

Nuno A Fonseca

List of Publications by Citations

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Version: 2024-04-27

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

97
papers

5,567
citations

27
h-index

74
g-index

106
ext. papers

7,916
ext. citations

9.6
avg, IF

7.15
L-index

#	Paper	IF	Citations
97	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020 , 578, 82-93	50.4	840
96	Two independent modes of chromatin organization revealed by cohesin removal. <i>Nature</i> , 2017 , 551, 51-56	50.4	589
95	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013 , 2, 10	7.6	461
94	Expression Atlas update--an integrated database of gene and protein expression in humans, animals and plants. <i>Nucleic Acids Research</i> , 2016 , 44, D746-52	20.1	404
93	Assemblathon 1: a competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011 , 21, 2224-41	9.7	364
92	ArrayExpress update - from bulk to single-cell expression data. <i>Nucleic Acids Research</i> , 2019 , 47, D711-D715	20.1	256
91	Expression Atlas update--a database of gene and transcript expression from microarray- and sequencing-based functional genomics experiments. <i>Nucleic Acids Research</i> , 2014 , 42, D926-32	20.1	247
90	Expression Atlas: gene and protein expression across multiple studies and organisms. <i>Nucleic Acids Research</i> , 2018 , 46, D246-D251	20.1	222
89	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020 , 578, 102-111	50.4	220
88	Tools for mapping high-throughput sequencing data. <i>Bioinformatics</i> , 2012 , 28, 3169-77	7.2	211
87	Expression Atlas update: from tissues to single cells. <i>Nucleic Acids Research</i> , 2020 , 48, D77-D83	20.1	159
86	Genomic basis for RNA alterations in cancer. <i>Nature</i> , 2020 , 578, 129-136	50.4	148
85	Gramene 2018: unifying comparative genomics and pathway resources for plant research. <i>Nucleic Acids Research</i> , 2018 , 46, D1181-D1189	20.1	107
84	Gramene 2016: comparative plant genomics and pathway resources. <i>Nucleic Acids Research</i> , 2016 , 44, D1133-40	20.1	102
83	Long-range enhancers regulating Myc expression are required for normal facial morphogenesis. <i>Nature Genetics</i> , 2014 , 46, 753-8	36.3	89
82	Transcription Factor Activities Enhance Markers of Drug Sensitivity in Cancer. <i>Cancer Research</i> , 2018 , 78, 769-780	10.1	87
81	Cancer LncRNA Census reveals evidence for deep functional conservation of long noncoding RNAs in tumorigenesis. <i>Communications Biology</i> , 2020 , 3, 56	6.7	77

80	RNA-Seq gene profiling--a systematic empirical comparison. <i>PLoS ONE</i> , 2014 , 9, e107026	3.7	61
79	A Pan-cancer Transcriptome Analysis Reveals Pervasive Regulation through Alternative Promoters. <i>Cell</i> , 2019 , 178, 1465-1477.e17	56.2	56
78	An S-RNase-based gametophytic self-incompatibility system evolved only once in eudicots. <i>Journal of Molecular Evolution</i> , 2008 , 67, 179-90	3.1	55
77	Integrative pathway enrichment analysis of multivariate omics data. <i>Nature Communications</i> , 2020 , 11, 735	17.4	53
76	Comparison of GENCODE and RefSeq gene annotation and the impact of reference geneset on variant effect prediction. <i>BMC Genomics</i> , 2015 , 16 Suppl 8, S2	4.5	53
75	High-resolution mapping of transcriptional dynamics across tissue development reveals a stable mRNA-tRNA interface. <i>Genome Research</i> , 2014 , 24, 1797-807	9.7	53
74	Convergent evolution at the gametophytic self-incompatibility system in Malus and Prunus. <i>PLoS ONE</i> , 2015 , 10, e0126138	3.7	39
73	Pathway and network analysis of more than 2500 whole cancer genomes. <i>Nature Communications</i> , 2020 , 11, 729	17.4	38
72	PopAffiliator: online calculator for individual affiliation to a major population group based on 17 autosomal short tandem repeat genotype profile. <i>International Journal of Legal Medicine</i> , 2011 , 125, 629-36	3.1	36
71	High-coverage whole-genome analysis of 1220 cancers reveals hundreds of genes deregulated by rearrangement-mediated cis-regulatory alterations. <i>Nature Communications</i> , 2020 , 11, 736	17.4	32
70	Evolutionary patterns at the RNase based gametophytic self - incompatibility system in two divergent Rosaceae groups (Maloideae and Prunus). <i>BMC Evolutionary Biology</i> , 2010 , 10, 200	3	24
69	iRAP - an integrated RNA-seq Analysis Pipeline		22
68	RNase-based gametophytic self-incompatibility evolution: Questioning the hypothesis of multiple independent recruitments of the S-pollen gene. <i>Journal of Molecular Evolution</i> , 2009 , 69, 32-41	3.1	21
67	Parallel ILP for distributed-memory architectures. <i>Machine Learning</i> , 2009 , 74, 257-279	4	20
66	The RNASeq-er API-a gateway to systematically updated analysis of public RNA-seq data. <i>Bioinformatics</i> , 2017 , 33, 2218-2220	7.2	19
65	Amino acid pairing at the N- and C-termini of helical segments in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 70, 188-96	4.2	19
64	Tumors induce de novo steroid biosynthesis in T cells to evade immunity. <i>Nature Communications</i> , 2020 , 11, 3588	17.4	19
63	Drosophila americana as a model species for comparative studies on the molecular basis of phenotypic variation. <i>Genome Biology and Evolution</i> , 2013 , 5, 661-79	3.9	18

