

Derek Gatherer

List of Publications by Year in descending order

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Version: 2024-02-01

98
papers

4,488
citations

126858

33
h-index

110317

64
g-index

105
all docs

105
docs citations

105
times ranked

6268
citing authors

#	ARTICLE	IF	CITATIONS
1	The family Parvoviridae. Archives of Virology, 2014, 159, 1239-1247.	0.9	555
2	Genetic content of wild-type human cytomegalovirus. Journal of General Virology, 2004, 85, 1301-1312.	1.3	500
3	Zika virus: a previously slow pandemic spreads rapidly through the Americas. Journal of General Virology, 2016, 97, 269-273.	1.3	246
4	High-resolution human cytomegalovirus transcriptome. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 19755-19760.	3.3	209
5	The 2014 Ebola virus disease outbreak in West Africa. Journal of General Virology, 2014, 95, 1619-1624.	1.3	198
6	Evolution and Diversity in Human Herpes Simplex Virus Genomes. Journal of Virology, 2014, 88, 1209-1227.	1.5	187
7	The 2009 H1N1 influenza outbreak in its historical context. Journal of Clinical Virology, 2009, 45, 174-178.	1.6	168
8	Comparative Genomics of Carp Herpesviruses. Journal of Virology, 2013, 87, 2908-2922.	1.5	117
9	The genome of Epstein-Barr virus type 2 strain AG876. Virology, 2006, 350, 164-170.	1.1	116
10	Integrating Reptilian Herpesviruses into the Family Herpesviridae. Journal of Virology, 2005, 79, 725-731.	1.5	114
11	Sequences of complete human cytomegalovirus genomes from infected cell cultures and clinical specimens. Journal of General Virology, 2010, 91, 605-615.	1.3	108
12	Sequence-independent characterization of viruses based on the pattern of viral small RNAs produced by the host. Nucleic Acids Research, 2015, 43, 6191-6206.	6.5	104
13	High-throughput sequence analysis of variants of human cytomegalovirus strains Towne and AD169. Journal of General Virology, 2009, 90, 2375-2380.	1.3	101
14	Correlation between bacterial G+C content, genome size and the G+C content of associated plasmids and bacteriophages. Microbial Genomics, 2018, 4, .	1.0	95
15	IL-10 encoded by viruses: a remarkable example of independent acquisition of a cellular gene by viruses and its subsequent evolution in the viral genome. Journal of General Virology, 2014, 95, 245-262.	1.3	80
16	On phylogenetic relationships among major lineages of the Gammaherpesvirinae. Journal of General Virology, 2005, 86, 307-316.	1.3	77
17	Lymphocryptovirus phylogeny and the origins of Epstein-Barr virus. Journal of General Virology, 2010, 91, 630-642.	1.3	70
18	Nitrogen-Fixing Aerobic Bacteria have Higher Genomic GC Content than Non-Fixing Species within the Same Genus. Hereditas, 2004, 128, 173-178.	0.5	65

