

Mark A Jensen

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

5,740
citations

236612

25
h-index

454577

30
g-index

30
all docs

30
docs citations

30
times ranked

9287
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015, 372, 2481-2498.	13.9	2,582
2	A Practical Guide to The Cancer Genome Atlas (TCGA). <i>Methods in Molecular Biology</i> , 2016, 1418, 111-141.	0.4	463
3	Improved Coreceptor Usage Prediction and Genotypic Monitoring of R5-to-X4 Transition by Motif Analysis of Human Immunodeficiency Virus Type 1 env V3 Loop Sequences. <i>Journal of Virology</i> , 2003, 77, 13376-13388.	1.5	390
4	The NCI Genomic Data Commons as an engine for precision medicine. <i>Blood</i> , 2017, 130, 453-459.	0.6	226
5	Dual HIV-1 infection associated with rapid disease progression. <i>Lancet</i> , 2004, 363, 619-622.	6.3	189
6	Changes in Human Immunodeficiency Virus Type 1 Fitness and Genetic Diversity during Disease Progression. <i>Journal of Virology</i> , 2005, 79, 9006-9018.	1.5	182
7	Modeling the role of bacteriophage in the control of cholera outbreaks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 4652-4657.	3.3	173
8	Potential impact of recombination on sitewise approaches for detecting positive natural selection. <i>Genetical Research</i> , 2003, 81, 115-121.	0.3	158
9	Deep Sequencing to Infer HIV-1 Co-Receptor Usage: Application to Three Clinical Trials of Maraviroc in Treatment-Experienced Patients. <i>Journal of Infectious Diseases</i> , 2011, 203, 237-245.	1.9	137
10	A Reliable Phenotype Predictor for Human Immunodeficiency Virus Type 1 Subtype C Based on Envelope V3 Sequences. <i>Journal of Virology</i> , 2006, 80, 4698-4704.	1.5	124
11	Consensus and Ancestral State HIV Vaccines. <i>Science</i> , 2003, 299, 1515c-1518.	6.0	121
12	Evolutionary Indicators of Human Immunodeficiency Virus Type 1 Reservoirs and Compartments. <i>Journal of Virology</i> , 2003, 77, 5540-5546.	1.5	97
13	HIV-Specific Probabilistic Models of Protein Evolution. <i>PLoS ONE</i> , 2007, 2, e503.	1.1	96
14	Predicting HIV-1 coreceptor usage with sequence analysis. <i>AIDS Reviews</i> , 2003, 5, 104-12.	0.5	95
15	Deep V3 Sequencing for HIV Type 1 Tropism in Treatment-Naive Patients: A Reanalysis of the MERIT Trial of Maraviroc. <i>Clinical Infectious Diseases</i> , 2011, 53, 732-742.	2.9	85
16	Coping with Viral Diversity in HIV Vaccine Design. <i>PLoS Computational Biology</i> , 2007, 3, e75.	1.5	83
17	Clinical and immunological impact of HIV envelope V3 sequence variation after starting initial triple antiretroviral therapy. <i>Aids</i> , 2004, 18, F1-F9.	1.0	80
18	Patterns of Genetic Variation at a Chromosome 4 Locus of <i>Drosophila melanogaster</i> and <i>D. simulans</i> . <i>Genetics</i> , 2002, 160, 493-507.	1.2	77

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19	Improved Detection of CXCR4-Using HIV by V3 Genotyping: Application of Population-Based and "Deep" Sequencing to Plasma RNA and Proviral DNA. <i>Journal of Acquired Immune Deficiency Syndromes</i> (1999), 2010, 54, 506-510.	0.9	66
20	Influence of Random Genetic Drift on Human Immunodeficiency Virus Type 1 env Evolution During Chronic Infection. <i>Genetics</i> , 2004, 166, 1155-1164.	1.2	65
21	Molecular Population Genetics and Evolution of a Prion-like Protein in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2001, 159, 527-535.	1.2	54
22	Reconstruction and Function of Ancestral Center-of-Tree Human Immunodeficiency Virus Type 1 Proteins. <i>Journal of Virology</i> , 2007, 81, 8507-8514.	1.5	53
23	BIO::Phylo-phyloinformatic analysis using perl. <i>BMC Bioinformatics</i> , 2011, 12, 63.	1.2	44
24	Genetic Characterization of Rebounding Human Immunodeficiency Virus Type 1 in Plasma during Multiple Interruptions of Highly Active Antiretroviral Therapy. <i>Journal of Virology</i> , 2003, 77, 3229-3237.	1.5	42
25	HIV Type 1 Superinfection with a Dual-Tropic Virus and Rapid Progression to AIDS: A Case Report. <i>Clinical Infectious Diseases</i> , 2007, 45, 501-509.	2.9	35
26	Molecular clock-like evolution of human immunodeficiency virus type 1. <i>Virology</i> , 2004, 329, 101-108.	1.1	15
27	HIV-1 with Predicted CXCR4 Genotype Identified in Clade C from India. <i>Molecular Diagnosis and Therapy</i> , 2009, 13, 19-24.	1.6	3
28	A Comparison of Interpretation by Three Different HIV Type 1 Genotypic Drug Resistance Algorithms Using Sequences from Non-Clade B HIV Type 1 Strains. <i>AIDS Research and Human Retroviruses</i> , 2009, 25, 315-318.	0.5	3
29	Sources of Variation in Ancestral Sequence Reconstruction for HIV-1 Envelope Genes. <i>Evolutionary Bioinformatics</i> , 2006, 2, 117693430600200.	0.6	1
30	Predicting disease outcomes in the clinic. <i>Nature Biotechnology</i> , 2008, 26, 611-612.	9.4	1