

Ettore Mosca

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

1,087
citations

516710

16
h-index

434195

31
g-index

51
all docs

51
docs citations

51
times ranked

2543
citing authors

#	ARTICLE	IF	CITATIONS
1	Analysis of Faecal Microbiota and Small ncRNAs in Autism: Detection of miRNAs and piRNAs with Possible Implications in Host-Gut Microbiota Cross-Talk. <i>Nutrients</i> , 2022, 14, 1340.	4.1	6
2	A novel expressed prostatic secretion (EPS)-urine metabolomic signature for the diagnosis of clinically significant prostate cancer. <i>Cancer Biology and Medicine</i> , 2021, 18, 604-615.	3.0	4
3	Multi-omic analyses in Abyssinian cats with primary renal amyloid deposits. <i>Scientific Reports</i> , 2021, 11, 8339.	3.3	6
4	Classification and Personalized Prognostic Assessment on the Basis of Clinical and Genomic Features in Myelodysplastic Syndromes. <i>Journal of Clinical Oncology</i> , 2021, 39, 1223-1233.	1.6	127
5	Characterization and comparison of gene-centered human interactomes. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	9
6	Clinical relevance of clonal hematopoiesis in persons aged ≥ 80 years. <i>Blood</i> , 2021, 138, 2093-2105.	1.4	37
7	Gene relevance based on multiple evidences in complex networks. <i>Bioinformatics</i> , 2020, 36, 865-871.	4.1	6
8	Profiling the Course of Resolving vs. Persistent Inflammation in Human Monocytes: The Role of IL-1 Family Molecules. <i>Frontiers in Immunology</i> , 2020, 11, 1426.	4.8	18
9	Assessment of haptoglobin alleles in autism spectrum disorders. <i>Scientific Reports</i> , 2020, 10, 7758.	3.3	2
10	Network Diffusion Promotes the Integrative Analysis of Multiple Omics. <i>Frontiers in Genetics</i> , 2020, 11, 106.	2.3	21
11	Frailness and resilience of gene networks predicted by detection of co-occurring mutations via a stochastic perturbative approach. <i>Scientific Reports</i> , 2020, 10, 2643.	3.3	3
12	Network-Based Integrative Analysis of Genomics, Epigenomics and Transcriptomics in Autism Spectrum Disorders. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3363.	4.1	8
13	The role of extracellular matrix in mouse and human corneal neovascularization. <i>Scientific Reports</i> , 2019, 9, 14272.	3.3	20
14	isma: an R package for the integrative analysis of mutations detected by multiple pipelines. <i>BMC Bioinformatics</i> , 2019, 20, 107.	2.6	5
15	Network Diffusion-Based Prioritization of Autism Risk Genes Identifies Significantly Connected Gene Modules. <i>Frontiers in Genetics</i> , 2017, 8, 129.	2.3	20
16	Network diffusion-based analysis of high-throughput data for the detection of differentially enriched modules. <i>Scientific Reports</i> , 2016, 6, 34841.	3.3	31
17	Methods for the integration of multi-omics data: mathematical aspects. <i>BMC Bioinformatics</i> , 2016, 17, 15.	2.6	316
18	Stochastic neutral modelling of the Gut Microbiota's relative species abundance from next generation sequencing data. <i>BMC Bioinformatics</i> , 2016, 17, 16.	2.6	19

