Geir Kjetil Sandve

List of Publications by Year
in descending order

68	2,572	257429 24	233409 45
papers	citations	h-index	g-index

92	92	92	4693
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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
2	In silico proof of principle of machine learning-based antibody design at unconstrained scale. MAbs, 2022, 14, 2031482.	5.2	40
3	Profiling the baseline performance and limits of machine learning models for adaptive immune receptor repertoire classification. GigaScience, 2022, 11, .	6.4	10
4	T cell receptor repertoire as a potential diagnostic marker for celiac disease. Clinical Immunology, 2021, 222, 108621.	3.2	11
5	Ten simple rules for quick and dirty scientific programming. PLoS Computational Biology, 2021, 17, e1008549.	3.2	9
6	A compact vocabulary of paratope-epitope interactions enables predictability of antibody-antigen binding. Cell Reports, 2021, 34, 108856.	6.4	101
7	Chromatin occupancy and target genes of the haematopoietic master transcription factor MYB. Scientific Reports, 2021, 11, 9008.	3.3	12
8	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
9	Differential expression profile of gluten-specific T cells identified by single-cell RNA-seq. PLoS ONE, 2021, 16, e0258029.	2.5	4
10	The immuneML ecosystem for machine learning analysis of adaptive immune receptor repertoires. Nature Machine Intelligence, 2021, 3, 936-944.	16.0	35
11	Individualized VDJ recombination predisposes the available Ig sequence space. Genome Research, 2021, 31, 2209-2224.	5.5	22
12	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
13	B cell tolerance and antibody production to the celiac disease autoantigen transglutaminase 2. Journal of Experimental Medicine, 2020, 217, .	8.5	38
14	immuneSIM: tunable multi-feature simulation of B- and T-cell receptor repertoires for immunoinformatics benchmarking. Bioinformatics, 2020, 36, 3594-3596.	4.1	48
15	NucBreak: location of structural errors in a genome assembly by using paired-end Illumina reads. BMC Bioinformatics, 2020, 21, 66.	2.6	5
16	Assessing graph-based read mappers against a baseline approach highlights strengths and weaknesses of current methods. BMC Genomics, 2020, 21, 282.	2.8	13
17	Editorial: Genomic Colocalization and Enrichment Analyses. Frontiers in Genetics, 2020, 11, 617876.	2.3	0
18	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

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19	Colocalization analyses of genomic elements: approaches, recommendations and challenges. Bioinformatics, 2019, 35, 1615-1624.	4.1	53
20	Graph Peak Caller: Calling ChIP-seq peaks on graph-based reference genomes. PLoS Computational Biology, 2019, 15, e1006731.	3.2	23
21	Transcriptional profiling of human intestinal plasma cells reveals effector functions beyond antibody production. United European Gastroenterology Journal, 2019, 7, 1399-1407.	3.8	8
22	A map of direct TFâ€“DNA interactions in the human genome. Nucleic Acids Research, 2019, 47, e21-e21.	14.5	72
23	Mind the gaps: overlooking inaccessible regions confounds statistical testing in genome analysis. BMC Bioinformatics, 2018, 19, 481.	2.6	9
24	Exploiting antigen receptor information to quantify index switching in single-cell transcriptome sequencing experiments. PLoS ONE, 2018, 13, e0208484.	2.5	4
25	Coloc-stats: a unified web interface to perform colocalization analysis of genomic features. Nucleic Acids Research, 2018, 46, W186-W193.	14.5	23
26	Disease-driving CD4+ T cell clonotypes persist for decades in celiac disease. Journal of Clinical Investigation, 2018, 128, 2642-2650.	8.2	90
27	GSuite HyperBrowser: integrative analysis of dataset collections across the genome and epigenome. GigaScience, 2017, 6, 1-12.	6.4	22
28	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
29	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
30	Coordinates and intervals in graph-based reference genomes. BMC Bioinformatics, 2017, 18, 263.	2.6	22
31	The rainfall plot: its motivation, characteristics and pitfalls. BMC Bioinformatics, 2017, 18, 264.	2.6	5
32	Complex patterns of concomitant medication use: A study among Norwegian women using paracetamol during pregnancy. PLoS ONE, 2017, 12, e0190101.	2.5	3
33	Genome build information is an essential part of genomic track files. Genome Biology, 2017, 18, 175.	8.8	6
34	NucDiff: in-depth characterization and annotation of differences between two sets of DNA sequences. BMC Bioinformatics, 2017, 18, 338.	2.6	43
35	In the loop: promoterâ€“enhancer interactions and bioinformatics. Briefings in Bioinformatics, 2016, 17, bbv097.	6.5	115
36	Galaxy Portal: interacting with the galaxy platform through mobile devices. Bioinformatics, 2016, 32, 1743-1745.	4.1	5