62	The <i>Drosophila melanogaster</i> methuselah gene: a novel gene with ancient functions. <i>PLoS ONE</i> , 2013 , 8, e63747	3.7	18
61	Combined burden and functional impact tests for cancer driver discovery using DriverPower. <i>Nature Communications</i> , 2020 , 11, 734	17.4	16
60	Patterns of evolution at the gametophytic self-incompatibility <i>Sorbus aucuparia</i> (Pyrinae) S pollen genes support the non-self recognition by multiple factors model. <i>Journal of Experimental Botany</i> , 2013 , 64, 2423-34	7	16
59	The number, age, sharing and relatedness of S-locus specificities in <i>Prunus</i> . <i>Genetical Research</i> , 2008 , 90, 17-26	1.1	16
58	ADOPS--Automatic Detection Of Positively Selected Sites. <i>Journal of Integrative Bioinformatics</i> , 2012 , 9, 200	3.8	16
57	Phylogeny of the teashirt-related zinc finger (tshz) gene family and analysis of the developmental expression of tshz2 and tshz3b in the zebrafish. <i>Developmental Dynamics</i> , 2010 , 239, 1010-8	2.9	15
56	Inferences on specificity recognition at the <i>Malus domestica</i> gametophytic self-incompatibility system. <i>Scientific Reports</i> , 2018 , 8, 1717	4.9	14
55	ADOPS - Automatic Detection Of Positively Selected Sites. <i>Journal of Integrative Bioinformatics</i> , 2012 , 9, 18-32	3.8	14
54	April ¶An Inductive Logic Programming System. <i>Lecture Notes in Computer Science</i> , 2006 , 481-484	0.9	12
53	Discovery and characterization of coding and non-coding driver mutations in more than 2,500 whole cancer genomes		12
52	The DAIBAM MITE element is involved in the origin of one fixed and two polymorphic <i>Drosophila virilis</i> phylad inversions. <i>Fly</i> , 2012 , 6, 71-4	1.3	11
51	An RNA-seq Based Machine Learning Approach Identifies Latent Tuberculosis Patients With an Active Tuberculosis Profile. <i>Frontiers in Immunology</i> , 2020 , 11, 1470	8.4	11
50	Genomic basis for RNA alterations revealed by whole-genome analyses of 27 cancer types		10
49	Strategies to Parallelize ILP Systems. <i>Lecture Notes in Computer Science</i> , 2005 , 136-153	0.9	10
48	On Applying Tabling to Inductive Logic Programming. <i>Lecture Notes in Computer Science</i> , 2005 , 707-714	0.9	10
47	Butler enables rapid cloud-based analysis of thousands of human genomes. <i>Nature Biotechnology</i> , 2020 , 38, 288-292	44.5	9
46	A user guide for the online exploration and visualization of PCAWG data. <i>Nature Communications</i> , 2020 , 11, 3400	17.4	7
45	Predicting malignancy from mammography findings and image-guided core biopsies. <i>International Journal of Data Mining and Bioinformatics</i> , 2015 , 11, 257-76	0.5	7

44	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. <i>Microorganisms</i> , 2020 , 8,	4.9	7
43	Improving the performance of Transposable Elements detection tools. <i>Journal of Integrative Bioinformatics</i> , 2013 , 10, 40-50	3.8	6
42	Amino acid pair- and triplet-wise groupings in the interior of Helical segments in proteins. <i>Journal of Theoretical Biology</i> , 2011 , 271, 136-44	2.3	6
41	Protein evolution of ANTP and PRD homeobox genes. <i>BMC Evolutionary Biology</i> , 2008 , 8, 200	3	6
40	Improving the performance of Transposable Elements detection tools. <i>Journal of Integrative Bioinformatics</i> , 2013 , 10, 231	3.8	6
39	Tumour gene expression signature in primary melanoma predicts long-term outcomes. <i>Nature Communications</i> , 2021 , 12, 1137	17.4	5
38	A Relational Learning Approach to Structure-Activity Relationships in Drug Design Toxicity Studies. <i>Journal of Integrative Bioinformatics</i> , 2011 , 8, 176-194	3.8	4
37	Improving the efficiency of inductive logic programming systems. <i>Software - Practice and Experience</i> , 2009 , 39, 189-219	2.5	4
36	Conceptual Clustering of Multi-Relational Data. <i>Lecture Notes in Computer Science</i> , 2012 , 145-159	0.9	4
35	Complete Genome Sequences of Walnut-Associated Strains CPBF 367 and CPBF 426 Obtained by Illumina/Nanopore Hybrid Assembly. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	4
34	The InBIO Barcoding Initiative Database: contribution to the knowledge on DNA barcodes of Iberian Plecoptera. <i>Biodiversity Data Journal</i> , 2020 , 8, e55137	1.8	4
33	Comparative Study of Classification Algorithms Using Molecular Descriptors in Toxicological DataBases. <i>Lecture Notes in Computer Science</i> , 2009 , 121-132	0.9	4
32	Whole genome and RNA sequencing of 1,220 cancers reveals hundreds of genes deregulated by rearrangement of cis-regulatory elements		4
31	Speeding up the detection of invasive aquatic species using environmental DNA and nanopore sequencing		4
30	Shedding Light on the African Enigma: In Vitro Testing of Coevolution. <i>Microorganisms</i> , 2021 , 9,	4.9	4
29	Boosting the Detection of Transposable Elements Using Machine Learning. <i>Advances in Intelligent Systems and Computing</i> , 2013 , 85-91	0.4	3
28	LogCHEM: Interactive Discriminative Mining of Chemical Structure 2008 ,		3
27	A pipelined data-parallel algorithm for ILP 2005 ,		3

