

# Jan Christian Kssens

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

19  
papers

1,067  
citations

8  
h-index

23  
g-index

23  
ext. papers

1,607  
ext. citations

8.2  
avg, IF

3.03  
L-index

#	Paper	IF	Citations
19	BIGwas: Single-command quality control and association testing for multi-cohort and biobank-scale GWAS/PheWAS data. <i>GigaScience</i> , <b>2021</b> , 10,	7.6	1
18	Genome-wide study of a Neolithic Wartberg grave community reveals distinct HLA variation and hunter-gatherer ancestry. <i>Communications Biology</i> , <b>2021</b> , 4, 113	6.7	5
17	Genome-wide association study in 8,956 German individuals identifies influence of ABO histo-blood groups on gut microbiome. <i>Nature Genetics</i> , <b>2021</b> , 53, 147-155	36.3	19
16	SNPInt-GPU: Tool for Epistasis Testing with Multiple Methods and GPU Acceleration. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2212, 17-35	1.4	1
15	Genomewide Association Study of Severe Covid-19 with Respiratory Failure. <i>New England Journal of Medicine</i> , <b>2020</b> , 383, 1522-1534	59.2	913
14	Reference-Based Haplotype Phasing with FPGAs. <i>Lecture Notes in Computer Science</i> , <b>2020</b> , 481-495	0.9	0
13	Protein-coding variants contribute to the risk of atopic dermatitis and skin-specific gene expression. <i>Journal of Allergy and Clinical Immunology</i> , <b>2020</b> , 145, 1208-1218	11.5	19
12	1000x Faster than PLINK: Combined FPGA and GPU accelerators for logistic regression-based detection of epistasis. <i>Journal of Computational Science</i> , <b>2019</b> , 30, 183-193	3.4	7
11	1,000x Faster Than PLINK: Genome-Wide Epistasis Detection with Logistic Regression Using Combined FPGA and GPU Accelerators. <i>Lecture Notes in Computer Science</i> , <b>2018</b> , 368-381	0.9	1
10	Fast Genome-Wide Third-order SNP Interaction Tests with Information Gain on a Low-cost Heterogeneous Parallel FPGA-GPU Computing Architecture. <i>Procedia Computer Science</i> , <b>2017</b> , 108, 596-605	1.6	8
9	Combining GPU and FPGA technology for efficient exhaustive interaction analysis in GWAS <b>2016</b> ,		3
8	Genome-wide Association Interaction Studies with MB-MDR and maxT Multiple Testing Correction on FPGAs. <i>Procedia Computer Science</i> , <b>2016</b> , 80, 639-649	1.6	3
7	Large-scale genome-wide association studies on a GPU cluster using a CUDA-accelerated PGAS programming model. <i>International Journal of High Performance Computing Applications</i> , <b>2015</b> , 29, 506-510	1.8	7
6	High-speed exhaustive 3-locus interaction epistasis analysis on FPGAs. <i>Journal of Computational Science</i> , <b>2015</b> , 9, 131-136	3.4	18
5	Parallelizing Epistasis Detection in GWAS on FPGA and GPU-Accelerated Computing Systems. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2015</b> , 12, 982-94	3	15
4	FPGA-based Acceleration of Detecting Statistical Epistasis in GWAS. <i>Procedia Computer Science</i> , <b>2014</b> , 29, 220-230	1.6	15
3	Hybrid CPU/GPU Acceleration of Detection of 2-SNP Epistatic Interactions in GWAS. <i>Lecture Notes in Computer Science</i> , <b>2014</b> , 680-691	0.9	6

2	The ABO blood group locus and a chromosome 3 gene cluster associate with SARS-CoV-2 respiratory failure in an Italian-Spanish genome-wide association analysis	23
1	Genome-wide association study in 8,956 German individuals identifies influence of ABO histo-blood groups on gut microbiome	1