Chris Upton

List of Publications by Year
in descending order

93 papers	7,199 citations	94269 37 h-index	58464 82 g-index
94 all docs	94 docs citations	94 times ranked	6442 citing authors

#	Article	IF	Citations
1	Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. Briefings in Bioinformatics, 2021, 22, 642-663.	3.2	110
2	The first genotype II African swine fever virus isolated in Africa provides insight into the current Eurasian pandemic. Scientific Reports, 2021, 11, 13081.	1.6	34
3	Bioinformatics for Analysis of Poxvirus Genomes. Methods in Molecular Biology, 2019, 2023, 29-62.	0.4	9
4	Isolation and Characterization of Akhmeta Virus from Wild-Caught Rodents (<i>Apodemus</i> spp.) in Georgia. Journal of Virology, 2019, 93, .	1.5	9
5	Bioinformatic Approaches for Comparative Analysis of Viruses. Methods in Molecular Biology, 2018, 1704, 401-417.	0.4	1
6	Base-By-Base Version 3: New Comparative Tools for Large Virus Genomes. Viruses, 2018, 10, 637.	1.5	24
7	Complete genome sequence of a novel sea otterpox virus. Virus Genes, 2018, 54, 756-767.	0.7	5
8	Genomic characterization of two novel pathogenic avipoxviruses isolated from pacific shearwaters (Ardenna spp.). BMC Genomics, 2017, 18, 298.	1.2	51
9	Complete genomic characterisation of two novel poxviruses (WKPV and EKPV) from western and eastern grey kangaroos. Virus Research, 2017, 242, 106-121.	1.1	8
10	Two novel poxviruses with unusual genome rearrangements: NY_014 and Murmansk. Virus Genes, 2017, 53, 883-897.	0.7	15
11	Characterization of Eptesipoxvirus, a novel poxvirus from a microchiropteran bat. Virus Genes, 2017, 53, 856-867.	0.7	16
12	Three novel Pseudomonas phages isolated from composting provide insights into the evolution and diversity of tailed phages. BMC Genomics, 2017, 18, 346.	1.2	32
13	The genomes of three North American orthopoxviruses. Virus Genes, 2017, 53, 21-34.	0.7	15
14	Virus Databases â˜†. , 2017, , .		2
15	Re-Assembly and Analysis of an Ancient Variola Virus Genome. Viruses, 2017, 9, 253.	1.5	14
16	Genomic characterization of a novel poxvirus from a flying fox: evidence for a new genus?. Journal of General Virology, 2016, 97, 2363-2375.	1.3	18
17	Comparative analysis of the complete genome sequences of Kenyan African swine fever virus isolates within p72 genotypes IX and X. Virus Genes, 2015, 50, 303-309.	0.7	49
18	Novel Poxvirus Infection in an Immune Suppressed Patient. Clinical Infectious Diseases, 2015, 61, 1543-1548.	2.9	16

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19	Related strains of African swine fever virus with different virulence: genome comparison and analysis. Journal of General Virology, 2015, 96, 408-419.	1.3	98
20	Genome sequence and comparative virulence of raccoonpox virus: the first North American poxvirus sequence. Journal of General Virology, 2015, 96, 2806-2821.	1.3	11
21	Incongruencies in Vaccinia Virus Phylogenetic Trees. Computation, 2014, 2, 182-198.	1.0	12
22	Expression of a non-coding RNA in ectromelia virus is required for normal plaque formation. Virus Genes, 2014, 48, 38-47.	0.7	2
23	Suffix tree searcher: exploration of common substrings in large DNA sequence sets. BMC Research Notes, 2014, 7, 466.	0.6	3
24	Prediction of Steps in the Evolution of Variola Virus Host Range. PLoS ONE, 2014, 9, e91520.	1.1	21
25	African swine fever virus replication and genomics. Virus Research, 2013, 173, 3-14.	1.1	460
26	Paramecium bursaria Chlorella Virus 1 Proteome Reveals Novel Architectural and Regulatory Features of a Giant Virus. Journal of Virology, 2012, 86, 8821-8834.	1.5	64
27	Bioinformatics for Analysis of Poxvirus Genomes. Methods in Molecular Biology, 2012, 890, 233-258.	0.4	8
28	It's a small world after all—viral genomics and the global dominance of viruses. Current Opinion in Virology, 2011, 1, 280-281.	2.6	0
29	Characterization of indels in poxvirus genomes. Virus Genes, 2011, 42, 171-177.	0.7	36
30	Prediction of a novel RNA binding domain in crocodilepox Zimbabwe Gene 157. Microbial Informatics and Experimentation, 2011, 1, 12.	7.6	1
31	Base-By-Base version 2: single nucleotide-level analysis of whole viral genome alignments. Microbial Informatics and Experimentation, 2011, 1, 2.	7.6	36
32	Genomic Analysis of Highly Virulent Georgia 2007/1 Isolate of African Swine Fever Virus. Emerging Infectious Diseases, 2011, 17, 599-605.	2.0	186
33	The Genome of Yoka Poxvirus. Journal of Virology, 2011, 85, 10230-10238.	1.5	30
34	Genomic Analysis of the Vaccinia Virus Strain Variants Found in Dryvax Vaccine. Journal of Virology, 2011, 85, 13049-13060.	1.5	63
35	Phylogenomic analysis of 11 complete African swine fever virus genome sequences. Virology, 2010, 400, 128-136.	1.1	134
36	JaPaFi: A Novel Program for the Identification of Highly Conserved DNA Sequences. Viruses, 2010, 2, 1867-1885.	1.5	2

