

Audrey Lemaçon

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3265858/publications.pdf>

Version: 2024-02-01

13
papers

1,657
citations

1307594

7
h-index

1125743

13
g-index

15
all docs

15
docs citations

15
times ranked

3921
citing authors

#	ARTICLE	IF	CITATIONS
1	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	27.8	1,099
2	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	21.4	289
3	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	21.4	120
4	Two single-nucleotide polymorphisms in the human vitamin D receptor promoter change protein-DNA complex formation and are associated with height and vitamin D status in adolescent girls. <i>Human Molecular Genetics</i> , 2005, 14, 3539-3548.	2.9	61
5	Association of breast cancer risk with genetic variants showing differential allelic expression: Identification of a novel breast cancer susceptibility locus at 4q21. <i>Oncotarget</i> , 2016, 7, 80140-80163.	1.8	31
6	Association of breast cancer risk in BRCA1 and BRCA2 mutation carriers with genetic variants showing differential allelic expression: identification of a modifier of breast cancer risk at locus 11q22.3. <i>Breast Cancer Research and Treatment</i> , 2017, 161, 117-134.	2.5	18
7	metagene Profiles Analyses Reveal Regulatory Element's Factor-Specific Recruitment Patterns. <i>PLoS Computational Biology</i> , 2016, 12, e1004751.	3.2	12
8	Pharmacogenomics of the Efficacy and Safety of Colchicine in COLCOT. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e003183.	3.6	7
9	DSNetwork: An Integrative Approach to Visualize Predictions of Variants' Deleteriousness. <i>Frontiers in Genetics</i> , 2019, 10, 1349.	2.3	5
10	LD-annot: A Bioinformatics Tool to Automatically Provide Candidate SNPs With Annotations for Genetically Linked Genes. <i>Frontiers in Genetics</i> , 2019, 10, 1192.	2.3	4
11	Genetic meta-analysis of cancer diagnosis following statin use identifies new associations and implicates human leukocyte antigen (HLA) in women. <i>Pharmacogenomics Journal</i> , 2021, 21, 446-457.	2.0	4
12	VEXOR: an integrative environment for prioritization of functional variants in fine-mapping analysis. <i>Bioinformatics</i> , 2017, 33, 1389-1391.	4.1	2
13	Uncovering the Contribution of Moderate-Penetrance Susceptibility Genes to Breast Cancer by Whole-Exome Sequencing and Targeted Enrichment Sequencing of Candidate Genes in Women of European Ancestry. <i>Cancers</i> , 2022, 14, 3363.	3.7	2