Dick de Ridder

List of Publications by Year
in descending order

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	Domestication Shapes Recombination Patterns in Tomato. Molecular Biology and Evolution, 2022, 39, .	8.9	14
2	Machine learning in plant science and plant breeding. IScience, 2021, 24, 101890.	4.1	127
3	BiG-SLiCE: A highly scalable tool maps the diversity of 1.2 million biosynthetic gene clusters. GigaScience, 2021, 10, .	6.4	98
4	Integrating structure-based machine learning and co-evolution to investigate specificity in plant sesquiterpene synthases. PLoS Computational Biology, 2021, 17, e1008197.	3.2	11
5	Accelerated discovery of functional genomic variation in pigs. Genomics, 2021, 113, 2229-2239.	2.9	16
6	Signal-based optical map alignment. PLoS ONE, 2021, 16, e0253102.	2.5	1
7	Uncovering the Role of Metabolism in Oomyceteâ€"Host Interactions Using Genome-Scale Metabolic Models. Frontiers in Microbiology, 2021, 12, 748178.	3.5	3
8	Evaluation of FRET X for single-molecule protein fingerprinting. IScience, 2021, 24, 103239.	4.1	18
9	Chasing breeding footprints through structural variations in Cucumis melo and wild relatives. G3: Genes, Genomes, Genetics, 2021, 11, 1-12.	1.8	7
10	Designing Eukaryotic Gene Expression Regulation Using Machine Learning. Trends in Biotechnology, 2020, 38, 191-201.	9.3	30
11	Meiotic recombination profiling of interspecific hybrid F1 tomato pollen by linked read sequencing. Plant Journal, 2020, 102, 480-492.	5.7	14
12	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>. G3: Genes, Genomes, Genetics, 2020, 10, 4215-4226.	1.8	6
13	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. PLoS Genetics, 2020, 16, e1009027.	3.5	7
14	The santalene synthase from Cinnamomum camphora: Reconstruction of a sesquiterpene synthase from a monoterpene synthase. Archives of Biochemistry and Biophysics, 2020, 695, 108647.	3.0	10
15	pCADD: SNV prioritisation in Sus scrofa. Genetics Selection Evolution, 2020, 52, 4.	3.0	21
16	WormQTL2: an interactive platform for systems genetics in Caenorhabditis elegans. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	39
17	Prior Biological Knowledge Improves Genomic Prediction of Growth-Related Traits in Arabidopsis thaliana. Frontiers in Genetics, 2020, 11, 609117.	2.3	4
18	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. , 2020, 16, e1009027.		0

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19	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. , 2020, 16, e1009027.		0
20	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. , 2020, 16, e1009027.		0
21	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. , 2020, 16, e1009027.		0
22	Metabolic Model of the <i>Phytophthora infestans</i> -Tomato Interaction Reveals Metabolic Switches during Host Colonization. MBio, 2019, 10, .	4.1	23
23	Hecaton: reliably detecting copy number variation in plant genomes using short read sequencing data. BMC Genomics, 2019, 20, 818.	2.8	4
24	Improved inference of intermolecular contacts through protein–protein interaction prediction using coevolutionary analysis. Bioinformatics, 2019, 35, 2036-2042.	4.1	9
25	An analysis of characterized plant sesquiterpene synthases. Phytochemistry, 2019, 158, 157-165.	2.9	67
26	Artificial intelligence in the lab: ask not what your computer can do for you. Microbial Biotechnology, 2019, 12, 38-40.	4.2	5
27	Exploiting next-generation sequencing to solve the haplotyping puzzle in polyploids: a simulation study. Briefings in Bioinformatics, 2018, 19, bbw126.	6.5	49
28	A survey of functional genomic variation in domesticated chickens. Genetics Selection Evolution, 2018, 50, 17.	3.0	27
29	Genome–wide characterization of <i>Phytophthora infestans</i> metabolism: a systems biology approach. Molecular Plant Pathology, 2018, 19, 1403-1413.	4.2	33
30	Correcting palindromes in long reads after whole-genome amplification. BMC Genomics, 2018, 19, 798.	2.8	16
31	Predicting variant deleteriousness in non-human species: applying the CADD approach in mouse. BMC Bioinformatics, 2018, 19, 373.	2.6	10
32	Efficient inference of homologs in large eukaryotic pan-proteomes. BMC Bioinformatics, 2018, 19, 340.	2.6	10
33	<scp>DNA</scp> sequence and shape are predictive for meiotic crossovers throughout the plant kingdom. Plant Journal, 2018, 95, 686-699.	5.7	24
34	TriPoly: haplotype estimation for polyploids using sequencing data of related individuals. Bioinformatics, 2018, 34, 3864-3872.	4.1	28
35	Global DNA Compaction in Stationary-Phase Bacteria Does Not Affect Transcription. Cell, 2018, 174, 1188-1199.e14.	28.9	81
36	Genome Sequences of Cyberlindnera fabianii 65, Pichia kudriavzevii 129, and Saccharomyces cerevisiae 131 Isolated from Fermented Masau Fruits in Zimbabwe. Genome Announcements, 2017, 5, .	0.8	9

