

Nuno A Fonseca

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/9494911/nuno-a-fonseca-publications-by-year.pdf>

Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	Tumour gene expression signature in primary melanoma predicts long-term outcomes. <i>Nature Communications</i> , 2021 , 12, 1137	17.4	5
96	Comparative Genomics of and pv. Strains Isolated from a Single Walnut Host Tree. <i>Microorganisms</i> , 2021 , 9,	4.9	3
95	Complete Genome Sequence Obtained by Nanopore and Illumina Hybrid Assembly of <i>Xanthomonas arboricola</i> pv. <i>juglandis</i> CPBF 427, Isolated from Buds of a Walnut Tree. <i>Microbiology Resource Announcements</i> , 2021 , 10,	1.3	2
94	Shedding Light on the African Enigma: In Vitro Testing of Coevolution. <i>Microorganisms</i> , 2021 , 9,	4.9	4
93	A user guide for the online exploration and visualization of PCAWG data. <i>Nature Communications</i> , 2020 , 11, 3400	17.4	7
92	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
91	Combined burden and functional impact tests for cancer driver discovery using DriverPower. <i>Nature Communications</i> , 2020 , 11, 734	17.4	16
90	Integrative pathway enrichment analysis of multivariate omics data. <i>Nature Communications</i> , 2020 , 11, 735	17.4	53
89	Pathway and network analysis of more than 2500 whole cancer genomes. <i>Nature Communications</i> , 2020 , 11, 729	17.4	38
88	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020 , 578, 102-111	50.4	220
87	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020 , 578, 82-93	50.4	840
86	Genomic basis for RNA alterations in cancer. <i>Nature</i> , 2020 , 578, 129-136	50.4	148
85	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
84	Expression Atlas update: from tissues to single cells. <i>Nucleic Acids Research</i> , 2020 , 48, D77-D83	20.1	159
83	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
82	The InBIO Barcoding Initiative Database: DNA barcodes of Portuguese Diptera 01. <i>Biodiversity Data Journal</i> , 2020 , 8, e49985	1.8	3
81	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

80	Butler enables rapid cloud-based analysis of thousands of human genomes. <i>Nature Biotechnology</i> , 2020 , 38, 288-292	44.5	9
79	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
78	Tumors induce de novo steroid biosynthesis in T cells to evade immunity. <i>Nature Communications</i> , 2020 , 11, 3588	17.4	19
77	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
76	A Pan-cancer Transcriptome Analysis Reveals Pervasive Regulation through Alternative Promoters. <i>Cell</i> , 2019 , 178, 1465-1477.e17	56.2	56
75	ArrayExpress update - from bulk to single-cell expression data. <i>Nucleic Acids Research</i> , 2019 , 47, D711-D715	256	256
74	Gramene 2018: unifying comparative genomics and pathway resources for plant research. <i>Nucleic Acids Research</i> , 2018 , 46, D1181-D1189	20.1	107
73	Inferences on specificity recognition at the <i>Malus domestica</i> gametophytic self-incompatibility system. <i>Scientific Reports</i> , 2018 , 8, 1717	4.9	14
72	Expression Atlas: gene and protein expression across multiple studies and organisms. <i>Nucleic Acids Research</i> , 2018 , 46, D246-D251	20.1	222
71	Transcription Factor Activities Enhance Markers of Drug Sensitivity in Cancer. <i>Cancer Research</i> , 2018 , 78, 769-780	10.1	87
70	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
69	Two independent modes of chromatin organization revealed by cohesin removal. <i>Nature</i> , 2017 , 551, 51-56	50.4	589
68	QmihR: Pipeline for Quantification of Microbiome in Human RNA-seq. <i>Advances in Intelligent Systems and Computing</i> , 2017 , 173-179	0.4	2
67	Parallel Algorithms for Multirelational Data Mining: Application to Life Science Problems. <i>Computer Communications and Networks</i> , 2016 , 339-363	0.5	
66	Gramene 2016: comparative plant genomics and pathway resources. <i>Nucleic Acids Research</i> , 2016 , 44, D1133-40	20.1	102
65	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
64	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
63	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

