Paul M Sharp

List of Publications by Year in descending order

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26613 13099 28,257 109 68 107 citations h-index g-index papers 110 110 110 17863 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	CD4 receptor diversity represents an ancient protection mechanism against primate lentiviruses. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	9
2	Heightened resistance to host type 1 interferons characterizes HIV-1 at transmission and after antiretroviral therapy interruption. Science Translational Medicine, 2021, 13 , .	12.4	54
3	CD4 receptor diversity in chimpanzees protects against SIV infection. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 3229-3238.	7.1	21
4	Investigating zoonotic infection barriers to ape Plasmodium parasites using faecal DNA analysis. International Journal for Parasitology, 2018, 48, 531-542.	3.1	9
5	Resistance to type 1 interferons is a major determinant of HIV-1 transmission fitness. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E590-E599.	7.1	137
6	Effective treatment of SIVcpz-induced immunodeficiency in a captive western chimpanzee. Retrovirology, 2017, 14, 35.	2.0	12
7	Multigenomic Delineation of <i>Plasmodium </i> Species of the <i>Laverania </i> Subgenus Infecting Wild-Living Chimpanzees and Gorillas. Genome Biology and Evolution, 2016, 8, 1929-1939.	2.5	38
8	Origin of the HIV-1 group O epidemic in western lowland gorillas. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1343-52.	7.1	136
9	Nef Proteins of Epidemic HIV-1 Group O Strains Antagonize Human Tetherin. Cell Host and Microbe, 2014, 16, 639-650.	11.0	77
10	African origin of the malaria parasite Plasmodium vivax. Nature Communications, 2014, 5, 3346.	12.8	167
11	Gene Loss and Adaptation to Hominids Underlie the Ancient Origin of HIV-1. Cell Host and Microbe, 2013, 14, 85-92.	11.0	93
12	<i>Plasmodium falciparum</i> -like parasites infecting wild apes in southern Cameroon do not represent a recurrent source of human malaria. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 7020-7025.	7.1	53
13	Great Apes and Zoonoses. Science, 2013, 340, 284-286.	12.6	27
14	The Malagarasi River Does Not Form an Absolute Barrier to Chimpanzee Movement in Western Tanzania. PLoS ONE, 2013, 8, e58965.	2.5	18
15	Eastern Chimpanzees, but Not Bonobos, Represent a Simian Immunodeficiency Virus Reservoir. Journal of Virology, 2012, 86, 10776-10791.	3.4	73
16	Efficient SIVcpz replication in human lymphoid tissue requires viral matrix protein adaptation. Journal of Clinical Investigation, 2012, 122, 1644-1652.	8.2	44
17	Evaluating the evidence for virus/host co-evolution. Current Opinion in Virology, 2011, 1, 436-441.	5.4	84
18	The evolution of infectious agents in relation to sex in animals and humans: brief discussions of some individual organisms. Annals of the New York Academy of Sciences, 2011, 1230, 74-107.	3.8	5

