

Dick de Ridder

List of Publications by Year in descending order

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Version: 2024-02-01

108
papers

6,792
citations

87888

38
h-index

69250

77
g-index

129
all docs

129
docs citations

129
times ranked

9765
citing authors

#	ARTICLE	IF	CITATIONS
1	Insertional mutagenesis combined with acquired somatic mutations causes leukemogenesis following gene therapy of SCID-X1 patients. <i>Journal of Clinical Investigation</i> , 2008, 118, 3143-3150.	8.2	1,069
2	Shifts in growth strategies reflect tradeoffs in cellular economics. <i>Molecular Systems Biology</i> , 2009, 5, 323.	7.2	535
3	Exploring genetic variation in the tomato (<i>Solanum</i> section <i>Lycopersicon</i>) clade by whole-genome sequencing. <i>Plant Journal</i> , 2014, 80, 136-148.	5.7	397
4	New insights on human T cell development by quantitative T cell receptor gene rearrangement studies and gene expression profiling. <i>Journal of Experimental Medicine</i> , 2005, 201, 1715-1723.	8.5	318
5	A Discriminating Messenger RNA Signature for Bipolar Disorder Formed by an Aberrant Expression of Inflammatory Genes in Monocytes. <i>Archives of General Psychiatry</i> , 2008, 65, 395.	12.3	308
6	De novo sequencing, assembly and analysis of the genome of the laboratory strain <i>Saccharomyces cerevisiae</i> CEN.PK113-7D, a model for modern industrial biotechnology. <i>Microbial Cell Factories</i> , 2012, 11, 36.	4.0	238
7	Vector integration is nonrandom and clustered and influences the fate of lymphopoiesis in SCID-X1 gene therapy. <i>Journal of Clinical Investigation</i> , 2007, 117, 2225-2232.	8.2	221
8	Gammaretrovirus-mediated correction of SCID-X1 is associated with skewed vector integration site distribution in vivo. <i>Journal of Clinical Investigation</i> , 2007, 117, 2241-2249.	8.2	185
9	Supervised Locally Linear Embedding. <i>Lecture Notes in Computer Science</i> , 2003, , 333-341.	1.3	160
10	Ig Gene Rearrangement Steps Are Initiated in Early Human Precursor B Cell Subsets and Correlate with Specific Transcription Factor Expression. <i>Journal of Immunology</i> , 2005, 175, 5912-5922.	0.8	158
11	Effective Treatment of Psoriasis with Narrow-Band UVB Phototherapy Is Linked to Suppression of the IFN and Th17 Pathways. <i>Journal of Investigative Dermatology</i> , 2011, 131, 1547-1558.	0.7	129
12	The PLETHORA Gene Regulatory Network Guides Growth and Cell Differentiation in Arabidopsis Roots. <i>Plant Cell</i> , 2016, 28, 2937-2951.	6.6	127
13	Machine learning in plant science and plant breeding. <i>IScience</i> , 2021, 24, 101890.	4.1	127
14	Topology of molecular interaction networks. <i>BMC Systems Biology</i> , 2013, 7, 90.	3.0	119
15	Genome duplication and mutations in <i>ACE2</i> cause multicellular, fast-sedimenting phenotypes in evolved <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E4223-31.	7.1	100
16	Circulating Human CD27 ^{hi} IgA ⁺ Memory B Cells Recognize Bacteria with Polyreactive Igs. <i>Journal of Immunology</i> , 2015, 195, 1417-1426.	0.8	99
17	BiG-SLiCE: A highly scalable tool maps the diversity of 1.2 million biosynthetic gene clusters. <i>GigaScience</i> , 2021, 10, .	6.4	98
18	Retroviral vector insertion sites associated with dominant hematopoietic clones mark stemness pathways. <i>Blood</i> , 2007, 109, 1897-1907.	1.4	87

