

# Alberto De La Fuente

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11773784/publications.pdf>

Version: 2024-02-01

27  
papers

2,349  
citations

430874

18  
h-index

610901

24  
g-index

28  
all docs

28  
docs citations

28  
times ranked

4124  
citing authors

#	ARTICLE	IF	CITATIONS
1	Discovery of meaningful associations in genomic data using partial correlation coefficients. <i>Bioinformatics</i> , 2004, 20, 3565-3574.	4.1	476
2	From “differential expression” to “differential networking” – identification of dysfunctional regulatory networks in diseases. <i>Trends in Genetics</i> , 2010, 26, 326-333.	6.7	417
3	The origin of correlations in metabolomics data. <i>Metabolomics</i> , 2005, 1, 53-63.	3.0	248
4	Gene networks: how to put the function in genomics. <i>Trends in Biotechnology</i> , 2002, 20, 467-472.	9.3	241
5	Linking the genes: inferring quantitative gene networks from microarray data. <i>Trends in Genetics</i> , 2002, 18, 395-398.	6.7	149
6	Gene Network Inference via Structural Equation Modeling in Genetical Genomics Experiments. <i>Genetics</i> , 2008, 178, 1763-1776.	2.9	104
7	Methylomics of gene expression in human monocytes. <i>Human Molecular Genetics</i> , 2013, 22, 5065-5074.	2.9	95
8	Verification of systems biology research in the age of collaborative competition. <i>Nature Biotechnology</i> , 2011, 29, 811-815.	17.5	83
9	Alterations of a Cellular Cholesterol Metabolism Network Are a Molecular Feature of Obesity-Related Type 2 Diabetes and Cardiovascular Disease. <i>Diabetes</i> , 2015, 64, 3464-3474.	0.6	82
10	Protein networking: insights into global functional organization of proteomes. <i>Proteomics</i> , 2008, 8, 799-816.	2.2	74
11	From Knockouts to Networks: Establishing Direct Cause-Effect Relationships through Graph Analysis. <i>PLoS ONE</i> , 2010, 5, e12912.	2.5	68
12	Transcriptomic profiles of aging in purified human immune cells. <i>BMC Genomics</i> , 2015, 16, 333.	2.8	58
13	Towards functional phosphoproteomics by mapping differential phosphorylation events in signaling networks. <i>Proteomics</i> , 2008, 8, 4453-4465.	2.2	51
14	Simulating systems genetics data with SysGenSIM. <i>Bioinformatics</i> , 2011, 27, 2459-2462.	4.1	31
15	Dissecting the dynamics of dysregulation of cellular processes in mouse mammary gland tumor. <i>BMC Genomics</i> , 2009, 10, 601.	2.8	28
16	Integrating Omics Data for Signaling Pathways, Interactome Reconstruction, and Functional Analysis. <i>Methods in Molecular Biology</i> , 2011, 719, 415-433.	0.9	24
17	Inferring Gene Networks: Dream or Nightmare?. <i>Annals of the New York Academy of Sciences</i> , 2009, 1158, 246-256.	3.8	23
18	Linking the proteins – Elucidation of proteome-scale networks using mass spectrometry. <i>Mass Spectrometry Reviews</i> , 2011, 30, 268-297.	5.4	23

#	ARTICLE	IF	CITATIONS
19	Silence on the relevant literature and errors in implementation. <i>Nature Biotechnology</i> , 2015, 33, 336-339.	17.5	14
20	Quantifying gene networks with regulatory strengths. <i>Molecular Biology Reports</i> , 2002, 29, 73-77.	2.3	13
21	Inferring Gene Networks: Dream or Nightmare?. <i>Annals of the New York Academy of Sciences</i> , 2009, 1158, 287-301.	3.8	12
22	Network-Assisted Disease Classification and Biomarker Discovery. <i>Methods in Molecular Biology</i> , 2016, 1386, 353-374.	0.9	11
23	Reconstruction of large-scale regulatory networks based on perturbation graphs and transitive reduction: improved methods and their evaluation. <i>BMC Systems Biology</i> , 2013, 7, 73.	3.0	9
24	What are Gene Regulatory Networks?. , 2010, , 1-27.		9
25	Inferring Gene Regulatory Networks from Genetical Genomics Data. , 2010, , 79-107.		4
26	sbv IMPROVER Diagnostic Signature Challenge. <i>Systems Biomedicine (Austin, Tex )</i> , 2013, 1, 208-216.	0.7	2
27	Condensing Biochemistry into Gene Regulatory Networks. <i>International Journal of Natural Computing Research</i> , 2014, 4, 1-25.	0.5	0