26	The InBIO Barcoding Initiative Database: DNA barcodes of Portuguese Diptera 01. <i>Biodiversity Data Journal</i> , 2020 , 8, e49985	1.8	3
25	Transcription factor activities enhance markers of drug response in cancer		3
24	A user-friendly guide to the online resources for data exploration, visualization, and discovery for the Pan-Cancer Analysis of Whole Genomes project (PCAWG)		3
23	Assessing the Gene Regulatory Landscape in 1,188 Human Tumors		3
22	A Pan-Cancer Transcriptome Analysis Reveals Pervasive Regulation through Tumor-Associated Alternative Promoters		3
21	Comparative Genomics of <i>and pv.</i> Strains Isolated from a Single Walnut Host Tree. <i>Microorganisms</i> , 2021 , 9,	4.9	3
20	Predicting Malignancy from Mammography Findings and Surgical Biopsies 2011 , 2011,	0.8	2
19	On the Development of a Pipeline for the Automatic Detection of Positively Selected Sites. <i>Advances in Intelligent and Soft Computing</i> , 2012 , 225-229		2
18	Predicting the secondary structure of proteins using machine learning algorithms. <i>International Journal of Data Mining and Bioinformatics</i> , 2012 , 6, 571-84	0.5	2
17	k-RNN 2008 ,		2
16	QmihR: Pipeline for Quantification of Microbiome in Human RNA-seq. <i>Advances in Intelligent Systems and Computing</i> , 2017 , 173-179	0.4	2
15	BIORED - A Genetic Algorithm for Pattern Detection in Biosequences. <i>Advances in Soft Computing</i> , 2009 , 156-165		2
14	Interactive Discriminative Mining of Chemical Fragments. <i>Lecture Notes in Computer Science</i> , 2011 , 59-66	0.9	2
13	Comprehensive genome and transcriptome analysis reveals genetic basis for gene fusions in cancer		2
12	Complete Genome Sequence Obtained by Nanopore and Illumina Hybrid Assembly of <i>Xanthomonas arboricola pv. juglandis</i> CPBF 427, Isolated from Buds of a Walnut Tree. <i>Microbiology Resource Announcements</i> , 2021 , 10,	1.3	2
11	Gene classification based on amino acid motifs and residues: the DLX (distal-less) test case. <i>PLoS ONE</i> , 2009 , 4, e5748	3.7	1
10	Induction as a Search Procedure 2008 , 166-216		1
9	ILP :- Just Trie It 2007 , 78-87		1

8	AND Parallelism for ILP: The APIS System. <i>Lecture Notes in Computer Science</i> , 2014 , 93-106	0.9	1
7	A relational learning approach to Structure-Activity Relationships in drug design toxicity studies. <i>Journal of Integrative Bioinformatics</i> , 2011 , 8, 182	3.8	1
6	Parallel Algorithms for Multirelational Data Mining: Application to Life Science Problems. <i>Computer Communications and Networks</i> , 2016 , 339-363	0.5	
5	Efficient and Scalable Induction of Logic Programs Using a Deductive Database System. <i>Lecture Notes in Computer Science</i> , 2006 , 184-198	0.9	
4	Visually Guiding and Controlling the Search While Mining Chemical Structures. <i>Lecture Notes in Computer Science</i> , 2009 , 1043-1046	0.9	
3	Partitional Clustering of Protein Sequences: An Inductive Logic Programming Approach. <i>Lecture Notes in Computer Science</i> , 2009 , 1001-1004	0.9	
2	Predicting the Start of Protein α -Helices Using Machine Learning Algorithms. <i>Advances in Intelligent and Soft Computing</i> , 2010 , 33-41		
1	Assessing the Effect of 2D Fingerprint Filtering on ILP-Based Structure-Activity Relationships Toxicity Studies in Drug Design. <i>Advances in Intelligent and Soft Computing</i> , 2011 , 355-363		