

Chris Upton

List of Publications by Year in descending order

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93
papers

7,199
citations

94433

37
h-index

58581

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. <i>Briefings in Bioinformatics</i> , 2021, 22, 642-663.	6.5	110
2	The first genotype II African swine fever virus isolated in Africa provides insight into the current Eurasian pandemic. <i>Scientific Reports</i> , 2021, 11, 13081.	3.3	34
3	Bioinformatics for Analysis of Poxvirus Genomes. <i>Methods in Molecular Biology</i> , 2019, 2023, 29-62.	0.9	9
4	Isolation and Characterization of Akhmeta Virus from Wild-Caught Rodents (<i>Apodemus</i> spp.) in Georgia. <i>Journal of Virology</i> , 2019, 93, .	3.4	9
5	Bioinformatic Approaches for Comparative Analysis of Viruses. <i>Methods in Molecular Biology</i> , 2018, 1704, 401-417.	0.9	1
6	Base-By-Base Version 3: New Comparative Tools for Large Virus Genomes. <i>Viruses</i> , 2018, 10, 637.	3.3	24
7	Complete genome sequence of a novel sea otterpox virus. <i>Virus Genes</i> , 2018, 54, 756-767.	1.6	5
8	Genomic characterization of two novel pathogenic avipoxviruses isolated from pacific shearwaters (<i>Ardenna</i> spp.). <i>BMC Genomics</i> , 2017, 18, 298.	2.8	51
9	Complete genomic characterisation of two novel poxviruses (WKPV and EKPV) from western and eastern grey kangaroos. <i>Virus Research</i> , 2017, 242, 106-121.	2.2	8
10	Two novel poxviruses with unusual genome rearrangements: NY_014 and Murmansk. <i>Virus Genes</i> , 2017, 53, 883-897.	1.6	15
11	Characterization of Eptesipoxvirus, a novel poxvirus from a microchiropteran bat. <i>Virus Genes</i> , 2017, 53, 856-867.	1.6	16
12	Three novel <i>Pseudomonas</i> phages isolated from composting provide insights into the evolution and diversity of tailed phages. <i>BMC Genomics</i> , 2017, 18, 346.	2.8	32
13	The genomes of three North American orthopoxviruses. <i>Virus Genes</i> , 2017, 53, 21-34.	1.6	15
14	Virus Databases \hat{t} . , 2017, , .		2
15	Re-Assembly and Analysis of an Ancient Variola Virus Genome. <i>Viruses</i> , 2017, 9, 253.	3.3	14
16	Genomic characterization of a novel poxvirus from a flying fox: evidence for a new genus?. <i>Journal of General Virology</i> , 2016, 97, 2363-2375.	2.9	18
17	Comparative analysis of the complete genome sequences of Kenyan African swine fever virus isolates within p72 genotypes IX and X. <i>Virus Genes</i> , 2015, 50, 303-309.	1.6	49
18	Novel Poxvirus Infection in an Immune Suppressed Patient. <i>Clinical Infectious Diseases</i> , 2015, 61, 1543-1548.	5.8	16

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19	Related strains of African swine fever virus with different virulence: genome comparison and analysis. <i>Journal of General Virology</i> , 2015, 96, 408-419.	2.9	98
20	Genome sequence and comparative virulence of raccoonpox virus: the first North American poxvirus sequence. <i>Journal of General Virology</i> , 2015, 96, 2806-2821.	2.9	11
21	Incongruencies in Vaccinia Virus Phylogenetic Trees. <i>Computation</i> , 2014, 2, 182-198.	2.0	12
22	Expression of a non-coding RNA in ectromelia virus is required for normal plaque formation. <i>Virus Genes</i> , 2014, 48, 38-47.	1.6	2
23	Suffix tree searcher: exploration of common substrings in large DNA sequence sets. <i>BMC Research Notes</i> , 2014, 7, 466.	1.4	3
24	Prediction of Steps in the Evolution of Variola Virus Host Range. <i>PLoS ONE</i> , 2014, 9, e91520.	2.5	21
25	African swine fever virus replication and genomics. <i>Virus Research</i> , 2013, 173, 3-14.	2.2	460
26	Paramecium bursaria Chlorella Virus 1 Proteome Reveals Novel Architectural and Regulatory Features of a Giant Virus. <i>Journal of Virology</i> , 2012, 86, 8821-8834.	3.4	64
27	Bioinformatics for Analysis of Poxvirus Genomes. <i>Methods in Molecular Biology</i> , 2012, 890, 233-258.	0.9	8
28	It's a small world after all—viral genomics and the global dominance of viruses. <i>Current Opinion in Virology</i> , 2011, 1, 280-281.	5.4	0
29	Characterization of indels in poxvirus genomes. <i>Virus Genes</i> , 2011, 42, 171-177.	1.6	36
30	Prediction of a novel RNA binding domain in crocodilepox Zimbabwe Gene 157. <i>Microbial Informatics and Experimentation</i> , 2011, 1, 12.	7.6	1
31	Base-By-Base version 2: single nucleotide-level analysis of whole viral genome alignments. <i>Microbial Informatics and Experimentation</i> , 2011, 1, 2.	7.6	36
32	Genomic Analysis of Highly Virulent Georgia 2007/1 Isolate of African Swine Fever Virus. <i>Emerging Infectious Diseases</i> , 2011, 17, 599-605.	4.3	186
33	The Genome of Yoka Poxvirus. <i>Journal of Virology</i> , 2011, 85, 10230-10238.	3.4	30
34	Genomic Analysis of the Vaccinia Virus Strain Variants Found in Dryvax Vaccine. <i>Journal of Virology</i> , 2011, 85, 13049-13060.	3.4	63
35	Phylogenomic analysis of 11 complete African swine fever virus genome sequences. <i>Virology</i> , 2010, 400, 128-136.	2.4	134
36	JaPaFi: A Novel Program for the Identification of Highly Conserved DNA Sequences. <i>Viruses</i> , 2010, 2, 1867-1885.	3.3	2

