Geir Kjetil Sandve

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4769706/publications.pdf

Version: 2024-02-01

68 papers	2,572 citations	257450 24 h-index	233421 45 g-index
92 all docs	92 docs citations	92 times ranked	4693 citing authors

#	Article	IF	Citations
1	Ten Simple Rules for Reproducible Computational Research. PLoS Computational Biology, 2013, 9, e1003285.	3.2	509
2	A survey of motif discovery methods in an integrated framework. Biology Direct, 2006, 1, 11.	4.6	135
3	In the loop: promoterâ€“enhancer interactions and bioinformatics. Briefings in Bioinformatics, 2016, 17, bbv097.	6.5	115
4	A compact vocabulary of paratope-epitope interactions enables predictability of antibody-antigen binding. Cell Reports, 2021, 34, 108856.	6.4	101
5	Disease-driving CD4+ T cell clonotypes persist for decades in celiac disease. Journal of Clinical Investigation, 2018, 128, 2642-2650.	8.2	90
6	The Genomic HyperBrowser: inferential genomics at the sequence level. Genome Biology, 2010, 11, R121.	9.6	78
7	A map of direct TFâ€“DNA interactions in the human genome. Nucleic Acids Research, 2019, 47, e21-e21.	14.5	72
8	High-Throughput Single-Cell Analysis of B Cell Receptor Usage among Autoantigen-Specific Plasma Cells in Celiac Disease. Journal of Immunology, 2017, 199, 782-791.	0.8	62
9	Improved benchmarks for computational motif discovery. BMC Bioinformatics, 2007, 8, 193.	2.6	61
10	Vitamin D receptor ChIP-seq in primary CD4+ cells: relationship to serum 25-hydroxyvitamin D levels and autoimmune disease. BMC Medicine, 2013, 11, 163.	5.5	59
11	Augmenting adaptive immunity: progress and challenges in the quantitative engineering and analysis of adaptive immune receptor repertoires. Molecular Systems Design and Engineering, 2019, 4, 701-736.	3.4	57
12	Colocalization analyses of genomic elements: approaches, recommendations and challenges. Bioinformatics, 2019, 35, 1615-1624.	4.1	53
13	Vitamin D receptor binding, chromatin states and association with multiple sclerosis. Human Molecular Genetics, 2012, 21, 3575-3586.	2.9	50
14	EBNA2 Binds to Genomic Intervals Associated with Multiple Sclerosis and Overlaps with Vitamin D Receptor Occupancy. PLoS ONE, 2015, 10, e0119605.	2.5	49
15	immuneSIM: tunable multi-feature simulation of B- and T-cell receptor repertoires for immunoinformatics benchmarking. Bioinformatics, 2020, 36, 3594-3596.	4.1	48
16	Assessment of composite motif discovery methods. BMC Bioinformatics, 2008, 9, 123.	2.6	44
17	Uracil Accumulation and Mutagenesis Dominated by Cytosine Deamination in CpG Dinucleotides in Mice Lacking UNG and SMUG1. Scientific Reports, 2017, 7, 7199.	3.3	43
18	NucDiff: in-depth characterization and annotation of differences between two sets of DNA sequences. BMC Bioinformatics, 2017, 18, 338.	2.6	43

#	Article	IF	Citations
19	In silico proof of principle of machine learning-based antibody design at unconstrained scale. MAbs, 2022, 14, 2031482.	5.2	40
20	B cell tolerance and antibody production to the celiac disease autoantigen transglutaminase 2. Journal of Experimental Medicine, 2020, 217, .	8.5	38
21	HiBrowse: multi-purpose statistical analysis of genome-wide chromatin 3D organization. Bioinformatics, 2014, 30, 1620-1622.	4.1	37
22	Transcriptionally Active Regions Are the Preferred Targets for Chromosomal HPV Integration in Cervical Carcinogenesis. PLoS ONE, 2015, 10, e0119566.	2.5	36
23	The immuneML ecosystem for machine learning analysis of adaptive immune receptor repertoires. Nature Machine Intelligence, 2021, 3, 936-944.	16.0	35
24	Sequential Monte Carlo multiple testing. Bioinformatics, 2011, 27, 3235-3241.	4.1	33
25	The Genomic HyperBrowser: an analysis web server for genome-scale data. Nucleic Acids Research, 2013, 41, W133-W141.	14.5	32
26	Human somatic cell mutagenesis creates genetically tractable sarcomas. Nature Genetics, 2014, 46, 964-972.	21.4	29
27	Increased expression of IRF4 and ETS1 in CD4⁺ cells from patients with intermittent allergic rhinitis. Allergy: European Journal of Allergy and Clinical Immunology, 2012, 67, 33-40.	5.7	25
28	Beware the Jaccard: the choice of similarity measure is important and non-trivial in genomic colocalisation analysis. Briefings in Bioinformatics, 2020, 21, 1523-1530.	6.5	24
29	Coloc-stats: a unified web interface to perform colocalization analysis of genomic features. Nucleic Acids Research, 2018, 46, W186-W193.	14.5	23
30	Graph Peak Caller: Calling ChIP-seq peaks on graph-based reference genomes. PLoS Computational Biology, 2019, 15, e1006731.	3.2	23
31	Comprehensive Analysis of CDR3 Sequences in Gluten-Specific T-Cell Receptors Reveals a Dominant R-Motif and Several New Minor Motifs. Frontiers in Immunology, 2021, 12, 639672.	4.8	23
32	Handling realistic assumptions in hypothesis testing of 3D co-localization of genomic elements. Nucleic Acids Research, 2013, 41, 5164-5174.	14.5	22
33	GSuite HyperBrowser: integrative analysis of dataset collections across the genome and epigenome. GigaScience, 2017, 6, 1-12.	6.4	22
34	Coordinates and intervals in graph-based reference genomes. BMC Bioinformatics, 2017, 18, 263.	2.6	22
35	Individualized VDJ recombination predisposes the available Ig sequence space. Genome Research, 2021, 31, 2209-2224.	5.5	22
36	DNase hypersensitive sites and association with multiple sclerosis. Human Molecular Genetics, 2014, 23, 942-948.	2.9	21

