

Derek Gatherer

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

95
papers

3,554
citations

30
h-index

58
g-index

105
ext. papers

4,108
ext. citations

4.9
avg, IF

5.6
L-index

#	Paper	IF	Citations
95	Chromosome-Scale Assembly of the Complete Genome Sequence of <i>Porcisia hertigi</i> , Isolate C119, Strain LV43. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0065121	1.3	
94	Chromosome-Scale Assembly of the Complete Genome Sequence of () , Isolate LSCM1, Strain LV760. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0005821	1.3	1
93	Mitochondrial DNA Profiling Reveals Two Lineages of Sun Bears in East and West Malaysia. <i>Journal of Heredity</i> , 2021 , 112, 214-220	2.4	1
92	LGAAP: Genome Assembly and Annotation Pipeline. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0043921	1.3	6
91	Chromosome-scale genome sequencing, assembly and annotation of six genomes from subfamily Leishmaniinae. <i>Scientific Data</i> , 2021 , 8, 234	8.2	0
90	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	1.3	0
89	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	1.3	
88	Chromosome-Scale Assembly of the Complete Genome Sequence of () sp. Ghana, Isolate GH5, Strain LV757. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0059121	1.3	
87	Reflections on integrating bioinformatics into the undergraduate curriculum: The Lancaster experience. <i>Biochemistry and Molecular Biology Education</i> , 2020 , 48, 118-127	1.3	6
86	Visualization of protein sequence space with force-directed graphs, and their application to the choice of target-template pairs for homology modelling. <i>Journal of Molecular Graphics and Modelling</i> , 2019 , 92, 180-191	2.8	
85	Delineating the Plausible Molecular Vaccine Candidates and Drug Targets of Multidrug-Resistant. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019 , 9, 203	5.9	11
84	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. <i>Scientific Reports</i> , 2019 , 9, 5427	4.9	1
83	Modelling versus Realisation: Rival Philosophies of Computational Theory in Systems Biology 2019 , 33-57		
82	In silico design of Mycobacterium tuberculosis epitope ensemble vaccines. <i>Molecular Immunology</i> , 2018 , 97, 56-62	4.3	20
81	Correlation between bacterial G+C content, genome size and the G+C content of associated plasmids and bacteriophages. <i>Microbial Genomics</i> , 2018 , 4,	4.4	42
80	Paradigm Shift in Drug Re-purposing From Phenalenone to Phenaleno-Furanone to Combat Multi-Drug Resistant Serovar Typhi. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018 , 8, 402	5.9	2
79	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	23.4	38

78	Influenza C in Lancaster, UK, in the winter of 2014-2015. <i>Scientific Reports</i> , 2017 , 7, 46578	4.9	6
77	Genome Sequence of Human Papillomavirus 23 Strain HPV-23/Lancaster/2015. <i>Genome Announcements</i> , 2017 , 5,		1
76	Genome Sequence of Human Rhinovirus A22, Strain Lancaster/2015. <i>Genome Announcements</i> , 2017 , 5,		1
75	Nasopharyngeal metagenomic deep sequencing data, Lancaster, UK, 2014-2015. <i>Scientific Data</i> , 2017 , 4, 170161	8.2	1
74	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,	6.6	29
73	In silico design of knowledge-based Plasmodium falciparum epitope ensemble vaccines. <i>Journal of Molecular Graphics and Modelling</i> , 2017 , 78, 195-205	2.8	14
72	Genome Sequence of Human Papillomavirus Type 20, Strain HPV-20/Lancaster/2015. <i>Genome Announcements</i> , 2017 , 5,		1
71	Towards the knowledge-based design of universal influenza epitope ensemble vaccines. <i>Bioinformatics</i> , 2016 , 32, 3233-3239	7.2	32
70	RosenS (M,R) system as an X-machine. <i>Journal of Theoretical Biology</i> , 2016 , 408, 97-104	2.3	11
69	RosenS (M,R) system in Unified Modelling Language. <i>BioSystems</i> , 2016 , 139, 29-36	1.9	12
68	Zika virus: a previously slow pandemic spreads rapidly through the Americas. <i>Journal of General Virology</i> , 2016 , 97, 269-273	4.9	194
67	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	4.9	13
66	Viral forensic genomics reveals the relatedness of classic herpes simplex virus strains KOS, KOS63, and KOS79. <i>Virology</i> , 2016 , 492, 179-86	3.6	22
65	Sequence-independent characterization of viruses based on the pattern of viral small RNAs produced by the host. <i>Nucleic Acids Research</i> , 2015 , 43, 6191-206	20.1	72
64	Viral genotype correlates with distinct liver gene transcription signatures in chronic hepatitis C virus infection. <i>Liver International</i> , 2015 , 35, 2256-64	7.9	9
63	The Genome of a Tortoise Herpesvirus (Testudinid Herpesvirus 3) Has a Novel Structure and Contains a Large Region That Is Not Required for Replication In Vitro or Virulence In Vivo. <i>Journal of Virology</i> , 2015 , 89, 11438-56	6.6	20
62	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		10
61	An N-terminal extension to the hepatitis B virus core protein forms a poorly ordered trimeric spike in assembled virus-like particles. <i>Journal of Structural Biology</i> , 2015 , 189, 73-80	3.4	5

