Jennifer Listgarten

List of Publications by Year
in descending order

31	7,312	304368 22	500791 28
papers	citations	h-index	g-index
37	37	37	13714
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Optimized sgRNA design to maximize activity and minimize off-target effects of CRISPR-Cas9. Nature Biotechnology, 2016, 34, 184-191.	9.4	3,168
2	FaST linear mixed models for genome-wide association studies. Nature Methods, 2011, 8, 833-835.	9.0	1,021
3	Rethinking drug design in the artificial intelligence era. Nature Reviews Drug Discovery, 2020, 19, 353-364.	21.5	394
4	Improved linear mixed models for genome-wide association studies. Nature Methods, 2012, 9, 525-526.	9.0	292
5	Statistical and Computational Methods for Comparative Proteomic Profiling Using Liquid Chromatography-Tandem Mass Spectrometry. Molecular and Cellular Proteomics, 2005, 4, 419-434.	2.5	264
6	Prediction of off-target activities for the end-to-end design of CRISPR guide RNAs. Nature Biomedical Engineering, 2018, 2, 38-47.	11.6	230
7	Orthologous CRISPR–Cas9 enzymes for combinatorial genetic screens. Nature Biotechnology, 2018, 36, 179-189.	9.4	216
8	Epigenome-wide association studies without the need for cell-type composition. Nature Methods, 2014, 11, 309-311.	9.0	205
9	Predictive Models for Breast Cancer Susceptibility from Multiple Single Nucleotide Polymorphisms. Clinical Cancer Research, 2004, 10, 2725-2737.	3.2	171
10	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
11	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
12	A genome-to-genome analysis of associations between human genetic variation, HIV-1 sequence diversity, and viral control. ELife, 2013, 2, e01123.	2.8	126
13	Extensive HLA class I allele promiscuity among viral CTL epitopes. European Journal of Immunology, 2007, 37, 2419-2433.	1.6	120
14	Widespread Impact of HLA Restriction on Immune Control and Escape Pathways of HIV-1. Journal of Virology, 2012, 86, 5230-5243.	1.5	114
15	Lymphovascular Invasion Is Associated With Poor Survival in Gastric Cancer. Annals of Surgery, 2006, 243, 64-73.	2.1	109
16	Correlates of Protective Cellular Immunity Revealed by Analysis of Population-Level Immune Escape Pathways in HIV-1. Journal of Virology, 2012, 86, 13202-13216.	1.5	99
17	Learning protein fitness models from evolutionary and assay-labeled data. Nature Biotechnology, 2022, 40, 1114-1122.	9.4	90
18	FaST-LMM-Select for addressing confounding from spatial structure and rare variants. Nature Genetics, 2013, 45, 470-471.	9.4	88

#	Article	IF	Citations
19	Leveraging Information Across HLA Alleles/Supertypes Improves Epitope Prediction. Journal of Computational Biology, 2007, 14, 736-746.	0.8	54
20	Statistical Resolution of Ambiguous HLA Typing Data. PLoS Computational Biology, 2008, 4, e1000016.	1.5	50
21	HLA-A*7401â€"Mediated Control of HIV Viremia Is Independent of Its Linkage Disequilibrium with HLA-B*5703. Journal of Immunology, 2011, 186, 5675-5686.	0.4	49
22	Patterns of methylation heritability in a genome-wide analysis of four brain regions. Nucleic Acids Research, 2013, 41, 2095-2104.	6.5	44
23	On the sparsity of fitness functions and implications for learning. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	21
24	Practical proteomic biomarker discovery: taking a step back to leap forward. Drug Discovery Today, 2005, 10, 1697-1702.	3.2	19
25	Epistatic Net allows the sparse spectral regularization of deep neural networks for inferring fitness functions. Nature Communications, 2021, 12, 5225.	5.8	18
26	Rare HLA Drive Additional HIV Evolution Compared to More Frequent Alleles. AIDS Research and Human Retroviruses, 2009, 25, 297-303.	0.5	10
27	A view of estimation of distribution algorithms through the lens of expectation-maximization. , 2020, , .		5
28	Clinically validated benchmarking of normalisation techniques for two-colour oligonucleotide spotted microarray slides. Applied Bioinformatics, 2003, 2, 219-28.	1.7	5
29	Learning Transcriptional Regulatory Relationships Using Sparse Graphical Models. PLoS ONE, 2012, 7, e35762.	1.1	3
30	PERSONALIZED MEDICINE: FROM GENOTYPES AND MOLECULAR PHENOTYPES TOWARDS THERAPY- SESSION INTRODUCTION. , 2013, 19, 224-8.		2
31	Flexible Modeling of Genetic Effects on Function-Valued Traits. Journal of Computational Biology, 2017, 24, 524-535.	0.8	0