

Tobias Sing

List of Publications by Year in descending order

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Version: 2024-02-01

17
papers

3,614
citations

623734

14
h-index

888059

17
g-index

17
all docs

17
docs citations

17
times ranked

7522
citing authors

#	ARTICLE	IF	CITATIONS
1	ROCR: visualizing classifier performance in R. <i>Bioinformatics</i> , 2005, 21, 3940-3941.	4.1	2,677
2	Predicting HIV Coreceptor Usage on the Basis of Genetic and Clinical Covariates. <i>Antiviral Therapy</i> , 2007, 12, 1097-1106.	1.0	137
3	Current V3 genotyping algorithms are inadequate for predicting X4 co-receptor usage in clinical isolates. <i>Aids</i> , 2007, 21, F17-F24.	2.2	127
4	Determining Human Immunodeficiency Virus Coreceptor Use in a Clinical Setting: Degree of Correlation between Two Phenotypic Assays and a Bioinformatic Model. <i>Journal of Clinical Microbiology</i> , 2007, 45, 279-284.	3.9	90
5	Bioinformatics-assisted anti-HIV therapy. <i>Nature Reviews Microbiology</i> , 2006, 4, 790-797.	28.6	82
6	Estimating HIV Evolutionary Pathways and the Genetic Barrier to Drug Resistance. <i>Journal of Infectious Diseases</i> , 2005, 191, 1953-1960.	4.0	76
7	Structural Descriptors of gp120 V3 Loop for the Prediction of HIV-1 Coreceptor Usage. <i>PLoS Computational Biology</i> , 2007, 3, e58.	3.2	76
8	Involvement of Novel Human Immunodeficiency Virus Type 1 Reverse Transcriptase Mutations in the Regulation of Resistance to Nucleoside Inhibitors. <i>Journal of Virology</i> , 2006, 80, 7186-7198.	3.4	64
9	Characterization and Structural Analysis of Novel Mutations in Human Immunodeficiency Virus Type 1 Reverse Transcriptase Involved in the Regulation of Resistance to Nonnucleoside Inhibitors. <i>Journal of Virology</i> , 2007, 81, 11507-11519.	3.4	62
10	HIV-1 gp120 V3 Loop for Structure-Based Drug Design. <i>Current Protein and Peptide Science</i> , 2005, 6, 413-422.	1.4	59
11	Compensatory Mutations at the HIV Cleavage Sites P7/P1 and P1/P6-Gag in Therapy-Naive and Therapy-Experienced Patients. <i>Antiviral Therapy</i> , 2006, 11, 879-888.	1.0	58
12	Improved Prediction of Response to Antiretroviral Combination Therapy using the Genetic Barrier to Drug Resistance. <i>Antiviral Therapy</i> , 2007, 12, 169-178.	1.0	42
13	Characterization of Novel HIV Drug Resistance Mutations Using Clustering, Multidimensional Scaling and SVM-Based Feature Ranking. <i>Lecture Notes in Computer Science</i> , 2005, , 285-296.	1.3	18
14	Docking Analysis and Resistance Evaluation of Clinically Relevant Mutations Associated with the HIV-1 Non-nucleoside Reverse Transcriptase Inhibitors Nevirapine, Efavirenz and Etravirine. <i>ChemMedChem</i> , 2011, 6, 2203-2213.	3.2	14
15	Dynamics of NRTI Resistance Mutations during Therapy Interruption. <i>AIDS Research and Human Retroviruses</i> , 2009, 25, 57-64.	1.1	11
16	Arevir: A Secure Platform for Designing Personalized Antiretroviral Therapies Against HIV. <i>Lecture Notes in Computer Science</i> , 2006, , 185-194.	1.3	11
17	Advantages of predicted phenotypes and statistical learning models in inferring virological response to antiretroviral therapy from HIV genotype. <i>Antiviral Therapy</i> , 2009, 14, 273-283.	1.0	10