Nuno A Fonseca

List of Publications by Year
in descending order

91 papers	9,283 citations	172386 29 h-index	66879 78 g-index
106 all docs	106 docs citations	106 times ranked	18908 citing authors

#	Article	IF	Citations
1	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	13.7	1,966
2	Two independent modes of chromatin organization revealed by cohesin removal. Nature, 2017, 551, 51-56.	13.7	935
3	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. GigaScience, 2013, 2, 10.	3.3	582
4	Expression Atlas update—an integrated database of gene and protein expression in humans, animals and plants. Nucleic Acids Research, 2016, 44, D746-D752.	6.5	526
5	ArrayExpress update – from bulk to single-cell expression data. Nucleic Acids Research, 2019, 47, D711-D715.	6.5	497
6	Assemblathon 1: A competitive assessment of de novo short read assembly methods. Genome Research, 2011, 21, 2224-2241.	2.4	443
7	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. Nature, 2020, 578, 102-111.	13.7	424
8	Expression Atlas: gene and protein expression across multiple studies and organisms. Nucleic Acids Research, 2018, 46, D246-D251.	6.5	365
9	Expression Atlas update: from tissues to single cells. Nucleic Acids Research, 2020, 48, D77-D83.	6.5	363
10	Expression Atlas update—a database of gene and transcript expression from microarray- and sequencing-based functional genomics experiments. Nucleic Acids Research, 2014, 42, D926-D932.	6.5	293
11	Genomic basis for RNA alterations in cancer. Nature, 2020, 578, 129-136.	13.7	280
12	Tools for mapping high-throughput sequencing data. Bioinformatics, 2012, 28, 3169-3177.	1.8	269
13	Transcription Factor Activities Enhance Markers of Drug Sensitivity in Cancer. Cancer Research, 2018, 78, 769-780.	0.4	161
14	Gramene 2018: unifying comparative genomics and pathway resources for plant research. Nucleic Acids Research, 2018, 46, D1181-D1189.	6.5	147
15	A Pan-cancer Transcriptome Analysis Reveals Pervasive Regulation through Alternative Promoters. Cell, 2019, 178, 1465-1477.e17.	13.5	144
16	Cancer LncRNA Census reveals evidence for deep functional conservation of long noncoding RNAs in tumorigenesis. Communications Biology, 2020, 3, 56.	2.0	140
17	Gramene 2016: comparative plant genomics and pathway resources. Nucleic Acids Research, 2016, 44, D1133-D1140.	6.5	138
18	Integrative pathway enrichment analysis of multivariate omics data. Nature Communications, 2020, 11, 735.	5.8	125

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19	Long-range enhancers regulating Myc expression are required for normal facial morphogenesis. Nature Genetics, 2014, 46, 753-758.	9.4	118
20	High-resolution mapping of transcriptional dynamics across tissue development reveals a stable mRNA–tRNA interface. Genome Research, 2014, 24, 1797-1807.	2.4	89
21	Comparison of GENCODE and RefSeq gene annotation and the impact of reference geneset on variant effect prediction. BMC Genomics, 2015, 16, S2.	1.2	80
22	Pathway and network analysis of more than 2500 whole cancer genomes. Nature Communications, 2020, 11, 729.	5.8	73
23	RNA-Seq Gene Profiling - A Systematic Empirical Comparison. PLoS ONE, 2014, 9, e107026.	1.1	72
24	An S-RNase-Based Gametophytic Self-Incompatibility System Evolved Only Once in Eudicots. Journal of Molecular Evolution, 2008, 67, 179-190.	0.8	70
25	Convergent Evolution at the Gametophytic Self-Incompatibility System in Malus and Prunus. PLoS ONE, 2015, 10, e0126138.	1.1	63
26	Tumors induce de novo steroid biosynthesis in T cells to evade immunity. Nature Communications, 2020, 11, 3588.	5.8	54
27	High-coverage whole-genome analysis of 1220 cancers reveals hundreds of genes deregulated by rearrangement-mediated cis-regulatory alterations. Nature Communications, 2020, 11, 736.	5.8	50
28	PopAffiliator: online calculator for individual affiliation to a major population group based on 17 autosomal short tandem repeat genotype profile. International Journal of Legal Medicine, 2011, 125, 629-636.	1.2	44
29	Combined burden and functional impact tests for cancer driver discovery using DriverPower. Nature Communications, 2020, 11, 734.	5.8	39
30	The RNASeq-er API—a gateway to systematically updated analysis of public RNA-seq data. Bioinformatics, 2017, 33, 2218-2220.	1.8	35
31	Tumour gene expression signature in primary melanoma predicts long-term outcomes. Nature Communications, 2021, 12, 1137.	5.8	33
32	Inferences on specificity recognition at the Malus—domestica gametophytic self-incompatibility system. Scientific Reports, 2018, 8, 1717.	1.6	30
33	Evolutionary patterns at the RNase based gametophytic self - incompatibility system in two divergent Rosaceae groups (Maloideae and Prunus). BMC Evolutionary Biology, 2010, 10, 200.	3.2	29
34	Amino acid pairing at the N•and C•termini of helical segments in proteins. Proteins: Structure, Function and Bioinformatics, 2008, 70, 188-196.	1.5	26
35	RNase-Based Gametophytic Self-Incompatibility Evolution: Questioning the Hypothesis of Multiple Independent Recruitments of the S-Pollen Gene. Journal of Molecular Evolution, 2009, 69, 32-41.	0.8	26
36	An RNA-seq Based Machine Learning Approach Identifies Latent Tuberculosis Patients With an Active Tuberculosis Profile. Frontiers in Immunology, 2020, 11, 1470.	2.2	25

