Gregory D Ebel

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	American alligators are capable of West Nile virus amplification, mosquito infection and transmission. Virology, 2022, 568, 49-55.	1.1	6
2	Balanced T and B cell responses are required for immune protection against Powassan virus in virus-like particle vaccination. Cell Reports, 2022, 38, 110388.	2.9	9
3	Electrochemical Immunoassay for the Detection of SARS-CoV-2 Nucleocapsid Protein in Nasopharyngeal Samples. Analytical Chemistry, 2022, 94, 4712-4719.	3.2	31
4	Correction for Riemersma et al., "Rapid Evolution of Enhanced Zika Virus Virulence during Direct Vertebrate Transmission Chains― Journal of Virology, 2022, , e0050122.	1.5	0
5	Impact of Prior Infection on SARS-CoV-2 Antibody Responses in Vaccinated Long-Term Care Facility Staff. MSphere, 2022, 7, .	1.3	3
6	Mutation, Selection, and Bottlenecks in Polio Vaccine Reversion. Cell Host and Microbe, 2021, 29, 3-5.	5.1	4
7	Genome Number and Size Polymorphism in Zika Virus Infectious Units. Journal of Virology, 2021, 95, .	1.5	14
8	Rapid Evolution of Enhanced Zika Virus Virulence during Direct Vertebrate Transmission Chains. Journal of Virology, 2021, 95, .	1.5	10
9	Towards a method for cryopreservation of mosquito vectors of human pathogens. Cryobiology, 2021, 99, 1-10.	0.3	5
10	SARS-CoV-2 infection, neuropathogenesis and transmission among deer mice: Implications for spillback to New World rodents. PLoS Pathogens, 2021, 17, e1009585.	2.1	96
11	Infection, dissemination, and transmission efficiencies of Zika virus in Aedes aegypti after serial passage in mosquito or mammalian cell lines or alternating passage in both cell types. Parasites and Vectors, 2021, 14, 261.	1.0	7
12	A longitudinal SARS-CoV-2 biorepository for COVID-19 survivors with and without post-acute sequelae. BMC Infectious Diseases, 2021, 21, 677.	1.3	41
13	Durable Antibody Responses in Staff at Two Long-Term Care Facilities, during and Post SARS-CoV-2 Outbreaks. Microbiology Spectrum, 2021, 9, e0022421.	1.2	8
14	Early Adoption of Longitudinal Surveillance for SARS-CoV-2 among Staff in Long-Term Care Facilities: Prevalence, Virologic and Sequence Analysis. Microbiology Spectrum, 2021, 9, e0100321.	1.2	18
15	Impact of extrinsic incubation temperature on natural selection during Zika virus infection of Aedes aegypti and Aedes albopictus. PLoS Pathogens, 2021, 17, e1009433.	2.1	11
16	A Hyperactive Kunjin Virus NS3 Helicase Mutant Demonstrates Increased Dissemination and Mortality in Mosquitoes. Journal of Virology, 2020, 94, .	1.5	2
17	Zika Virus Replication in Myeloid Cells during Acute Infection Is Vital to Viral Dissemination and Pathogenesis in a Mouse Model. Journal of Virology, 2020, 94, .	1.5	14
18	Comparative Pathology of West Nile Virus in Humans and Non-Human Animals. Pathogens, 2020, 9, 48.	1.2	38

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19	Comparison of Chikungunya Virus and Zika Virus Replication and Transmission Dynamics in Aedes aegypti Mosquitoes. American Journal of Tropical Medicine and Hygiene, 2020, 103, 869-875.	0.6	15
20	Effects of Arbovirus Multi-Host Life Cycles on Dinucleotide and Codon Usage Patterns. Viruses, 2019, 11, 643.	1.5	25
21	Endless Forms: Within-Host Variation in the Structure of the West Nile Virus RNA Genome during Serial Passage in Bird Hosts. MSphere, 2019, 4, .	1.3	5
22	Bat influenza viruses transmit among bats but are poorly adapted to non-bat species. Nature Microbiology, 2019, 4, 2298-2309.	5.9	42
23	On the Fly: Interactions Between Birds, Mosquitoes, and Environment That Have Molded West Nile Virus Genomic Structure Over Two Decades. Journal of Medical Entomology, 2019, 56, 1467-1474.	0.9	17
