

Birte Kehr

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4032196/publications.pdf>

Version: 2024-02-01

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	Population-scale detection of non-reference sequence variants using colored de Bruijn graphs. <i>Bioinformatics</i> , 2022, 38, 604-611.	4.1	4
2	Lifelong Reduction in LDL (Low-Density Lipoprotein) Cholesterol due to a Gain-of-Function Mutation in <i>LDLR</i> . <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e003029.	3.6	12
3	PopDel identifies medium-size deletions simultaneously in tens of thousands of genomes. <i>Nature Communications</i> , 2021, 12, 730.	12.8	9
4	GAMIBHEAR: whole-genome haplotype reconstruction from Genome Architecture Mapping data. <i>Bioinformatics</i> , 2021, 37, 3128-3135.	4.1	1
5	Novel sequencing technologies and bioinformatic tools for deciphering the non-coding genome. <i>Medizinische Genetik</i> , 2021, 33, 133-145.	0.2	1
6	Sequence variants associating with urinary biomarkers. <i>Human Molecular Genetics</i> , 2019, 28, 1199-1211.	2.9	28
7	Multiple transmissions of de novo mutations in families. <i>Nature Genetics</i> , 2018, 50, 1674-1680.	21.4	89
8	popSTR: population-scale detection of STR variants. <i>Bioinformatics</i> , 2017, 33, 4041-4048.	4.1	34
9	Diversity in non-repetitive human sequences not found in the reference genome. <i>Nature Genetics</i> , 2017, 49, 588-593.	21.4	70
10	Comprehensive population-wide analysis of Lynch syndrome in Iceland reveals founder mutations in <i>MSH6</i> and <i>PMS2</i> . <i>Nature Communications</i> , 2017, 8, 14755.	12.8	96
11	A rare splice donor mutation in the haptoglobin gene associates with blood lipid levels and coronary artery disease. <i>Human Molecular Genetics</i> , 2017, 26, 2364-2376.	2.9	17
12	Whole genome characterization of sequence diversity of 15,220 Icelanders. <i>Scientific Data</i> , 2017, 4, 170115.	5.3	98
13	GraphTyper enables population-scale genotyping using pangenome graphs. <i>Nature Genetics</i> , 2017, 49, 1654-1660.	21.4	189
14	Parental influence on human germline de novo mutations in 1,548 trios from Iceland. <i>Nature</i> , 2017, 549, 519-522.	27.8	410
15	A sequence variant associating with educational attainment also affects childhood cognition. <i>Scientific Reports</i> , 2016, 6, 36189.	3.3	2
16	The rate of meiotic gene conversion varies by sex and age. <i>Nature Genetics</i> , 2016, 48, 1377-1384.	21.4	85
17	chopBAM: BAM index reduction solves I/O bottlenecks in the joint analysis of large sequencing cohorts. <i>Bioinformatics</i> , 2016, 32, 2202-2204.	4.1	0
18	Insertion of an SVA-E retrotransposon into the <i>CASP8</i> gene is associated with protection against prostate cancer. <i>Human Molecular Genetics</i> , 2016, 25, 1008-1018.	2.9	22

#	ARTICLE	IF	CITATIONS
19	PopIns: population-scale detection of novel sequence insertions. <i>Bioinformatics</i> , 2016, 32, 961-967.	4.1	33
20	New basal cell carcinoma susceptibility loci. <i>Nature Communications</i> , 2015, 6, 6825.	12.8	59
21	PopAlu: population-scale detection of Alu polymorphisms. <i>PeerJ</i> , 2015, 3, e1269.	2.0	6
22	NetCoffee: a fast and accurate global alignment approach to identify functionally conserved proteins in multiple networks. <i>Bioinformatics</i> , 2014, 30, 540-548.	4.1	56
23	Genome alignment with graph data structures: a comparison. <i>BMC Bioinformatics</i> , 2014, 15, 99.	2.6	32
24	Determination of Glycan Structure from Tandem Mass Spectra. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 976-986.	3.0	19
25	STELLAR: fast and exact local alignments. <i>BMC Bioinformatics</i> , 2011, 12, S15.	2.6	28