Arend Sidow

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6361214/publications.pdf

Version: 2024-02-01

42 papers	8,790 citations	186265 28 h-index	289244 40 g-index
52 all docs	52 docs citations	52 times ranked	19575 citing authors

#	Article	IF	Citations
1	Benchmarking challenging small variants with linked and long reads. Cell Genomics, 2022, 2, 100128.	6.5	77
2	Aquila enables reference-assisted diploid personal genome assembly and comprehensive variant detection based on linked reads. Nature Communications, 2021, 12, 1077.	12.8	11
3	De novo mutational signature discovery in tumor genomes using SparseSignatures. PLoS Computational Biology, 2021, 17, e1009119.	3.2	20
4	Aquila_stLFR: diploid genome assembly based structural variant calling package for stLFR linked-reads. Bioinformatics Advances, 2021, 1, .	2.4	8
5	De novo diploid genome assembly for genome-wide structural variant detection. NAR Genomics and Bioinformatics, 2020, 2, lqz018.	3.2	9
6	Comprehensive genomic characterization of breast tumors with BRCA1 and BRCA2 mutations. BMC Medical Genomics, 2019, 12, 84.	1.5	20
7	Assessment of human diploid genome assembly with 10x Linked-Reads data. GigaScience, 2019, 8, .	6.4	20
8	Multi-omic tumor data reveal diversity of molecular mechanisms that correlate with survival. Nature Communications, 2018, 9, 4453.	12.8	123
9	High-quality genome sequences of uncultured microbes by assembly of read clouds. Nature Biotechnology, 2018, 36, 1067-1075.	17.5	103
10	HAPDeNovo: a haplotype-based approach for filtering and phasing de novo mutations in linked read sequencing data. BMC Genomics, 2018, 19, 467.	2.8	11
11	Genome-wide reconstruction of complex structural variants using read clouds. Nature Methods, 2017, 14, 915-920.	19.0	96
12	Extensive sequencing of seven human genomes to characterize benchmark reference materials. Scientific Data, 2016, 3, 160025.	5.3	575
13	A research roadmap for next-generation sequencing informatics. Science Translational Medicine, 2016, 8, 335ps10.	12.4	37
14	Lineage-specific enhancers activate self-renewal genes in macrophages and embryonic stem cells. Science, 2016, 351, aad5510.	12.6	194
15	Cell-lineage heterogeneity and driver mutation recurrence in pre-invasive breast neoplasia. Genome Medicine, 2015, 7, 28.	8.2	17
16	Concepts in solid tumor evolution. Trends in Genetics, 2015, 31, 208-214.	6.7	51
17	Read clouds uncover variation in complex regions of the human genome. Genome Research, 2015, 25, 1570-1580.	5.5	70
18	svviz: a read viewer for validating structural variants. Bioinformatics, 2015, 31, 3994-3996.	4.1	46

#	Article	IF	Citations
19	Constraint and divergence of global gene expression in the mammalian embryo. ELife, 2015, 4, e05538.	6.0	3
20	Maternal bias and escape from X chromosome imprinting in the midgestation mouse placenta. Developmental Biology, 2014, 390, 80-92.	2.0	30
21	Genome evolution during progression to breast cancer. Genome Research, 2013, 23, 1097-1108.	5.5	98
22	Identification Of The Disease-Causing Mutation In Autosomal Dominant Familial Immune Thrombocytopenia By Genome-Wide Linkage Analysis and Whole Genome Sequencing. Blood, 2013, 122, 565-565.	1.4	0
23	Architecture of the human regulatory network derived from ENCODE data. Nature, 2012, 489, 91-100.	27.8	1,384
24	ProPhylER: A curated online resource for protein function and structure based on evolutionary constraint analyses. Genome Research, 2010, 20, 142-154.	5.5	28
25	Identifying a High Fraction of the Human Genome to be under Selective Constraint Using GERP++. PLoS Computational Biology, 2010, 6, e1001025.	3.2	1,443
26	Genome-wide analysis of transcription factor binding sites based on ChIP-Seq data. Nature Methods, 2008, 5, 829-834.	19.0	627
27	Fruit Fly Family Fun. Cell, 2007, 131, 1222-1223.	28.9	0
28	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. Genome Research, 2007, 17, 760-774.	5.5	184
29	Distribution and intensity of constraint in mammalian genomic sequence. Genome Research, 2005, 15, 901-913.	5.5	1,230
30	TRADE-OFFS IN DETECTING EVOLUTIONARILY CONSTRAINED SEQUENCE BY COMPARATIVE GENOMICS. Annual Review of Genomics and Human Genetics, 2005, 6, 143-164.	6.2	41
31	Characterization of Evolutionary Rates and Constraints in Three Mammalian Genomes. Genome Research, 2004, 14, 539-548.	5.5	125
32	ABC: software for interactive browsing of genomic multiple sequence alignment data. BMC Bioinformatics, 2004, 5, 192.	2.6	12
33	Title is missing!. Journal of Structural and Functional Genomics, 2003, 3, 45-52.	1.2	42
34	Genomic regulatory regions: insights from comparative sequence analysis. Current Opinion in Genetics and Development, 2003, 13, 604-610.	3.3	57
35	Quantitative Estimates of Sequence Divergence for Comparative Analyses of Mammalian Genomes. Genome Research, 2003, 13, 813-820.	5.5	106
36	LAGAN and Multi-LAGAN: Efficient Tools for Large-Scale Multiple Alignment of Genomic DNA. Genome Research, 2003, 13, 721-731.	5.5	960

#	Article	IF	Citations
37	Inference of functional regions in proteins by quantification of evolutionary constraints. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 2912-2917.	7.1	68
38	Sequence First. Ask Questions Later.. Cell, 2002, 111, 13-16.	28.9	34
39	A Double-Deletion Mutation in the Pitx3 Gene Causes Arrested Lens Development in Aphakia Mice. Genomics, 2001, 72, 61-72.	2.9	139
40	A novel member of the F-box/WD40 gene family, encoding dactylin, is disrupted in the mouse dactylaplasia mutant. Nature Genetics, 1999, 23, 104-107.	21.4	85
41	Serrate2 is disrupted in the mouse limb-development mutant syndactylism. Nature, 1997, 389, 722-725.	27.8	110
42	Gen(om)e duplications in the evolution of early vertebrates. Current Opinion in Genetics and Development, 1996, 6, 715-722.	3.3	438