24	Arbovirus coinfection and co-transmission: A neglected public health concern?. PLoS Biology, 2019, 17, e3000130.	2.6	106
25	Zika viruses of African and Asian lineages cause fetal harm in a mouse model of vertical transmission. PLoS Neglected Tropical Diseases, 2019, 13, e0007343.	1.3	70
26	Evaluation of a novel West Nile virus transmission control strategy that targets Culex tarsalis with endectocide-containing blood meals. PLoS Neglected Tropical Diseases, 2019, 13, e0007210.	1.3	12
27	Small RNA responses of Culex mosquitoes and cell lines during acute and persistent virus infection. Insect Biochemistry and Molecular Biology, 2019, 109, 13-23.	1.2	47
28	Mutations present in a low-passage Zika virus isolate result in attenuated pathogenesis in mice. Virology, 2019, 530, 19-26.	1.1	45
29	A reverse-transcription/RNase H based protocol for depletion of mosquito ribosomal RNA facilitates viral intrahost evolution analysis, transcriptomics and pathogen discovery. Virology, 2019, 528, 181-197.	1.1	21
30	Dengue type 1 viruses circulating in humans are highly infectious and poorly neutralized by human antibodies. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 227-232.	3.3	69
31	Capturing sequence diversity in metagenomes with comprehensive and scalable probe design. Nature Biotechnology, 2019, 37, 160-168.	9.4	96
32	Discrete viral E2 lysine residues and scavenger receptor MARCO are required for clearance of circulating alphaviruses. ELife, 2019, 8, .	2.8	25
33	How Do Virus–Mosquito Interactions Lead to Viral Emergence?. Trends in Parasitology, 2018, 34, 310-321.	1.5	80
34	Mosquito-borne and sexual transmission of Zika virus: Recent developments and future directions. Virus Research, 2018, 254, 1-9.	1.1	33
35	An mRNA Vaccine Protects Mice against Multiple Tick-Transmitted Flavivirus Infections. Cell Reports, 2018, 25, 3382-3392.e3.	2.9	79
36	Sequential Infection of Aedes aegypti Mosquitoes with Chikungunya Virus and Zika Virus Enhances Early Zika Virus Transmission. Insects, 2018, 9, 177.	1.0	34

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37	Adventitious viruses persistently infect three commonly used mosquito cell lines. Virology, 2018, 521, 175-180.	1.1	29
38	Co-Infection Patterns in Individual Ixodes scapularis Ticks Reveal Associations between Viral, Eukaryotic and Bacterial Microorganisms. Viruses, 2018, 10, 388.	1.5	44
39	Variation in competence for ZIKV transmission by Aedes aegypti and Aedes albopictus in Mexico. PLoS Neglected Tropical Diseases, 2018, 12, e0006599.	1.3	36
40	An Immunocompetent Mouse Model of Zika Virus Infection. Cell Host and Microbe, 2018, 23, 672-685.e6.	5.1	192
41	Did Zika Virus Mutate to Cause Severe Outbreaks?. Trends in Microbiology, 2018, 26, 877-885.	3.5	43
42	Using barcoded Zika virus to assess virus population structure in vitro and in Aedes aegypti mosquitoes. Virology, 2018, 521, 138-148.	1.1	43
43	Xenosurveillance reflects traditional sampling techniques for the identification of human pathogens: A comparative study in West Africa. PLoS Neglected Tropical Diseases, 2018, 12, e0006348.	1.3	20
44	Molecularly barcoded Zika virus libraries to probe in vivo evolutionary dynamics. PLoS Pathogens, 2018, 14, e1006964.	2.1	38
45	Rapid and specific detection of Asian- and African-lineage Zika viruses. Science Translational Medicine, 2017, 9, .	5.8	86
46	Mosquitoes Transmit Unique West Nile Virus Populations during Each Feeding Episode. Cell Reports, 2017, 19, 709-718.	2.9	67
47	Impact of simultaneous exposure to arboviruses on infection and transmission by Aedes aegypti mosquitoes. Nature Communications, 2017, 8, 15412.	5.8	164
48	Rescue and Characterization of Recombinant Virus from a New World Zika Virus Infectious Clone. Journal of Visualized Experiments, 2017, , .	0.2	8