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37	Vaccinia Virus–Encoded Ribonucleotide Reductase Subunits Are Differentially Required for Replication and Pathogenesis. PLoS Pathogens, 2010, 6, e1000984.	2.1	66
38	Vaccinia Virus G8R Protein: A Structural Ortholog of Proliferating Cell Nuclear Antigen (PCNA). PLoS ONE, 2009, 4, e5479.	1.1	13
39	Sequence Searcher: A Java tool to perform regular expression and fuzzy searches of multiple DNA and protein sequences. BMC Research Notes, 2009, 2, 14.	0.6	11
40	KISSa: a strategy to build multiple sequence alignments from pairwise comparisons of very closely related sequences. BMC Research Notes, 2009, 2, 91.	0.6	0
41	Evidence for a novel gene associated with human influenza A viruses. Virology Journal, 2009, 6, 198.	1.4	26
42	Cowpox Virus Inhibits the Transporter Associated with Antigen Processing to Evade T Cell Recognition. Cell Host and Microbe, 2009, 6, 433-445.	5.1	68
43	Comparison of the genome sequences of non-pathogenic and pathogenic African swine fever virus isolates. Journal of General Virology, 2008, 89, 397-408.	1.3	244
44	A new method for indexing genomes using on-disk suffix trees. , 2008, , .		18
45	Comparative Genomics of Viruses Using Bioinformatics Tools. , 2007, , 49-72.		0
46	Genomic differences of Vaccinia virus clones from Dryvax smallpox vaccine: The Dryvax-like ACAM2000 and the mouse neurovirulent Clone-3. Vaccine, 2007, 25, 8807-8832.	1.7	40
47	Role of phages in the pathogenesis of Burkholderia, or 'Where are the toxin genes in Burkholderia phages?'. Current Opinion in Microbiology, 2007, 10, 410-417.	2.3	50
48	An ectromelia virus profilin homolog interacts with cellular tropomyosin and viral A-type inclusion protein. Virology Journal, 2007, 4, 76.	1.4	12
49	Comparative genomic analysis of the family Iridoviridae: re-annotating and defining the core set of iridovirus genes. Virology Journal, 2007, 4, 11.	1.4	152
50	Shortest Path Approaches for the Longest Common Subsequence of a Set of Strings. , 2007, , .		2
51	GraphDNA: a Java program for graphical display of DNA composition analyses. BMC Bioinformatics, 2007, 8, 21.	1.2	41
52	Organizing and Updating Whole Genome BLAST Searches with ReHAB. Methods in Molecular Biology, 2007, 395, 187-194.	0.4	1
53	Genomic sequence and analysis of a vaccinia virus isolate from a patient with a smallpox vaccine-related complication. Virology Journal, 2006, 3, 88.	1.4	24
54	Poxviruses: past, present and future. Virus Research, 2006, 117, 105-118.	1.1	164

