H5N1 Viruses Suggests Separate Introductions in 2006 and 2007. <i>Avian Diseases</i> , 2010, 54, 335-339.	0.4	11
61	Genetic data from avian influenza and avian paramyxoviruses generated by the European network of excellence (EPIZONE) between 2006 and 2011 – Review and recommendations for surveillance. <i>Veterinary Microbiology</i> , 2012, 154, 209-221.	0.8	11
62	Incorporating heterogeneous sampling probabilities in continuous phylogeographic inference – Application to H5N1 spread in the Mekong region. <i>Bioinformatics</i> , 2020, 36, 2098-2104.	1.8	11
63	Evolutionary Dynamics of H5 Highly Pathogenic Avian Influenza Viruses (Clade 2.3.4.4B) Circulating in Bulgaria in 2019–2021. <i>Viruses</i> , 2021, 13, 2086.	1.5	11
64	Modelling the species jump: towards assessing the risk of human infection from novel avian influenzas. <i>Royal Society Open Science</i> , 2015, 2, 150173.	1.1	10
65	Vaccine immune pressure influences viral population complexity of avian influenza virus during infection. <i>Veterinary Microbiology</i> , 2017, 203, 88-94.	0.8	10
66	Avian influenza overview February – August 2019. <i>EFSA Journal</i> , 2019, 17, e05843.	0.9	10
67	First detection of highly pathogenic H5N6 avian influenza virus on the African continent. <i>Emerging Microbes and Infections</i> , 2020, 9, 886-888.	3.0	10
68	Live Bird Markets in Nigeria: A Potential Reservoir for H9N2 Avian Influenza Viruses. <i>Viruses</i> , 2021, 13, 1445.	1.5	10
69	Gene segment reassortment between Eurasian and American clades of avian influenza virus in Italy. <i>Archives of Virology</i> , 2010, 155, 77-81.	0.9	9
70	Unexpected rabies variant identified in kinkajou (<i>Potos flavus</i>), Mato Grosso, Brazil. <i>Emerging Microbes and Infections</i> , 2020, 9, 851-854.	3.0	9
71	Characterization of novel, pathogenic field strains of infectious bronchitis virus (IBV) in poultry in Trinidad and Tobago. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 2775-2788.	1.3	9
72	Circulation of multiple genotypes of H1N2 viruses in a swine farm in Italy over a two-month period. <i>Veterinary Microbiology</i> , 2016, 195, 25-29.	0.8	8

#	ARTICLE	IF	CITATIONS
73	Complete Genome Sequence of Psittacine Adenovirus 1, Identified from <i>Poicephalus senegalus</i> in Italy. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	8
74	Identification of a zoonotic genotype 3 hepatitis E subtype in wildlife in north-eastern Italy. <i>Infection, Genetics and Evolution</i> , 2019, 71, 16-20.	1.0	8
75	Genetic Variability among Swine Influenza Viruses in Italy: Data Analysis of the Period 2017â€“2020. <i>Viruses</i> , 2022, 14, 47.	1.5	8
76	Different environmental gradients associated to the spatiotemporal and genetic pattern of the H5N8 highly pathogenic avian influenza outbreaks in poultry in Italy. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 152-167.	1.3	7
77	Spatiotemporal reconstruction and transmission dynamics during the 2016â€“17 H5N8 highly pathogenic avian influenza epidemic in Italy. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 37-50.	1.3	7
78	Genetic characterization of highly pathogenic avian Influenza H5Nx clade 2.3.4.4b reveals independent introductions in nigeria. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 423-433.	1.3	7
79	Clade-level Spatial Modelling of HPAI H5N1 Dynamics in the Mekong Region Reveals New Patterns and Associations with Agro-Ecological Factors. <i>Scientific Reports</i> , 2016, 6, 30316.	1.6	6
80	A two-year monitoring period of the genetic properties of clade 2.3.2.1c H5N1 viruses in Nigeria reveals the emergence and co-circulation of distinct genotypes. <i>Infection, Genetics and Evolution</i> , 2018, 57, 98-105.	1.0	6
81	Highly pathogenic avian influenza A/H5N1 Clade 2.3.2.1c virus in poultry in Cameroon, 2016â€“2017. <i>Avian Pathology</i> , 2018, 47, 559-575.	0.8	6
82	Spatial spread and emergence of reassortant H5 highly pathogenic avian influenza viruses in Iran. <i>Infection, Genetics and Evolution</i> , 2020, 83, 104342.	1.0	5
83	Spatiotemporal Dynamics, Evolutionary History and Zoonotic Potential of Moroccan H9N2 Avian Influenza Viruses from 2016 to 2021. <i>Viruses</i> , 2022, 14, 509.	1.5	5
84	Highly Pathogenic Avian Influenza H5N1 Clade 2.3.2.1c Virus in Lebanon, 2016. <i>Avian Diseases</i> , 2017, 61, 271.	0.4	4
85	Avian influenza overview August â€“ November 2019. <i>EFSA Journal</i> , 2019, 17, e05988.	0.9	4
86	Pathogenicity and Full Genome Sequencing of the Avian Influenza H9N2 Moroccan Isolate 2016. <i>Avian Diseases</i> , 2018, 63, 24.	0.4	4
87	Molecular Detection of Avian Influenza Virus in Wild Birds in Morocco, 2016â€“2019. <i>Avian Diseases</i> , 2021, 66, .	0.4	4
88	Spillover transmission of European H1N1 avian-like swine influenza viruses to turkeys: A strain-dependent possibility?. <i>Veterinary Microbiology</i> , 2016, 186, 102-110.	0.8	3
89	Viral population diversity in vaccinated poultry host infected with H5N1 highly pathogenic avian influenza virus. <i>International Journal of Infectious Diseases</i> , 2016, 53, 104.	1.5	2
90	Impact of host immunity in the mammalian adaptation of an H3N6 avian influenza virus. <i>International Journal of Infectious Diseases</i> , 2016, 53, 104.	1.5	2

#	ARTICLE	IF	CITATIONS
91	Global origins of African highly pathogenic avian influenza H5Nx viruses and intracontinental spread. International Journal of Infectious Diseases, 2019, 79, 9-10.	1.5	2
92	Co-circulation of multiple reassortant influenza viruses in a swine farm. International Journal of Infectious Diseases, 2016, 53, 103-104.	1.5	0
93	Genetic characterization of HPAI H5N8 viruses identified in wild and domestic birds in Uganda, 2017. International Journal of Infectious Diseases, 2019, 79, 97.	1.5	0
94	A27â€fWhole genome characterization of influenza D viruses detected in cattle herds in northern Italy between 2015 and 2017. Virus Evolution, 2019, 5, .	2.2	0
95	A28â€fSpatial spread of highly pathogenic avian influenza A (H5N8) virus in Italy, 2017â€8. Virus Evolution, 2019, 5, .	2.2	0
96	Complete Genome Sequences of Three Rabbit Endogenous Lentivirus Type K Viruses Obtained from Commercial Meat Rabbits in Italy. Microbiology Resource Announcements, 2019, 8, .	0.3	0