62	Convergent evolution at the gametophytic self-incompatibility system in Malus and Prunus. <i>PLoS ONE</i> , 2015 , 10, e0126138	3.7	39
61	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
60	Long-range enhancers regulating Myc expression are required for normal facial morphogenesis. <i>Nature Genetics</i> , 2014 , 46, 753-8	36.3	89
59	RNA-Seq gene profiling--a systematic empirical comparison. <i>PLoS ONE</i> , 2014 , 9, e107026	3.7	61
58	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
57	AND Parallelism for ILP: The APIS System. <i>Lecture Notes in Computer Science</i> , 2014 , 93-106	0.9	1
56	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013 , 2, 10	7.6	461
55	<i>Drosophila americana</i> 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
54	Boosting the Detection of Transposable Elements Using Machine Learning. <i>Advances in Intelligent Systems and Computing</i> , 2013 , 85-91	0.4	3
53	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
52	Improving the performance of Transposable Elements detection tools. <i>Journal of Integrative Bioinformatics</i> , 2013 , 10, 40-50	3.8	6
51	The <i>Drosophila melanogaster</i> methuselah gene: a novel gene with ancient functions. <i>PLoS ONE</i> , 2013 , 8, e63747	3.7	18
50	Improving the performance of Transposable Elements detection tools. <i>Journal of Integrative Bioinformatics</i> , 2013 , 10, 231	3.8	6
49	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
48	Tools for mapping high-throughput sequencing data. <i>Bioinformatics</i> , 2012 , 28, 3169-77	7.2	211
47	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
46	Conceptual Clustering of Multi-Relational Data. <i>Lecture Notes in Computer Science</i> , 2012 , 145-159	0.9	4
45	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

44	ADOPS - Automatic Detection Of Positively Selected Sites. <i>Journal of Integrative Bioinformatics</i> , 2012 , 9, 18-32	3.8	14
43	ADOPS--Automatic Detection Of Positively Selected Sites. <i>Journal of Integrative Bioinformatics</i> , 2012 , 9, 200	3.8	16
42	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
41	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
40	Predicting Malignancy from Mammography Findings and Surgical Biopsies 2011 , 2011,	0.8	2
39	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
38	Assemblathon 1: a competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011 , 21, 2224-41	9.7	364
37	Interactive Discriminative Mining of Chemical Fragments. <i>Lecture Notes in Computer Science</i> , 2011 , 59-66.9		2
36	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		
35	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
34	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
33	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
32	Predicting the Start of Protein Helices Using Machine Learning Algorithms. <i>Advances in Intelligent and Soft Computing</i> , 2010 , 33-41		
31	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
30	Parallel ILP for distributed-memory architectures. <i>Machine Learning</i> , 2009 , 74, 257-279	4	20
29	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
28	Improving the efficiency of inductive logic programming systems. <i>Software - Practice and Experience</i> , 2009 , 39, 189-219	2.5	4
27	BIORED - A Genetic Algorithm for Pattern Detection in Biosequences. <i>Advances in Soft Computing</i> , 2009 , 156-165		2

26	Comparative Study of Classification Algorithms Using Molecular Descriptors in Toxicological DataBases. <i>Lecture Notes in Computer Science</i> , 2009 , 121-132	0.9	4
25	Visually Guiding and Controlling the Search While Mining Chemical Structures. <i>Lecture Notes in Computer Science</i> , 2009 , 1043-1046	0.9	
24	Partitional Clustering of Protein Sequences [An Inductive Logic Programming Approach. <i>Lecture Notes in Computer Science</i> , 2009 , 1001-1004	0.9	
23	Protein evolution of ANTP and PRD homeobox genes. <i>BMC Evolutionary Biology</i> , 2008 , 8, 200	3	6
22	LogCHEM: Interactive Discriminative Mining of Chemical Structure 2008 ,		3
21	k-RNN 2008 ,		2
20	The number, age, sharing and relatedness of S-locus specificities in Prunus. <i>Genetical Research</i> , 2008 , 90, 17-26	1.1	16
19	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
18	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
17	Induction as a Search Procedure 2008 , 166-216		1
16	ILP :- Just Trie It 2007 , 78-87		1
15	April [An Inductive Logic Programming System. <i>Lecture Notes in Computer Science</i> , 2006 , 481-484	0.9	12
14	Efficient and Scalable Induction of Logic Programs Using a Deductive Database System. <i>Lecture Notes in Computer Science</i> , 2006 , 184-198	0.9	
13	A pipelined data-parallel algorithm for ILP 2005 ,		3
12	Strategies to Parallelize ILP Systems. <i>Lecture Notes in Computer Science</i> , 2005 , 136-153	0.9	10
11	On Applying Tabling to Inductive Logic Programming. <i>Lecture Notes in Computer Science</i> , 2005 , 707-714	0.9	10
10	iRAP - an integrated RNA-seq Analysis Pipeline		22
9	Whole genome and RNA sequencing of 1,220 cancers reveals hundreds of genes deregulated by rearrangement of cis-regulatory elements		4

8	Transcription factor activities enhance markers of drug response in cancer	3
7	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
6	Genomic basis for RNA alterations revealed by whole-genome analyses of 27 cancer types	10
5	Speeding up the detection of invasive aquatic species using environmental DNA and nanopore sequencing	4
4	Assessing the Gene Regulatory Landscape in 1,188 Human Tumors	3
3	Discovery and characterization of coding and non-coding driver mutations in more than 2,500 whole cancer genomes	12
2	Comprehensive genome and transcriptome analysis reveals genetic basis for gene fusions in cancer	2
1	A Pan-Cancer Transcriptome Analysis Reveals Pervasive Regulation through Tumor-Associated Alternative Promoters	3