Freerk Van Dijk

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/10663683/publications.pdf

Version: 2024-02-01

22 papers	2,331 citations	567281 15 h-index	677142 22 g-index
25 all docs	25 docs citations	25 times ranked	7811 citing authors

#	Article	IF	Citations
1	Posttranscriptional Regulation of the Human LDL Receptor by the U2-Spliceosome. Circulation Research, 2022, 130, 80-95.	4.5	9
2	DNA methylation in peripheral tissues and left-handedness. Scientific Reports, 2022, 12, 5606.	3.3	12
3	DNA methylation signatures of aggression and closely related constructs: A meta-analysis of epigenome-wide studies across the lifespan. Molecular Psychiatry, 2021, 26, 2148-2162.	7.9	21
4	Feasibility of predicting allele specific expression from DNA sequencing using machine learning. Scientific Reports, 2021, 11, 10606.	3.3	4
5	A common variant in CCDC93 protects against myocardial infarction and cardiovascular mortality by regulating endosomal trafficking of low-density lipoprotein receptor. European Heart Journal, 2020, 41, 1040-1053.	2.2	20
6	Genome-wide identification of genes regulating DNA methylation using genetic anchors for causal inference. Genome Biology, 2020, 21, 220.	8.8	27
7	Epigenome-wide Association Study of Attention-Deficit/Hyperactivity Disorder Symptoms in Adults. Biological Psychiatry, 2019, 86, 599-607.	1.3	47
8	Genetics, Lifestyle, and Low-Density Lipoprotein Cholesterol in Young and Apparently Healthy Women. Circulation, 2018, 137, 820-831.	1.6	30
9	NIPTeR: an R package for fast and accurate trisomy prediction in non-invasive prenatal testing. BMC Bioinformatics, 2018, 19, 531.	2.6	7
10	Disease variants alter transcription factor levels and methylation of their binding sites. Nature Genetics, 2017, 49, 131-138.	21.4	390
11	Identification of context-dependent expression quantitative trait loci in whole blood. Nature Genetics, 2017, 49, 139-145.	21.4	363
12	Meta-GWAS and Meta-Analysis of Exome Array Studies Do Not Reveal Genetic Determinants of Serum Hepcidin. PLoS ONE, 2016, 11, e0166628.	2.5	2
13	CoNVaDING: Single Exon Variation Detection in Targeted NGS Data. Human Mutation, 2016, 37, 457-464.	2.5	79
14	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	21.4	66
15	A high-quality human reference panel reveals the complexity and distribution of genomic structural variants. Nature Communications, 2016, 7, 12989.	12.8	99
16	Refined mapping of autoimmune disease associated genetic variants with gene expression suggests an important role for non-coding RNAs. Journal of Autoimmunity, 2016, 68, 62-74.	6.5	64
17	Cohort Profile: LifeLines, a three-generation cohort study and biobank. International Journal of Epidemiology, 2015, 44, 1172-1180.	1.9	578
18	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. American Journal of Human Genetics, 2015, 97, 75-85.	6.2	116

#	Article	IF	Citations
19	Molgenis-impute: imputation pipeline in a box. BMC Research Notes, 2015, 8, 359.	1.4	8
20	Genome of the Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. Nature Communications, 2015, 6, 6065.	12.8	45
21	Improved imputation quality of low-frequency and rare variants in European samples using the â€˜Genome of The Netherlandsâ€™. European Journal of Human Genetics, 2014, 22, 1321-1326.	2.8	92
22	The Genome of the Netherlands: design, and project goals. European Journal of Human Genetics, 2014, 22, 221-227.	2.8	246