

Nicolas Carels

List of Publications by Year in descending order

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Version: 2024-02-01

67
papers

2,067
citations

279487

23
h-index

243296

44
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68
all docs

68
docs citations

68
times ranked

2695
citing authors

#	ARTICLE	IF	CITATIONS
1	A Data Science Approach for the Identification of Molecular Signatures of Aggressive Cancers. <i>Cancers</i> , 2022, 14, 2325.	1.7	3
2	Galaxy and MEAN Stack to Create a User-Friendly Workflow for the Rational Optimization of Cancer Chemotherapy. <i>Frontiers in Genetics</i> , 2021, 12, 624259.	1.1	6
3	SARS-CoV-2 Proteins Bind to Hemoglobin and Its Metabolites. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9035.	1.8	41
4	Data-Driven Modeling of Breast Cancer Tumors Using Boolean Networks. <i>Frontiers in Big Data</i> , 2021, 4, 656395.	1.8	4
5	Atazanavir, Alone or in Combination with Ritonavir, Inhibits SARS-CoV-2 Replication and Proinflammatory Cytokine Production. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	109
6	Modeling Basins of Attraction for Breast Cancer Using Hopfield Networks. <i>Frontiers in Genetics</i> , 2020, 11, 314.	1.1	14
7	Challenges for the Optimization of Drug Therapy in the Treatment of Cancer. <i>Computational Biology</i> , 2020, , 163-198.	0.1	2
8	Proteome of the Triatomine Digestive Tract: From Catalytic to Immune Pathways; Focusing on Annexin Expression. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 589435.	1.6	8
9	Cellular Regulatory Network Modeling Applied to Breast Cancer. <i>Computational Biology</i> , 2020, , 339-365.	0.1	0
10	Signaling Complexity Measured by Shannon Entropy and Its Application in Personalized Medicine. <i>Frontiers in Genetics</i> , 2019, 10, 930.	1.1	22
11	Pervasive System Biology for Active Compound Valorization in <i>Jatropha</i> . , 2019, , 199-251.		0
12	Specific enzyme functionalities of <i>Fusarium oxysporum</i> compared to host plants. <i>Gene</i> , 2018, 676, 219-226.	1.0	3
13	System Biology to Access Target Relevance in the Research and Development of Molecular Inhibitors. <i>Computational Biology</i> , 2018, , 221-242.	0.1	2
14	The Challenge of Translating System Biology into Targeted Therapy of Cancer. <i>Computational Biology</i> , 2018, , 175-194.	0.1	1
15	In vitro Trypanocidal Activity, Genomic Analysis of Isolates, and in vivo Transcription of Type VI Secretion System of <i>Serratia marcescens</i> Belonging to the Microbiota of <i>Rhodnius prolixus</i> Digestive Tract. <i>Frontiers in Microbiology</i> , 2018, 9, 3205.	1.5	33
16	Cellular Reprogramming. <i>Computational Biology</i> , 2018, , 41-55.	0.1	1
17	A Metagenomic Analysis of Bacterial Microbiota in the Digestive Tract of Triatomines. <i>Bioinformatics and Biology Insights</i> , 2017, 11, 117793221773342.	1.0	14
18	A Computational Methodology to Overcome the Challenges Associated With the Search for Specific Enzyme Targets to Develop Drugs Against <i>Leishmania major</i> . <i>Bioinformatics and Biology Insights</i> , 2017, 11, 117793221771247.	1.0	3

