Arend Sidow

List of Publications by Year
in descending order

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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	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
2	Architecture of the human regulatory network derived from ENCODE data. Nature, 2012, 489, 91-100.	27.8	1,384
3	Distribution and intensity of constraint in mammalian genomic sequence. Genome Research, 2005, 15, 901-913.	5.5	1,230
4	LAGAN and Multi-LAGAN: Efficient Tools for Large-Scale Multiple Alignment of Genomic DNA. Genome Research, 2003, 13, 721-731.	5.5	960
5	Genome-wide analysis of transcription factor binding sites based on ChIP-Seq data. Nature Methods, 2008, 5, 829-834.	19.0	627
6	Extensive sequencing of seven human genomes to characterize benchmark reference materials. Scientific Data, 2016, 3, 160025.	5.3	575
7	Gen(om)e duplications in the evolution of early vertebrates. Current Opinion in Genetics and Development, 1996, 6, 715-722.	3.3	438
8	Lineage-specific enhancers activate self-renewal genes in macrophages and embryonic stem cells. Science, 2016, 351, aad5510.	12.6	194
9	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. Genome Research, 2007, 17, 760-774.	5.5	184
10	A Double-Deletion Mutation in the Pitx3 Gene Causes Arrested Lens Development in Aphakia Mice. Genomics, 2001, 72, 61-72.	2.9	139
11	Characterization of Evolutionary Rates and Constraints in Three Mammalian Genomes. Genome Research, 2004, 14, 539-548.	5.5	125
12	Multi-omic tumor data reveal diversity of molecular mechanisms that correlate with survival. Nature Communications, 2018, 9, 4453.	12.8	123
13	Serrate2 is disrupted in the mouse limb-development mutant syndactylism. Nature, 1997, 389, 722-725.	27.8	110
14	Quantitative Estimates of Sequence Divergence for Comparative Analyses of Mammalian Genomes. Genome Research, 2003, 13, 813-820.	5.5	106
15	High-quality genome sequences of uncultured microbes by assembly of read clouds. Nature Biotechnology, 2018, 36, 1067-1075.	17.5	103
16	Genome evolution during progression to breast cancer. Genome Research, 2013, 23, 1097-1108.	5.5	98
17	Genome-wide reconstruction of complex structural variants using read clouds. Nature Methods, 2017, 14, 915-920.	19.0	96
18	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

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19	Benchmarking challenging small variants with linked and long reads. Cell Genomics, 2022, 2, 100128.	6.5	77
20	Read clouds uncover variation in complex regions of the human genome. Genome Research, 2015, 25, 1570-1580.	5.5	70
21	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
22	Genomic regulatory regions: insights from comparative sequence analysis. Current Opinion in Genetics and Development, 2003, 13, 604-610.	3.3	57
23	Concepts in solid tumor evolution. Trends in Genetics, 2015, 31, 208-214.	6.7	51
24	svviz: a read viewer for validating structural variants. Bioinformatics, 2015, 31, 3994-3996.	4.1	46
25	Title is missing!. Journal of Structural and Functional Genomics, 2003, 3, 45-52.	1.2	42
26	TRADE-OFFS IN DETECTING EVOLUTIONARILY CONSTRAINED SEQUENCE BY COMPARATIVE GENOMICS. Annual Review of Genomics and Human Genetics, 2005, 6, 143-164.	6.2	41
27	A research roadmap for next-generation sequencing informatics. Science Translational Medicine, 2016, 8, 335ps10.	12.4	37
28	Sequence First. Ask Questions Later.. Cell, 2002, 111, 13-16.	28.9	34
29	Maternal bias and escape from X chromosome imprinting in the midgestation mouse placenta. Developmental Biology, 2014, 390, 80-92.	2.0	30
30	ProPhylER: A curated online resource for protein function and structure based on evolutionary constraint analyses. Genome Research, 2010, 20, 142-154.	5.5	28
31	Comprehensive genomic characterization of breast tumors with BRCA1 and BRCA2 mutations. BMC Medical Genomics, 2019, 12, 84.	1.5	20
32	Assessment of human diploid genome assembly with 10x Linked-Reads data. GigaScience, 2019, 8, .	6.4	20
33	De novo mutational signature discovery in tumor genomes using SparseSignatures. PLoS Computational Biology, 2021, 17, e1009119.	3.2	20
34	Cell-lineage heterogeneity and driver mutation recurrence in pre-invasive breast neoplasia. Genome Medicine, 2015, 7, 28.	8.2	17
35	ABC: software for interactive browsing of genomic multiple sequence alignment data. BMC Bioinformatics, 2004, 5, 192.	2.6	12
36	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

#	Article	IF	Citations
37	Aquila enables reference-assisted diploid personal genome assembly and comprehensive variant detection based on linked reads. Nature Communications, 2021, 12, 1077.	12.8	11
38	De novo diploid genome assembly for genome-wide structural variant detection. NAR Genomics and Bioinformatics, 2020, 2, lqz018.	3.2	9
39	Aquila_stLFR: diploid genome assembly based structural variant calling package for stLFR linked-reads. Bioinformatics Advances, 2021, 1, .	2.4	8
40	Constraint and divergence of global gene expression in the mammalian embryo. ELife, 2015, 4, e05538.	6.0	3
41	Fruit Fly Family Fun. Cell, 2007, 131, 1222-1223.	28.9	0
42	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