Nicolas Carels

List of Publications by Year
in descending order

67 papers	2,067 citations	279487 23 h-index	243296 44 g-index
68 all docs	68 docs citations	68 times ranked	2695 citing authors

#	Article	IF	Citations
1	Genome size, base composition and karyotype of Jatropha curcas L., an important biofuel plant. Plant Science, 2008, 174, 613-617.	1.7	182
2	The distribution of genes in the genomes of Gramineae. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 6857-6861.	3.3	162
3	Two Classes of Genes in Plants. Genetics, 2000, 154, 1819-1825.	1.2	162
4	Genome Properties of the Diatom Phaeodactylum tricornutum. Plant Physiology, 2002, 129, 993-1002.	2.3	119
5	Atazanavir, Alone or in Combination with Ritonavir, Inhibits SARS-CoV-2 Replication and Proinflammatory Cytokine Production. Antimicrobial Agents and Chemotherapy, 2020, 64, .	1.4	109
6	Cultivation-Independent Methods Reveal Differences among Bacterial Gut Microbiota in Triatomine Vectors of Chagas Disease. PLoS Neglected Tropical Diseases, 2012, 6, e1631.	1.3	92
7	Chapter 2 Jatropha curcas. Advances in Botanical Research, 2009, 50, 39-86.	0.5	91
8	The mitochondrial genome of the phytopathogenic basidiomycete Moniliophthora perniciosa is 109kb in size and contains a stable integrated plasmid. Mycological Research, 2008, 112, 1136-1152.	2.5	87
9	Characterization of the microbiota in the guts of Triatoma brasiliensis and Triatoma pseudomaculata infected by Trypanosoma cruzi in natural conditions using culture independent methods. Parasites and Vectors, 2015, 8, 245.	1.0	75
10	Comparative Analysis of Expressed Genes from Cacao Meristems Infected by Moniliophthora perniciosa. Annals of Botany, 2007, 100, 129-140.	1.4	74
11	Compositional Properties of Homologous Coding Sequences from Plants. Journal of Molecular Evolution, 1998, 46, 45-53.	0.8	65
12	Compositional mapping of chicken chromosomes and identification of the gene-richest regions. Chromosome Research, 2001, 9, 521-532.	1.0	54
13	The gene distribution of the maize genome.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 11057-11060.	3.3	53
14	Validation of a network-based strategy for the optimization of combinatorial target selection in breast cancer therapy: siRNA knockdown of network targets in MDA-MB-231 cells as an *in vitro* model for inhibition of tumor development. Oncotarget, 2016, 7, 63189-63203.	0.8	49
15	Toward precision medicine of breast cancer. Theoretical Biology and Medical Modelling, 2016, 13, 7.	2.1	48
16	A strategy to identify housekeeping genes suitable for analysis in breast cancer diseases. BMC Genomics, 2016, 17, 639.	1.2	47
17	Metabolic Signatures of Triatomine Vectors of Trypanosoma cruzi Unveiled by Metabolomics. PLoS ONE, 2013, 8, e77283.	1.1	43
18	SARS-CoV-2 Proteins Bind to Hemoglobin and Its Metabolites. International Journal of Molecular Sciences, 2021, 22, 9035.	1.8	41

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19	A Computational Strategy to Select Optimized Protein Targets for Drug Development toward the Control of Cancer Diseases. PLoS ONE, 2015, 10, e0115054.	1.1	40
20	Compositional heterogeneity within and among isochores in mammalian genomes. Gene, 2001, 276, 15-24.	1.0	34
21	In vitro Trypanocidal Activity, Genomic Analysis of Isolates, and in vivo Transcription of Type VI Secretion System of Serratia marcescens Belonging to the Microbiota of Rhodnius prolixus Digestive Tract. Frontiers in Microbiology, 2018, 9, 3205.	1.5	33
22	Towards the Domestication of Jatropha: The Integration of Sciences. , 2013, , 263-299.		32
23	The pig genome: compositional analysis and identification of the gene-richest regions in chromosomes and nuclei. Gene, 2004, 343, 245-251.	1.0	31
24	ESTs from Seeds to Assist the Selective Breeding of <i>Jatropha curcas</i> L. for Oil and Active Compounds. Genomics Insights, 2010, 3, GEI.S4340.	3.0	26
25	EST profiling of resistant and susceptible Hevea infected by Microcyclus ulei. Physiological and Molecular Plant Pathology, 2011, 76, 126-136.	1.3	22
26	Optimization of combination chemotherapy based on the calculation of network entropy for protein-protein interactions in breast cancer cell lines. EPJ Nonlinear Biomedical Physics, 2015, 3, .	0.8	22
27	Signaling Complexity Measured by Shannon Entropy and Its Application in Personalized Medicine. Frontiers in Genetics, 2019, 10, 930.	1.1	22
28	Single nucleotide polymorphisms from Theobroma cacao expressed sequence tags associated with witches' broom disease in cacao. Genetics and Molecular Research, 2009, 8, 799-808.	0.3	21
29	Using analytical ultracentrifugation to study compositional variation in vertebrate genomes. European Biophysics Journal, 2003, 32, 418-426.	1.2	20
30	Development, characterization, validation, and mapping of SSRs derived from Theobroma cacao L.–Moniliophthora perniciosa interaction ESTs. Tree Genetics and Genomes, 2010, 6, 663-676.	0.6	20
31	Diversity and Phylogenetic Implications of CsCl Profiles from Rodent DNAs. Molecular Phylogenetics and Evolution, 2000, 17, 219-230.	1.2	19
32	The compositional organization and the expression of the Arabidopsis genome. FEBS Letters, 2000, 472, 302-306.	1.3	15
33	Perennial plants for biofuel production: Bridging genomics and field research. Biotechnology Journal, 2015, 10, 505-507.	1.8	15
34	A Metagenomic Analysis of Bacterial Microbiota in the Digestive Tract of Triatomines. Bioinformatics and Biology Insights, 2017, 11, 117793221773342.	1.0	14
35	Modeling Basins of Attraction for Breast Cancer Using Hopfield Networks. Frontiers in Genetics, 2020, 11, 314.	1.1	14
36	Synonymous and Nonsynonymous Substitutions in Genes from Gramineae: Intragenic Correlations. Journal of Molecular Evolution, 1999, 49, 330-342.	0.8	12