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19	Beyond genomic variation - comparison and functional annotation of three Brassica rapagenomes: a turnip, a rapid cycling and a Chinese cabbage. BMC Genomics, 2014, 15, 250.	2.8	87
20	Sammon's mapping using neural networks: A comparison. Pattern Recognition Letters, 1997, 18, 1307-1316.	4.2	82
21	Global DNA Compaction in Stationary-Phase Bacteria Does Not Affect Transcription. Cell, 2018, 174, 1188-1199.e14.	28.9	81
22	Gross Deletions Involving IGHM, BTK, or Artemis: A Model for Genomic Lesions Mediated by Transposable Elements. American Journal of Human Genetics, 2008, 82, 320-332.	6.2	77
23	The Genome of Winter Moth (<i>Operophtera brumata</i>) Provides a Genomic Perspective on Sexual Dimorphism and Phenology. Genome Biology and Evolution, 2015, 7, 2321-2332.	2.5	70
24	<i>De novo</i> detection of copy number variation by co-assembly. Bioinformatics, 2012, 28, 3195-3202.	4.1	69
25	Classification in the presence of class noise using a probabilistic Kernel Fisher method. Pattern Recognition, 2007, 40, 3349-3357.	8.1	68
26	An analysis of characterized plant sesquiterpene synthases. Phytochemistry, 2019, 158, 157-165.	2.9	67
27	Pattern recognition in bioinformatics. Briefings in Bioinformatics, 2013, 14, 633-647.	6.5	65
28	Experiments with a featureless approach to pattern recognition. Pattern Recognition Letters, 1997, 18, 1159-1166.	4.2	57
29	Laboratory evolution of new lactate transporter genes in a <i>jen1^Δ</i> mutant of <i>Saccharomyces cerevisiae</i> and their identification as ADY2 alleles by whole-genome resequencing and transcriptome analysis. FEMS Yeast Research, 2012, 12, 359-374.	2.3	56
30	Single-molecule protein sequencing through fingerprinting: computational assessment. Physical Biology, 2015, 12, 055003.	1.8	53
31	Predicting Metabolic Fluxes Using Gene Expression Differences As Constraints. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 206-216.	3.0	52
32	Making the difference: integrating structural variation detection tools. Briefings in Bioinformatics, 2015, 16, 852-864.	6.5	52
33	GRASS: a generic algorithm for scaffolding next-generation sequencing assemblies. Bioinformatics, 2012, 28, 1429-1437.	4.1	49
34	Exploiting next-generation sequencing to solve the haplotyping puzzle in polyploids: a simulation study. Briefings in Bioinformatics, 2018, 19, bbw126.	6.5	49
35	Is IL2RG oncogenic in T-cell development?. Nature, 2006, 443, E5-E5.	27.8	48
36	B-cell polyclonal lymphocytic leukemia: a specific subgroup of mantle cell lymphoma. Blood, 2014, 124, 412-419.	1.4	48

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37	Relational discriminant analysis. <i>Pattern Recognition Letters</i> , 1999, 20, 1175-1181.	4.2	47
38	PanTools: representation, storage and exploration of pan-genomic data. <i>Bioinformatics</i> , 2016, 32, i487-i493.	4.1	46
39	Distribution, position and genomic characteristics of crossovers in tomato recombinant inbred lines derived from an interspecific cross between <i>Solanum lycopersicum</i> and <i>Solanum pimpinellifolium</i> . <i>Plant Journal</i> , 2017, 89, 554-564.	5.7	46
40	Integrating genome assemblies with MAIA. <i>Bioinformatics</i> , 2010, 26, i433-i439.	4.1	45
41	GATA3 Expression Is Decreased in Psoriasis and during Epidermal Regeneration; Induction by Narrow-Band UVB and IL-4. <i>PLoS ONE</i> , 2011, 6, e19806.	2.5	44
42	How Biochemical Constraints of Cellular Growth Shape Evolutionary Adaptations in Metabolism. <i>Genetics</i> , 2013, 194, 505-512.	2.9	40
43	WormQTL2: an interactive platform for systems genetics in <i>Caenorhabditis elegans</i> . <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	3.0	39
44	Laboratory evolution of new lactate transporter genes in a <i>jen1^Δ</i> mutant of <i>Saccharomyces cerevisiae</i> and their identification as ADY2 alleles by whole-genome resequencing and transcriptome analysis. <i>FEMS Yeast Research</i> , 2012, 12, n/a-n/a.	2.3	33
45	Genome-wide characterization of <i>Phytophthora infestans</i> metabolism: a systems biology approach. <i>Molecular Plant Pathology</i> , 2018, 19, 1403-1413.	4.2	33
46	Unbiased Quantitative Models of Protein Translation Derived from Ribosome Profiling Data. <i>PLoS Computational Biology</i> , 2015, 11, e1004336.	3.2	31
47	Designing Eukaryotic Gene Expression Regulation Using Machine Learning. <i>Trends in Biotechnology</i> , 2020, 38, 191-201.	9.3	30
48	The diversity of protein turnover and abundance under nitrogen-limited steady-state conditions in <i>Saccharomyces cerevisiae</i> . <i>Molecular BioSystems</i> , 2011, 7, 3316.	2.9	29
49	Exploring variation-aware contig graphs for (comparative) metagenomics using MaryGold. <i>Bioinformatics</i> , 2013, 29, 2826-2834.	4.1	29
50	IL-7R expression and IL-7 signaling confer a distinct phenotype on developing human B-lineage cells. <i>Blood</i> , 2011, 118, 2116-2127.	1.4	28
51	TriPoly: haplotype estimation for polyploids using sequencing data of related individuals. <i>Bioinformatics</i> , 2018, 34, 3864-3872.	4.1	28
52	A survey of functional genomic variation in domesticated chickens. <i>Genetics Selection Evolution</i> , 2018, 50, 17.	3.0	27
53	A note on core research issues for statistical pattern recognition. <i>Pattern Recognition Letters</i> , 2002, 23, 493-499.	4.2	25
54	AraQTL – workbench and archive for systems genetics in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2017, 89, 1225-1235.	5.7	24