49	Development and Characterization of Recombinant Virus Generated from a New World Zika Virus Infectious Clone. Journal of Virology, 2017, 91, .	1.5	91
50	Lack of evidence for Zika virus transmission by Culex mosquitoes. Emerging Microbes and Infections, 2017, 6, 1-2.	3.0	24
51	Promiscuous viruses—how do viruses survive multiple unrelated hosts?. Current Opinion in Virology, 2017, 23, 125-129.	2.6	5
52	American Aedes vexans Mosquitoes are Competent Vectors of Zika Virus. American Journal of Tropical Medicine and Hygiene, 2017, 96, 1338-1340.	0.6	44
53	The Use of Xenosurveillance to Detect Human Bacteria, Parasites, and Viruses in Mosquito Bloodmeals. American Journal of Tropical Medicine and Hygiene, 2017, 97, 324-329.	0.6	26
54	Vector Competence of American Mosquitoes for Three Strains of Zika Virus. PLoS Neglected Tropical Diseases, 2016, 10, e0005101.	1.3	172

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55	Transmission bottlenecks and RNAi collectively influence tick-borne flavivirus evolution. Virus Evolution, 2016, 2, vew033.	2.2	35
56	Genetic Drift during Systemic Arbovirus Infection of Mosquito Vectors Leads to Decreased Relative Fitness during Host Switching. Cell Host and Microbe, 2016, 19, 481-492.	5.1	125
57	Zika Virus Infection in Mice Causes Panuveitis with Shedding of Virus in Tears. Cell Reports, 2016, 16, 3208-3218.	2.9	243
58	West African Anopheles gambiae mosquitoes harbor a taxonomically diverse virome including new insect-specific flaviviruses, mononegaviruses, and totiviruses. Virology, 2016, 498, 288-299.	1.1	112
59	Dynamics of West Nile virus evolution in mosquito vectors. Current Opinion in Virology, 2016, 21, 132-138.	2.6	39
60	West Nile Virus Population Structure, Injury, and Interferon-Stimulated Gene Expression in the Brain From a Fatal Case of Encephalitis. Open Forum Infectious Diseases, 2016, 3, ofv182.	0.4	11
61	Isolation of a Novel Insect-Specific Flavivirus from <i>Culiseta melanura</i> in the Northeastern United States. Vector-Borne and Zoonotic Diseases, 2016, 16, 181-190.	0.6	15
62	Temporal and Spatial Variability of Entomological Risk Indices for West Nile Virus Infection in Northern Colorado: 2006–2013. Journal of Medical Entomology, 2016, 53, 425-434.	0.9	16
63	Potential for Co-Infection of a Mosquito-Specific Flavivirus, Nhumirim Virus, to Block West Nile Virus Transmission in Mosquitoes. Viruses, 2015, 7, 5801-5812.	1.5	112
64	Modulation of Flavivirus Population Diversity by RNA Interference. Journal of Virology, 2015, 89, 4035-4039.	1.5	36
65	Experimental Evolution of an RNA Virus in Wild Birds: Evidence for Host-Dependent Impacts on Population Structure and Competitive Fitness. PLoS Pathogens, 2015, 11, e1004874.	2.1	51
66	Xenosurveillance: A Novel Mosquito-Based Approach for Examining the Human-Pathogen Landscape. PLoS Neglected Tropical Diseases, 2015, 9, e0003628.	1.3	67
67	Genotype-specific variation in West Nile virus dispersal in California. Virology, 2015, 485, 79-85.	1.1	37
68	Flavivirus sfRNA suppresses antiviral RNA interference in cultured cells and mosquitoes and directly interacts with the RNAi machinery. Virology, 2015, 485, 322-329.	1.1	129
69	A positively selected mutation in the WNV 2K peptide confers resistance to superinfection exclusion in vivo. Virology, 2014, 464-465, 228-232.	1.1	15
70	Toward an Activist Agenda for Monitoring Virus Emergence. Cell Host and Microbe, 2014, 15, 655-656.	5.1	2
71	The Role of Innate Immunity in Conditioning Mosquito Susceptibility to West Nile Virus. Viruses, 2013, 5, 3142-3170.	1.5	21
72	Powassan Virus in Mammals, Alaska and New Mexico, USA, and Russia, 2004–2007. Emerging Infectious Diseases, 2013, 19, 2012-2016.	2.0	52

