

# Alice Fusaro

## List of Publications by Year in descending order

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96  
papers

3,020  
citations

172207

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182168

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96  
docs citations

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times ranked

2832  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Avian influenza overview May â€“ September 2021. <i>EFSA Journal</i> , 2022, 20, e07122.	0.9	18
3	Intercontinental Spread of Eurasian Highly Pathogenic Avian Influenza A(H5N1) to Senegal. <i>Emerging Infectious Diseases</i> , 2022, 28, 234-237.	2.0	23
4	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
5	Avian influenza overview December 2021 â€“ March 2022. <i>EFSA Journal</i> , 2022, 20, e07289.	0.9	45
6	Genetic Variability among Swine Influenza Viruses in Italy: Data Analysis of the Period 2017â€“2020. <i>Viruses</i> , 2022, 14, 47.	1.5	8
7	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
8	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
9	Avian influenza overview December 2020 â€“ February 2021. <i>EFSA Journal</i> , 2021, 19, e06497.	0.9	35
10	Live Bird Markets in Nigeria: A Potential Reservoir for H9N2 Avian Influenza Viruses. <i>Viruses</i> , 2021, 13, 1445.	1.5	10
11	Evolutionary Dynamics of H5 Highly Pathogenic Avian Influenza Viruses (Clade 2.3.4.4B) Circulating in Bulgaria in 2019â€“2021. <i>Viruses</i> , 2021, 13, 2086.	1.5	11
12	Avian influenza overview September â€“ December 2021. <i>EFSA Journal</i> , 2021, 19, e07108.	0.9	34
13	Molecular Detection of Avian Influenza Virus in Wild Birds in Morocco, 2016â€“2019. <i>Avian Diseases</i> , 2021, 66, .	0.4	4
14	Avian influenza overview February â€“ May 2021. <i>EFSA Journal</i> , 2021, 19, e06951.	0.9	22
15	Incorporating heterogeneous sampling probabilities in continuous phylogeographic inference â€” Application to H5N1 spread in the Mekong region. <i>Bioinformatics</i> , 2020, 36, 2098-2104.	1.8	11
16	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
17	Avian influenza overview November 2019â€“ February2020. <i>EFSA Journal</i> , 2020, 18, e06096.	0.9	19
18	Avian influenza overview â€“ update on 19 November 2020, EU/EEA and the UK. <i>EFSA Journal</i> , 2020, 18, e06341.	0.9	12

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19	Avian influenza overview May – August 2020. EFSA Journal, 2020, 18, e06270.	0.9	16
20	Unexpected rabies variant identified in kinkajou ( <i>Potos flavus</i> ), Mato Grosso, Brazil. Emerging Microbes and Infections, 2020, 9, 851-854.	3.0	9
21	Two waves of canine distemper virus showing different spatio-temporal dynamics in Alpine wildlife (2006–2018). Infection, Genetics and Evolution, 2020, 84, 104359.	1.0	15
22	Characterization of novel, pathogenic field strains of infectious bronchitis virus (IBV) in poultry in Trinidad and Tobago. Transboundary and Emerging Diseases, 2020, 67, 2775-2788.	1.3	9
23	Sub-Saharan Africa and Eurasia Ancestry of Reassortant Highly Pathogenic Avian Influenza A(H5N8) Virus, Europe, December 2019. Emerging Infectious Diseases, 2020, 26, 1557-1561.	2.0	20
24	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. Frontiers in Microbiology, 2020, 11, 1136.	1.5	15
25	Avian influenza overview February – May 2020. EFSA Journal, 2020, 18, e06194.	0.9	13
26	First detection of highly pathogenic H5N6 avian influenza virus on the African continent. Emerging Microbes and Infections, 2020, 9, 886-888.	3.0	10
27	Spatial spread and emergence of reassortant H5 highly pathogenic avian influenza viruses in Iran. Infection, Genetics and Evolution, 2020, 83, 104342.	1.0	5
28	Avian influenza overview August – December 2020. EFSA Journal, 2020, 18, e06379.	0.9	29
29	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
30	A27 – Whole genome characterization of influenza D viruses detected in cattle herds in northern Italy between 2015 and 2017. Virus Evolution, 2019, 5, .	2.2	0
31	A28 – Spatial spread of highly pathogenic avian influenza A (H5N8) virus in Italy, 2017–8. Virus Evolution, 2019, 5, .	2.2	0
32	Avian influenza overview February – August 2019. EFSA Journal, 2019, 17, e05843.	0.9	10
33	Avian influenza H9N2 subtype in Ghana: virus characterization and evidence of co-infection. Avian Pathology, 2019, 48, 470-476.	0.8	44
34	Updated unified phylogenetic classification system and revised nomenclature for Newcastle disease virus. Infection, Genetics and Evolution, 2019, 74, 103917.	1.0	227
35	Identification of a zoonotic genotype 3 hepatitis E subtype in wildlife in north-eastern Italy. Infection, Genetics and Evolution, 2019, 71, 16-20.	1.0	8
36	Avian influenza overview August – November 2019. EFSA Journal, 2019, 17, e05988.	0.9	4

