Jeroen de Ridder

List of Publications by Year
in descending order

61 papers	3,934 citations	279487 23 h-index	143772 57 g-index
76 all docs	76 docs citations	76 times ranked	7563 citing authors

#	Article	IF	Citations
1	Integration of multiple lineage measurements from the same cell reconstructs parallel tumor evolution. Cell Genomics, 2022, 2, 100096.	3.0	13
2	Cancer Type Classification in Liquid Biopsies Based on Sparse Mutational Profiles Enabled through Data Augmentation and Integration. Life, 2022, 12, 1.	1.1	15
3	PolarMorphism enables discovery of shared genetic variants across multiple traits from GWAS summary statistics. Bioinformatics, 2022, 38, i212-i219.	1.8	4
4	Adavosertib in combination with carboplatin in advanced TP53-mutated platinum-resistant ovarian cancer.. Journal of Clinical Oncology, 2022, 40, 5516-5516.	0.8	1
5	Allele-specific expression of GATA2 due to epigenetic dysregulation in CEBPA double-mutant AML. Blood, 2021, 138, 160-177.	0.6	13
6	Predicting pathogenic non-coding SVs disrupting the 3D genome in 1646 whole cancer genomes using multiple instance learning. Scientific Reports, 2021, 11, 14411.	1.6	1
7	Accurate detection of circulating tumor DNA using nanopore consensus sequencing. Npj Genomic Medicine, 2021, 6, 106.	1.7	14
8	Multi-contact 4C: long-molecule sequencing of complex proximity ligation products to uncover local cooperative and competitive chromatin topologies. Nature Protocols, 2020, 15, 364-397.	5.5	25
9	Gene Networks Constructed Through Simulated Treatment Learning can Predict Proteasome Inhibitor Benefit in Multiple Myeloma. Clinical Cancer Research, 2020, 26, 5952-5961.	3.2	5
10	MetaboShiny: interactive analysis and metabolite annotation of mass spectrometry-based metabolomics data. Metabolomics, 2020, 16, 99.	1.4	15
11	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	3.8	742
12	Alternate approach to stroke phenotyping identifies a genetic risk locus for small vessel stroke. European Journal of Human Genetics, 2020, 28, 963-972.	1.4	12
13	A deep learning system accurately classifies primary and metastatic cancers using passenger mutation patterns. Nature Communications, 2020, 11, 728.	5.8	140
14	RAINFOREST: a random forest approach to predict treatment benefit in data from (failed) clinical drug trials. Bioinformatics, 2020, 36, i601-i609.	1.8	20
15	svMIL: predicting the pathogenic effect of TAD boundary-disrupting somatic structural variants throughÂmultiple instance learning. Bioinformatics, 2020, 36, i692-i699.	1.8	4
16	sv-callers: a highly portable parallel workflow for structural variant detection in whole-genome sequence data. PeerJ, 2020, 8, e8214.	0.9	17
17	A data-driven interactome of synergistic genes improves network-based cancer outcome prediction. PLoS Computational Biology, 2019, 15, e1006657.	1.5	13
18	Molecular heterogeneity and early metastatic clone selection in testicular germ cell cancer development. British Journal of Cancer, 2019, 120, 444-452.	2.9	35

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19	Three-dimensional analysis of single molecule FISH in human colon organoids. Biology Open, 2019, 8, .	0.6	9
20	TargetClone: A multi-sample approach for reconstructing subclonal evolution of tumors. PLoS ONE, 2018, 13, e0208002.	1.1	7
21	A portable and scalable workflow for detecting structural variants in whole-genome sequencing data. , 2018, , .		1
22	A Single Complex Agpat2 Allele in a Patient With Partial Lipodystrophy. Frontiers in Physiology, 2018, 9, 1363.	1.3	7
23	Predicting treatment benefit in multiple myeloma through simulation of alternative treatment effects. Nature Communications, 2018, 9, 2943.	5.8	23
24	From squiggle to basepair: computational approaches for improving nanopore sequencing read accuracy. Genome Biology, 2018, 19, 90.	3.8	485
25	Enhancer hubs and loop collisions identified from single-allele topologies. Nature Genetics, 2018, 50, 1151-1160.	9.4	189
26	Mapping and phasing of structural variation in patient genomes using nanopore sequencing. Nature Communications, 2017, 8, 1326.	5.8	315
27	Gamma-Retrovirus Integration Marks Cell Type-Specific Cancer Genes: A Novel Profiling Tool in Cancer Genomics. PLoS ONE, 2016, 11, e0154070.	1.1	8
28	ECCB 2016: The 15th European Conference on Computational Biology. Bioinformatics, 2016, 32, i389-i392.	1.8	2
29	PAX5 is a tumor suppressor in mouse mutagenesis models of acute lymphoblastic leukemia. Blood, 2015, 125, 3609-3617.	0.6	72
30	Integration of gene expression and DNA-methylation profiles improves molecular subtype classification in acute myeloid leukemia. BMC Bioinformatics, 2015, 16, S5.	1.2	24
31	Genome Wide DNA Methylation Profiles Provide Clues to the Origin and Pathogenesis of Germ Cell Tumors. PLoS ONE, 2015, 10, e0122146.	1.1	63
32	3D hotspots of recurrent retroviral insertions reveal long-range interactions with cancer genes. Nature Communications, 2015, 6, 6381.	5.8	34
33	Hi-C Chromatin Interaction Networks Predict Co-expression in the Mouse Cortex. PLoS Computational Biology, 2015, 11, e1004221.	1.5	45
34	FERAL: network-based classifier with application to breast cancer outcome prediction. Bioinformatics, 2015, 31, i311-i319.	1.8	36
35	Insertional Mutagenesis and Deep Profiling Reveals Gene Hierarchies and a Myc/p53-Dependent Bottleneck in Lymphomagenesis. PLoS Genetics, 2014, 10, e1004167.	1.5	17
36	Soft Skills: An Important Asset Acquired from Organizing Regional Student Group Activities. PLoS Computational Biology, 2014, 10, e1003708.	1.5	15