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19	Agrobacterium-mediated transformation of <i>Jatropha curcas</i> leaf explants with a fungal chitinase gene. <i>African Journal of Biotechnology</i> , 2016, 15, 2006-2016.	0.3	9
20	A strategy to identify housekeeping genes suitable for analysis in breast cancer diseases. <i>BMC Genomics</i> , 2016, 17, 639.	1.2	47
21	In silico structural characterization of protein targets for drug development against <i>Trypanosoma cruzi</i> . <i>Journal of Molecular Modeling</i> , 2016, 22, 244.	0.8	7
22	Toward precision medicine of breast cancer. <i>Theoretical Biology and Medical Modelling</i> , 2016, 13, 7.	2.1	48
23	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 <i>in vitro</i> model for inhibition of tumor development. <i>Oncotarget</i> , 2016, 7, 63189-63203.	0.8	49
24	Editorial: Sustainable production of renewable energy from non-food crops. <i>Biotechnology Journal</i> , 2015, 10, 503-503.	1.8	3
25	Optimization of combination chemotherapy based on the calculation of network entropy for protein-protein interactions in breast cancer cell lines. <i>EPJ Nonlinear Biomedical Physics</i> , 2015, 3, .	0.8	22
26	An Interpretation of the Ancestral Codon from Miller's Amino Acids and Nucleotide Correlations in Modern Coding Sequences. <i>Bioinformatics and Biology Insights</i> , 2015, 9, BBI.S24021.	1.0	5
27	A Computational Strategy to Select Optimized Protein Targets for Drug Development toward the Control of Cancer Diseases. <i>PLoS ONE</i> , 2015, 10, e0115054.	1.1	40
28	Characterization of the microbiota in the guts of <i>Triatoma brasiliensis</i> and <i>Triatoma pseudomaculata</i> infected by <i>Trypanosoma cruzi</i> in natural conditions using culture independent methods. <i>Parasites and Vectors</i> , 2015, 8, 245.	1.0	75
29	Perennial plants for biofuel production: Bridging genomics and field research. <i>Biotechnology Journal</i> , 2015, 10, 505-507.	1.8	15
30	Functional Genomics. , 2015, , 223-245.		0
31	A History of Genomic Structures: The Big Picture. , 2015, , 131-178.		0
32	ENTROPY MEASURES BASED METHOD FOR THE CLASSIFICATION OF PROTEIN DOMAINS INTO FAMILIES AND CLANS. , 2014, , .		0
33	The Purine Bias of Coding Sequences is Determined by Physicochemical Constraints on Proteins. <i>Bioinformatics and Biology Insights</i> , 2014, 8, BBI.S13161.	1.0	4
34	Karyology and Genomics of <i>Jatropha</i> : Current Status and Future Prospects. , 2013, , 301-320.		3
35	Towards the Domestication of <i>Jatropha</i> : The Integration of Sciences. , 2013, , 263-299.		32
36	A Statistical Method without Training Step for the Classification of Coding Frame in Transcriptome Sequences. <i>Bioinformatics and Biology Insights</i> , 2013, 7, BBI.S10053.	1.0	8

