

# Frederic Hospital

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7576114/publications.pdf>

Version: 2024-02-01

26  
papers

3,601  
citations

394421

19  
h-index

552781

26  
g-index

26  
all docs

26  
docs citations

26  
times ranked

4220  
citing authors

#	ARTICLE	IF	CITATIONS
1	Assessing the Impact of Transgenerational Epigenetic Variation on Complex Traits. PLoS Genetics, 2009, 5, e1000530.	3.5	669
2	The use of molecular genetics in the improvement of agricultural populations. Nature Reviews Genetics, 2002, 3, 22-32.	16.3	519
3	Mapping the Epigenetic Basis of Complex Traits. Science, 2014, 343, 1145-1148.	12.6	403
4	Marker-Assisted Introgression of Quantitative Trait Loci. Genetics, 1997, 147, 1469-1485.	2.9	268
5	More on the efficiency of marker-assisted selection. Theoretical and Applied Genetics, 1997, 95, 1181-1189.	3.6	190
6	Selective Sweep at a Quantitative Trait Locus in the Presence of Background Genetic Variation. Genetics, 2008, 180, 1645-1660.	2.9	173
7	Toward a Theory of Marker-Assisted Gene Pyramiding. Genetics, 2004, 168, 513-523.	2.9	156
8	Marker-Assisted Introgression of Favorable Alleles at Quantitative Trait Loci Between Maize Elite Lines. Genetics, 2002, 162, 1945-1959.	2.9	150
9	Marker-Assisted Selection Efficiency in Populations of Finite Size. Genetics, 1998, 148, 1353-1365.	2.9	146
10	Size of Donor Chromosome Segments Around Introgressed Loci and Reduction of Linkage Drag in Marker-Assisted Backcross Programs. Genetics, 2001, 158, 1363-1379.	2.9	128
11	Selection in backcross programmes. Philosophical Transactions of the Royal Society B: Biological Sciences, 2005, 360, 1503-1511.	4.0	124
12	Challenges for effective marker-assisted selection in plants. Genetica, 2009, 136, 303-310.	1.1	114
13	Genome-Wide Epigenetic Perturbation Jump-Starts Patterns of Heritable Variation Found in Nature. Genetics, 2011, 188, 1015-1017.	2.9	109
14	quantiNemo: an individual-based program to simulate quantitative traits with explicit genetic architecture in a dynamic metapopulation. Bioinformatics, 2008, 24, 1552-1553.	4.1	102
15	Both additivity and epistasis control the genetic variation for fruit quality traits in tomato. Theoretical and Applied Genetics, 2007, 115, 429-442.	3.6	79
16	Genetic and Nongenetic Bases for the L-Shaped Distribution of Quantitative Trait Loci Effects. Genetics, 2001, 157, 1773-1787.	2.9	65
17	Rapid Rise and Fall of Selfish Sex-Ratio X Chromosomes in Drosophila simulans: Spatiotemporal Analysis of Phenotypic and Molecular Data. Molecular Biology and Evolution, 2011, 28, 2461-2470.	8.9	54
18	Hitchhiking Both Ways: Effect of Two Interfering Selective Sweeps on Linked Neutral Variation. Genetics, 2008, 180, 301-316.	2.9	39

#	ARTICLE	IF	CITATIONS
19	Interactions of selection, linkage and drift in the dynamics of polygenic characters. <i>Genetical Research</i> , 1996, 67, 77-87.	0.9	31
20	Two- and Three-Locus Tests for Linkage Analysis Using Recombinant Inbred Lines. <i>Genetics</i> , 2006, 173, 451-459.	2.9	21
21	The Hitchhiking Effect of an Autosomal Meiotic Drive Gene. <i>Genetics</i> , 2006, 173, 1829-1832.	2.9	17
22	Contribution of an additive locus to genetic variance when inheritance is multi-factorial with implications on interpretation of GWAS. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1457-1472.	3.6	17
23	Genomic contributions in livestock gene introgression programmes. <i>Genetics Selection Evolution</i> , 2005, 37, 291-313.	3.0	11
24	Distribution of Parental Genome Blocks in Recombinant Inbred Lines. <i>Genetics</i> , 2011, 189, 645-654.	2.9	10
25	Molecular signature of epistatic selection: interrogating genetic interactions in the <i>sex-ratio</i> meiotic drive of <i>Drosophila simulans</i> . <i>Genetical Research</i> , 2009, 91, 171-182.	0.9	3
26	Blocks of chromosomes identical by descent in a population: Models and predictions. <i>PLoS ONE</i> , 2017, 12, e0187416.	2.5	3