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37	ADOPS--Automatic Detection Of Positively Selected Sites. Journal of Integrative Bioinformatics, 2012, 9, 200.	1.0	25
38	Parallel ILP for distributed-memory architectures. Machine Learning, 2009, 74, 257-279.	3.4	24
39	Drosophila americana as a Model Species for Comparative Studies on the Molecular Basis of Phenotypic Variation. Genome Biology and Evolution, 2013, 5, 661-679.	1.1	24
40	Patterns of evolution at the gametophytic self-incompatibility Sorbus aucuparia (Pyrinae) S pollen genes support the non-self recognition by multiple factors model. Journal of Experimental Botany, 2013, 64, 2423-2434.	2.4	24
41	The Drosophila melanogaster methuselah Gene: A Novel Gene with Ancient Functions. PLoS ONE, 2013, 8, e63747.	1.1	23
42	A user guide for the online exploration and visualization of PCAWG data. Nature Communications, 2020, 11, 3400.	5.8	23
43	The number, age, sharing and relatedness of *S*-locus specificities in *Prunus*. Genetical Research, 2008, 90, 17-26.	0.3	17
44	ADOPS - Automatic Detection Of Positively Selected Sites. Journal of Integrative Bioinformatics, 2012, 9, 18-32.	1.0	17
45	Phylogeny of the teashirtâ€related zinc finger (tshz) gene family and analysis of the developmental expression of *tshz2* and *tshz3b* in the zebrafish. Developmental Dynamics, 2010, 239, 1010-1018.	0.8	16
46	Speeding up the detection of invasive bivalve species using environmental DNA: A Nanopore and Illumina sequencing comparison. Molecular Ecology Resources, 2022, 22, 2232-2247.	2.2	16
47	Gastric Microbiome Diversities in Gastric Cancer Patients from Europe and Asia Mimic the Human Population Structure and Are Partly Driven by Microbiome Quantitative Trait Loci. Microorganisms, 2020, 8, 1196.	1.6	14
48	April â€" An Inductive Logic Programming System. Lecture Notes in Computer Science, 2006, , 481-484.	1.0	13
49	The DAIBAM MITE element is involved in the origin of one fixed and two polymorphic Drosophila virilis phylad inversions. Fly, 2012, 6, 71-74.	0.9	13
50	Improving the performance of Transposable Elements detection tools. Journal of Integrative Bioinformatics, 2013, 10, 40-50.	1.0	11
51	On Applying Tabling to Inductive Logic Programming. Lecture Notes in Computer Science, 2005, , 707-714.	1.0	11
52	Butler enables rapid cloud-based analysis of thousands of human genomes. Nature Biotechnology, 2020, 38, 288-292.	9.4	11
53	Comparative Genomics of Xanthomonas euroxanthea and Xanthomonas arboricola pv. juglandis Strains Isolated from a Single Walnut Host Tree. Microorganisms, 2021, 9, 624.	1.6	10
54	Shedding Light on the African Enigma: In Vitro Testing of Homo sapiens-Helicobacter pylori Coevolution. Microorganisms, 2021, 9, 240.	1.6	10

