Earl A Hubbell

List of Publications by Year
in descending order

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Version: 2024-02-01

27 papers	9,002 citations	331670 21 h-index	526287 27 g-index
28 all docs	28 docs citations	28 times ranked	12459 citing authors

#	Article	IF	Citations
1	Large-Scale Identification, Mapping, and Genotyping of Single-Nucleotide Polymorphisms in the Human Genome. Science, 1998, 280, 1077-1082.	12.6	1,993
2	Accessing Genetic Information with High-Density DNA Arrays. Science, 1996, 274, 610-614.	12.6	1,512
3	Integrated detection and population-genetic analysis of SNPs and copy number variation. Nature Genetics, 2008, 40, 1166-1174.	21.4	838
4	Sensitive and specific multi-cancer detection and localization using methylation signatures in cell-free DNA. Annals of Oncology, 2020, 31, 745-759.	1.2	770
5	Integrated genotype calling and association analysis of SNPs, common copy number polymorphisms and rare CNVs. Nature Genetics, 2008, 40, 1253-1260.	21.4	712
6	Extensive polymorphisms observed in HIVâ€“1 clade B protease gene using highâ€“density oligonucleotide arrays. Nature Medicine, 1996, 2, 753-759.	30.7	558
7	Robust estimators for expression analysis. Bioinformatics, 2002, 18, 1585-1592.	4.1	545
8	High-intensity sequencing reveals the sources of plasma circulating cell-free DNA variants. Nature Medicine, 2019, 25, 1928-1937.	30.7	485
9	Genotyping over 100,000 SNPs on a pair of oligonucleotide arrays. Nature Methods, 2004, 1, 109-111.	19.0	392
10	Genome-wide mapping with biallelic markers in Arabidopsis thaliana. Nature Genetics, 1999, 23, 203-207.	21.4	260
11	Next generation genome-wide association tool: Design and coverage of a high-throughput European-optimized SNP array. Genomics, 2011, 98, 79-89.	2.9	186
12	Dynamic model based algorithms for screening and genotyping over 100K SNPs on oligonucleotide microarrays. Bioinformatics, 2005, 21, 1958-1963.	4.1	167
13	Probe selection for high-density oligonucleotide arrays. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 11237-11242.	7.1	117
14	Gene structure-based splice variant deconvolution using a microarry platform. Bioinformatics, 2003, 19, i315-i322.	4.1	88
15	NetAffx Gene Ontology Mining Tool: a visual approach for microarray data analysis. Bioinformatics, 2004, 20, 1462-1463.	4.1	75
16	Modeled Reductions in Late-stage Cancer with a Multi-Cancer Early Detection Test. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 460-468.	2.5	68
17	Prognostic Significance of Blood-Based Multi-cancer Detection in Plasma Cell-Free DNA. Clinical Cancer Research, 2021, 27, 4221-4229.	7.0	61
18	Prevalence of clonal hematopoiesis of indeterminate potential (CHIP) measured by an ultra-sensitive sequencing assay: Exploratory analysis of the Circulating Cancer Genome Atlas (CCGA) study.. Journal of Clinical Oncology, 2018, 36, 12003-12003.	1.6	40

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19	Projected Reductions in Absolute Cancerâ€“Related Deaths from Diagnosing Cancers Before Metastasis, 2006â€“2015. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 895-902.	2.5	36
20	Combinatorial Algorithms for Design of DNA Arrays. Advances in Biochemical Engineering/Biotechnology, 2002, 77, 1-19.	1.1	31
21	Infrared absorption features for tetrahedral ammonia ice crystals. Icarus, 1989, 80, 220-223.	2.5	25
22	Multi-cancer early detection: A new paradigm for reducing cancer-specific and all-cause mortality. Cancer Cell, 2021, 39, 447-448.	16.8	14
23	Multiplex Sequencing by Hybridization. Journal of Computational Biology, 2001, 8, 141-149.	1.6	7
24	Alignment-free filtering for cfNA fusion fragments. Bioinformatics, 2019, 35, i225-i232.	4.1	7
25	Racial/ethnic differences in cancer diagnosed after metastasis: absolute burden and deaths potentially avoidable through earlier detection. Cancer Epidemiology Biomarkers and Prevention, 2021, , cebp.0823.2021.	2.5	7
26	Resolving deconvolution ambiguity in gene alternative splicing. BMC Bioinformatics, 2009, 10, 237.	2.6	5
27	Tumor methylation patterns to measure tumor fraction in cell-free DNA.. Journal of Clinical Oncology, 2020, 38, 3052-3052.	1.6	3