60	The 2014 Ebola virus disease outbreak in West Africa. <i>Journal of General Virology</i> , 2014 , 95, 1619-1624	4.9	155
59	Evolution and diversity in human herpes simplex virus genomes. <i>Journal of Virology</i> , 2014 , 88, 1209-27	6.6	141
58	Modelling the structure of full-length Epstein-Barr virus nuclear antigen 1. <i>Virus Genes</i> , 2014 , 49, 358-72	2.3	11
57	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, 3826-36	6.6	31
56	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	7.6	46
55	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. <i>Journal of General Virology</i> , 2014 , 95, 245-262	4.9	65
54	The family Parvoviridae. <i>Archives of Virology</i> , 2014 , 159, 1239-47	2.6	424
53	RosenS (M,R) system in process algebra. <i>BMC Systems Biology</i> , 2013 , 7, 128	3.5	8
52	Comparative genomics of carp herpesviruses. <i>Journal of Virology</i> , 2013 , 87, 2908-22	6.6	86
51	Molecular methods of virus detection in lymphoma. <i>Methods in Molecular Biology</i> , 2013 , 971, 277-93	1.4	5
50	Anguillid herpesvirus 1 transcriptome. <i>Journal of Virology</i> , 2012 , 86, 10150-61	6.6	12
49	Functional characterization of residues required for the herpes simplex virus 1 E3 ubiquitin ligase ICP0 to interact with the cellular E2 ubiquitin-conjugating enzyme UBE2D1 (UbcH5a). <i>Journal of Virology</i> , 2012 , 86, 6323-33	6.6	24
48	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, 679-90	6.6	16
47	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, 572-7	6.6	12
46	High-resolution human cytomegalovirus transcriptome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 19755-60	11.5	161
45	Lymphocryptovirus phylogeny and the origins of Epstein-Barr virus. <i>Journal of General Virology</i> , 2010 , 91, 630-42	4.9	60
44	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, 5494-507	6.6	56
43	The Little Ice Age and the emergence of influenza A. <i>Medical Hypotheses</i> , 2010 , 75, 359-62	3.8	3

42	So what do we really mean when we say that systems biology is holistic?. <i>BMC Systems Biology</i> , 2010 , 4, 22	3.5	39
41	Passage in egg culture is a major cause of apparent positive selection in influenza B hemagglutinin. <i>Journal of Medical Virology</i> , 2010 , 82, 123-7	19.7	13
40	Tempo and mode in the molecular evolution of influenza C. <i>PLOS Currents</i> , 2010 , 2, RRN1199		10
39	Sequences of complete human cytomegalovirus genomes from infected cell cultures and clinical specimens. <i>Journal of General Virology</i> , 2010 , 91, 605-15	4.9	91
38	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	4.9	36
37	Patterns of divergence in the vCXCL and vGPCR gene clusters in primate cytomegalovirus genomes. <i>Virology</i> , 2009 , 395, 21-32	3.6	23
36	On the origin of influenza A hemagglutinin. <i>Indian Journal of Microbiology</i> , 2009 , 49, 352-7	3.7	2
35	The 2009 H1N1 influenza outbreak in its historical context. <i>Journal of Clinical Virology</i> , 2009 , 45, 174-8	14.5	134
34	Peptide vocabulary analysis reveals ultra-conservation and homonymity in protein sequences. <i>Bioinformatics and Biology Insights</i> , 2009 , 1, 101-26	5.3	4
33	High-throughput sequence analysis of variants of human cytomegalovirus strains Towne and AD169. <i>Journal of General Virology</i> , 2009 , 90, 2375-2380	4.9	86
32	A captured viral interleukin 10 gene with cellular exon structure. <i>Journal of General Virology</i> , 2008 , 89, 2447-2455	4.9	30
31	Molecular Evolution of the Herpesvirales 2008 , 447-475		12
30	Structural insights into calicivirus attachment and uncoating. <i>Journal of Virology</i> , 2008 , 82, 8051-8	6.6	48
29	Genotypic analysis of two hypervariable human cytomegalovirus genes. <i>Journal of Medical Virology</i> , 2008 , 80, 1615-23	19.7	48
28	Finite Universe of Discourse: The Systems Biology of Walter Elsasser (1904-1991). <i>The Open Biology Journal</i> , 2008 , 1, 9-20	0.5	5
27	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,	3.5	3
26	Lineage structures in the genome sequences of three Epstein-Barr virus strains. <i>Virology</i> , 2007 , 359, 1-5	3.6	30
25	The genome of Epstein-Barr virus type 2 strain AG876. <i>Virology</i> , 2006 , 350, 164-70	3.6	102

