

# Ellen E Paxinos

## List of Publications by Year in descending order

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39  
papers

4,852  
citations

185998

28  
h-index

301761

39  
g-index

39  
all docs

39  
docs citations

39  
times ranked

7498  
citing authors

#	ARTICLE	IF	CITATIONS
1	Origins of the <i>E. coli</i> Strain Causing an Outbreak of Hemolytic-Uremic Syndrome in Germany. <i>New England Journal of Medicine</i> , 2011, 365, 709-717.	13.9	778
2	The Origin of the Haitian Cholera Outbreak Strain. <i>New England Journal of Medicine</i> , 2011, 364, 33-42.	13.9	676
3	Assembly and diploid architecture of an individual human genome via single-molecule technologies. <i>Nature Methods</i> , 2015, 12, 780-786.	9.0	465
4	Development and Characterization of a Novel Single-Cycle Recombinant-Virus Assay To Determine Human Immunodeficiency Virus Type 1 Coreceptor Tropism. <i>Antimicrobial Agents and Chemotherapy</i> , 2007, 51, 566-575.	1.4	320
5	Neutralizing antibody responses drive the evolution of human immunodeficiency virus type 1 envelope during recent HIV infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 18514-18519.	3.3	313
6	Defective HIV-1 proviruses produce novel protein-coding RNA species in HIV-infected patients on combination antiretroviral therapy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8783-8788.	3.3	282
7	A hybrid approach for the automated finishing of bacterial genomes. <i>Nature Biotechnology</i> , 2012, 30, 701-707.	9.4	178
8	The Diversity, Structure, and Function of Heritable Adaptive Immunity Sequences in the <i>Aedes aegypti</i> Genome. <i>Current Biology</i> , 2017, 27, 3511-3519.e7.	1.8	167
9	Coreceptor Tropism in Human Immunodeficiency Virus Type 1 Subtype D: High Prevalence of CXCR4 Tropism and Heterogeneous Composition of Viral Populations. <i>Journal of Virology</i> , 2007, 81, 7885-7893.	1.5	149
10	Cerebrospinal fluid HIV infection and pleocytosis: Relation to systemic infection and antiretroviral treatment. <i>BMC Infectious Diseases</i> , 2005, 5, 98.	1.3	138
11	Evolutionary Dynamics of <i>Vibrio cholerae</i> O1 following a Single-Source Introduction to Haiti. <i>MBio</i> , 2013, 4, .	1.8	118
12	mtDNA from fossils reveals a radiation of Hawaiian geese recently derived from the Canada goose ( <i>Branta canadensis</i> ). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 1399-1404.	3.3	116
13	Mutation D30N Is Not Preferentially Selected by Human Immunodeficiency Virus Type 1 Subtype C in the Development of Resistance to Nelfinavir. <i>Antimicrobial Agents and Chemotherapy</i> , 2004, 48, 2159-2165.	1.4	110
14	Differences in disease progression in a cohort of long-term non-progressors after more than 16 years of HIV-1 infection. <i>Aids</i> , 2004, 18, 1109-1116.	1.0	93
15	Hypersusceptibility to non-nucleoside reverse transcriptase inhibitors in HIV-1. <i>Aids</i> , 2002, 16, F41-F47.	1.0	85
16	Relationships of the extinct moa-nalos, flightless Hawaiian waterfowl, based on ancient DNA. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1999, 266, 2187-2193.	1.2	81
17	Persistence of drug-resistant HIV-1 after a structured treatment interruption and its impact on treatment response. <i>Aids</i> , 2003, 17, 361-370.	1.0	80
18	Use of Four Next-Generation Sequencing Platforms to Determine HIV-1 Coreceptor Tropism. <i>PLoS ONE</i> , 2012, 7, e49602.	1.1	78

