Birte Kehr

List of Publications by Year
in descending order

25 papers	1,408 citations	516710 16 h-index	677142 22 g-index
30 all docs	30 docs citations	30 times ranked	3484 citing authors

#	Article	IF	Citations
1	Parental influence on human germline de novo mutations in 1,548 trios from Iceland. Nature, 2017, 549, 519-522.	27.8	410
2	Graphtyper enables population-scale genotyping using pangenome graphs. Nature Genetics, 2017, 49, 1654-1660.	21.4	189
3	Whole genome characterization of sequence diversity of 15,220 Icelanders. Scientific Data, 2017, 4, 170115.	5.3	98
4	Comprehensive population-wide analysis of Lynch syndrome in Iceland reveals founder mutations in MSH6 and PMS2. Nature Communications, 2017, 8, 14755.	12.8	96
5	Multiple transmissions of de novo mutations in families. Nature Genetics, 2018, 50, 1674-1680.	21.4	89
6	The rate of meiotic gene conversion varies by sex and age. Nature Genetics, 2016, 48, 1377-1384.	21.4	85
7	Diversity in non-repetitive human sequences not found in the reference genome. Nature Genetics, 2017, 49, 588-593.	21.4	70
8	New basal cell carcinoma susceptibility loci. Nature Communications, 2015, 6, 6825.	12.8	59
9	NetCoffee: a fast and accurate global alignment approach to identify functionally conserved proteins in multiple networks. Bioinformatics, 2014, 30, 540-548.	4.1	56
10	popSTR: population-scale detection of STR variants. Bioinformatics, 2017, 33, 4041-4048.	4.1	34
11	PopIns: population-scale detection of novel sequence insertions. Bioinformatics, 2016, 32, 961-967.	4.1	33
12	Genome alignment with graph data structures: a comparison. BMC Bioinformatics, 2014, 15, 99.	2.6	32
13	STELLAR: fast and exact local alignments. BMC Bioinformatics, 2011, 12, S15.	2.6	28
14	Sequence variants associating with urinary biomarkers. Human Molecular Genetics, 2019, 28, 1199-1211.	2.9	28
15	Insertion of an SVA-E retrotransposon into the *CASP8* gene is associated with protection against prostate cancer. Human Molecular Genetics, 2016, 25, 1008-1018.	2.9	22
16	Determination of Glycan Structure from Tandem Mass Spectra. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 976-986.	3.0	19
17	A rare splice donor mutation in the haptoglobin gene associates with blood lipid levels and coronary artery disease. Human Molecular Genetics, 2017, 26, 2364-2376.	2.9	17
18	Lifelong Reduction in LDL (Low-Density Lipoprotein) Cholesterol due to a Gain-of-Function Mutation in *LDLR*. Circulation Genomic and Precision Medicine, 2021, 14, e003029.	3.6	12

#	Article	IF	Citations
19	PopDel identifies medium-size deletions simultaneously in tens of thousands of genomes. Nature Communications, 2021, 12, 730.	12.8	9
20	PopAlu: population-scale detection of Alu polymorphisms. PeerJ, 2015, 3, e1269.	2.0	6
21	Population-scale detection of non-reference sequence variants using colored de Bruijn graphs. Bioinformatics, 2022, 38, 604-611.	4.1	4
22	A sequence variant associating with educational attainment also affects childhood cognition. Scientific Reports, 2016, 6, 36189.	3.3	2
23	GAMIBHEAR: whole-genome haplotype reconstruction from Genome Architecture Mapping data. Bioinformatics, 2021, 37, 3128-3135.	4.1	1
24	Novel sequencing technologies and bioinformatic tools for deciphering the non-coding genome. Medizinische Genetik, 2021, 33, 133-145.	0.2	1
25	chopBAI: BAM index reduction solves I/O bottlenecks in the joint analysis of large sequencing cohorts. Bioinformatics, 2016, 32, 2202-2204.	4.1	0