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55	Genomics of Adaptation Depends on the Rate of Environmental Change in Experimental Yeast Populations. <i>Molecular Biology and Evolution</i> , 2017, 34, 2613-2626.	8.9	24
56	<scp>DNA</scp> sequence and shape are predictive for meiotic crossovers throughout the plant kingdom. <i>Plant Journal</i> , 2018, 95, 686-699.	5.7	24
57	Metabolic Model of the <i>Phytophthora infestans</i> -Tomato Interaction Reveals Metabolic Switches during Host Colonization. <i>MBio</i> , 2019, 10, .	4.1	23
58	Sequence features of viral and human Internal Ribosome Entry Sites predictive of their activity. <i>PLoS Computational Biology</i> , 2017, 13, e1005734.	3.2	23
59	The effect of oligonucleotide microarray data pre-processing on the analysis of patient-cohort studies. <i>BMC Bioinformatics</i> , 2006, 7, 105.	2.6	22
60	pCADD: SNV prioritisation in <i>Sus scrofa</i> . <i>Genetics Selection Evolution</i> , 2020, 52, 4.	3.0	21
61	Exploring Sequence Characteristics Related to High-Level Production of Secreted Proteins in <i>Aspergillus niger</i> . <i>PLoS ONE</i> , 2012, 7, e45869.	2.5	20
62	Evaluation of FRET X for single-molecule protein fingerprinting. <i>IScience</i> , 2021, 24, 103239.	4.1	18
63	Metabolic pathway alignment between species using a comprehensive and flexible similarity measure. <i>BMC Systems Biology</i> , 2008, 2, 111.	3.0	17
64	Introgression browser: high-throughput whole-genome <scp>SNP</scp> visualization. <i>Plant Journal</i> , 2015, 82, 174-182.	5.7	17
65	Heritable gene expression differences between apomictic clone members in <i>Taraxacum officinale</i> : Insights into early stages of evolutionary divergence in asexual plants. <i>BMC Genomics</i> , 2016, 17, 203.	2.8	16
66	Correcting palindromes in long reads after whole-genome amplification. <i>BMC Genomics</i> , 2018, 19, 798.	2.8	16
67	Accelerated discovery of functional genomic variation in pigs. <i>Genomics</i> , 2021, 113, 2229-2239.	2.9	16
68	Nonlinear image processing using artificial neural networks. <i>Advances in Imaging and Electron Physics</i> , 2003, 126, 351-450.	0.2	15
69	SPiCE: a web-based tool for sequence-based protein classification and exploration. <i>BMC Bioinformatics</i> , 2014, 15, 93.	2.6	15
70	Sequence-based analysis of protein degradation rates. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1593-1601.	2.6	14
71	Meiotic recombination profiling of interspecific hybrid F1 tomato pollen by linked read sequencing. <i>Plant Journal</i> , 2020, 102, 480-492.	5.7	14
72	Domestication Shapes Recombination Patterns in Tomato. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	14