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19	Impact of translational selection on codon usage bias in the archaeon <i>Methanococcus maripaludis</i> . Biology Letters, 2011, 7, 131-135.	2.3	12
20	Origins of HIV and the AIDS Pandemic. Cold Spring Harbor Perspectives in Medicine, 2011, 1, a006841-a006841.	6.2	937
21	High Prevalence of Simian Immunodeficiency Virus Infection in a Community of Savanna Chimpanzees. Journal of Virology, 2011, 85, 9918-9928.	3.4	94
22	Intercompartmental Recombination of HIV-1 Contributes to <i>env</i> li>lntrahost Diversity and Modulates Viral Tropism and Sensitivity to Entry Inhibitors. Journal of Virology, 2011, 85, 6024-6037.	3.4	50
23	Origin of the human malaria parasite Plasmodium falciparum in gorillas. Nature, 2010, 467, 420-425.	27.8	445
24	Forces that influence the evolution of codon bias. Philosophical Transactions of the Royal Society B: Biological Sciences, 2010, 365, 1203-1212.	4.0	301
25	The evolution of HIV-1 and the origin of AIDS. Philosophical Transactions of the Royal Society B: Biological Sciences, 2010, 365, 2487-2494.	4.0	241
26	Origin and Biology of Simian Immunodeficiency Virus in Wild-Living Western Gorillas. Journal of Virology, 2009, 83, 1635-1648.	3.4	106
27	Increased mortality and AIDS-like immunopathology in wild chimpanzees infected with SIVcpz. Nature, 2009, 460, 515-519.	27.8	315
28	Tetherin-Driven Adaptation of Vpu and Nef Function and the Evolution of Pandemic and Nonpandemic HIV-1 Strains. Cell Host and Microbe, 2009, 6, 409-421.	11.0	391
29	Prehistory of HIV-1. Nature, 2008, 455, 605-606.	27.8	33
30	Deciphering Human Immunodeficiency Virus Type 1 Transmission and Early Envelope Diversification by Single-Genome Amplification and Sequencing. Journal of Virology, 2008, 82, 3952-3970.	3.4	540
31	Molecular Ecology and Natural History of Simian Foamy Virus Infection in Wild-Living Chimpanzees. PLoS Pathogens, 2008, 4, e1000097.	4.7	122
32	Predicting Gene Expression Level from Codon Usage Bias. Molecular Biology and Evolution, 2007, 24, 10-12.	8.9	62
33	Generation of Infectious Molecular Clones of Simian Immunodeficiency Virus from Fecal Consensus Sequences of Wild Chimpanzees. Journal of Virology, 2007, 81, 7463-7475.	3.4	62
34	Adaptation of HIV-1 to Its Human Host. Molecular Biology and Evolution, 2007, 24, 1853-1860.	8.9	100
35	Full-length sequence analysis of SIVmus in wild populations of mustached monkeys (Cercopithecus) Tj ETQq1 1 407-418.	0.784314 2.4	rgBT /Overlo 43
36	Genetic diversity and phylogeographic clustering of SIVcpzPtt in wild chimpanzees in Cameroon. Virology, 2007, 368, 155-171.	2.4	118

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37	Chimpanzee Reservoirs of Pandemic and Nonpandemic HIV-1. Science, 2006, 313, 523-526.	12.6	723
38	Nef-Mediated Suppression of T Cell Activation Was Lost in a Lentiviral Lineage that Gave Rise to HIV-1. Cell, 2006, 125, 1055-1067.	28.9	359
39	SIV infection in wild gorillas. Nature, 2006, 444, 164-164.	27.8	315
40	Enterobacterial Repetitive Intergenic Consensus (ERIC) Sequences in Escherichia coli: Evolution and Implications for ERIC-PCR. Molecular Biology and Evolution, 2006, 23, 1156-1168.	8.9	106
41	Simian Immunodeficiency Virus Infection in Wild-Caught Chimpanzees from Cameroon. Journal of Virology, 2005, 79, 1312-1319.	3.4	45
42	Simian Immunodeficiency Virus Infection of Chimpanzees. Journal of Virology, 2005, 79, 3891-3902.	3.4	173
43	Variation in the strength of selected codon usage bias among bacteria. Nucleic Acids Research, 2005, 33, 1141-1153.	14.5	348
44	Simian Immunodeficiency Virus Infection in Free-Ranging Sooty Mangabeys (Cercocebus atys atys) from the Tail` Forest, Col,te d'Ivoire: Implications for the Origin of Epidemic Human Immunodeficiency Virus Type 2. Journal of Virology, 2005, 79, 12515-12527.	3.4	274
45	New Simian Immunodeficiency Virus Infecting De Brazza's Monkeys (Cercopithecus neglectus): Evidence for a Cercopithecus Monkey Virus Clade. Journal of Virology, 2004, 78, 7748-7762.	3.4	121
46	Contaminated polio vaccine theory refuted. Nature, 2004, 428, 820-820.	27.8	74
47	Complete Genome Analysis of One of the Earliest SIVcpzPtt Strains from Gabon (SIVcpzGAB2). AIDS Research and Human Retroviruses, 2004, 20, 1377-1381.	1.1	22
48	Foci of Endemic Simian Immunodeficiency Virus Infection in Wild-Living Eastern Chimpanzees (Pan) Tj ETQq0 0	0 rgBT /Ov	erlock 10 Tf 5
49	Hybrid Origin of SIV in Chimpanzees. Science, 2003, 300, 1713-1713.	12.6	337
50	Amplification of a Complete Simian Immunodeficiency Virus Genome from Fecal RNA of a Wild Chimpanzee. Journal of Virology, 2003, 77, 2233-2242.	3.4	80
51	Noninvasive Detection of Simian Immunodeficiency Virus Infection in a Wild-Living L'Hoest's Monkey (Cercopithecus lhoesti). AIDS Research and Human Retroviruses, 2003, 19, 1163-1166.	1.1	40
52	The Evolution of Primate Lentiviruses and the Origins of AIDS. , 2002, , 65-96.		10
53	SIVcpz in Wild Chimpanzees. Science, 2002, 295, 465-465.	12.6	207
54	Origins of Human Virus Diversity. Cell, 2002, 108, 305-312.	28.9	86

