

# Chris Upton

## List of Publications by Year in descending order

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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	The Genome Sequence of the SARS-Associated Coronavirus. <i>Science</i> , 2003, 300, 1399-1404.	6.0	1,842
2	African swine fever virus replication and genomics. <i>Virus Research</i> , 2013, 173, 3-14.	1.1	460
3	Virulence differences between monkeypox virus isolates from West Africa and the Congo basin. <i>Virology</i> , 2005, 340, 46-63.	1.1	342
4	Encoding of a homolog of the IFN-gamma receptor by myxoma virus. <i>Science</i> , 1992, 258, 1369-1372.	6.0	319
5	A new family of lipolytic enzymes?. <i>Trends in Biochemical Sciences</i> , 1995, 20, 178-179.	3.7	286
6	Poxvirus Orthologous Clusters: toward Defining the Minimum Essential Poxvirus Genome. <i>Journal of Virology</i> , 2003, 77, 7590-7600.	1.5	254
7	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.	1.3	244
8	Genome Annotation Transfer Utility (GATU): rapid annotation of viral genomes using a closely related reference genome. <i>BMC Genomics</i> , 2006, 7, 150.	1.2	212
9	Genomic Analysis of Highly Virulent Georgia 2007/1 Isolate of African Swine Fever Virus. <i>Emerging Infectious Diseases</i> , 2011, 17, 599-605.	2.0	186
10	Poxviruses: past, present and future. <i>Virus Research</i> , 2006, 117, 105-118.	1.1	164
11	SERP1, a Serine Proteinase Inhibitor Encoded by Myxoma Virus, Is a Secreted Glycoprotein That Interferes with Inflammation. <i>Virology</i> , 1993, 195, 348-363.	1.1	152
12	Comparative genomic analysis of the family Iridoviridae: re-annotating and defining the core set of iridovirus genes. <i>Virology Journal</i> , 2007, 4, 11.	1.4	152
13	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.	1.5	142
14	Phylogenomic analysis of 11 complete African swine fever virus genome sequences. <i>Virology</i> , 2010, 400, 128-136.	1.1	134
15	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.	3.2	110
16	JDotter: a Java interface to multiple dotplots generated by dotter. <i>Bioinformatics</i> , 2004, 20, 279-281.	1.8	102
17	Related strains of African swine fever virus with different virulence: genome comparison and analysis. <i>Journal of General Virology</i> , 2015, 96, 408-419.	1.3	98
18	A new family of lipolytic plant enzymes with members in rice, arabidopsis and maize. <i>FEBS Letters</i> , 1995, 377, 475-480.	1.3	97

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19	The Myxoma Virus-soluble Interferon- $\beta$ Receptor Homolog, M-T7, Inhibits Interferon- $\beta$ in a Species-specific Manner. <i>Journal of Biological Chemistry</i> , 1995, 270, 3031-3038.	1.6	91
20	The genomic sequence of ectromelia virus, the causative agent of mousepox. <i>Virology</i> , 2003, 317, 165-186.	1.1	86
21	Cowpox Virus Inhibits the Transporter Associated with Antigen Processing to Evade T Cell Recognition. <i>Cell Host and Microbe</i> , 2009, 6, 433-445.	5.1	68
22	Vaccinia Virus-Encoded Ribonucleotide Reductase Subunits Are Differentially Required for Replication and Pathogenesis. <i>PLoS Pathogens</i> , 2010, 6, e1000984.	2.1	66
23	Base-By-Base: single nucleotide-level analysis of whole viral genome alignments. <i>BMC Bioinformatics</i> , 2004, 5, 96.	1.2	64
24	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.	1.5	64
25	Genomic Analysis of the Vaccinia Virus Strain Variants Found in Dryvax Vaccine. <i>Journal of Virology</i> , 2011, 85, 13049-13060.	1.5	63
26	Poxvirus Orthologous Clusters (POCs). <i>Bioinformatics</i> , 2002, 18, 1544-1545.	1.8	62
27	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.	1.1	56
28	Poxvirus Bioinformatics Resource Center: a comprehensive Poxviridae informational and analytical resource. <i>Nucleic Acids Research</i> , 2004, 33, D311-D316.	6.5	53
29	Genomic characterization of two novel pathogenic avipoxviruses isolated from pacific shearwaters ( <i>Ardenna</i> spp.). <i>BMC Genomics</i> , 2017, 18, 298.	1.2	51
30	Viral genome organizer: a system for analyzing complete viral genomes. <i>Virus Research</i> , 2000, 70, 55-64.	1.1	50
31	Role of phages in the pathogenesis of Burkholderia, or "Where are the toxin genes in Burkholderia phages?" <i>Current Opinion in Microbiology</i> , 2007, 10, 410-417.	2.3	50
32	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.	0.7	49
33	Organization of two genes encoding cytotoxic T lymphocyte-specific serine proteases CCPI and CCPII. <i>Biochemistry</i> , 1988, 27, 6941-6946.	1.2	42
34	Shope Fibroma Virus RING Finger Protein N1R Binds DNA and Inhibits Apoptosis. <i>Virology</i> , 1998, 249, 42-51.	1.1	42
35	Complete coding sequences of the rabbitpox virus genome. <i>Journal of General Virology</i> , 2005, 86, 2969-2977.	1.3	41
36	GraphDNA: a Java program for graphical display of DNA composition analyses. <i>BMC Bioinformatics</i> , 2007, 8, 21.	1.2	41