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19	Mutations within a Conserved Region of the Hepatitis C Virus E2 Glycoprotein That Influence Virus-Receptor Interactions and Sensitivity to Neutralizing Antibodies. <i>Journal of Virology</i> , 2010, 84, 5494-5507.	1.5	65
20	Conserved Fever Pathways across Vertebrates: A Herpesvirus Expressed Decoy TNF- α Receptor Delays Behavioral Fever in Fish. <i>Cell Host and Microbe</i> , 2017, 21, 244-253.	5.1	57
21	So what do we really mean when we say that systems biology is holistic?. <i>BMC Systems Biology</i> , 2010, 4, 22.	3.0	55
22	Non-random Escape Pathways from a Broadly Neutralizing Human Monoclonal Antibody Map to a Highly Conserved Region on the Hepatitis C Virus E2 Glycoprotein Encompassing Amino Acids 412-423. <i>PLoS Pathogens</i> , 2014, 10, e1004297.	2.1	55
23	Genotypic analysis of two hypervariable human cytomegalovirus genes. <i>Journal of Medical Virology</i> , 2008, 80, 1615-1623.	2.5	54
24	Structural Insights into Calicivirus Attachment and Uncoating. <i>Journal of Virology</i> , 2008, 82, 8051-8058.	1.5	53
25	Transforming growth factor betas in mammalian embryogenesis. <i>Progress in Growth Factor Research</i> , 1990, 2, 153-168.	1.7	51
26	Correlation of examination performance with lecture attendance: a comparative study of first-year biological sciences undergraduates. <i>Biochemical Education</i> , 1998, 26, 121-123.	0.1	50
27	RNA-Seq Analysis of Differentiated Keratinocytes Reveals a Massive Response to Late Events during Human Papillomavirus 16 Infection, Including Loss of Epithelial Barrier Function. <i>Journal of Virology</i> , 2017, 91, .	1.5	47
28	Towards the knowledge-based design of universal influenza epitope ensemble vaccines. <i>Bioinformatics</i> , 2016, 32, 3233-3239.	1.8	46
29	Novel cytomegaloviruses in free-ranging and captive great apes: phylogenetic evidence for bidirectional horizontal transmission. <i>Journal of General Virology</i> , 2009, 90, 2386-2394.	1.3	42
30	The Role of TGF β in Mouse Development. <i>Annals of the New York Academy of Sciences</i> , 1990, 593, 259-271.	1.8	40
31	Stability of the Parainfluenza Virus 5 Genome Revealed by Deep Sequencing of Strains Isolated from Different Hosts and following Passage in Cell Culture. <i>Journal of Virology</i> , 2014, 88, 3826-3836.	1.5	40
32	Small regions of preferential codon usage and their effect on overall codon bias - The case of the plp gene. <i>IUBMB Life</i> , 1997, 43, 107-114.	1.5	39
33	Viral forensic genomics reveals the relatedness of classic herpes simplex virus strains KOS, KOS63, and KOS79. <i>Virology</i> , 2016, 492, 179-186.	1.1	36
34	Lineage structures in the genome sequences of three Epstein-Barr virus strains. <i>Virology</i> , 2007, 359, 1-5.	1.1	34
35	A captured viral interleukin 10 gene with cellular exon structure. <i>Journal of General Virology</i> , 2008, 89, 2447-2455.	1.3	33
36	The role of TGF- β s in mammalian development and neoplasia. <i>Molecular Reproduction and Development</i> , 1992, 32, 127-135.	1.0	31

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37	In silico design of Mycobacterium tuberculosis epitope ensemble vaccines. <i>Molecular Immunology</i> , 2018, 97, 56-62.	1.0	30
38	The Genome of a Tortoise Herpesvirus (Testudinid Herpesvirus 3) Has a Novel Structure and Contains a Large Region That Is Not Required for Replication <i>In Vitro</i> or Virulence <i>In Vivo</i> . <i>Journal of Virology</i> , 2015, 89, 11438-11456.	1.5	27
39	Patterns of divergence in the vCXCL and vGPCR gene clusters in primate cytomegalovirus genomes. <i>Virology</i> , 2009, 395, 21-32.	1.1	26
40	Functional Characterization of Residues Required for the Herpes Simplex Virus 1 E3 Ubiquitin Ligase ICPO To Interact with the Cellular E2 Ubiquitin-Conjugating Enzyme UBE2D1 (UbcH5a). <i>Journal of Virology</i> , 2012, 86, 6323-6333.	1.5	26
41	In silico design of knowledge-based Plasmodium falciparum epitope ensemble vaccines. <i>Journal of Molecular Graphics and Modelling</i> , 2017, 78, 195-205.	1.3	20
42	Delineating the Plausible Molecular Vaccine Candidates and Drug Targets of Multidrug-Resistant <i>Acinetobacter baumannii</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 203.	1.8	19
43	Conserved Glycine 33 Residue in Flexible Domain I of Hepatitis C Virus Core Protein Is Critical for Virus Infectivity. <i>Journal of Virology</i> , 2012, 86, 679-690.	1.5	17
44	The serology of Ebolavirus – a wider geographical range, a wider genus of viruses or a wider range of virulence?. <i>Journal of General Virology</i> , 2016, 97, 3120-3130.	1.3	17
45	Codon indices as a predictor of gene functionality in a <i>Frankia</i> operon. <i>Canadian Journal of Botany</i> , 1999, 77, 1287-1292.	1.2	16
46	Passage in egg culture is a major cause of apparent positive selection in influenza B hemagglutinin. <i>Journal of Medical Virology</i> , 2010, 82, 123-127.	2.5	15
47	Developmental effects of over-expression of normal and mutated forms of a <i>Xenopus</i> NF- κ B homologue. <i>Mechanisms of Development</i> , 1995, 52, 165-177.	1.7	14
48	Anguillid Herpesvirus 1 Transcriptome. <i>Journal of Virology</i> , 2012, 86, 10150-10161.	1.5	14
49	Epstein-Barr Virus Isolates Retain Their Capacity To Evade T Cell Immunity through BNLF2a despite Extensive Sequence Variation. <i>Journal of Virology</i> , 2012, 86, 572-577.	1.5	14
50	Modelling the structure of full-length Epstein-Barr virus nuclear antigen 1. <i>Virus Genes</i> , 2014, 49, 358-372.	0.7	14
51	Rosen's (M,R) system in Unified Modelling Language. <i>BioSystems</i> , 2016, 139, 29-36.	0.9	14
52	The unprecedented scale of the West African Ebola virus disease outbreak is due to environmental and sociological factors, not special attributes of the currently circulating strain of the virus. <i>Evidence-Based Medicine</i> , 2015, 20, 28-28.	0.6	13
53	Viral genotype correlates with distinct liver gene transcription signatures in chronic hepatitis C virus infection. <i>Liver International</i> , 2015, 35, 2256-2264.	1.9	13
54	Rosen's (M,R) system as an X-machine. <i>Journal of Theoretical Biology</i> , 2016, 408, 97-104.	0.8	13