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37	EBNA2 Binds to Genomic Intervals Associated with Multiple Sclerosis and Overlaps with Vitamin D Receptor Occupancy. PLoS ONE, 2015, 10, e0119605.	2.5	49
38	ClusTrack: Feature Extraction and Similarity Measures for Clustering of Genome-Wide Data Sets. PLoS ONE, 2015, 10, e0123261.	2.5	3
39	c-Myb Binding Sites in Haematopoietic Chromatin Landscapes. PLoS ONE, 2015, 10, e0133280.	2.5	20
40	Monte Carlo Null Models for Genomic Data. Statistical Science, 2015, 30, .	2.8	13
41	Transcriptionally Active Regions Are the Preferred Targets for Chromosomal HPV Integration in Cervical Carcinogenesis. PLoS ONE, 2015, 10, e0119566.	2.5	36
42	HiBrowse: multi-purpose statistical analysis of genome-wide chromatin 3D organization. Bioinformatics, 2014, 30, 1620-1622.	4.1	37
43	DNase hypersensitive sites and association with multiple sclerosis. Human Molecular Genetics, 2014, 23, 942-948.	2.9	21
44	Human somatic cell mutagenesis creates genetically tractable sarcomas. Nature Genetics, 2014, 46, 964-972.	21.4	29
45	Chromatin states reveal functional associations for globally defined transcription start sites in four human cell lines. BMC Genomics, 2014, 15, 120.	2.8	17
46	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
47	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
48	The Genomic HyperBrowser: an analysis web server for genome-scale data. Nucleic Acids Research, 2013, 41, W133-W141.	14.5	32
49	Ten Simple Rules for Reproducible Computational Research. PLoS Computational Biology, 2013, 9, e1003285.	3.2	509
50	Handling realistic assumptions in hypothesis testing of 3D co-localization of genomic elements. Nucleic Acids Research, 2013, 41, 5164-5174.	14.5	22
51	Vitamin D receptor binding, chromatin states and association with multiple sclerosis. Human Molecular Genetics, 2012, 21, 3575-3586.	2.9	50
52	Genomic Regions Associated with Multiple Sclerosis Are Active in B Cells. PLoS ONE, 2012, 7, e32281.	2.5	16
53	Age-Associated Hyper-Methylated Regions in the Human Brain Overlap with Bivalent Chromatin Domains. PLoS ONE, 2012, 7, e43840.	2.5	18
54	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

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55	Identifying elemental genomic track types and representing them uniformly. BMC Bioinformatics, 2011, 12, 494.	2.6	20
56	The differential disease regulome. BMC Genomics, 2011, 12, 353.	2.8	9
57	Sequential Monte Carlo multiple testing. Bioinformatics, 2011, 27, 3235-3241.	4.1	33
58	The Genomic HyperBrowser: inferential genomics at the sequence level. Genome Biology, 2010, 11, R121.	9.6	78
59	Segmentation of DNA sequences into twostate regions and melting fork regions. Journal of Physics Condensed Matter, 2009, 21, 034109.	1.8	3
60	Assessment of composite motif discovery methods. BMC Bioinformatics, 2008, 9, 123.	2.6	44
61	Compo: composite motif discovery using discrete models. BMC Bioinformatics, 2008, 9, 527.	2.6	11
62	BayCis: A Bayesian Hierarchical HMM for Cis-Regulatory Module Decoding in Metazoan Genomes. , 2008, , 66-81.		11
63	False Discovery Rates in Identifying Functional DNA Motifs. , 2007, , .		0
64	Improved benchmarks for computational motif discovery. BMC Bioinformatics, 2007, 8, 193.	2.6	61
65	A survey of motif discovery methods in an integrated framework. Biology Direct, 2006, 1, 11.	4.6	135
66	Accelerating Motif Discovery: Motif Matching on Parallel Hardware. Lecture Notes in Computer Science, 2006, , 197-206.	1.3	10
67	A METHODOLOGY FOR MOTIF DISCOVERY EMPLOYING ITERATED CLUSTER RE-ASSIGNMENT. , 2006, , .		0
68	Generalized Composite Motif Discovery. Lecture Notes in Computer Science, 2005, , 763-769.	1.3	3