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37	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.	1.7	40
38	Deletion of the growth factor gene related to EGF and TGF $\beta$ reduces virulence of malignant rabbit fibroma virus. <i>Virology</i> , 1992, 186, 175-191.	1.1	39
39	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.	1.3	37
40	Characterization of indels in poxvirus genomes. <i>Virus Genes</i> , 2011, 42, 171-177.	0.7	36
41	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
42	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.	1.6	34
43	Three novel Pseudomonas phages isolated from composting provide insights into the evolution and diversity of tailed phages. <i>BMC Genomics</i> , 2017, 18, 346.	1.2	32
44	The Genome of Yoka Poxvirus. <i>Journal of Virology</i> , 2011, 85, 10230-10238.	1.5	30
45	Analysis of host response modifier ORFs of ectromelia virus, the causative agent of mousepox. <i>Virus Research</i> , 2000, 66, 155-173.	1.1	26
46	Evidence for a novel gene associated with human influenza A viruses. <i>Virology Journal</i> , 2009, 6, 198.	1.4	26
47	Transcriptional regulation of two cytotoxic T lymphocyte-specific serine protease gene. <i>Nucleic Acids Research</i> , 1989, 17, 5765-5779.	6.5	24
48	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.	1.4	24
49	Base-By-Base Version 3: New Comparative Tools for Large Virus Genomes. <i>Viruses</i> , 2018, 10, 637.	1.5	24
50	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.	1.1	23
51	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.	1.0	23
52	Prediction of Steps in the Evolution of Variola Virus Host Range. <i>PLoS ONE</i> , 2014, 9, e91520.	1.1	21
53	Predicted function of the vaccinia virus G5R protein. <i>Bioinformatics</i> , 2006, 22, 2846-2850.	1.8	19
54	A new method for indexing genomes using on-disk suffix trees. , 2008, , .		18

