Carl Kadie

List of Publications by Year
in descending order

24 papers	2,068 citations	393982 19 h-index	610482 24 g-index
24 all docs	24 docs citations	24 times ranked	2888 citing authors

#	Article	IF	Citations
1	Uganda Genome Resource Enables Insights into Population History and Genomic Discovery in Africa. Cell, 2019, 179, 984-1002.e36.	13.5	152
2	Linear mixed model for heritability estimation that explicitly addresses environmental variation. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7377-7382.	3.3	75
3	HIV Control Is Mediated in Part by CD8$^+$ T-Cell Targeting of Specific Epitopes. Journal of Virology, 2014, 88, 12937-12948.	1.5	69
4	Widespread Impact of HLA Restriction on Immune Control and Escape Pathways of HIV-1. Journal of Virology, 2012, 86, 5230-5243.	1.5	114
5	Translation of HLA–HIV Associations to the Cellular Level: HIV Adapts To Inflate CD8 T Cell Responses against Nef and HLA-Adapted Variant Epitopes. Journal of Immunology, 2011, 187, 2502-2513.	0.4	25
6	Variable HIV peptide stability in human cytosol is critical to epitope presentation and immune escape. Journal of Clinical Investigation, 2011, 121, 2480-2492.	3.9	41
7	Conditional Random Fields for Fast, Large-Scale Genome-Wide Association Studies. PLoS ONE, 2011, 6, e21591.	1.1	1
8	Correction for hidden confounders in the genetic analysis of gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 16465-16470.	3.3	135
9	Additive Contribution of HLA Class I Alleles in the Immune Control of HIV-1 Infection. Journal of Virology, 2010, 84, 9879-9888.	1.5	148
10	Exploiting knowledge of immune selection in HIV-1 to detect HIV-specific CD8 T-cell responses. Vaccine, 2010, 28, 6052-6057.	1.7	9
11	Rare HLA Drive Additional HIV Evolution Compared to More Frequent Alleles. AIDS Research and Human Retroviruses, 2009, 25, 297-303.	0.5	10
12	Marked Epitope- and Allele-Specific Differences in Rates of Mutation in Human Immunodeficiency Type 1 (HIV-1) Gag, Pol, and Nef Cytotoxic T-Lymphocyte Epitopes in Acute/Early HIV-1 Infection. Journal of Virology, 2008, 82, 9216-9227.	1.5	162
13	Design, Expression, and Processing of Epitomized Hepatitis C Virus-Encoded CTL Epitopes. Journal of Immunology, 2008, 181, 6361-6370.	0.4	17
14	HLA Class I-Driven Evolution of Human Immunodeficiency Virus Type 1 Subtype C Proteome: Immune Escape and Viral Load. Journal of Virology, 2008, 82, 6434-6446.	1.5	126
15	Phylogenetic Dependency Networks: Inferring Patterns of CTL Escape and Codon Covariation in HIV-1 Gag. PLoS Computational Biology, 2008, 4, e1000225.	1.5	116
16	Statistical Resolution of Ambiguous HLA Typing Data. PLoS Computational Biology, 2008, 4, e1000016.	1.5	50
17	Central Role of Reverting Mutations in HLA Associations with Human Immunodeficiency Virus Set Point. Journal of Virology, 2008, 82, 8548-8559.	1.5	152
18	Human leukocyte antigen-specific polymorphisms in HIV-1 Gag and their association with viral load in chronic untreated infection. Aids, 2008, 22, 1277-1286.	1.0	67

#	Article	IF	Citations
19	Evidence of Differential HLA Class I-Mediated Viral Evolution in Functional and Accessory/Regulatory Genes of HIV-1. PLoS Pathogens, 2007, 3, e94.	2.1	153
20	A Statistical Framework for Modeling HLA-Dependent T Cell Response Data. PLoS Computational Biology, 2007, 3, e188.	1.5	5
21	Leveraging Information Across HLA Alleles/Supertypes Improves Epitope Prediction. Journal of Computational Biology, 2007, 14, 736-746.	0.8	54
22	Founder Effects in the Assessment of HIV Polymorphisms and HLA Allele Associations. Science, 2007, 315, 1583-1586.	6.0	234
23	Extensive HLA class I allele promiscuity among viral CTL epitopes. European Journal of Immunology, 2007, 37, 2419-2433.	1.6	120
24	Leveraging Hierarchical Population Structure in Discrete Association Studies. PLoS ONE, 2007, 2, e591.	1.1	33