

# Martin Shumway

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11103534/publications.pdf>

Version: 2024-02-01

16  
papers

14,397  
citations

516710

16  
h-index

940533

16  
g-index

16  
all docs

16  
docs citations

16  
times ranked

26253  
citing authors

#	ARTICLE	IF	CITATIONS
1	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2012, 40, D13-D25.	14.5	510
2	The sequence read archive: explosive growth of sequencing data. <i>Nucleic Acids Research</i> , 2012, 40, D54-D56.	14.5	841
3	The 1000 Genomes Project: data management and community access. <i>Nature Methods</i> , 2012, 9, 459-462.	19.0	308
4	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2011, 39, D38-D51.	14.5	582
5	Two New Complete Genome Sequences Offer Insight into Host and Tissue Specificity of Plant Pathogenic <i>Xanthomonas</i> spp. <i>Journal of Bacteriology</i> , 2011, 193, 5450-5464.	2.2	189
6	The Sequence Read Archive. <i>Nucleic Acids Research</i> , 2011, 39, D19-D21.	14.5	2,298
7	Sequencing of <i>Culex quinquefasciatus</i> Establishes a Platform for Mosquito Comparative Genomics. <i>Science</i> , 2010, 330, 86-88.	12.6	424
8	Archiving next generation sequencing data. <i>Nucleic Acids Research</i> , 2010, 38, D870-D871.	14.5	101
9	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2010, 38, D5-D16.	14.5	417
10	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2009, 37, D5-D15.	14.5	797
11	Genome sequence and rapid evolution of the rice pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99A. <i>BMC Genomics</i> , 2008, 9, 204.	2.8	327
12	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2007, 36, D13-D21.	14.5	757
13	Genome Sequence of <i>Aedes aegypti</i> , a Major Arbovirus Vector. <i>Science</i> , 2007, 316, 1718-1723.	12.6	1,025
14	Large-scale sequencing of human influenza reveals the dynamic nature of viral genome evolution. <i>Nature</i> , 2005, 437, 1162-1166.	27.8	419
15	Versatile and open software for comparing large genomes. <i>Genome Biology</i> , 2004, 5, R12.	9.6	4,989
16	Comparative Genome Sequencing for Discovery of Novel Polymorphisms in <i>Bacillus anthracis</i> . <i>Science</i> , 2002, 296, 2028-2033.	12.6	413