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37	Vaccinia Virus Encoded Ribonucleotide Reductase Subunits Are Differentially Required for Replication and Pathogenesis. <i>PLoS Pathogens</i> , 2010, 6, e1000984.	4.7	66
38	Vaccinia Virus G8R Protein: A Structural Ortholog of Proliferating Cell Nuclear Antigen (PCNA). <i>PLoS ONE</i> , 2009, 4, e5479.	2.5	13
39	Sequence Searcher: A Java tool to perform regular expression and fuzzy searches of multiple DNA and protein sequences. <i>BMC Research Notes</i> , 2009, 2, 14.	1.4	11
40	KISSa: a strategy to build multiple sequence alignments from pairwise comparisons of very closely related sequences. <i>BMC Research Notes</i> , 2009, 2, 91.	1.4	0
41	Evidence for a novel gene associated with human influenza A viruses. <i>Virology Journal</i> , 2009, 6, 198.	3.4	26
42	Cowpox Virus Inhibits the Transporter Associated with Antigen Processing to Evade T Cell Recognition. <i>Cell Host and Microbe</i> , 2009, 6, 433-445.	11.0	68
43	Comparison of the genome sequences of non-pathogenic and pathogenic African swine fever virus isolates. <i>Journal of General Virology</i> , 2008, 89, 397-408.	2.9	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. <i>Vaccine</i> , 2007, 25, 8807-8832.	3.8	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.	5.1	50
48	An ectromelia virus profilin homolog interacts with cellular tropomyosin and viral A-type inclusion protein. <i>Virology Journal</i> , 2007, 4, 76.	3.4	12
49	Comparative genomic analysis of the family Iridoviridae: re-annotating and defining the core set of iridovirus genes. <i>Virology Journal</i> , 2007, 4, 11.	3.4	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. <i>BMC Bioinformatics</i> , 2007, 8, 21.	2.6	41
52	Organizing and Updating Whole Genome BLAST Searches with ReHAB. <i>Methods in Molecular Biology</i> , 2007, 395, 187-194.	0.9	1
53	Genomic sequence and analysis of a vaccinia virus isolate from a patient with a smallpox vaccine-related complication. <i>Virology Journal</i> , 2006, 3, 88.	3.4	24
54	Poxviruses: past, present and future. <i>Virus Research</i> , 2006, 117, 105-118.	2.2	164

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55	Java GUI for InterProScan (JIPS): A tool to help process multiple InterProScans and perform ortholog analysis. <i>BMC Bioinformatics</i> , 2006, 7, 462.	2.6	7
56	Genome Annotation Transfer Utility (GATU): rapid annotation of viral genomes using a closely related reference genome. <i>BMC Genomics</i> , 2006, 7, 150.	2.8	212
57	Predicted function of the vaccinia virus G5R protein. <i>Bioinformatics</i> , 2006, 22, 2846-2850.	4.1	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. <i>Journal of Virology</i> , 2006, 80, 9850-9860.	3.4	142
59	Using purine skews to predict genes in AT-rich poxviruses. <i>BMC Genomics</i> , 2005, 6, 22.	2.8	14
60	Virulence differences between monkeypox virus isolates from West Africa and the Congo basin. <i>Virology</i> , 2005, 340, 46-63.	2.4	342
61	Genome segment RNA-1 of a flat apple isolate of Cherry rasp leaf virus: nucleotide sequence analysis and RT-PCR detection. <i>Archives of Virology</i> , 2005, 150, 1469-1476.	2.1	9
62	Complete coding sequences of the rabbitpox virus genome. <i>Journal of General Virology</i> , 2005, 86, 2969-2977.	2.9	41
63	Recent Hits Acquired by BLAST (ReHAB): a tool to identify new hits in sequence similarity searches. <i>BMC Bioinformatics</i> , 2005, 6, 23.	2.6	10
64	New bioinformatics tools for viral genome analyses at Viral Bioinformatics "Canada". <i>Pharmacogenomics</i> , 2005, 6, 271-280.	1.3	11
65	Host-derived pathogenicity islands in poxviruses. <i>Virology Journal</i> , 2005, 2, 30.	3.4	7
66	Poxvirus Bioinformatics. , 2004, 269, 347-370.		3
67	JDotter: a Java interface to multiple dotplots generated by dotter. <i>Bioinformatics</i> , 2004, 20, 279-281.	4.1	102
68	Poxvirus Bioinformatics Resource Center: a comprehensive Poxviridae informational and analytical resource. <i>Nucleic Acids Research</i> , 2004, 33, D311-D316.	14.5	53
69	Base-By-Base: single nucleotide-level analysis of whole viral genome alignments. <i>BMC Bioinformatics</i> , 2004, 5, 96.	2.6	64
70	The genomic sequence of ectromelia virus, the causative agent of mousepox. <i>Virology</i> , 2003, 317, 165-186.	2.4	86
71	The Genome Sequence of the SARS-Associated Coronavirus. <i>Science</i> , 2003, 300, 1399-1404.	12.6	1,842
72	Poxvirus Orthologous Clusters: toward Defining the Minimum Essential Poxvirus Genome. <i>Journal of Virology</i> , 2003, 77, 7590-7600.	3.4	254

