

Geir Kjetil Sandve

List of Publications by Year in descending order

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Version: 2024-02-01

68
papers

2,572
citations

257450

24
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233421

45
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92
all docs

92
docs citations

92
times ranked

4693
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. <i>Briefings in Bioinformatics</i> , 2022, 23, . | 6.5 | 5 |
| 2 | In silico proof of principle of machine learning-based antibody design at unconstrained scale. <i>MAbs</i> , 2022, 14, 2031482. | 5.2 | 40 |
| 3 | Profiling the baseline performance and limits of machine learning models for adaptive immune receptor repertoire classification. <i>GigaScience</i> , 2022, 11, . | 6.4 | 10 |
| 4 | T cell receptor repertoire as a potential diagnostic marker for celiac disease. <i>Clinical Immunology</i> , 2021, 222, 108621. | 3.2 | 11 |
| 5 | Ten simple rules for quick and dirty scientific programming. <i>PLoS Computational Biology</i> , 2021, 17, e1008549. | 3.2 | 9 |
| 6 | A compact vocabulary of paratope-epitope interactions enables predictability of antibody-antigen binding. <i>Cell Reports</i> , 2021, 34, 108856. | 6.4 | 101 |
| 7 | Chromatin occupancy and target genes of the haematopoietic master transcription factor MYB. <i>Scientific Reports</i> , 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. <i>Frontiers in Immunology</i> , 2021, 12, 639672. | 4.8 | 23 |
| 9 | Differential expression profile of gluten-specific T cells identified by single-cell RNA-seq. <i>PLoS ONE</i> , 2021, 16, e0258029. | 2.5 | 4 |
| 10 | The immuneML ecosystem for machine learning analysis of adaptive immune receptor repertoires. <i>Nature Machine Intelligence</i> , 2021, 3, 936-944. | 16.0 | 35 |
| 11 | Individualized VDJ recombination predisposes the available Ig sequence space. <i>Genome Research</i> , 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. <i>Briefings in Bioinformatics</i> , 2020, 21, 1523-1530. | 6.5 | 24 |
| 13 | B cell tolerance and antibody production to the celiac disease autoantigen transglutaminase 2. <i>Journal of Experimental Medicine</i> , 2020, 217, . | 8.5 | 38 |
| 14 | immuneSIM: tunable multi-feature simulation of B- and T-cell receptor repertoires for immunoinformatics benchmarking. <i>Bioinformatics</i> , 2020, 36, 3594-3596. | 4.1 | 48 |
| 15 | NucBreak: location of structural errors in a genome assembly by using paired-end Illumina reads. <i>BMC Bioinformatics</i> , 2020, 21, 66. | 2.6 | 5 |
| 16 | Assessing graph-based read mappers against a baseline approach highlights strengths and weaknesses of current methods. <i>BMC Genomics</i> , 2020, 21, 282. | 2.8 | 13 |
| 17 | Editorial: Genomic Colocalization and Enrichment Analyses. <i>Frontiers in Genetics</i> , 2020, 11, 617876. | 2.3 | 0 |
| 18 | Augmenting adaptive immunity: progress and challenges in the quantitative engineering and analysis of adaptive immune receptor repertoires. <i>Molecular Systems Design and Engineering</i> , 2019, 4, 701-736. | 3.4 | 57 |

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|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 19 | Colocalization analyses of genomic elements: approaches, recommendations and challenges. <i>Bioinformatics</i> , 2019, 35, 1615-1624. | 4.1 | 53 |
| 20 | Graph Peak Caller: Calling ChIP-seq peaks on graph-based reference genomes. <i>PLoS Computational Biology</i> , 2019, 15, e1006731. | 3.2 | 23 |
| 21 | Transcriptional profiling of human intestinal plasma cells reveals effector functions beyond antibody production. <i>United European Gastroenterology Journal</i> , 2019, 7, 1399-1407. | 3.8 | 8 |
| 22 | A map of direct TF-DNA interactions in the human genome. <i>Nucleic Acids Research</i> , 2019, 47, e21-e21. | 14.5 | 72 |
| 23 | Mind the gaps: overlooking inaccessible regions confounds statistical testing in genome analysis. <i>BMC Bioinformatics</i> , 2018, 19, 481. | 2.6 | 9 |
| 24 | Exploiting antigen receptor information to quantify index switching in single-cell transcriptome sequencing experiments. <i>PLoS ONE</i> , 2018, 13, e0208484. | 2.5 | 4 |
| 25 | Coloc-stats: a unified web interface to perform colocalization analysis of genomic features. <i>Nucleic Acids Research</i> , 2018, 46, W186-W193. | 14.5 | 23 |
| 26 | Disease-driving CD4+ T cell clonotypes persist for decades in celiac disease. <i>Journal of Clinical Investigation</i> , 2018, 128, 2642-2650. | 8.2 | 90 |
| 27 | GSuite HyperBrowser: integrative analysis of dataset collections across the genome and epigenome. <i>GigaScience</i> , 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. <i>Journal of Immunology</i> , 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. <i>Scientific Reports</i> , 2017, 7, 7199. | 3.3 | 43 |
| 30 | Coordinates and intervals in graph-based reference genomes. <i>BMC Bioinformatics</i> , 2017, 18, 263. | 2.6 | 22 |
| 31 | The rainfall plot: its motivation, characteristics and pitfalls. <i>BMC Bioinformatics</i> , 2017, 18, 264. | 2.6 | 5 |
| 32 | Complex patterns of concomitant medication use: A study among Norwegian women using paracetamol during pregnancy. <i>PLoS ONE</i> , 2017, 12, e0190101. | 2.5 | 3 |
| 33 | Genome build information is an essential part of genomic track files. <i>Genome Biology</i> , 2017, 18, 175. | 8.8 | 6 |
| 34 | NucDiff: in-depth characterization and annotation of differences between two sets of DNA sequences. <i>BMC Bioinformatics</i> , 2017, 18, 338. | 2.6 | 43 |
| 35 | In the loop: promoter-enhancer interactions and bioinformatics. <i>Briefings in Bioinformatics</i> , 2016, 17, bbv097. | 6.5 | 115 |
| 36 | Galaxy Portal: interacting with the galaxy platform through mobile devices. <i>Bioinformatics</i> , 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 |