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73	Seroprevalence of Powassan Virus in New England Deer, 1979–2010. American Journal of Tropical Medicine and Hygiene, 2013, 88, 1159-1162.	0.6	39
74	Complete viral RNA genome sequencing of ultra-low copy samples by sequence-independent amplification. Nucleic Acids Research, 2013, 41, e13-e13.	6.5	75
75	Highly Sensitive and Specific Detection of Rare Variants in Mixed Viral Populations from Massively Parallel Sequence Data. PLoS Computational Biology, 2012, 8, e1002417.	1.5	107
76	Dispersal of <i>Culex</i> Mosquitoes (Diptera: Culicidae) From a Wastewater Treatment Facility. Journal of Medical Entomology, 2012, 49, 35-42.	0.9	55
77	West Nile virus population genetics and evolution. Infection, Genetics and Evolution, 2012, 12, 181-190.	1.0	61
78	Internally deleted WNV genomes isolated from exotic birds in New Mexico: Function in cells, mosquitoes, and mice. Virology, 2012, 427, 10-17.	1.1	35
79	Emergence of Culex pipiens from Overwintering Hibernacula. Journal of the American Mosquito Control Association, 2011, 27, 21-29.	0.2	22
80	West Nile Virus Genetic Diversity is Maintained during Transmission by Culex pipiens quinquefasciatus Mosquitoes. PLoS ONE, 2011, 6, e24466.	1.1	42
81	Molecular evolution of West Nile virus in a northern temperate region: Connecticut, USA 1999–2008. Virology, 2011, 417, 203-210.	1.1	34
82	Small RNA profiling of Dengue virus-mosquito interactions implicates the PIWI RNA pathway in anti-viral defense. BMC Microbiology, 2011, 11, 45.	1.3	155
83	Nonconsensus West Nile Virus Genomes Arising during Mosquito Infection Suppress Pathogenesis and Modulate Virus Fitness <i>In Vivo</i> . Journal of Virology, 2011, 85, 12605-12613.	1.5	21
84	Heparan sulfate binding by natural eastern equine encephalitis viruses promotes neurovirulence. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 16026-16031.	3.3	110
85	West Nile Virus Experimental Evolution in vivo and the Trade-off Hypothesis. PLoS Pathogens, 2011, 7, e1002335.	2.1	98
86	Homogeneity of Powassan virus populations in naturally infected Ixodes scapularis. Virology, 2010, 402, 366-371.	1.1	26
87	Population variation of West Nile virus confers a host-specific fitness benefit in mosquitoes. Virology, 2010, 404, 89-95.	1.1	42
88	C6/36 Aedes albopictus Cells Have a Dysfunctional Antiviral RNA Interference Response. PLoS Neglected Tropical Diseases, 2010, 4, e856.	1.3	276
89	Spatial and Temporal Variation in Vector Competence of Culex pipiens and Cx. restuans Mosquitoes for West Nile Virus. American Journal of Tropical Medicine and Hygiene, 2010, 83, 607-613.	0.6	88
90	Update on Powassan Virus: Emergence of a North American Tick-Borne Flavivirus. Annual Review of Entomology, 2010, 55, 95-110.	5.7	200

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91	Persistence of Pathogens with Short Infectious Periods in Seasonal Tick Populations: The Relative Importance of Three Transmission Routes. PLoS ONE, 2010, 5, e11745.	1.1	39
92	Prevalence of West Nile Virus in Migratory Birds during Spring and Fall Migration. American Journal of Tropical Medicine and Hygiene, 2009, 81, 1151-1158.	0.6	58
93	Fatal Case of Deer Tick Virus Encephalitis. New England Journal of Medicine, 2009, 360, 2099-2107.	13.9	104
94	RNAi Targeting of West Nile Virus in Mosquito Midguts Promotes Virus Diversification. PLoS Pathogens, 2009, 5, e1000502.	2.1	202
95	Genetic diversity and purifying selection in West Nile virus populations are maintained during host switching. Virology, 2008, 374, 256-260.	1.1	76
96	A Global Perspective on the Epidemiology of West Nile Virus. Annual Review of Entomology, 2008, 53, 61-81.	5.7	434