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73	Poxvirus Orthologous Clusters (POCs). <i>Bioinformatics</i> , 2002, 18, 1544-1545.	4.1	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. <i>Virus Research</i> , 2000, 70, 55-64.	2.2	50
76	Analysis of host response modifier ORFs of ectromelia virus, the causative agent of mousepox. <i>Virus Research</i> , 2000, 66, 155-173.	2.2	26
77	Ectromelia virus virulence factor p28 acts upstream of caspase-3 in response to UV light-induced apoptosis. <i>Journal of General Virology</i> , 2000, 81, 1087-1097.	2.9	37
78	Single primer pair designs that facilitate simultaneous detection and differentiation of peach mosaic virus and cherry mottle leaf virus. <i>Journal of Virological Methods</i> , 1999, 83, 103-111.	2.1	23
79	Shope Fibroma Virus RING Finger Protein N1R Binds DNA and Inhibits Apoptosis. <i>Virology</i> , 1998, 249, 42-51.	2.4	42
80	Subversion of Cytokine Networks by Viruses. <i>International Reviews of Immunology</i> , 1998, 17, 121-155.	3.3	17
81	A human homolog of the vaccinia virus HindIII K4L gene is a member of the phospholipase D superfamily. <i>Virus Research</i> , 1997, 48, 11-18.	2.2	23
82	A novel poxvirus gene and its human homolog are similar to an E. coli Lysophospholipase. <i>Virus Research</i> , 1997, 52, 157-167.	2.2	17
83	gpt-gus Fusion Gene for Selection and Marker in Recombinant Poxviruses. <i>BioTechniques</i> , 1997, 22, 276-278.	1.8	16
84	A new family of lipolytic enzymes?. <i>Trends in Biochemical Sciences</i> , 1995, 20, 178-179.	7.5	286
85	The Myxoma Virus-soluble Interferon- γ Receptor Homolog, M-T7, Inhibits Interferon- γ in a Species-specific Manner. <i>Journal of Biological Chemistry</i> , 1995, 270, 3031-3038.	3.4	91
86	A new family of lipolytic plant enzymes with members in rice, arabidopsis and maize. <i>FEBS Letters</i> , 1995, 377, 475-480.	2.8	97
87	SERP1, a Serine Proteinase Inhibitor Encoded by Myxoma Virus, Is a Secreted Glycoprotein That Interferes with Inflammation. <i>Virology</i> , 1993, 195, 348-363.	2.4	152
88	Encoding of a homolog of the IFN-gamma receptor by myxoma virus. <i>Science</i> , 1992, 258, 1369-1372.	12.6	319
89	Deletion of the growth factor gene related to EGF and TGF β reduces virulence of malignant rabbit fibroma virus. <i>Virology</i> , 1992, 186, 175-191.	2.4	39
90	Myxoma virus M11L ORF encodes a protein for which cell surface localization is critical in manifestation of viral virulence. <i>Virology</i> , 1992, 191, 112-124.	2.4	56

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91	Utilization of the second polyadenylation signal at the 3' end of the chicken carbonic anhydrase II gene. Nucleic Acids Research, 1990, 18, 1049-1049.	14.5	3
92	Transcriptional regulation of two cytotoxic T lymphocyte-specific serine protease gene. Nucleic Acids Research, 1989, 17, 5765-5779.	14.5	24
93	Organization of two genes encoding cytotoxic T lymphocyte-specific serine proteases CCPI and CCP II. Biochemistry, 1988, 27, 6941-6946.	2.5	42