Karim Oualkacha

List of Publications by Year
in descending order

37 papers	1,295 citations	1039406 9 h-index	454577 30 g-index
39 all docs	39 docs citations	39 times ranked	4807 citing authors

#	Article	IF	Citations
1	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	13.7	1,014
2	Adjusted Sequence Kernel Association Test for Rare Variants Controlling for Cryptic and Family Relatedness. Genetic Epidemiology, 2013, 37, 366-376.	0.6	50
3	Specific expression of novel long non-coding RNAs in high-hyperdiploid childhood acute lymphoblastic leukemia. PLoS ONE, 2017, 12, e0174124.	1.1	24
4	On Path to Informing Hierarchy of Eplet Mismatches as Determinants of Kidney Transplant Loss. Kidney International Reports, 2021, 6, 1567-1579.	0.4	24
5	Gene Coexpression Analyses Differentiate Networks Associated with Diverse Cancers Harboring TP53 Missense or Null Mutations. Frontiers in Genetics, 2016, 7, 137.	1.1	23
6	A method for analyzing multiple continuous phenotypes in rare variant association studies allowing for flexible correlations in variant effects. European Journal of Human Genetics, 2016, 24, 1344-1351.	1.4	21
7	Constrained instruments and their application to Mendelian randomization with pleiotropy. Genetic Epidemiology, 2019, 43, 373-401.	0.6	15
8	Principal Components of Heritability for High Dimension Quantitative Traits and General Pedigrees. Statistical Applications in Genetics and Molecular Biology, 2012, 11, .	0.2	13
9	A coordinate descent algorithm for computing penalized smooth quantile regression. Statistics and Computing, 2017, 27, 865-883.	0.8	9
10	Causal modeling in a multi-omic setting: insights from GAW20. BMC Genetics, 2018, 19, 74.	2.7	9
11	A new statistical model for random unit vectors. Journal of Multivariate Analysis, 2009, 100, 70-80.	0.5	8
12	Performance of an alleleâ€level multiâ€locus HLA genotype imputation tool in hematopoietic stem cell donors from Quebec. Immunity, Inflammation and Disease, 2017, 5, 551-559.	1.3	8
13	The cluster correlation-network support vector machine for high-dimensional binary classification. Journal of Statistical Computation and Simulation, 2019, 89, 1020-1043.	0.7	8
14	A rare variant association test in familyâ€based designs and nonâ€normal quantitative traits. Statistics in Medicine, 2016, 35, 905-921.	0.8	7
15	Principal component of explained variance: An efficient and optimal data dimension reduction framework for association studies. Statistical Methods in Medical Research, 2018, 27, 1331-1350.	0.7	7
16	On the estimation of an average rigid body motion. Biometrika, 2012, 99, 585-598.	1.3	6
17	Joint analysis of multiple blood pressure phenotypes in GAW19 data by using a multivariate rare-variant association test. BMC Proceedings, 2016, 10, 309-313.	1.8	6
18	Simultaneous SNP selection and adjustment for population structure in high dimensional prediction models. PLoS Genetics, 2020, 16, e1008766.	1.5	5

#	Article	IF	Citations
19	Block coordinate descent algorithm improves variable selection and estimation in errorâ€inâ€variables regression. Genetic Epidemiology, 2021, 45, 874-890.	0.6	5
20	The Kendall interaction filter for variable interaction screening in high dimensional classification problems. Journal of Applied Statistics, 0, , 1-19.	0.6	5
21	A smoothed EM-algorithm for DNA methylation profiles from sequencing-based methods in cell lines or for a single cell type. Statistical Applications in Genetics and Molecular Biology, 2017, 16, 333-347.	0.2	4
22	A new GEE method to account for heteroscedasticity using asymmetric least-square regressions. Journal of Applied Statistics, 2022, 49, 3564-3590.	0.6	4
23	Investigating potential causal relationships between SNPs, DNA methylation and HDL. BMC Proceedings, 2018, 12, 20.	1.8	3
24	A flexible copulaâ€based approach for the analysis of secondary phenotypes in ascertained samples. Statistics in Medicine, 2020, 39, 517-543.	0.8	3
25	A novel statistical method for modeling covariate effects in bisulfite sequencing derived measures of DNA methylation. Biometrics, 2021, 77, 424-438.	0.8	3
26	Pathway analysis for genetic association studies: to do, or not to do? That is the question. BMC Proceedings, 2014, 8, S103.	1.8	2
27	Software Application Profile: RVPedigree: a suite of family-based rare variant association tests for normally and non-normally distributed quantitative traits. International Journal of Epidemiology, 2016, 45, 402-407.	0.9	2
28	Exome-wide rare variant analyses of two bone mineral density phenotypes: the challenges of analyzing rare genetic variation. Scientific Reports, 2018, 8, 220.	1.6	2
29	CpG-set association assessment of lipid concentration changes and DNA methylation. BMC Proceedings, 2018, 12, 30.	1.8	2
30	Group penalized quantile regression. Statistical Methods and Applications, 2022, 31, 495-529.	0.7	1
31	Multivariate association test for rare variants controlling for cryptic and family relatedness. Canadian Journal of Statistics, 2019, 47, 90-107.	0.6	1
32	Title is missing!. , 2020, 16, e1008766.		0
33	Title is missing!. , 2020, 16, e1008766.		0
34	Title is missing!. , 2020, 16, e1008766.		0
35	Title is missing!. , 2020, 16, e1008766.		0
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