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37	Sequence-based analysis of protein degradation rates. Proteins: Structure, Function and Bioinformatics, 2017, 85, 1593-1601.	2.6	14
38	Ara<scp>QTL</scp> â€" workbench and archive for systems genetics in *Arabidopsis thaliana*. Plant Journal, 2017, 89, 1225-1235.	5.7	24
39	Genomics of Adaptation Depends on the Rate of Environmental Change in Experimental Yeast Populations. Molecular Biology and Evolution, 2017, 34, 2613-2626.	8.9	24
40	Distribution, position and genomic characteristics of crossovers in tomato recombinant inbred lines derived from an interspecific cross between *Solanum lycopersicum* and *Solanum pimpinellifolium*. Plant Journal, 2017, 89, 554-564.	5.7	46
41	Sequence features of viral and human Internal Ribosome Entry Sites predictive of their activity. PLoS Computational Biology, 2017, 13, e1005734.	3.2	23
42	The PLETHORA Gene Regulatory Network Guides Growth and Cell Differentiation in Arabidopsis Roots. Plant Cell, 2016, 28, 2937-2951.	6.6	127
43	Selected proceedings of Machine Learning in Systems Biology: MLSB 2016. BMC Bioinformatics, 2016, 17, 437.	2.6	3
44	PanTools: representation, storage and exploration of pan-genomic data. Bioinformatics, 2016, 32, i487-i493.	4.1	46
45	Heritable gene expression differences between apomictic clone members in Taraxacum officinale: Insights into early stages of evolutionary divergence in asexual plants. BMC Genomics, 2016, 17, 203.	2.8	16
46	CyLineUp: A Cytoscape app for visualizing data in network small multiples. F1000Research, 2016, 5, 635.	1.6	3
47	Cnidaria: fast, reference-free clustering of raw and assembled genome and transcriptome NGS data. BMC Bioinformatics, 2015, 16, 352.	2.6	11
48	Insight into Neutral and Disease-Associated Human Genetic Variants through Interpretable Predictors. PLoS ONE, 2015, 10, e0120729.	2.5	2
49	Unbiased Quantitative Models of Protein Translation Derived from Ribosome Profiling Data. PLoS Computational Biology, 2015, 11, e1004336.	3.2	31
50	ACE: accurate correction of errors using *K*-mer tries. Bioinformatics, 2015, 31, 3216-3218.	4.1	13
51	Circulating Human CD27â^'IgA+ Memory B Cells Recognize Bacteria with Polyreactive Igs. Journal of Immunology, 2015, 195, 1417-1426.	0.8	99
52	Introgression browser: highâ€throughput wholeâ€genome <scp>SNP</scp> visualization. Plant Journal, 2015, 82, 174-182.	5.7	17
53	The Genome of Winter Moth (*Operophtera brumata*) Provides a Genomic Perspective on Sexual Dimorphism and Phenology. Genome Biology and Evolution, 2015, 7, 2321-2332.	2.5	70
54	Single-molecule protein sequencing through fingerprinting: computational assessment. Physical Biology, 2015, 12, 055003.	1.8	53

