

# Jeremy D Volkening

## 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.

30  
papers

920  
citations

13  
h-index

30  
g-index

31  
ext. papers

1,213  
ext. citations

7.1  
avg, IF

3.77  
L-index

| #  | Paper   | IF   | Citations |
|----|---|------|-----------|
| 30 | Runting and Stunting Syndrome in Broiler Chickens: Histopathology and Association With a Novel Picornavirus. <i>Veterinary Pathology</i> , <b>2021</b> , 58, 123-135  | 2.8  | 2         |
| 29 | Surveillance and Genetic Characterization of Virulent Newcastle Disease Virus Subgenotype V.3 in Indigenous Chickens from Backyard Poultry Farms and Live Bird Markets in Kenya. <i>Viruses</i> , <b>2021</b> , 13, | 6.2  | 2         |
| 28 | Comparative Molecular Characterization of Three Type 3 Strains 301B/1, HPRS24, and SB-1. <i>Avian Diseases</i> , <b>2020</b> , 64, 174-182  | 1.6  | 0         |
| 27 | Presence of Newcastle disease viruses of sub-genotypes Vc and VIn in backyard chickens and in apparently healthy wild birds from Mexico in 2017. <i>Virus Genes</i> , <b>2019</b> , 55, 479-489                     | 2.3  | 8         |
| 26 | MinION sequencing to genotype US strains of infectious laryngotracheitis virus. <i>Avian Pathology</i> , <b>2019</b> , 48, 255-269  | 2.4  | 7         |
| 25 | Rapid, multiplexed, whole genome and plasmid sequencing of foodborne pathogens using long-read nanopore technology. <i>Scientific Reports</i> , <b>2019</b> , 9, 16350  | 4.9  | 22        |
| 24 | Proteome-wide Analysis of Protein Thermal Stability in the Model Higher Plant. <i>Molecular and Cellular Proteomics</i> , <b>2019</b> , 18, 308-319   | 7.6  | 23        |
| 23 | Draft Genome Sequences of Five Novel Ochrobactrum spp. Isolated from Different Avian Hosts in Nigeria. <i>Genome Announcements</i> , <b>2018</b> , 6,   |      | 2         |
| 22 | Draft Genome Sequences of Three Ochrobactrum spp. Isolated from Different Avian Hosts in Pakistan. <i>Genome Announcements</i> , <b>2018</b> , 6,   |      | 1         |
| 21 | Rapid virulence prediction and identification of Newcastle disease virus genotypes using third-generation sequencing. <i>Virology Journal</i> , <b>2018</b> , 15, 179   | 6.1  | 13        |
| 20 | A robust and cost-effective approach to sequence and analyze complete genomes of small RNA viruses. <i>Virology Journal</i> , <b>2017</b> , 14, 72  | 6.1  | 53        |
| 19 | A proteomic atlas of the legume <i>Medicago truncatula</i> and its nitrogen-fixing endosymbiont <i>Sinorhizobium meliloti</i> . <i>Nature Biotechnology</i> , <b>2016</b> , 34, 1198-1205                           | 44.5 | 68        |
| 18 | Attenuation and protection efficacy of ORF C gene-deleted recombinant of infectious laryngotracheitis virus. <i>Journal of General Virology</i> , <b>2016</b> , 97, 2352-2362                                       | 4.9  | 15        |
| 17 | Complete Genome Sequence of a Genotype XVII Newcastle Disease Virus, Isolated from an Apparently Healthy Domestic Duck in Nigeria. <i>Genome Announcements</i> , <b>2016</b> , 4,                                   |      | 12        |
| 16 | Identification and Complete Genome Sequence Analysis of a Genotype XIV Newcastle Disease Virus from Nigeria. <i>Genome Announcements</i> , <b>2016</b> , 4,   |      | 3         |
| 15 | Potential regulatory phosphorylation sites in a <i>Medicago truncatula</i> plasma membrane proton pump implicated during early symbiotic signaling in roots. <i>FEBS Letters</i> , <b>2015</b> , 589, 2186-93       | 3.8  | 7         |
| 14 | Unique patterns of transcript and miRNA expression in the South American strong voltage electric eel ( <i>Electrophorus electricus</i> ). <i>BMC Genomics</i> , <b>2015</b> , 16, 243                               | 4.5  | 13        |

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|----|--|------|-----|
| 13 | Algal ancestor of land plants was preadapted for symbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 13390-5  | 11.5 | 197 |
| 12 | Molecular characterization of the complete genome of falconid herpesvirus strain S-18. <i>Virus Research</i> , <b>2014</b> , 188, 109-21   | 6.4  | 5   |
| 11 | Nonhuman genetics. Genomic basis for the convergent evolution of electric organs. <i>Science</i> , <b>2014</b> , 344, 1522-5   | 33.3 | 128 |
| 10 | Expression of chicken parvovirus VP2 in chicken embryo fibroblasts requires codon optimization for production of naked DNA and vectored meleagrid herpesvirus type 1 vaccines. <i>Virus Genes</i> , <b>2013</b> , 47, 259-67                       | 2.3  | 5   |
| 9  | Symbiosis and the social network of higher plants. <i>Current Opinion in Plant Biology</i> , <b>2013</b> , 16, 118-27  | 9.9  | 98  |
| 8  | Genomic sequence analysis of the United States infectious laryngotracheitis vaccine strains chicken embryo origin (CEO) and tissue culture origin (TCO). <i>Virology</i> , <b>2013</b> , 440, 64-74  | 3.6  | 37  |
| 7  | Identification and characterization of the genomic termini and cleavage/packaging signals of gallid herpesvirus type 2. <i>Avian Diseases</i> , <b>2013</b> , 57, 401-8  | 1.6  | 6   |
| 6  | Comparative full genome analysis of four infectious laryngotracheitis virus (Gallid herpesvirus-1) virulent isolates from the United States. <i>Virus Genes</i> , <b>2012</b> , 44, 273-85   | 2.3  | 35  |
| 5  | Dynamic equilibrium of Marek's disease genomes during in vitro serial passage. <i>Virus Genes</i> , <b>2012</b> , 45, 526-36   | 2.3  | 13  |
| 4  | A proteogenomic survey of the <i>Medicago truncatula</i> genome. <i>Molecular and Cellular Proteomics</i> , <b>2012</b> , 11, 933-44   | 7.6  | 24  |
| 3  | Rapid phosphoproteomic and transcriptomic changes in the rhizobia-legume symbiosis. <i>Molecular and Cellular Proteomics</i> , <b>2012</b> , 11, 724-44  | 7.6  | 91  |
| 2  | Purification of DNA from the cell-associated herpesvirus Marek's disease virus for 454 pyrosequencing using micrococcal nuclease digestion and polyethylene glycol precipitation. <i>Journal of Virological Methods</i> , <b>2009</b> , 157, 55-61 | 2.6  | 27  |
| 1  | Rapid and sensitive virulence prediction and identification of Newcastle disease virus genotypes using third-generation sequencing   |      | 3   |