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37	Chromatin Landscapes of Retroviral and Transposon Integration Profiles. PLoS Genetics, 2014, 10, e1004250.	1.5	80
38	Scale-space measures for graph topology link protein network architecture to function. Bioinformatics, 2014, 30, i237-i245.	1.8	12
39	Identifying regulatory mechanisms underlying tumorigenesis using locus expression signature analysis. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5747-5752.	3.3	7
40	Applications of DNA integrating elements: Facing the bias bully. Mobile Genetic Elements, 2014, 4, 1-6.	1.8	5
41	Detecting recurrent gene mutation in interaction network context using multi-scale graph diffusion. BMC Bioinformatics, 2013, 14, 29.	1.2	31
42	Chromatin Position Effects Assayed by Thousands of Reporters Integrated in Parallel. Cell, 2013, 154, 914-927.	13.5	283
43	Pattern recognition in bioinformatics. Briefings in Bioinformatics, 2013, 14, 633-647.	3.2	65
44	Don't Wear Your New Shoes (Yet): Taking the Right Steps to Become a Successful Principal Investigator. PLoS Computational Biology, 2013, 9, e1002834.	1.5	3
45	The Young PI Buzz: Learning from the Organizers of the Junior Principal Investigator Meeting at ISMB-ECCB 2013. PLoS Computational Biology, 2013, 9, e1003350.	1.5	2
46	The genetic heterogeneity and mutational burden of engineered melanomas in zebrafish models. Genome Biology, 2013, 14, R113.	13.9	40
47	Mutational Genomics for Cancer Pathway Discovery. Lecture Notes in Computer Science, 2013, , 35-46.	1.0	0
48	The deubiquitinase USP9X suppresses pancreatic ductal adenocarcinoma. Nature, 2012, 486, 266-270.	13.7	297
49	Insertional mutagenesis identifies multiple networks of cooperating genes driving intestinal tumorigenesis. Nature Genetics, 2011, 43, 1202-1209.	9.4	172
50	Computational identification of insertional mutagenesis targets for cancer gene discovery. Nucleic Acids Research, 2011, 39, e105-e105.	6.5	24
51	Integrating Protein Family Sequence Similarities with Gene Expression to Find Signature Gene Networks in Breast Cancer Metastasis. Lecture Notes in Computer Science, 2011, , 247-259.	1.0	4
52	HAT: Hypergeometric Analysis of Tiling-arrays with application to promoter-GeneChip data. BMC Bioinformatics, 2010, 11, 275.	1.2	6
53	Insertional Mutagenesis in Mice Deficient for p15Ink4b, p16Ink4a, p21Cip1, and p27Kip1 Reveals Cancer Gene Interactions and Correlations with Tumor Phenotypes. Cancer Research, 2010, 70, 520-531.	0.4	31
54	Novel Candidate Cancer Genes Identified by a Large-Scale Cross-Species Comparative Oncogenomics Approach. Cancer Research, 2010, 70, 883-895.	0.4	40

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55	Highlights from the 5th International Society for Computational Biology Student Council Symposium at the 17th Annual International Conference on Intelligent Systems for Molecular Biology and the 8th European Conference on Computational Biology. BMC Bioinformatics, 2009, 10, I1.	1.2	10
56	Large-Scale Mutagenesis in p19ARF- and p53-Deficient Mice Identifies Cancer Genes and Their Collaborative Networks. Cell, 2008, 133, 727-741.	13.5	167
57	Identification of cancer genes using a statistical framework for multiexperiment analysis of nondiscretized array CGH data. Nucleic Acids Research, 2008, 36, e13-e13.	6.5	62
58	Co-occurrence analysis of insertional mutagenesis data reveals cooperating oncogenes. Bioinformatics, 2007, 23, i133-i141.	1.8	20
59	Detecting Statistically Significant Common Insertion Sites in Retroviral Insertional Mutagenesis Screens. PLoS Computational Biology, 2006, 2, e166.	1.5	111
60	Detecting Statistically Significant Common Insertion Sites in Retroviral Insertional Mutagenesis Screens. PLoS Computational Biology, 2005, preprint, e166.	1.5	1
61	An Electronic Throttle Simulation Model with Automatic Parameter Tuning. , 0, , .		9