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55	Java GUI for InterProScan (JIPS): A tool to help process multiple InterProScans and perform ortholog analysis. BMC Bioinformatics, 2006, 7, 462.	1.2	7
56	Genome Annotation Transfer Utility (GATU): rapid annotation of viral genomes using a closely related reference genome. BMC Genomics, 2006, 7, 150.	1.2	212
57	Predicted function of the vaccinia virus G5R protein. Bioinformatics, 2006, 22, 2846-2850.	1.8	19
58	A Full-Genome Phylogenetic Analysis of Varicella-Zoster Virus Reveals a Novel Origin of Replication-Based Genotyping Scheme and Evidence of Recombination between Major Circulating Clades. Journal of Virology, 2006, 80, 9850-9860.	1.5	142
59	Using purine skews to predict genes in AT-rich poxviruses. BMC Genomics, 2005, 6, 22.	1.2	14
60	Virulence differences between monkeypox virus isolates from West Africa and the Congo basin. Virology, 2005, 340, 46-63.	1.1	342
61	Genome segment RNA-1 of a flat apple isolate of Cherry rasp leaf virus: nucleotide sequence analysis and RT-PCR detection. Archives of Virology, 2005, 150, 1469-1476.	0.9	9
62	Complete coding sequences of the rabbitpox virus genome. Journal of General Virology, 2005, 86, 2969-2977.	1.3	41
63	Recent Hits Acquired by BLAST (ReHAB): a tool to identify new hits in sequence similarity searches. BMC Bioinformatics, 2005, 6, 23.	1.2	10
64	New bioinformatics tools for viral genome analyses at Viral Bioinformatics – Canada. Pharmacogenomics, 2005, 6, 271-280.	0.6	11
65	Host-derived pathogenicity islands in poxviruses. Virology Journal, 2005, 2, 30.	1.4	7
66	Poxvirus Bioinformatics. , 2004, 269, 347-370.		3
67	JDotter: a Java interface to multiple dotplots generated by dotter. Bioinformatics, 2004, 20, 279-281.	1.8	102
68	Poxvirus Bioinformatics Resource Center: a comprehensive Poxviridae informational and analytical resource. Nucleic Acids Research, 2004, 33, D311-D316.	6.5	53
69	Base-By-Base: single nucleotide-level analysis of whole viral genome alignments. BMC Bioinformatics, 2004, 5, 96.	1.2	64
70	The genomic sequence of ectromelia virus, the causative agent of mousepox. Virology, 2003, 317, 165-186.	1.1	86
71	The Genome Sequence of the SARS-Associated Coronavirus. Science, 2003, 300, 1399-1404.	6.0	1,842
72	Poxvirus Orthologous Clusters: toward Defining the Minimum Essential Poxvirus Genome. Journal of Virology, 2003, 77, 7590-7600.	1.5	254

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73	Poxvirus Orthologous Clusters (POCs). Bioinformatics, 2002, 18, 1544-1545.	1.8	62
74	Screening predicted coding regions in poxvirus genomes. , 2000, 20, 159-164.		15
75	Viral genome organizer: a system for analyzing complete viral genomes. Virus Research, 2000, 70, 55-64.	1.1	50
76	Analysis of host response modifier ORFs of ectromelia virus, the causative agent of mousepox. Virus Research, 2000, 66, 155-173.	1.1	26
77	Ectromelia virus virulence factor p28 acts upstream of caspase-3 in response to UV light-induced apoptosis. Journal of General Virology, 2000, 81, 1087-1097.	1.3	37
78	Single primer pair designs that facilitate simultaneous detection and differentiation of peach mosaic virus and cherry mottle leaf virus. Journal of Virological Methods, 1999, 83, 103-111.	1.0	23
79	Shope Fibroma Virus RING Finger Protein N1R Binds DNA and Inhibits Apoptosis. Virology, 1998, 249, 42-51.	1.1	42
80	Subversion of Cytokine Networks by Viruses. International Reviews of Immunology, 1998, 17, 121-155.	1.5	17
81	A human homolog of the vaccinia virus HindIII K4L gene is a member of the phospholipase D superfamily. Virus Research, 1997, 48, 11-18.	1.1	23
82	A novel poxvirus gene and its human homolog are similar to an E. coli Lysophospholipase. Virus Research, 1997, 52, 157-167.	1.1	17
83	gpt-gus Fusion Gene for Selection and Marker in Recombinant Poxviruses. BioTechniques, 1997, 22, 276-278.	0.8	16
84	A new family of lipolytic enzymes?. Trends in Biochemical Sciences, 1995, 20, 178-179.	3.7	286
85	The Myxoma Virus-soluble Interferon- Î³ Receptor Homolog, M-T7, Inhibits Interferon- Î³ in a Species-specific Manner. Journal of Biological Chemistry, 1995, 270, 3031-3038.	1.6	91
86	A new family of lipolytic plant enzymes with members in rice, arabidopsis and maize. FEBS Letters, 1995, 377, 475-480.	1.3	97
87	SERP1, a Serine Proteinase Inhibitor Encoded by Myxoma Virus, Is a Secreted Glycoprotein That Interferes with Inflammation. Virology, 1993, 195, 348-363.	1.1	152
88	Encoding of a homolog of the IFN-gamma receptor by myxoma virus. Science, 1992, 258, 1369-1372.	6.0	319
89	Deletion of the growth factor gene related to EGF and TGFÎ± reduces virulence of malignant rabbit fibroma virus. Virology, 1992, 186, 175-191.	1.1	39
90	Myxoma virus M11L ORF encodes a protein for which cell surface localization is critical in manifestation of viral virulence. Virology, 1992, 191, 112-124.	1.1	56

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91	Utilization of the second polyadenylation signal at the 3â€² end of the chicken carbonic anhydrase II gene. Nucleic Acids Research, 1990, 18, 1049-1049.	6.5	3
92	Transcriptional regulation of two cytotoxk T lymphocyte-specific serine protease gene. Nucleic Acids Research, 1989, 17, 5765-5779.	6.5	24
93	Organization of two genes encoding cytotoxic T lymphocyte-specific serine proteases CCPI and CCPII. Biochemistry, 1988, 27, 6941-6946.	1.2	42