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55	Synonymous codon usage in Pseudomonas aeruginosa PA01. Gene, 2002, 289, 131-139.	2.2	71
56	Synonymous codon usage in Cryptosporidium parvum: identification of two distinct trends among genes. International Journal for Parasitology, 2001, 31, 402-412.	3.1	31
57	The origins of acquired immune deficiency syndrome viruses: where and when?. Philosophical Transactions of the Royal Society B: Biological Sciences, 2001, 356, 867-876.	4.0	263
58	Patterns of Genomic Sequence Diversity among Their Simian Immunodeficiency Viruses Suggest that L'Hoest Monkeys (Cercopithecus Ihoesti) Are a Natural Lentivirus Reservoir. Journal of Virology, 2000, 74, 3892-3898.	3.4	42
59	AIDS as a Zoonosis: Scientific and Public Health Implications. Science, 2000, 287, 607-614.	12.6	1,012
60	Absence of translationally selected synonymous codon usage bias in Helicobacter pylori. Microbiology (United Kingdom), 2000, 146, 851-860.	1.8	86
61	Proteome composition and codon usage in spirochaetes: species-specific and DNA strand-specific mutational biases. Nucleic Acids Research, 1999, 27, 1642-1649.	14.5	130
62	Origin of HIV-1 in the chimpanzee Pan troglodytes troglodytes. Nature, 1999, 397, 436-441.	27.8	1,405
63	Chromosomal location effects on gene sequence evolution in mammals. Current Biology, 1999, 9, 786-791.	3.9	123
64	Characterization of a Novel Simian Immunodeficiency Virus (SIV) from L'Hoest Monkeys () Tj ETQq0 0 0 rgB1 Journal of Virology, 1999, 73, 1036-1045.	Overlock 3.4	2 10 Tf 50 38 80
65	Simian Immunodeficiency Virus (SIV) from Sun-Tailed Monkeys (<i>Cercopithecus solatus </i>): Evidence for Host-Dependent Evolution of SIV within the <i>C. Ihoesti </i> Superspecies. Journal of Virology, 1999, 73, 7734-7744.	3.4	87
66	An African HIV-1 sequence from 1959 and implications for the origin of the epidemic. Nature, 1998, 391, 594-597.	27.8	479
67	An Isolate of Human Immunodeficiency Virus Type 1 Originally Classified as Subtype I Represents a Complex Mosaic Comprising Three Different Group M Subtypes (A, G, and I). Journal of Virology, 1998, 72, 10234-10241.	3.4	90
68	A Comprehensive Panel of Near-Full-Length Clones and Reference Sequences for Non-Subtype B Isolates of Human Immunodeficiency Virus Type 1. Journal of Virology, 1998, 72, 5680-5698.	3.4	270
69	Sequence Analysis of a Highly Divergent HIV-1-Related Lentivirus Isolated from a Wild Captured Chimpanzee. Virology, 1996, 221, 346-350.	2.4	94
70	Codon usage and base composition inRickettsia prowazekii. Journal of Molecular Evolution, 1996, 42, 525-536.	1.8	82
71	Codon usage in the Mycobacterium tuberculosis complex. Microbiology (United Kingdom), 1996, 142, 915-925.	1.8	102
72	Recombination in AIDS viruses. Journal of Molecular Evolution, 1995, 40, 249-259.	1.8	408