97	Increased Recognition of Powassan Encephalitis in the United States, 1999–2005. Vector-Borne and Zoonotic Diseases, 2008, 8, 733-740.	0.6	114
98	Molecular Epidemiology of Eastern Equine Encephalitis Virus, New York. Emerging Infectious Diseases, 2008, 14, 454-460.	2.0	51
99	Stable Prevalence of Powassan Virus in Ixodes scapularis in a Northern Wisconsin Focus. American Journal of Tropical Medicine and Hygiene, 2008, 79, 971-973.	0.6	57
100	Stable prevalence of Powassan virus in Ixodes scapularis in a northern Wisconsin focus. American Journal of Tropical Medicine and Hygiene, 2008, 79, 971-3.	0.6	30
101	Declining Growth Rate of West Nile Virus in North America. Journal of Virology, 2007, 81, 2531-2534.	1.5	73
102	A Newly Emergent Genotype of West Nile Virus Is Transmitted Earlier and More Efficiently by Culex Mosquitoes. American Journal of Tropical Medicine and Hygiene, 2007, 77, 365-370.	0.6	228
103	Crow Deaths Caused by West Nile Virus during Winter. Emerging Infectious Diseases, 2007, 13, 1912-1914.	2.0	50
104	The West Nile virus mutant spectrum is host-dependant and a determinant of mortality in mice. Virology, 2007, 360, 469-476.	1.1	104
105	A newly emergent genotype of West Nile virus is transmitted earlier and more efficiently by Culex mosquitoes. American Journal of Tropical Medicine and Hygiene, 2007, 77, 365-70.	0.6	149
106	Development of a humanized monoclonal antibody with therapeutic potential against West Nile virus. Nature Medicine, 2005, 11, 522-530.	15.2	477
107	Phylogenetic analysis of North American West Nile virus isolates, 2001–2004: Evidence for the emergence of a dominant genotype. Virology, 2005, 342, 252-265.	1.1	231
108	<i>Culex restuans</i> (Diptera: Culicidae) Relative Abundance and Vector Competence for West Nile Virus. Journal of Medical Entomology, 2005, 42, 838-843.	0.9	78

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109	Genetic variation in West Nile virus from naturally infected mosquitoes and birds suggests quasispecies structure and strong purifying selection. Journal of General Virology, 2005, 86, 2175-2183.	1.3	177
110	GENETIC AND PHENOTYPIC VARIATION OF WEST NILE VIRUS IN NEW YORK, 2000–2003. American Journal of Tropical Medicine and Hygiene, 2004, 71, 493-500.	0.6	219
111	Short report: duration of tick attachment required for transmission of powassan virus by deer ticks. American Journal of Tropical Medicine and Hygiene, 2004, 71, 268-71.	0.6	98
112	Genetic and phenotypic variation of West Nile virus in New York, 2000-2003. American Journal of Tropical Medicine and Hygiene, 2004, 71, 493-500.	0.6	141
113	Dynamics of Flavivirus Infection in Mosquitoes. Advances in Virus Research, 2003, 60, 187-232.	0.9	171
114	Detection by Enzyme-Linked Immunosorbent Assay of Antibodies to <i>West Nile virus</i> in Birds. Emerging Infectious Diseases, 2002, 8, 979-982.	2.0	114
115	West Nile Virus Infection in Birds and Mosquitoes, New York State, 2000. Emerging Infectious Diseases, 2001, 7, 679-685.	2.0	151
116	Partial Genetic Characterization of West Nile Virus Strains, New York State, 2000. Emerging Infectious Diseases, 2001, 7, 650-653.	2.0	93
117	Sentinel Chickens as a Surveillance Tool for West Nile Virus in New York City, 2000. Annals of the New York Academy of Sciences, 2001, 951, 343-346.	1.8	14
118	Phylogeny of North American Powassan virus. Journal of General Virology, 2001, 82, 1657-1665.	1.3	92
119	A Focus of Deer Tick Virus Transmission in the Northcentral United States. Emerging Infectious Diseases, 1999, 5, 570-574.	2.0	77
120	Longitudinal Surveillance for SARS-CoV-2 Among Staff in Six Colorado Long Term Care Facilities: Epidemiologic, Virologic and Sequence Analysis. SSRN Electronic Journal, 0, , .	0.4	4