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55	Making the difference: integrating structural variation detection tools. Briefings in Bioinformatics, 2015, 16, 852-864.	6.5	52
56	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
57	Exploring genetic variation in the tomato (*Solanum* section *Lycopersicon*) clade by whole‑genome sequencing. Plant Journal, 2014, 80, 136-148.	5.7	397
58	B-cell prolymphocytic leukemia: a specific subgroup of mantle cell lymphoma. Blood, 2014, 124, 412-419.	1.4	48
59	Protein redesign by learning from data. Protein Engineering, Design and Selection, 2014, 27, 281-288.	2.1	8
60	Physiological and Transcriptional Responses of Anaerobic Chemostat Cultures of Saccharomyces cerevisiae Subjected to Diurnal Temperature Cycles. Applied and Environmental Microbiology, 2014, 80, 4433-4449.	3.1	6
61	SPiCE: a web-based tool for sequence-based protein classification and exploration. BMC Bioinformatics, 2014, 15, 93.	2.6	15
62	Pattern recognition in bioinformatics. Briefings in Bioinformatics, 2013, 14, 633-647.	6.5	65
63	Exploring variation-aware contig graphs for (comparative) metagenomics using MaryGold. Bioinformatics, 2013, 29, 2826-2834.	4.1	29
64	Topology of molecular interaction networks. BMC Systems Biology, 2013, 7, 90.	3.0	119
65	Genome duplication and mutations in *ACE2* cause multicellular, fast-sedimenting phenotypes in evolved *Saccharomyces cerevisiae*. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E4223-31.	7.1	100
66	How Biochemical Constraints of Cellular Growth Shape Evolutionary Adaptations in Metabolism. Genetics, 2013, 194, 505-512.	2.9	40
67	*De novo* detection of copy number variation by co-assembly. Bioinformatics, 2012, 28, 3195-3202.	4.1	69
68	Laboratory evolution of new lactate transporter genes in a jen1Î” mutant of Saccharomyces cerevisiae and their identification as ADY2 alleles by whole-genome resequencing and transcriptome analysis. FEMS Yeast Research, 2012, 12, n/a-n/a.	2.3	33
69	De novo sequencing, assembly and analysis of the genome of the laboratory strain Saccharomyces cerevisiae CEN.PK113-7D, a model for modern industrial biotechnology. Microbial Cell Factories, 2012, 11, 36.	4.0	238
70	Understanding Regulation of Metabolism through Feasibility Analysis. PLoS ONE, 2012, 7, e39396.	2.5	11
71	Exploring Sequence Characteristics Related to High-Level Production of Secreted Proteins in Aspergillus niger. PLoS ONE, 2012, 7, e45869.	2.5	20
72	GRASS: a generic algorithm for scaffolding next-generation sequencing assemblies. Bioinformatics, 2012, 28, 1429-1437.	4.1	49

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73	Laboratory evolution of new lactate transporter genes in a jen1Î" mutant of Saccharomyces cerevisiae and their identification as ADY2 alleles by whole-genome resequencing and transcriptome analysis. FEMS Yeast Research, 2012, 12, 359-374.	2.3	56
74	The diversity of protein turnover and abundance under nitrogen-limited steady-state conditions in Saccharomyces cerevisiae. Molecular BioSystems, 2011, 7, 3316.	2.9	29
75	Predicting Metabolic Fluxes Using Gene Expression Differences As Constraints. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 206-216.	3.0	52
76	GATA3 Expression Is Decreased in Psoriasis and during Epidermal Regeneration; Induction by Narrow-Band UVB and IL-4. PLoS ONE, 2011, 6, e19806.	2.5	44
77	IL-7R expression and IL-7 signaling confer a distinct phenotype on developing human B-lineage cells. Blood, 2011, 118, 2116-2127.	1.4	28
78	Effective Treatment of Psoriasis with Narrow-Band UVB Phototherapy Is Linked to Suppression of the IFN and Th17 Pathways. Journal of Investigative Dermatology, 2011, 131, 1547-1558.	0.7	129
79	Integrating genome assemblies with MAIA. Bioinformatics, 2010, 26, i433-i439.	4.1	45
80	Sequence-Based Prediction of Protein Secretion Success in Aspergillus niger. Lecture Notes in Computer Science, 2010, , 3-14.	1.3	2
81	Shifts in growth strategies reflect tradeoffs in cellular economics. Molecular Systems Biology, 2009, 5, 323.	7.2	535
82	Evolutionary Optimization of Kernel Weights Improves Protein Complex Comembership Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 427-437.	3.0	9
83	Integration of prior knowledge of measurement noise in kernel density classification. Pattern Recognition, 2008, 41, 320-330.	8.1	9
84	Erratum to â€œClassification in the presence of class noise using a probabilistic kernel fisher methodâ€. Pattern Recognition, 2008, 41, 1214.	8.1	0
85	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
86	Metabolic pathway alignment between species using a comprehensive and flexible similarity measure. BMC Systems Biology, 2008, 2, 111.	3.0	17
87	A Discriminating Messenger RNA Signature for Bipolar Disorder Formed by an Aberrant Expression of Inflammatory Genes in Monocytes. Archives of General Psychiatry, 2008, 65, 395.	12.3	308
88	Insertional mutagenesis combined with acquired somatic mutations causes leukemogenesis following gene therapy of SCID-X1 patients. Journal of Clinical Investigation, 2008, 118, 3143-3150.	8.2	1,069
89	Retroviral vector insertion sites associated with dominant hematopoietic clones mark â€œstemnessâ€ pathways. Blood, 2007, 109, 1897-1907.	1.4	87
90	Classification in the presence of class noise using a probabilistic Kernel Fisher method. Pattern Recognition, 2007, 40, 3349-3357.	8.1	68