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37	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
38	Detection of a New Genetic Cluster of Influenza D Virus in Italian Cattle. <i>Viruses</i> , 2019, 11, 1110.	1.5	25
39	Global origins of African highly pathogenic avian influenza H5Nx viruses and intracontinental spread. <i>International Journal of Infectious Diseases</i> , 2019, 79, 9-10.	1.5	2
40	Complete Genome Sequences of Three Rabbit Endogenous Lentivirus Type K Viruses Obtained from Commercial Meat Rabbits in Italy. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
41	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
42	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
43	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
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	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
46	Highly Pathogenic Avian Influenza A(H5N8) Virus, Cameroon, 2017. <i>Emerging Infectious Diseases</i> , 2018, 24, 1367-1370.	2.0	21
47	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
48	Pathogenicity and Full Genome Sequencing of the Avian Influenza H9N2 Moroccan Isolate 2016. <i>Avian Diseases</i> , 2018, 63, 24.	0.4	4
49	Vaccine immune pressure influences viral population complexity of avian influenza virus during infection. <i>Veterinary Microbiology</i> , 2017, 203, 88-94.	0.8	10
50	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
51	Highly Pathogenic Avian Influenza H5N1 Clade 2.3.2.1c Virus in Lebanon, 2016. <i>Avian Diseases</i> , 2017, 61, 271.	0.4	4
52	Influenza A(H9N2) Virus, Burkina Faso. <i>Emerging Infectious Diseases</i> , 2017, 23, 2118-2119.	2.0	44
53	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
54	Molecular Evolution and Phylogeography of Co-circulating IHNV and VHSV in Italy. <i>Frontiers in Microbiology</i> , 2016, 7, 1306.	1.5	33

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55	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
56	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
57	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
58	Co-circulation of multiple reassortant influenza viruses in a swine farm. <i>International Journal of Infectious Diseases</i> , 2016, 53, 103-104.	1.5	0
59	Unexpected Interfarm Transmission Dynamics during a Highly Pathogenic Avian Influenza Epidemic. <i>Journal of Virology</i> , 2016, 90, 6401-6411.	1.5	14
60	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
61	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
62	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
63	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
64	Poultry vaccination directed evolution of H9N2 low pathogenicity avian influenza viruses in Korea. <i>Virology</i> , 2016, 488, 225-231.	1.1	45
65	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
66	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
67	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
68	Highly Pathogenic Avian Influenza A(H5N1) Virus in Poultry, Nigeria, 2015. <i>Emerging Infectious Diseases</i> , 2015, 21, 1275-1277.	2.0	50
69	Evolutionary trajectories of two distinct avian influenza epidemics: Parallelisms and divergences. <i>Infection, Genetics and Evolution</i> , 2015, 34, 457-466.	1.0	16
70	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
71	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
72	Molecular evolution of H9N2 avian influenza viruses in Israel. <i>Virus Genes</i> , 2014, 48, 457-463.	0.7	25

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73	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
74	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
75	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
76	Antigenic characterization of recent H5N1 highly pathogenic avian influenza viruses circulating in Egyptian poultry. <i>Virology</i> , 2013, 435, 350-356.	1.1	21
77	The introduction of fox rabies into Italy (2008â€“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
78	Molecular epidemiology and evolutionary dynamics of betanodavirus in southern Europe. <i>Infection, Genetics and Evolution</i> , 2012, 12, 63-70.	1.0	122
79	Genetic data from avian influenza and avian paramyxoviruses generated by the European network of excellence (EPIZONE) between 2006 and 2011â€”Review and recommendations for surveillance. <i>Veterinary Microbiology</i> , 2012, 154, 209-221.	0.8	11
80	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
81	A distinct CDV genotype causing a major epidemic in Alpine wildlife. <i>Veterinary Microbiology</i> , 2011, 150, 63-69.	0.8	44
82	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
83	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
84	Viral encephalopathy and retinopathy outbreak in freshwater fish farmed in Italy. <i>Diseases of Aquatic Organisms</i> , 2011, 96, 45-54.	0.5	42
85	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
86	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
87	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
88	Phylogenetic Analysis of Rabies Viruses from Burkina Faso, 2007. <i>Zoonoses and Public Health</i> , 2010, 57, e42-6.	0.9	14
89	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
90	Introduction into Nigeria of a Distinct Genotype of Avian Influenza Virus (H5N1). <i>Emerging Infectious Diseases</i> , 2009, 15, 445-447.	2.0	41

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91	Highly Pathogenic Avian Influenza Virus Subtype H5N1 in Africa: A Comprehensive Phylogenetic Analysis and Molecular Characterization of Isolates. PLoS ONE, 2009, 4, e4842.	1.1	101
92	H5N1 Virus Evolution in Europe – An Updated Overview. Viruses, 2009, 1, 1351-1363.	1.5	30
93	Isolation and identification of highly pathogenic avian influenza H5N1 virus from Houbara bustards ( <i>Chlamydotis undulata macqueenii</i> ) and contact falcons. Avian Pathology, 2009, 38, 35-39.	0.8	20
94	Evidence of Infection by H5N2 Highly Pathogenic Avian Influenza Viruses in Healthy Wild Waterfowl. PLoS Pathogens, 2008, 4, e1000127.	2.1	110
95	Reassortant Avian Influenza Virus (H5N1) in Poultry, Nigeria, 2007. Emerging Infectious Diseases, 2008, 14, 637-640.	2.0	44
96	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. Journal of General Virology, 2008, 89, 2691-2697.	1.3	33