Mark A Jensen

List of Publications by Year
in descending order

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30 papers	5,740 citations	236925 25 h-index	454955 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. New England Journal of Medicine, 2015, 372, 2481-2498.	27.0	2,582
2	A Practical Guide to The Cancer Genome Atlas (TCGA). Methods in Molecular Biology, 2016, 1418, 111-141.	0.9	463
3	Improved Coreceptor Usage Prediction and GenotypicMonitoring of R5-to-X4 Transition by Motif Analysis of HumanImmunodeficiency Virus Type 1 env V3 LoopSequences. Journal of Virology, 2003, 77, 13376-13388.	3.4	390
4	The NCI Genomic Data Commons as an engine for precision medicine. Blood, 2017, 130, 453-459.	1.4	226
5	Dual HIV-1 infection associated with rapid disease progression. Lancet, The, 2004, 363, 619-622.	13.7	189
6	Changes in Human Immunodeficiency Virus Type 1 Fitness and Genetic Diversity during Disease Progression. Journal of Virology, 2005, 79, 9006-9018.	3.4	182
7	Modeling the role of bacteriophage in the control of cholera outbreaks. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 4652-4657.	7.1	173
8	Potential impact of recombination on sitewise approaches for detecting positive natural selection. Genetical Research, 2003, 81, 115-121.	0.9	158
9	Deep Sequencing to Infer HIV-1 Co-Receptor Usage: Application to Three Clinical Trials of Maraviroc in Treatment-Experienced Patients. Journal of Infectious Diseases, 2011, 203, 237-245.	4.0	137
10	A Reliable Phenotype Predictor for Human Immunodeficiency Virus Type 1 Subtype C Based on Envelope V3 Sequences. Journal of Virology, 2006, 80, 4698-4704.	3.4	124
11	Consensus and Ancestral State HIV Vaccines. Science, 2003, 299, 1515c-1518.	12.6	121
12	Evolutionary Indicators of Human Immunodeficiency Virus Type 1 Reservoirs and Compartments. Journal of Virology, 2003, 77, 5540-5546.	3.4	97
13	HIV-Specific Probabilistic Models of Protein Evolution. PLoS ONE, 2007, 2, e503.	2.5	96
14	Predicting HIV-1 coreceptor usage with sequence analysis. AIDS Reviews, 2003, 5, 104-12.	1.0	95
15	Deep V3 Sequencing for HIV Type 1 Tropism in Treatment-Naive Patients: A Reanalysis of the MERIT Trial of Maraviroc. Clinical Infectious Diseases, 2011, 53, 732-742.	5.8	85
16	Coping with Viral Diversity in HIV Vaccine Design. PLoS Computational Biology, 2007, 3, e75.	3.2	83
17	Clinical and immunological impact of HIV envelope V3 sequence variation after starting initial triple antiretroviral therapy. Aids, 2004, 18, F1-F9.	2.2	80
18	Patterns of Genetic Variation at a Chromosome 4 Locus of Drosophila melanogaster and D. simulans. Genetics, 2002, 160, 493-507.	2.9	77

#	Article	IF	Citations
19	Improved Detection of CXCR4-Using HIV by V3 Genotyping: Application of Population-Based and â€œDeepâ€• Sequencing to Plasma RNA and Proviral DNA. Journal of Acquired Immune Deficiency Syndromes (1999), 2010, 54, 506-510.	2.1	66
20	Influence of Random Genetic Drift on Human Immunodeficiency Virus Type 1 env Evolution During Chronic Infection. Genetics, 2004, 166, 1155-1164.	2.9	65
21	Molecular Population Genetics and Evolution of a Prion-like Protein in Saccharomyces cerevisiae. Genetics, 2001, 159, 527-535.	2.9	54
22	Reconstruction and Function of Ancestral Center-of-Tree Human Immunodeficiency Virus Type 1 Proteins. Journal of Virology, 2007, 81, 8507-8514.	3.4	53
23	BIO::Phylo-phyloinformatic analysis using perl. BMC Bioinformatics, 2011, 12, 63.	2.6	44
24	Genetic Characterization of Rebounding Human Immunodeficiency Virus Type 1 in Plasma during Multiple Interruptions of Highly Active Antiretroviral Therapy. Journal of Virology, 2003, 77, 3229-3237.	3.4	42
25	HIV Type 1 Superinfection with a Dual-Tropic Virus and Rapid Progression to AIDS: A Case Report. Clinical Infectious Diseases, 2007, 45, 501-509.	5.8	35
26	Molecular clock-like evolution of human immunodeficiency virus type 1. Virology, 2004, 329, 101-108.	2.4	15
27	HIV-1 with Predicted CXCR4 Genotype Identified in Clade C from India. Molecular Diagnosis and Therapy, 2009, 13, 19-24.	3.8	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. AIDS Research and Human Retroviruses, 2009, 25, 315-318.	1.1	3
29	Sources of Variation in Ancestral Sequence Reconstruction for HIV-1 Envelope Genes. Evolutionary Bioinformatics, 2006, 2, 117693430600200.	1.2	1
30	Predicting disease outcomes in the clinic. Nature Biotechnology, 2008, 26, 611-612.	17.5	1