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55	Gene Knockouts and Murine Development. (gene knockout/gene targeting/Mus/mammalian) Tj ETQq1 1 0.784314,rgBT /Overlock 10	0.6	12
56	Molecular Evolution of the Herpesvirales. , 2008, , 447-475.		12
57	Tempo and Mode in the Molecular Evolution of Influenza C. PLOS Currents, 2010, 2, RRN1199.	1.4	12
58	Codon indices as a predictor of gene functionality in a <i>Frankia</i> operon. Canadian Journal of Botany, 1999, 77, 1287-1292.	1.2	11
59	An Unusual Codon Usage Pattern in the Ciliate Family Ophryoscolecidae and its Implications for Determining the Source of Cloned DNA. Anaerobe, 2000, 6, 21-28.	1.0	11
60	Influenza C in Lancaster, UK, in the winter of 2014–2015. Scientific Reports, 2017, 7, 46578.	1.6	11
61	Adaptation of Standard Spreadsheet Software for the Analysis of DNA Sequences. BioTechniques, 1998, 24, 131-138.	0.8	10
62	Rosen's (M,R) system in process algebra. BMC Systems Biology, 2013, 7, 128.	3.0	10
63	An N-terminal extension to the hepatitis B virus core protein forms a poorly ordered trimeric spike in assembled virus-like particles. Journal of Structural Biology, 2015, 189, 73-80.	1.3	9
64	Analysis of Sequence Periodicity in E. coli Proteins: Empirical Investigation of the ?Duplication and Divergence? Theory of Protein Evolution. Journal of Molecular Evolution, 2003, 57, 149-158.	0.8	8
65	Reflections on integrating bioinformatics into the undergraduate curriculum: The Lancaster experience. Biochemistry and Molecular Biology Education, 2020, 48, 118-127.	0.5	8
66	LGAAP: Leishmaniinae Genome Assembly and Annotation Pipeline. Microbiology Resource Announcements, 2021, 10, e0043921.	0.3	8
67	The mutational-response index and codon bias in genes from a <i>Frankia</i> nif operon. Theoretical and Applied Genetics, 1998, 96, 716-718.	1.8	7
68	The evolution of music—A comparison of Darwinian and dialectical methods. Journal of Social and Evolutionary Systems, 1997, 20, 75-92.	0.2	6
69	Molecular Methods of Virus Detection in Lymphoma. Methods in Molecular Biology, 2013, 971, 277-293.	0.4	6
70	A decade of sustained selection pressure on two surface sites of the VP1 protein of Enterovirus A71 suggests that immune evasion may be an indirect driver for virulence. Scientific Reports, 2019, 9, 5427.	1.6	6
71	Finite Universe of Discourse: The Systems Biology of Walter Elsasser (1904-1991). The Open Biology Journal, 2008, 1, 9-20.	0.5	6
72	Cultural Evolution The Biological Perspective. Parallax, 2006, 12, 57-68.	0.3	5

