

Jennifer Listgarten

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

7,312
citations

304743

22
h-index

501196

28
g-index

37
all docs

37
docs citations

37
times ranked

13714
citing authors

#	ARTICLE	IF	CITATIONS
1	Learning protein fitness models from evolutionary and assay-labeled data. <i>Nature Biotechnology</i> , 2022, 40, 1114-1122.	17.5	90
2	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, .	7.1	21
3	Epistatic Net allows the sparse spectral regularization of deep neural networks for inferring fitness functions. <i>Nature Communications</i> , 2021, 12, 5225.	12.8	18
4	Rethinking drug design in the artificial intelligence era. <i>Nature Reviews Drug Discovery</i> , 2020, 19, 353-364.	46.4	394
5	A view of estimation of distribution algorithms through the lens of expectation-maximization. , 2020, , .		5
6	Orthologous CRISPR-Cas9 enzymes for combinatorial genetic screens. <i>Nature Biotechnology</i> , 2018, 36, 179-189.	17.5	216
7	Prediction of off-target activities for the end-to-end design of CRISPR guide RNAs. <i>Nature Biomedical Engineering</i> , 2018, 2, 38-47.	22.5	230
8	Flexible Modeling of Genetic Effects on Function-Valued Traits. <i>Journal of Computational Biology</i> , 2017, 24, 524-535.	1.6	0
9	Optimized sgRNA design to maximize activity and minimize off-target effects of CRISPR-Cas9. <i>Nature Biotechnology</i> , 2016, 34, 184-191.	17.5	3,168
10	Epigenome-wide association studies without the need for cell-type composition. <i>Nature Methods</i> , 2014, 11, 309-311.	19.0	205
11	FaST-LMM-Select for addressing confounding from spatial structure and rare variants. <i>Nature Genetics</i> , 2013, 45, 470-471.	21.4	88
12	Patterns of methylation heritability in a genome-wide analysis of four brain regions. <i>Nucleic Acids Research</i> , 2013, 41, 2095-2104.	14.5	44
13	PERSONALIZED MEDICINE: FROM GENOTYPES AND MOLECULAR PHENOTYPES TOWARDS THERAPY- SESSION INTRODUCTION. , 2013, 19, 224-8.		2
14	A genome-to-genome analysis of associations between human genetic variation, HIV-1 sequence diversity, and viral control. <i>ELife</i> , 2013, 2, e01123.	6.0	126
15	Correlates of Protective Cellular Immunity Revealed by Analysis of Population-Level Immune Escape Pathways in HIV-1. <i>Journal of Virology</i> , 2012, 86, 13202-13216.	3.4	99
16	Widespread Impact of HLA Restriction on Immune Control and Escape Pathways of HIV-1. <i>Journal of Virology</i> , 2012, 86, 5230-5243.	3.4	114
17	Improved linear mixed models for genome-wide association studies. <i>Nature Methods</i> , 2012, 9, 525-526.	19.0	292
18	Learning Transcriptional Regulatory Relationships Using Sparse Graphical Models. <i>PLoS ONE</i> , 2012, 7, e35762.	2.5	3

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19	FaST linear mixed models for genome-wide association studies. <i>Nature Methods</i> , 2011, 8, 833-835.	19.0	1,021
20	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, 5675-5686.	0.8	49
21	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, 16465-16470.	7.1	135
22	Additive Contribution of HLA Class I Alleles in the Immune Control of HIV-1 Infection. <i>Journal of Virology</i> , 2010, 84, 9879-9888.	3.4	148
23	Rare HLA Drive Additional HIV Evolution Compared to More Frequent Alleles. <i>AIDS Research and Human Retroviruses</i> , 2009, 25, 297-303.	1.1	10
24	Statistical Resolution of Ambiguous HLA Typing Data. <i>PLoS Computational Biology</i> , 2008, 4, e1000016.	3.2	50
25	Leveraging Information Across HLA Alleles/Supertypes Improves Epitope Prediction. <i>Journal of Computational Biology</i> , 2007, 14, 736-746.	1.6	54
26	Extensive HLA class I allele promiscuity among viral CTL epitopes. <i>European Journal of Immunology</i> , 2007, 37, 2419-2433.	2.9	120
27	Lymphovascular Invasion Is Associated With Poor Survival in Gastric Cancer. <i>Annals of Surgery</i> , 2006, 243, 64-73.	4.2	109
28	Practical proteomic biomarker discovery: taking a step back to leap forward. <i>Drug Discovery Today</i> , 2005, 10, 1697-1702.	6.4	19
29	Statistical and Computational Methods for Comparative Proteomic Profiling Using Liquid Chromatography-Tandem Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 419-434.	3.8	264
30	Predictive Models for Breast Cancer Susceptibility from Multiple Single Nucleotide Polymorphisms. <i>Clinical Cancer Research</i> , 2004, 10, 2725-2737.	7.0	171
31	Clinically validated benchmarking of normalisation techniques for two-colour oligonucleotide spotted microarray slides. <i>Applied Bioinformatics</i> , 2003, 2, 219-28.	1.6	5