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73	Recombination in HIV-1. Nature, 1995, 374, 124-126.	27.8	589
74	The molecular evolution of the human immunodeficiency viruses. , 1995, , 438-454.		2
75	Codon usage inCaenorhabditis elegans: delineation of translational selection and mutational biases. Nucleic Acids Research, 1994, 22, 2437-2446.	14.5	282
76	Codon usage and genome evolution. Current Opinion in Genetics and Development, 1994, 4, 851-860.	3.3	232
77	Synonymous codon usage inKluyveromyces lactis. Yeast, 1993, 9, 1219-1228.	1.7	31
78	Conservation of motifs within the unusually variable polypeptide sequences of type I restriction and modification enzymes. Molecular Microbiology, 1993, 9, 133-143.	2.5	59
79	Regional base composition variation along yeast chromosome III: evoluation of chormosome primary structure. Nucleic Acids Research, 1993, 21, 179-183.	14.5	114
80	Genetic Typing of HIV-2 from a Senegalese/German Heterosexual Transmission. AIDS Research and Human Retroviruses, 1993, 9, 703-704.	1.1	8
81	Codon usage: mutational bias, translational selection, or both?. Biochemical Society Transactions, 1993, 21, 835-841.	3.4	280
82	Structure, Expression, and Evolution of Guinea Pig Serum Amyloid P Component and C-Reactive Protein1. Journal of Biochemistry, 1993, 113, 277-284.	1.7	52
83	Evolution of codon usage patterns: the extent and nature of divergence betweenCandida albicansandSaccharomyces cerevisiae. Nucleic Acids Research, 1992, 20, 5289-5295.	14.5	119
84	Human infection by genetically diverse SIVSM-related HIV-2 in West Africa. Nature, 1992, 358, 495-499.	27.8	486
85	The salmon gene encoding apolipoprotein A-I: cDNA sequence, tissue expression and evolution. Gene, 1991, 104, 155-161.	2.2	39
86	Coelacanth's relationships. Nature, 1991, 353, 218-219.	27.8	18
87	Molecular evolution of bacteriophages: Discrete patterns of codon usage in T4 genes are related to the time of gene expression. Journal of Molecular Evolution, 1991, 33, 13-22.	1.8	17
88	Determinants of DNA sequence divergence between Escherichia coli and Salmonella typhimurium: Codon usage, map position, and concerted evolution. Journal of Molecular Evolution, 1991, 33, 23-33.	1.8	239
89	Synonymous codon usage inSaccharomyces cerevisiae. Yeast, 1991, 7, 657-678.	1.7	263
90	Codon usage in Aspergillus nidulans. Molecular Genetics and Genomics, 1991, 230, 288-294.	2.4	70

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91	Fast and sensitive multiple sequence alignments on a microcomputer. Bioinformatics, 1989, 5, 151-153.	4.1	799
92	Codon usage and gene expression level inDictyosteiium discoidtum: highly expressed genes do [prefer] optimal codons. Nucleic Acids Research, 1989, 17, 5029-5040.	14.5	170
93	Rates of synonymous substitution in plant nuclear genes. Journal of Molecular Evolution, 1989, 29, 208-211.	1.8	179
94	Malarial proteinase?. Nature, 1989, 340, 604-604.	27.8	60
95	Evidence that mutation patterns vary among Drosophila transposable elements. Journal of Molecular Biology, 1989, 207, 843-846.	4.2	24
96	Mutation rates differ among regions of the mammalian genome. Nature, 1989, 337, 283-285.	27.8	599
97	Understanding the origins of AIDS viruses. Nature, 1988, 336, 315-315.	27.8	66
98	Codon usage patterns in in in Escherichia coli, Bacillus subtilis, Saccharomyces cerevisiae, Schizosaccharomyces pombe, Drosophila melanogaster in and in Homo sapiens in a review of the considerable within-species diversity. Nucleic Acids Research, 1988, 16, 8207-8211.	14.5	569
99	CLUSTAL: a package for performing multiple sequence alignment on a microcomputer. Gene, 1988, 73, 237-244.	2.2	3,454
100	Selective differences among translation termination codons. Gene, 1988, 63, 141-145.	2.2	65
101	Molecular evolution of ubiquitin genes. Trends in Ecology and Evolution, 1987, 2, 328-332.	8.7	41
102	The codon adaptation index-a measure of directional synonymous codon usage bias, and its potential applications. Nucleic Acids Research, 1987, 15, 1281-1295.	14.5	3,290
103	Synonymous codon usage in <i>Bacillus subtilis</i> reflects both translational selection and mutational biases. Nucleic Acids Research, 1987, 15, 8023-8040.	14.5	277
104	An evaluation of the molecular clock hypothesis using mammalian DNA sequences. Journal of Molecular Evolution, 1987, 25, 330-342.	1.8	456
105	What can AIDS virus codon usage tell us?. Nature, 1986, 324, 114-114.	27.8	31
106	An evolutionary perspective on synonymous codon usage in unicellular organisms. Journal of Molecular Evolution, 1986, 24, 28-38.	1.8	801
107	Codon usage in yeast: cluster analysis clearly differentiates highly and lowly expressed genes. Nucleic Acids Research, 1986, 14, 5125-5143.	14.5	1,073
108	Selection pressures on codon usage in the complete genome of bacteriophage T7. Journal of Molecular Evolution, 1985, 21, 150-160.	1.8	60

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109	Does the â€~non-coding' strand code?. Nucleic Acids Research, 1985, 13, 1389-1397.	14.5	22