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73	Peptide Vocabulary Analysis Reveals Ultra-Conservation and Homonymity in Protein Sequences. <i>Bioinformatics and Biology Insights</i> , 2007, 1, BBI.S415.	1.0	5
74	Chromosome-Scale Assembly of the Complete Genome Sequence of <i>Leishmania</i> (<i>Mundinia</i>) Tj ETQq0 0 0 rgBT /Overlock e0005821.	0.3	5
75	Chromosome-scale genome sequencing, assembly and annotation of six genomes from subfamily Leishmaniinae. <i>Scientific Data</i> , 2021, 8, 234.	2.4	5
76	Chromosome-Scale Assembly of the Complete Genome Sequence of <i>Leishmania</i> (<i>Mundinia</i>) <i>orientalis</i> , Isolate LSCM4, Strain LV768. <i>Microbiology Resource Announcements</i> , 2021, 10, e0057421.	0.3	5
77	Meme Pools, World 3, and Averroës's Vision of Immortality. <i>Zygon</i> , 1998, 33, 203-219.	0.2	4
78	Phylogenetic Differences in Content and Intensity of Periodic Proteins. <i>Journal of Molecular Evolution</i> , 2005, 60, 447-461.	0.8	4
79	Less is more: the battle of Moore's law against Bremermann's limit on the field of systems biology. <i>BMC Systems Biology</i> , 2007, 1, .	3.0	4
80	On Units of Selection in Cultural Evolution. <i>Journal of Theoretical Biology</i> , 1998, 192, 409-413.	0.8	3
81	The Little Ice Age and the emergence of influenza A. <i>Medical Hypotheses</i> , 2010, 75, 359-362.	0.8	3
82	Mitochondrial DNA Profiling Reveals Two Lineages of Sun Bears in East and West Malaysia. <i>Journal of Heredity</i> , 2021, 112, 214-220.	1.0	3
83	N-acetyl-cysteine causes a late re-specification of the anteroposterior axis in the <i>Xenopus</i> embryo. , 1996, 205, 395-409.		2
84	On the origin of influenza A hemagglutinin. <i>Indian Journal of Microbiology</i> , 2009, 49, 352-357.	1.5	2
85	Nasopharyngeal metagenomic deep sequencing data, Lancaster, UK, 2014â€“2015. <i>Scientific Data</i> , 2017, 4, 170161.	2.4	2
86	Paradigm Shift in Drug Re-purposing From Phenalenone to Phenaleno-Furanone to Combat Multi-Drug Resistant <i>Salmonella enterica</i> Serovar Typhi. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 402.	1.8	2
87	Chromosome-Scale Assembly of the Complete Genome Sequence of <i>Leishmania</i> (<i>Mundinia</i>) <i>enriettii</i> , Isolate CUR178, Strain LV763. <i>Microbiology Resource Announcements</i> , 2021, 10, e0057521.	0.3	2
88	Ebola returns to its Congo Basin heartland. <i>Journal of General Virology</i> , 2018, 99, 861-863.	1.3	2
89	Genome Sequence of Human Papillomavirus 23 Strain HPV-23/Lancaster/2015. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
90	Genome Sequence of Human Rhinovirus A22, Strain Lancaster/2015. <i>Genome Announcements</i> , 2017, 5, .	0.8	1

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91	Genome Sequence of Human Papillomavirus Type 20, Strain HPV-20/Lancaster/2015. Genome Announcements, 2017, 5, .	0.8	1
92	Letter: TreeAdder: A Tool to Assist the Optimal Positioning of a New Leaf into an Existing Phylogenetic Tree. Open Bioinformatics Journal, 2007, 1, 1-2.	1.0	1
93	Chromosome-Scale Assembly of the Complete Genome Sequence of Porcisia hertigi, Isolate C119, Strain LV43. Microbiology Resource Announcements, 2021, 10, e0065121.	0.3	1
94	Sequence Variation in Multidrug-Resistant Plasmid pLUH01, Isolated from Human Nasopharyngeal Swabs. Microbiology Resource Announcements, 2018, 7, .	0.3	0
95	Visualization of protein sequence space with force-directed graphs, and their application to the choice of target-template pairs for homology modelling. Journal of Molecular Graphics and Modelling, 2019, 92, 180-191.	1.3	0
96	Insecticide-impregnated netting: A surface treatment for killing Lutzomyia longipalpis (Diptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 54 Diseases, 2021, 1, 100044.	0.7	0
97	Chromosome-Scale Assembly of the Complete Genome Sequence of Leishmania (Mundinia) sp. Ghana, Isolate GH5, Strain LV757. Microbiology Resource Announcements, 2021, 10, e0059121.	0.3	0
98	Modelling versus Realisation: Rival Philosophies of Computational Theory in Systems Biology. , 2019, , 33-57.		0