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91	Vector integration is nonrandom and clustered and influences the fate of lymphopoiesis in SCID-X1 gene therapy. Journal of Clinical Investigation, 2007, 117, 2225-2232.	8.2	221
92	Gammaretrovirus-mediated correction of SCID-X1 is associated with skewed vector integration site distribution in vivo. Journal of Clinical Investigation, 2007, 117, 2241-2249.	8.2	185
93	Is IL2RG oncogenic in T-cell development?. Nature, 2006, 443, E5-E5.	27.8	48
94	The effect of oligonucleotide microarray data pre-processing on the analysis of patient-cohort studies. BMC Bioinformatics, 2006, 7, 105.	2.6	22
95	Maximum significance clustering of oligonucleotide microarrays. Bioinformatics, 2006, 22, 326-331.	4.1	9
96	Computational estimation of the composition of fat/oil mixtures containing interesterifications from gas and liquid chromatography data. JAOCS, Journal of the American Oil Chemists' Society, 2005, 82, 707-716.	1.9	3
97	Ig Gene Rearrangement Steps Are Initiated in Early Human Precursor B Cell Subsets and Correlate with Specific Transcription Factor Expression. Journal of Immunology, 2005, 175, 5912-5922.	0.8	158
98	New insights on human T cell development by quantitative T cell receptor gene rearrangement studies and gene expression profiling. Journal of Experimental Medicine, 2005, 201, 1715-1723.	8.5	318
99	Almost autonomous training of mixtures of principal component analyzers. Pattern Recognition Letters, 2004, 25, 1085-1095.	4.2	6
100	Nonlinear image processing using artificial neural networks. Advances in Imaging and Electron Physics, 2003, 126, 351-450.	0.2	15
101	Supervised Locally Linear Embedding. Lecture Notes in Computer Science, 2003, , 333-341.	1.3	160
102	Texture Segmentation Using the Mixtures of Principal Component Analyzers. Lecture Notes in Computer Science, 2003, , 505-512.	1.3	3
103	A note on core research issues for statistical pattern recognition. Pattern Recognition Letters, 2002, 23, 493-499.	4.2	25
104	The Adaptive Subspace Map for Image Description and Image Database Retrieval. Lecture Notes in Computer Science, 2000, , 94-103.	1.3	8
105	Relational discriminant analysis. Pattern Recognition Letters, 1999, 20, 1175-1181.	4.2	47
106	Detection of vehicles in infrared imagery using shared-weight neural network feature detectors. , 1998, , .		1
107	Sammon's mapping using neural networks: A comparison. Pattern Recognition Letters, 1997, 18, 1307-1316.	4.2	82
108	Experiments with a featureless approach to pattern recognition. Pattern Recognition Letters, 1997, 18, 1159-1166.	4.2	57