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55	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.	1.3	18
56	A novel poxvirus gene and its human homolog are similar to an E. coli Lysophospholipase. <i>Virus Research</i> , 1997, 52, 157-167.	1.1	17
57	Subversion of Cytokine Networks by Viruses. <i>International Reviews of Immunology</i> , 1998, 17, 121-155.	1.5	17
58	gpt-gus Fusion Gene for Selection and Marker in Recombinant Poxviruses. <i>BioTechniques</i> , 1997, 22, 276-278.	0.8	16
59	Novel Poxvirus Infection in an Immune Suppressed Patient. <i>Clinical Infectious Diseases</i> , 2015, 61, 1543-1548.	2.9	16
60	Characterization of Eptesipoxvirus, a novel poxvirus from a microchiropteran bat. <i>Virus Genes</i> , 2017, 53, 856-867.	0.7	16
61	Screening predicted coding regions in poxvirus genomes. , 2000, 20, 159-164.		15
62	Two novel poxviruses with unusual genome rearrangements: NY_014 and Murmansk. <i>Virus Genes</i> , 2017, 53, 883-897.	0.7	15
63	The genomes of three North American orthopoxviruses. <i>Virus Genes</i> , 2017, 53, 21-34.	0.7	15
64	Using purine skews to predict genes in AT-rich poxviruses. <i>BMC Genomics</i> , 2005, 6, 22.	1.2	14
65	Re-Assembly and Analysis of an Ancient Variola Virus Genome. <i>Viruses</i> , 2017, 9, 253.	1.5	14
66	Vaccinia Virus G8R Protein: A Structural Ortholog of Proliferating Cell Nuclear Antigen (PCNA). <i>PLoS ONE</i> , 2009, 4, e5479.	1.1	13
67	An ectromelia virus profilin homolog interacts with cellular tropomyosin and viral A-type inclusion protein. <i>Virology Journal</i> , 2007, 4, 76.	1.4	12
68	Incongruencies in Vaccinia Virus Phylogenetic Trees. <i>Computation</i> , 2014, 2, 182-198.	1.0	12
69	New bioinformatics tools for viral genome analyses at Viral Bioinformatics “Canada. <i>Pharmacogenomics</i> , 2005, 6, 271-280.	0.6	11
70	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.	0.6	11
71	Genome sequence and comparative virulence of raccoonpox virus: the first North American poxvirus sequence. <i>Journal of General Virology</i> , 2015, 96, 2806-2821.	1.3	11
72	Recent Hits Acquired by BLAST (ReHAB): a tool to identify new hits in sequence similarity searches. <i>BMC Bioinformatics</i> , 2005, 6, 23.	1.2	10

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73	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
74	Bioinformatics for Analysis of Poxvirus Genomes. Methods in Molecular Biology, 2019, 2023, 29-62.	0.4	9
75	Isolation and Characterization of Akhmeta Virus from Wild-Caught Rodents ( <i>Apodemus</i> spp.) in Georgia. Journal of Virology, 2019, 93, .	1.5	9
76	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
77	Bioinformatics for Analysis of Poxvirus Genomes. Methods in Molecular Biology, 2012, 890, 233-258.	0.4	8
78	Host-derived pathogenicity islands in poxviruses. Virology Journal, 2005, 2, 30.	1.4	7
79	Java GUI for InterProScan (JIPS): A tool to help process multiple InterProScans and perform ortholog analysis. BMC Bioinformatics, 2006, 7, 462.	1.2	7
80	Complete genome sequence of a novel sea otterpox virus. Virus Genes, 2018, 54, 756-767.	0.7	5
81	Utilization of the second polyadenylation signal at the 3' end of the chicken carbonic anhydrase II gene. Nucleic Acids Research, 1990, 18, 1049-1049.	6.5	3
82	Poxvirus Bioinformatics. , 2004, 269, 347-370.		3
83	Suffix tree searcher: exploration of common substrings in large DNA sequence sets. BMC Research Notes, 2014, 7, 466.	0.6	3
84	Shortest Path Approaches for the Longest Common Subsequence of a Set of Strings. , 2007, , .		2
85	JaPaFi: A Novel Program for the Identification of Highly Conserved DNA Sequences. Viruses, 2010, 2, 1867-1885.	1.5	2
86	Expression of a non-coding RNA in ectromelia virus is required for normal plaque formation. Virus Genes, 2014, 48, 38-47.	0.7	2
87	Virus Databases . , 2017, , .		2
88	Prediction of a novel RNA binding domain in crocodilepox Zimbabwe Gene 157. Microbial Informatics and Experimentation, 2011, 1, 12.	7.6	1
89	Bioinformatic Approaches for Comparative Analysis of Viruses. Methods in Molecular Biology, 2018, 1704, 401-417.	0.4	1
90	Organizing and Updating Whole Genome BLAST Searches with ReHAB. Methods in Molecular Biology, 2007, 395, 187-194.	0.4	1

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91	Comparative Genomics of Viruses Using Bioinformatics Tools. , 2007, , 49-72.		0
92	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
93	It's a small world after allâ€”viral genomics and the global dominance of viruses. Current Opinion in Virology, 2011, 1, 280-281.	2.6	0