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37	Agrobacterium-mediated transformation of Jatropha curcas leaf explants with a fungal chitinase gene. African Journal of Biotechnology, 2016, 15, 2006-2016.	0.3	9
38	A Statistical Method without Training Step for the Classification of Coding Frame in Transcriptome Sequences. Bioinformatics and Biology Insights, 2013, 7, BBI.S10053.	1.0	8
39	Proteome of the Triatomine Digestive Tract: From Catalytic to Immune Pathways; Focusing on Annexin Expression. Frontiers in Molecular Biosciences, 2020, 7, 589435.	1.6	8
40	In silico structural characterization of protein targets for drug development against Trypanosoma cruzi. Journal of Molecular Modeling, 2016, 22, 244.	0.8	7
41	Universal Features for the Classification of Coding and Non-coding DNA Sequences. Bioinformatics and Biology Insights, 2009, 3, BBI.S2236.	1.0	6
42	Classifying Coding DNA with Nucleotide Statistics. Bioinformatics and Biology Insights, 2009, 3, BBI.S3030.	1.0	6
43	Galaxy and MEAN Stack to Create a User-Friendly Workflow for the Rational Optimization of Cancer Chemotherapy. Frontiers in Genetics, 2021, 12, 624259.	1.1	6
44	The mutual information theory for the certification of rice coding sequences. FEBS Letters, 2004, 568, 155-158.	1.3	5
45	An Interpretation of the Ancestral Codon from Miller's Amino Acids and Nucleotide Correlations in Modern Coding Sequences. Bioinformatics and Biology Insights, 2015, 9, BBI.S24021.	1.0	5
46	Symptomatological and Morphological Study of the Resistance of Wild Beet Species of the *Patellares* Section to *Cercospora beticola* Sacc.. Journal of Phytopathology, 1990, 130, 317-330.	0.5	4
47	The Purine Bias of Coding Sequences is Determined by Physicochemical Constraints on Proteins. Bioinformatics and Biology Insights, 2014, 8, BBI.S13161.	1.0	4
48	The Challenge of Bioenergies: An Overview. , 0, , .		4
49	Data-Driven Modeling of Breast Cancer Tumors Using Boolean Networks. Frontiers in Big Data, 2021, 4, 656395.	1.8	4
50	Karyology and Genomics of Jatropha: Current Status and Future Prospects. , 2013, , 301-320.		3
51	Editorial: Sustainable production of renewable energy from non-food crops. Biotechnology Journal, 2015, 10, 503-503.	1.8	3
52	A Computational Methodology to Overcome the Challenges Associated With the Search for Specific Enzyme Targets to Develop Drugs Against Leishmania major. Bioinformatics and Biology Insights, 2017, 11, 117793221771247.	1.0	3
53	Specific enzyme functionalities of Fusarium oxysporum compared to host plants. Gene, 2018, 676, 219-226.	1.0	3
54	A Data Science Approach for the Identification of Molecular Signatures of Aggressive Cancers. Cancers, 2022, 14, 2325.	1.7	3

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55	The maize gene space is compositionally compartimentalized. FEBS Letters, 2005, 579, 3867-3871.	1.3	2
56	System Biology to Access Target Relevance in the Research and Development of Molecular Inhibitors. Computational Biology, 2018, , 221-242.	0.1	2
57	Challenges for the Optimization of Drug Therapy in the Treatment of Cancer. Computational Biology, 2020, , 163-198.	0.1	2
58	THE CONTRIBUTION OF STOP CODON FREQUENCY AND PURINE BIAS TO THE CLASSIFICATION OF CODING SEQUENCES. , 2013, , .		2
59	The Challenge of Translating System Biology into Targeted Therapy of Cancer. Computational Biology, 2018, , 175-194.	0.1	1
60	The Birth of a New Energy Crop. , 2012, , 3-12.		1
61	Cellular Reprogramming. Computational Biology, 2018, , 41-55.	0.1	1
62	ENTROPY MEASURES BASED METHOD FOR THE CLASSIFICATION OF PROTEIN DOMAINS INTO FAMILIES AND CLANS. , 2014, , .		0
63	Functional Genomics. , 2015, , 223-245.		0
64	A History of Genomic Structures: The Big Picture. , 2015, , 131-178.		0
65	Pervasive System Biology for Active Compound Valorization in Jatropha. , 2019, , 199-251.		0
66	UNIVERSAL FEATURES FOR EXON PREDICTION. , 2011, , .		0
67	Cellular Regulatory Network Modeling Applied to Breast Cancer. Computational Biology, 2020, , 339-365.	0.1	0