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55	Improving the performance of Transposable Elements detection tools. Journal of Integrative Bioinformatics, 2013, 10, 231.	1.0	10
56	Amino acid pair- and triplet-wise groupings in the interior of α-helical segments in proteins. Journal of Theoretical Biology, 2011, 271, 136-144.	0.8	9
57	Predicting malignancy from mammography findings and image-guided core biopsies. International Journal of Data Mining and Bioinformatics, 2015, 11, 257.	0.1	9
58	The InBIO Barcoding Initiative Database: DNA barcodes of Portuguese Diptera 01. Biodiversity Data Journal, 2020, 8, e49985.	0.4	9
59	Boosting the Detection of Transposable Elements Using Machine Learning. Advances in Intelligent Systems and Computing, 2013, , 85-91.	0.5	8
60	Protein evolution of ANTP and PRD homeobox genes. BMC Evolutionary Biology, 2008, 8, 200.	3.2	7
61	The InBIO Barcoding Initiative Database: contribution to the knowledge on DNA barcodes of Iberian Plecoptera. Biodiversity Data Journal, 2020, 8, e55137.	0.4	7
62	A pipelined data-parallel algorithm for ILP. , 2005, , .		5
63	A Relational Learning Approach to Structure-Activity Relationships in Drug Design Toxicity Studies. Journal of Integrative Bioinformatics, 2011, 8, 176-194.	1.0	5
64	Comparative Study of Classification Algorithms Using Molecular Descriptors in Toxicological DataBases. Lecture Notes in Computer Science, 2009, , 121-132.	1.0	5
65	Complete Genome Sequences of Walnut-Associated <i>Xanthomonas euroxanthea</i> Strains CPBF 367 and CPBF 426 Obtained by Illumina/Nanopore Hybrid Assembly. Microbiology Resource Announcements, 2020, 9, .	0.3	5
66	LogCHEM: Interactive Discriminative Mining of Chemical Structure. , 2008, , .		4
67	Improving the efficiency of inductive logic programming systems. Software - Practice and Experience, 2009, 39, 189-219.	2.5	4
68	Conceptual Clustering of Multi-Relational Data. Lecture Notes in Computer Science, 2012, , 145-159.	1.0	4
69	Complete Genome Sequence Obtained by Nanopore and Illumina Hybrid Assembly of Xanthomonas arboricola pv. juglandis CPBF 427, Isolated from Buds of a Walnut Tree. Microbiology Resource Announcements, 2021, 10, .	0.3	4
70	k-RNN. , 2008, , .		3
71	Predicting the secondary structure of proteins using machine learning algorithms. International Journal of Data Mining and Bioinformatics, 2012, 6, 571.	0.1	3
72	BIORED - A Genetic Algorithm for Pattern Detection in Biosequences. Advances in Soft Computing, 2009, , 156-165.	0.4	3

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73	Predicting Malignancy from Mammography Findings and Surgical Biopsies. , 2011, 2011, .		2
74	On the Development of a Pipeline for the Automatic Detection of Positively Selected Sites. Advances in Intelligent and Soft Computing, 2012, , 225-229.	0.2	2
75	ILP :- Just Trie It. , 2007, , 78-87.		2
76	Interactive Discriminative Mining of Chemical Fragments. Lecture Notes in Computer Science, 2011, , 59-66.	1.0	2
77	Gene Classification Based on Amino Acid Motifs and Residues: The DLX (distal-less) Test Case. PLoS ONE, 2009, 4, e5748.	1.1	1
78	AND Parallelism for ILP: The APIS System. Lecture Notes in Computer Science, 2014, , 93-106.	1.0	1
79	Induction as a Search Procedure. , 2008, , 166-216.		1
80	Partitional Clustering of Protein Sequences â€" An Inductive Logic Programming Approach. Lecture Notes in Computer Science, 2009, , 1001-1004.	1.0	1
81	A relational learning approach to Structure-Activity Relationships in drug design toxicity studies. Journal of Integrative Bioinformatics, 2011, 8, 182.	1.0	1
82	On Predicting Protein Secondary Structure from their Aminoacid Sequences using Inductive Logic Programming. , 2005, , .		0
83	Parallel Algorithms for Multirelational Data Mining: Application to Life Science Problems. Computer Communications and Networks, 2016, , 339-363.	0.8	0
84	Evaluating the impact of sampling strategies and bioinformatics on ethanol-based DNA metabarcoding. ARPHA Conference Abstracts, 0, 4, .	0.0	0
85	Metabarcoding with MinION: Speeding up the detection of invasive aquatic species using environmental DNA and nanopore sequencing. ARPHA Conference Abstracts, 0, 4, .	0.0	0
86	Visually Guiding and Controlling the Search While Mining Chemical Structures. Lecture Notes in Computer Science, 2009, , 1043-1046.	1.0	0
87	Predicting the Start of Protein Î±-Helices Using Machine Learning Algorithms. Advances in Intelligent and Soft Computing, 2010, , 33-41.	0.2	0
88	Assessing the Effect of 2D Fingerprint Filtering on ILP-Based Structure-Activity Relationships Toxicity Studies in Drug Design. Advances in Intelligent and Soft Computing, 2011, , 355-363.	0.2	0
89	Abstract 389: Integrating diverse transcriptomic alterations to identify cancer-relevant genes. , 2017, , .		0
90	Abstract LB-274: Primary tumor gene expression signature predicts long-term outcomes in primary melanoma: A prospective multicenter study. , 2020, , .		0

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91	Efficient and Scalable Induction of Logic Programs Using a Deductive Database System. Lecture Notes in Computer Science, 2006, , 184-198.	1.0	0