#	Article	IF	Citations
37	Identifying elemental genomic track types and representing them uniformly. BMC Bioinformatics, 2011, 12, 494.	2.6	20
38	c-Myb Binding Sites in Haematopoietic Chromatin Landscapes. PLoS ONE, 2015, 10, e0133280.	2.5	20
39	Age-Associated Hyper-Methylated Regions in the Human Brain Overlap with Bivalent Chromatin Domains. PLoS ONE, 2012, 7, e43840.	2.5	18
40	Chromatin states reveal functional associations for globally defined transcription start sites in four human cell lines. BMC Genomics, 2014, 15, 120.	2.8	17
41	Genomic Regions Associated with Multiple Sclerosis Are Active in B Cells. PLoS ONE, 2012, 7, e32281.	2.5	16
42	Monte Carlo Null Models for Genomic Data. Statistical Science, 2015, 30, .	2.8	13
43	Assessing graph-based read mappers against a baseline approach highlights strengths and weaknesses of current methods. BMC Genomics, 2020, 21, 282.	2.8	13
44	Chromatin occupancy and target genes of the haematopoietic master transcription factor MYB. Scientific Reports, 2021, 11, 9008.	3.3	12
45	Compo: composite motif discovery using discrete models. BMC Bioinformatics, 2008, 9, 527.	2.6	11
46	T cell receptor repertoire as a potential diagnostic marker for celiac disease. Clinical Immunology, 2021, 222, 108621.	3.2	11
47	BayCis: A Bayesian Hierarchical HMM for Cis-Regulatory Module Decoding in Metazoan Genomes. , 2008, , 66-81.		11
48	Accelerating Motif Discovery: Motif Matching on Parallel Hardware. Lecture Notes in Computer Science, 2006, , 197-206.	1.3	10
49	Profiling the baseline performance and limits of machine learning models for adaptive immune receptor repertoire classification. GigaScience, 2022, 11, .	6.4	10
50	The differential disease regulome. BMC Genomics, 2011, 12, 353.	2.8	9
51	Mind the gaps: overlooking inaccessible regions confounds statistical testing in genome analysis. BMC Bioinformatics, 2018, 19, 481.	2.6	9
52	Ten simple rules for quick and dirty scientific programming. PLoS Computational Biology, 2021, 17, e1008549.	3.2	9
53	Transcriptional profiling of human intestinal plasma cells reveals effector functions beyond antibody production. United European Gastroenterology Journal, 2019, 7, 1399-1407.	3.8	8
54	Integrating multiple oestrogen receptor alpha ChIP studies: overlap with disease susceptibility regions, DNase I hypersensitivity peaks and gene expression. BMC Medical Genomics, 2013, 6, 45.	1.5	7

#	Article	IF	Citations
55	Genome build information is an essential part of genomic track files. Genome Biology, 2017, 18, 175.	8.8	6
56	Galaxy Portal: interacting with the galaxy platform through mobile devices. Bioinformatics, 2016, 32, 1743-1745.	4.1	5
57	The rainfall plot: its motivation, characteristics and pitfalls. BMC Bioinformatics, 2017, 18, 264.	2.6	5
58	NucBreak: location of structural errors in a genome assembly by using paired-end Illumina reads. BMC Bioinformatics, 2020, 21, 66.	2.6	5
59	TCRpower: quantifying the detection power of T-cell receptor sequencing with a novel computational pipeline calibrated by spike-in sequences. Briefings in Bioinformatics, 2022, 23, .	6.5	5
60	Exploiting antigen receptor information to quantify index switching in single-cell transcriptome sequencing experiments. PLoS ONE, 2018, 13, e0208484.	2.5	4
61	Differential expression profile of gluten-specific T cells identified by single-cell RNA-seq. PLoS ONE, 2021, 16, e0258029.	2.5	4
62	Segmentation of DNA sequences into twostate regions and melting fork regions. Journal of Physics Condensed Matter, 2009, 21, 034109.	1.8	3
63	ClusTrack: Feature Extraction and Similarity Measures for Clustering of Genome-Wide Data Sets. PLoS ONE, 2015, 10, e0123261.	2.5	3
64	Complex patterns of concomitant medication use: A study among Norwegian women using paracetamol during pregnancy. PLoS ONE, 2017, 12, e0190101.	2.5	3
65	Generalized Composite Motif Discovery. Lecture Notes in Computer Science, 2005, , 763-769.	1.3	3
66	False Discovery Rates in Identifying Functional DNA Motifs. , 2007, , .		0
67	Editorial: Genomic Colocalization and Enrichment Analyses. Frontiers in Genetics, 2020, 11, 617876.	2.3	0
68	A METHODOLOGY FOR MOTIF DISCOVERY EMPLOYING ITERATED CLUSTER RE-ASSIGNMENT. , 2006, , .		0