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73	ACE: accurate correction of errors using <i>k</i> -mer tries. <i>Bioinformatics</i> , 2015, 31, 3216-3218.	4.1	13
74	Understanding Regulation of Metabolism through Feasibility Analysis. <i>PLoS ONE</i> , 2012, 7, e39396.	2.5	11
75	Cnidaria: fast, reference-free clustering of raw and assembled genome and transcriptome NGS data. <i>BMC Bioinformatics</i> , 2015, 16, 352.	2.6	11
76	Integrating structure-based machine learning and co-evolution to investigate specificity in plant sesquiterpene synthases. <i>PLoS Computational Biology</i> , 2021, 17, e1008197.	3.2	11
77	Predicting variant deleteriousness in non-human species: applying the CADD approach in mouse. <i>BMC Bioinformatics</i> , 2018, 19, 373.	2.6	10
78	Efficient inference of homologs in large eukaryotic pan-proteomes. <i>BMC Bioinformatics</i> , 2018, 19, 340.	2.6	10
79	The santalene synthase from <i>Cinnamomum camphora</i> : Reconstruction of a sesquiterpene synthase from a monoterpene synthase. <i>Archives of Biochemistry and Biophysics</i> , 2020, 695, 108647.	3.0	10
80	Maximum significance clustering of oligonucleotide microarrays. <i>Bioinformatics</i> , 2006, 22, 326-331.	4.1	9
81	Integration of prior knowledge of measurement noise in kernel density classification. <i>Pattern Recognition</i> , 2008, 41, 320-330.	8.1	9
82	Evolutionary Optimization of Kernel Weights Improves Protein Complex Comembership Prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009, 6, 427-437.	3.0	9
83	Genome Sequences of <i>Cyberlindnera fabianii</i> 65, <i>Pichia kudriavzevii</i> 129, and <i>Saccharomyces cerevisiae</i> 131 Isolated from Fermented Masau Fruits in Zimbabwe. <i>Genome Announcements</i> , 2017, 5, .	0.8	9
84	Improved inference of intermolecular contacts through protein-protein interaction prediction using coevolutionary analysis. <i>Bioinformatics</i> , 2019, 35, 2036-2042.	4.1	9
85	Protein redesign by learning from data. <i>Protein Engineering, Design and Selection</i> , 2014, 27, 281-288.	2.1	8
86	The Adaptive Subspace Map for Image Description and Image Database Retrieval. <i>Lecture Notes in Computer Science</i> , 2000, , 94-103.	1.3	8
87	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. <i>PLoS Genetics</i> , 2020, 16, e1009027.	3.5	7
88	Chasing breeding footprints through structural variations in <i>Cucumis melo</i> and wild relatives. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, 1-12.	1.8	7
89	Almost autonomous training of mixtures of principal component analyzers. <i>Pattern Recognition Letters</i> , 2004, 25, 1085-1095.	4.2	6
90	Physiological and Transcriptional Responses of Anaerobic Chemostat Cultures of <i>Saccharomyces cerevisiae</i> Subjected to Diurnal Temperature Cycles. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4433-4449.	3.1	6

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91	Network Analysis Prioritizes <i>DEWAX</i> and <i>ICE1</i> as the Candidate Genes for Major eQTL Hotspots in Seed Germination of <i>Arabidopsis thaliana</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 4215-4226.	1.8	6
92	Artificial intelligence in the lab: ask not what your computer can do for you. <i>Microbial Biotechnology</i> , 2019, 12, 38-40.	4.2	5
93	Hecaton: reliably detecting copy number variation in plant genomes using short read sequencing data. <i>BMC Genomics</i> , 2019, 20, 818.	2.8	4
94	Prior Biological Knowledge Improves Genomic Prediction of Growth-Related Traits in <i>Arabidopsis thaliana</i> . <i>Frontiers in Genetics</i> , 2020, 11, 609117.	2.3	4
95	Computational estimation of the composition of fat/oil mixtures containing interesterifications from gas and liquid chromatography data. <i>JAOCs, Journal of the American Oil Chemists' Society</i> , 2005, 82, 707-716.	1.9	3
96	Selected proceedings of Machine Learning in Systems Biology: MLSB 2016. <i>BMC Bioinformatics</i> , 2016, 17, 437.	2.6	3
97	Texture Segmentation Using the Mixtures of Principal Component Analyzers. <i>Lecture Notes in Computer Science</i> , 2003, , 505-512.	1.3	3
98	CyLineUp: A Cytoscape app for visualizing data in network small multiples. <i>F1000Research</i> , 2016, 5, 635.	1.6	3
99	Uncovering the Role of Metabolism in Oomycete-Host Interactions Using Genome-Scale Metabolic Models. <i>Frontiers in Microbiology</i> , 2021, 12, 748178.	3.5	3
100	Sequence-Based Prediction of Protein Secretion Success in <i>Aspergillus niger</i> . <i>Lecture Notes in Computer Science</i> , 2010, , 3-14.	1.3	2
101	Insight into Neutral and Disease-Associated Human Genetic Variants through Interpretable Predictors. <i>PLoS ONE</i> , 2015, 10, e0120729.	2.5	2
102	Detection of vehicles in infrared imagery using shared-weight neural network feature detectors. , 1998, , .		1
103	Signal-based optical map alignment. <i>PLoS ONE</i> , 2021, 16, e0253102.	2.5	1
104	Erratum to "Classification in the presence of class noise using a probabilistic kernel fisher method". <i>Pattern Recognition</i> , 2008, 41, 1214.	8.1	0
105	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. , 2020, 16, e1009027.		0
106	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. , 2020, 16, e1009027.		0
107	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. , 2020, 16, e1009027.		0
108	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. , 2020, 16, e1009027.		0