

Jennifer Listgarten

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

35
papers

4,715
citations

21
h-index

37
g-index

37
ext. papers

6,225
ext. citations

15.7
avg, IF

5.25
L-index

#	Paper	IF	Citations
35	Optimized sgRNA design to maximize activity and minimize off-target effects of CRISPR-Cas9. <i>Nature Biotechnology</i> , 2016 , 34, 184-191	44.5	1790
34	FaST linear mixed models for genome-wide association studies. <i>Nature Methods</i> , 2011 , 8, 833-5	21.6	727
33	Statistical and computational methods for comparative proteomic profiling using liquid chromatography-tandem mass spectrometry. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 419-34	7.6	232
32	Improved linear mixed models for genome-wide association studies. <i>Nature Methods</i> , 2012 , 9, 525-6	21.6	228
31	Rethinking drug design in the artificial intelligence era. <i>Nature Reviews Drug Discovery</i> , 2020 , 19, 353-364	4.1	179
30	Epigenome-wide association studies without the need for cell-type composition. <i>Nature Methods</i> , 2014 , 11, 309-11	21.6	171
29	Orthologous CRISPR-Cas9 enzymes for combinatorial genetic screens. <i>Nature Biotechnology</i> , 2018 , 36, 179-189	44.5	144
28	Predictive models for breast cancer susceptibility from multiple single nucleotide polymorphisms. <i>Clinical Cancer Research</i> , 2004 , 10, 2725-37	12.9	131
27	Prediction of off-target activities for the end-to-end design of CRISPR guide RNAs. <i>Nature Biomedical Engineering</i> , 2018 , 2, 38-47	19	127
26	Additive contribution of HLA class I alleles in the immune control of HIV-1 infection. <i>Journal of Virology</i> , 2010 , 84, 9879-88	6.6	123
25	Correction for hidden confounders in the genetic analysis of gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 16465-70	11.5	107
24	Extensive HLA class I allele promiscuity among viral CTL epitopes. <i>European Journal of Immunology</i> , 2007 , 37, 2419-33	6.1	106
23	Lymphovascular invasion is associated with poor survival in gastric cancer: an application of gene-expression and tissue array techniques. <i>Annals of Surgery</i> , 2006 , 243, 64-73	7.8	94
22	Widespread impact of HLA restriction on immune control and escape pathways of HIV-1. <i>Journal of Virology</i> , 2012 , 86, 5230-43	6.6	90
21	A genome-to-genome analysis of associations between human genetic variation, HIV-1 sequence diversity, and viral control. <i>ELife</i> , 2013 , 2, e01123	8.9	85
20	Correlates of protective cellular immunity revealed by analysis of population-level immune escape pathways in HIV-1. <i>Journal of Virology</i> , 2012 , 86, 13202-16	6.6	81
19	FaST-LMM-Select for addressing confounding from spatial structure and rare variants. <i>Nature Genetics</i> , 2013 , 45, 470-1	36.3	54

18	Leveraging information across HLA alleles/supertypes improves epitope prediction. <i>Journal of Computational Biology</i> , 2007 , 14, 736-46	1.7	52
17	HLA-A*7401-mediated control of HIV viremia is independent of its linkage disequilibrium with HLA-B*5703. <i>Journal of Immunology</i> , 2011 , 186, 5675-86	5.3	45
16	Statistical resolution of ambiguous HLA typing data. <i>PLoS Computational Biology</i> , 2008 , 4, e1000016	5	43
15	Patterns of methylation heritability in a genome-wide analysis of four brain regions. <i>Nucleic Acids Research</i> , 2013 , 41, 2095-104	20.1	41
14	Practical proteomic biomarker discovery: taking a step back to leap forward. <i>Drug Discovery Today</i> , 2005 , 10, 1697-702	8.8	17
13	Rare HLA drive additional HIV evolution compared to more frequent alleles. <i>AIDS Research and Human Retroviruses</i> , 2009 , 25, 297-303	1.6	10
12	Combining evolutionary and assay-labelled data for protein fitness prediction		5
11	Epistatic Net allows the sparse spectral regularization of deep neural networks for inferring fitness functions. <i>Nature Communications</i> , 2021 , 12, 5225	17.4	5
10	Clinically validated benchmarking of normalisation techniques for two-colour oligonucleotide spotted microarray slides. <i>Applied Bioinformatics</i> , 2003 , 2, 219-28		5
9	Learning protein fitness models from evolutionary and assay-labeled data.. <i>Nature Biotechnology</i> , 2022 ,	44.5	4
8	On the sparsity of fitness functions and implications for learning.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	4
7	Learning transcriptional regulatory relationships using sparse graphical models. <i>PLoS ONE</i> , 2012 , 7, e35767		3
6	Predicting off-target effects for end-to-end CRISPR guide design		3
5	Sparse Epistatic Regularization of Deep Neural Networks for Inferring Fitness Functions		3
4	A view of estimation of distribution algorithms through the lens of expectation-maximization 2020 ,		2
3	Personalized medicine: from genotypes and molecular phenotypes towards therapy- session introduction. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2014 , 19, 224-8	1.3	1
2	On the sparsity of fitness functions and implications for learning		1
1	Flexible Modeling of Genetic Effects on Function-Valued Traits. <i>Journal of Computational Biology</i> , 2017 , 24, 524-535	1.7	