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37	Metabolic Signatures of Triatomine Vectors of <i>Trypanosoma cruzi</i> Unveiled by Metabolomics. <i>PLoS ONE</i> , 2013, 8, e77283.	1.1	43
38	THE CONTRIBUTION OF STOP CODON FREQUENCY AND PURINE BIAS TO THE CLASSIFICATION OF CODING SEQUENCES. , 2013, , .		2
39	Cultivation-Independent Methods Reveal Differences among Bacterial Gut Microbiota in Triatomine Vectors of Chagas Disease. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1631.	1.3	92
40	The Birth of a New Energy Crop. , 2012, , 3-12.		1
41	EST profiling of resistant and susceptible <i>Hevea</i> infected by <i>Microcyclus ulei</i> . <i>Physiological and Molecular Plant Pathology</i> , 2011, 76, 126-136.	1.3	22
42	UNIVERSAL FEATURES FOR EXON PREDICTION. , 2011, , .		0
43	Development, characterization, validation, and mapping of SSRs derived from <i>Theobroma cacao</i> L.â€™ <i>Moniliophthora perniciosa</i> interaction ESTs. <i>Tree Genetics and Genomes</i> , 2010, 6, 663-676.	0.6	20
44	ESTs from Seeds to Assist the Selective Breeding of <i>Jatropha curcas</i> L. for Oil and Active Compounds. <i>Genomics Insights</i> , 2010, 3, GEI.S4340.	3.0	26
45	Universal Features for the Classification of Coding and Non-coding DNA Sequences. <i>Bioinformatics and Biology Insights</i> , 2009, 3, BBI.S2236.	1.0	6
46	Classifying Coding DNA with Nucleotide Statistics. <i>Bioinformatics and Biology Insights</i> , 2009, 3, BBI.S3030.	1.0	6
47	Chapter 2 <i>Jatropha curcas</i> . <i>Advances in Botanical Research</i> , 2009, 50, 39-86.	0.5	91
48	Single nucleotide polymorphisms from <i>Theobroma cacao</i> expressed sequence tags associated with witchesâ€™ broom disease in cacao. <i>Genetics and Molecular Research</i> , 2009, 8, 799-808.	0.3	21
49	The mitochondrial genome of the phytopathogenic basidiomycete <i>Moniliophthora perniciosa</i> is 109kb in size and contains a stable integrated plasmid. <i>Mycological Research</i> , 2008, 112, 1136-1152.	2.5	87
50	Genome size, base composition and karyotype of <i>Jatropha curcas</i> L., an important biofuel plant. <i>Plant Science</i> , 2008, 174, 613-617.	1.7	182
51	Comparative Analysis of Expressed Genes from Cacao Meristems Infected by <i>Moniliophthora perniciosa</i> . <i>Annals of Botany</i> , 2007, 100, 129-140.	1.4	74
52	The maize gene space is compositionally compartmentalized. <i>FEBS Letters</i> , 2005, 579, 3867-3871.	1.3	2
53	The pig genome: compositional analysis and identification of the gene-richest regions in chromosomes and nuclei. <i>Gene</i> , 2004, 343, 245-251.	1.0	31
54	The mutual information theory for the certification of rice coding sequences. <i>FEBS Letters</i> , 2004, 568, 155-158.	1.3	5

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55	Using analytical ultracentrifugation to study compositional variation in vertebrate genomes. <i>European Biophysics Journal</i> , 2003, 32, 418-426.	1.2	20
56	Genome Properties of the Diatom <i>Phaeodactylum tricornutum</i> . <i>Plant Physiology</i> , 2002, 129, 993-1002.	2.3	119
57	Compositional heterogeneity within and among isochores in mammalian genomes. <i>Gene</i> , 2001, 276, 15-24.	1.0	34
58	Compositional mapping of chicken chromosomes and identification of the gene-richest regions. <i>Chromosome Research</i> , 2001, 9, 521-532.	1.0	54
59	Diversity and Phylogenetic Implications of CsCl Profiles from Rodent DNAs. <i>Molecular Phylogenetics and Evolution</i> , 2000, 17, 219-230.	1.2	19
60	The compositional organization and the expression of the <i>Arabidopsis</i> genome. <i>FEBS Letters</i> , 2000, 472, 302-306.	1.3	15
61	Two Classes of Genes in Plants. <i>Genetics</i> , 2000, 154, 1819-1825.	1.2	162
62	Synonymous and Nonsynonymous Substitutions in Genes from Gramineae: Intragenic Correlations. <i>Journal of Molecular Evolution</i> , 1999, 49, 330-342.	0.8	12
63	Compositional Properties of Homologous Coding Sequences from Plants. <i>Journal of Molecular Evolution</i> , 1998, 46, 45-53.	0.8	65
64	The distribution of genes in the genomes of Gramineae. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 6857-6861.	3.3	162
65	The gene distribution of the maize genome.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 11057-11060.	3.3	53
66	Symptomatological and Morphological Study of the Resistance of Wild Beet Species of the <i>Patellares</i> Section to <i>Cercospora beticola</i> Sacc.. <i>Journal of Phytopathology</i> , 1990, 130, 317-330.	0.5	4
67	The Challenge of Bioenergies: An Overview. , 0, , .		4