Carl Kadie

List of Publications by Year
in descending order

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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	Founder Effects in the Assessment of HIV Polymorphisms and HLA Allele Associations. Science, 2007, 315, 1583-1586.	6.0	234
2	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
3	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
4	Central Role of Reverting Mutations in HLA Associations with Human Immunodeficiency Virus Set Point. Journal of Virology, 2008, 82, 8548-8559.	1.5	152
5	Uganda Genome Resource Enables Insights into Population History and Genomic Discovery in Africa. Cell, 2019, 179, 984-1002.e36.	13.5	152
6	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
7	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
8	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
9	Extensive HLA class I allele promiscuity among viral CTL epitopes. European Journal of Immunology, 2007, 37, 2419-2433.	1.6	120
10	Phylogenetic Dependency Networks: Inferring Patterns of CTL Escape and Codon Covariation in HIV-1 Gag. PLoS Computational Biology, 2008, 4, e1000225.	1.5	116
11	Widespread Impact of HLA Restriction on Immune Control and Escape Pathways of HIV-1. Journal of Virology, 2012, 86, 5230-5243.	1.5	114
12	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
13	HIV Control Is Mediated in Part by CD8 ⁺ T-Cell Targeting of Specific Epitopes. Journal of Virology, 2014, 88, 12937-12948.	1.5	69
14	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
15	Leveraging Information Across HLA Alleles/Supertypes Improves Epitope Prediction. Journal of Computational Biology, 2007, 14, 736-746.	0.8	54
16	Statistical Resolution of Ambiguous HLA Typing Data. PLoS Computational Biology, 2008, 4, e1000016.	1.5	50
17	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
18	Leveraging Hierarchical Population Structure in Discrete Association Studies. PLoS ONE, 2007, 2, e591.	1.1	33

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19	Translation of HLAâ€“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
20	Design, Expression, and Processing of Epitomized Hepatitis C Virus-Encoded CTL Epitopes. Journal of Immunology, 2008, 181, 6361-6370.	0.4	17
21	Rare HLA Drive Additional HIV Evolution Compared to More Frequent Alleles. AIDS Research and Human Retroviruses, 2009, 25, 297-303.	0.5	10
22	Exploiting knowledge of immune selection in HIV-1 to detect HIV-specific CD8 T-cell responses. Vaccine, 2010, 28, 6052-6057.	1.7	9
23	A Statistical Framework for Modeling HLA-Dependent T Cell Response Data. PLoS Computational Biology, 2007, 3, e188.	1.5	5
24	Conditional Random Fields for Fast, Large-Scale Genome-Wide Association Studies. PLoS ONE, 2011, 6, e21591.	1.1	1