Freerk Van Dijk

List of Publications by Year in descending order

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FDEEDK VAN DUK

#	Article	IF	CITATIONS
1	Cohort Profile: LifeLines, a three-generation cohort study and biobank. International Journal of Epidemiology, 2015, 44, 1172-1180.	1.9	578
2	Disease variants alter transcription factor levels and methylation of their binding sites. Nature Genetics, 2017, 49, 131-138.	21.4	390
3	Identification of context-dependent expression quantitative trait loci in whole blood. Nature Genetics, 2017, 49, 139-145.	21.4	363
4	The Genome of the Netherlands: design, and project goals. European Journal of Human Genetics, 2014, 22, 221-227.	2.8	246
5	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. American Journal of Human Genetics, 2015, 97, 75-85.	6.2	116
6	A high-quality human reference panel reveals the complexity and distribution of genomic structural variants. Nature Communications, 2016, 7, 12989.	12.8	99
7	Improved imputation quality of low-frequency and rare variants in European samples using the â€~Genome of The Netherlands'. European Journal of Human Genetics, 2014, 22, 1321-1326.	2.8	92
8	CoNVaDING: Single Exon Variation Detection in Targeted NGS Data. Human Mutation, 2016, 37, 457-464.	2.5	79
9	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	21.4	66
10	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
11	Epigenome-wide Association Study of Attention-Deficit/Hyperactivity Disorder Symptoms in Adults. Biological Psychiatry, 2019, 86, 599-607.	1.3	47
12	Genome of the Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. Nature Communications, 2015, 6, 6065.	12.8	45
13	Genetics, Lifestyle, and Low-Density Lipoprotein Cholesterol in Young and Apparently Healthy Women. Circulation, 2018, 137, 820-831.	1.6	30
14	Genome-wide identification of genes regulating DNA methylation using genetic anchors for causal inference. Genome Biology, 2020, 21, 220.	8.8	27
15	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
16	A common variant in <i>CCDC93</i> 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
17	DNA methylation in peripheral tissues and left-handedness. Scientific Reports, 2022, 12, 5606.	3.3	12
18	Posttranscriptional Regulation of the Human LDL Receptor by the U2-Spliceosome. Circulation Research, 2022, 130, 80-95.	4.5	9

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19	Molgenis-impute: imputation pipeline in a box. BMC Research Notes, 2015, 8, 359.	1.4	8
20	NIPTeR: an R package for fast and accurate trisomy prediction in non-invasive prenatal testing. BMC Bioinformatics, 2018, 19, 531.	2.6	7
21	Feasibility of predicting allele specific expression from DNA sequencing using machine learning. Scientific Reports, 2021, 11, 10606.	3.3	4
22	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