24	Cultural Evolution The Biological Perspective. <i>Parallax</i> , 2006 , 12, 57-68	0.1	1
23	Phylogenetic differences in content and intensity of periodic proteins. <i>Journal of Molecular Evolution</i> , 2005 , 60, 447-61	3.1	4
22	On phylogenetic relationships among major lineages of the Gammaherpesvirinae. <i>Journal of General Virology</i> , 2005 , 86, 307-316	4.9	69
21	Integrating reptilian herpesviruses into the family herpesviridae. <i>Journal of Virology</i> , 2005 , 79, 725-31	6.6	102
20	Genetic content of wild-type human cytomegalovirus. <i>Journal of General Virology</i> , 2004 , 85, 1301-1312	4.9	439
19	Analysis of sequence periodicity in E. coli proteins: empirical investigation of the "duplication and divergence" theory of protein evolution. <i>Journal of Molecular Evolution</i> , 2003 , 57, 149-58	3.1	6
18	An Unusual Codon Usage Pattern in the Ciliate Family Ophryoscolecidae and its Implications for Determining the Source of Cloned DNA. <i>Anaerobe</i> , 2000 , 6, 21-28	2.8	7
17	Codon indices as a predictor of gene functionality in a Frankia operon. <i>Canadian Journal of Botany</i> , 1999 , 77, 1287-1292		10
16	Codon indices as a predictor of gene functionality in a Frankia operon. <i>Canadian Journal of Botany</i> , 1999 , 77, 1287-1292		13
15	Meme Pools, World 3, and Averroës's Vision of Immortality. <i>Zygon</i> , 1998 , 33, 203-219	0.3	2
14	On Units of Selection in Cultural Evolution. <i>Journal of Theoretical Biology</i> , 1998 , 192, 409-413	2.3	3
13	The mutational-response index and codon bias in genes from a Frankia nif operon. <i>Theoretical and Applied Genetics</i> , 1998 , 96, 716-718	6	7
12	Correlation of examination performance with lecture attendance: a comparative study of first-year biological sciences undergraduates. <i>Biochemical Education</i> , 1998 , 26, 121-123		40
11	Nitrogen-fixing aerobic bacteria have higher genomic GC content than non-fixing species within the same genus. <i>Hereditas</i> , 1998 , 128, 173-8	2.4	53
10	Adaptation of standard spreadsheet software for the analysis of DNA sequences. <i>BioTechniques</i> , 1998 , 24, 131-6, 138	2.5	10
9	The evolution of music: a comparison of Darwinian and dialectical methods. <i>Journal of Social and Evolutionary Systems</i> , 1997 , 20, 75-92		3
8	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, 107-14	4.7	30
7	N-acetyl-cysteine causes a late re-specification of the anteroposterior axis in the Xenopus embryo. <i>Developmental Dynamics</i> , 1996 , 205, 395-409	2.9	1

6	Developmental effects of over-expression of normal and mutated forms of a Xenopus NF-kappa B homologue. <i>Mechanisms of Development</i> , 1995 , 52, 165-77	1.7	14
5	Gene Knockouts and Murine Development. <i>Development Growth and Differentiation</i> , 1993 , 35, 365-370	3	9
4	The role of TGF-beta s in mammalian development and neoplasia. <i>Molecular Reproduction and Development</i> , 1992 , 32, 127-35	2.6	29
3	The role of TGF beta in mouse development. <i>Annals of the New York Academy of Sciences</i> , 1990 , 593, 259-71	6.5	34
2	Transforming growth factor betas in mammalian embryogenesis. <i>Progress in Growth Factor Research</i> , 1990 , 2, 153-68		45
1	Tempus et Locus: a tool for extracting precisely dated viral sequences from GenBank, and its application to the phylogenetics of primate erythroparvovirus 1 (B19V)		1