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19	Cerebrospinal fluid response to structured treatment interruption after virological failure. <i>Aids</i> , 2001, 15, 1251-1259.	1.0	59
20	Prehistoric Decline of Genetic Diversity in the Nene. <i>Science</i> , 2002, 296, 1827-1827.	6.0	57
21	Impact of frequent natural polymorphisms at the protease gene on the in vitro susceptibility to protease inhibitors in HIV-1 non-B subtypes. <i>Journal of Clinical Virology</i> , 2004, 31, 215-220.	1.6	56
22	High Prevalence of Antiretroviral Resistance in Treated Ugandans Infected with Non-subtype B Human Immunodeficiency Virus Type 1. <i>AIDS Research and Human Retroviruses</i> , 2004, 20, 355-364.	0.5	53
23	Combinations of Mutations in the Connection Domain of Human Immunodeficiency Virus Type 1 Reverse Transcriptase: Assessing the Impact on Nucleoside and Nonnucleoside Reverse Transcriptase Inhibitor Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 1973-1980.	1.4	46
24	Genotypic and Phenotypic Analyses of Human Immunodeficiency Virus Type 1 in Antiretroviral Drug-Naive Nigerian Patients. <i>AIDS Research and Human Retroviruses</i> , 2006, 22, 22-26.	0.5	41
25	Multiplexed highly-accurate DNA sequencing of closely-related HIV-1 variants using continuous long reads from single molecule, real-time sequencing. <i>Nucleic Acids Research</i> , 2015, 43, e129-e129.	6.5	41
26	Comparative Genomics Reveals the Diversity of Restriction-Modification Systems and DNA Methylation Sites in <i>Listeria monocytogenes</i> . <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	31
27	Discovery of a divergent HPIV4 from respiratory secretions using second and third generation metagenomic sequencing. <i>Scientific Reports</i> , 2013, 3, 2468.	1.6	30
28	Rapid Sequencing of Complete <i>env</i> Genes from Primary HIV-1 Samples. <i>Virus Evolution</i> , 2016, 2, vew018.	2.2	30
29	Characterization of a Subtype D Human Immunodeficiency Virus Type 1 Isolate That Was Obtained from an Untreated Individual and That Is Highly Resistant to Nonnucleoside Reverse Transcriptase Inhibitors. <i>Journal of Virology</i> , 2004, 78, 5390-5401.	1.5	29
30	Long-Term Survivors in Nairobi: Complete HIV-1 RNA Sequences and Immunogenetic Associations. <i>Journal of Infectious Diseases</i> , 2004, 190, 697-701.	1.9	28
31	Intraspecific Competition Influences Food Return-Predation Risk Trade-Off by White-Crowned Sparrows. <i>Condor</i> , 1997, 99, 642-650.	0.7	25
32	Phenotypic Drug Resistance Patterns in Subtype A HIV-1 Clones with Nonnucleoside Reverse Transcriptase Resistance Mutations. <i>AIDS Research and Human Retroviruses</i> , 2006, 22, 289-293.	0.5	20
33	Diagnosis and monitoring of HCV infection using the cobas <sup>®</sup> HCV test for use on the cobas <sup>®</sup> 6800/8800 systems. <i>Journal of Clinical Virology</i> , 2018, 102, 63-69.	1.6	18
34	Multicenter Comparison Study of both Analytical and Clinical Performance across Four Roche Hepatitis C Virus RNA Assays Utilizing Different Platforms. <i>Journal of Clinical Microbiology</i> , 2017, 55, 1131-1139.	1.8	15
35	Whole-Genome Sequences of <i>Burkholderia pseudomallei</i> Isolates Exhibiting Decreased Meropenem Susceptibility. <i>Genome Announcements</i> , 2017, 5, .	0.8	15
36	Commutability and concordance of four hepatitis B virus DNA assays in an international multicenter study. <i>Therapeutic Advances in Gastroenterology</i> , 2017, 10, 609-618.	1.4	10

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37	Analytical performance of four molecular platforms used for HIV-1, HBV and HCV viral load determinations. <i>Expert Review of Molecular Diagnostics</i> , 2019, 19, 941-949.	1.5	10
38	Multicenter evaluation of the cobas® HIV-1 quantitative nucleic acid test for use on the cobas® 4800 system for the quantification of HIV-1 plasma viral load. <i>Journal of Clinical Virology</i> , 2019, 114, 43-49.	1.6	9
39	Different Viral Rebound following Discontinuation of Antiretroviral Therapy in Cases of Infection with Viruses Carrying L74V or Thymidine-Associated Mutations. <i>Journal of Clinical Microbiology</i> , 2004, 42, 862-866.	1.8	2