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19	Systems medicine of inflammaging. <i>Briefings in Bioinformatics</i> , 2016, 17, 527-540.	6.5	35
20	Parallel Solutions for Voxel-Based Simulations of Reaction-Diffusion Systems. <i>BioMed Research International</i> , 2014, 2014, 1-10.	1.9	8
21	A CUDA Implementation of the Spatial TAU-Leaping in Crowded Compartments (STAUCC) Simulator. , 2014, , .		0
22	Geometric and Computational Models of Chromatin Fibre Folding for Human Embryonic Stem Cells. <i>Procedia, Social and Behavioral Sciences</i> , 2014, 108, 296-305.	0.5	1
23	Diffusion of Information throughout the Host Interactome Reveals Gene Expression Variations in Network Proximity to Target Proteins of Hepatitis C Virus. <i>PLoS ONE</i> , 2014, 9, e113660.	2.5	11
24	SNPranker 2.0: a gene-centric data mining tool for diseases associated SNP prioritization in GWAS. <i>BMC Bioinformatics</i> , 2013, 14, S9.	2.6	23
25	Decreased Transcriptional Activity of Calcium-sensing receptor Gene Promoter 1 Is Associated With Calcium Nephrolithiasis. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2013, 98, 3839-3847.	3.6	49
26	Network-based analysis of omics with multi-objective optimization. <i>Molecular BioSystems</i> , 2013, 9, 2971.	2.9	16
27	A Parallel Implementation of the Stau-DPP Stochastic Simulator for the Modelling of Biological Systems. , 2013, , .		2
28	SENSITIVITY ANALYSIS FOR STUDYING THE RELATION BETWEEN BIOCHEMICAL REACTIONS AND METABOLIC PHENOTYPES. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1340002.	0.8	2
29	Data Integration, Breast Cancer Database. , 2013, , 523-524.		0
30	Computational Modeling of the Metabolic States Regulated by the Kinase Akt. <i>Frontiers in Physiology</i> , 2012, 3, 418.	2.8	20
31	Systems biology of the metabolic network regulated by the Akt pathway. <i>Biotechnology Advances</i> , 2012, 30, 131-141.	11.7	37
32	Ontology-based resources for bioinformatics analysis. <i>International Journal of Metadata, Semantics and Ontologies</i> , 2011, 6, 35.	0.2	3
33	Modeling Biochemical Pathways. , 2011, , 111-126.		0
34	Overlapping Genes May Control Reprogramming of Mouse Somatic Cells into Induced Pluripotent Stem Cells (iPSCs) and Breast Cancer Stem Cells. <i>In Silico Biology</i> , 2010, 10, 207-221.	0.9	6
35	SNPranker: a tool for identification and scoring of SNPs associated to target genes. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, 331-345.	1.5	4
36	A multilevel data integration resource for breast cancer study. <i>BMC Systems Biology</i> , 2010, 4, 76.	3.0	85

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37	A systems biology approach for the identification of glycolysis key regulators in cancer cells. Journal of Biotechnology, 2010, 150, 545-546.	3.8	0
38	Calcium kidney stones are associated with a haplotype of the calcium-sensing receptor gene regulatory region. Nephrology Dialysis Transplantation, 2010, 25, 2245-2252.	0.7	47
39	A Novel Variant of P Systems for the Modelling and Simulation of Biochemical Systems. Lecture Notes in Computer Science, 2010, , 210-226.	1.3	3
40	Modelling Spatial Heterogeneity and Macromolecular Crowding with Membrane Systems. Lecture Notes in Computer Science, 2010, , 285-304.	1.3	6
41	SNPRanker: a tool for identification and scoring of SNPs associated to target genes. Journal of Integrative Bioinformatics, 2010, 7, .	1.5	4
42	Identification of functionally related genes using data mining and data integration: a breast cancer case study. BMC Bioinformatics, 2009, 10, S8.	2.6	20
43	Stochastic Simulations on a Grid Framework for Parameter Sweep Applications in Biological Models. , 2009, , .		5
44	Ontological Enrichment of the Genes-to-Systems Breast Cancer Database. Communications in Computer and Information Science, 2009, , 171-182.	0.5	1
45	The cell cycle DB: a systems biology approach to cell cycle analysis. Nucleic Acids Research, 2007, 36, D641-D645.	14.5	12
46	A data integration approach for cell cycle analysis oriented to model simulation in systems biology. BMC Systems Biology, 2007, 1, 35.	3.0	23
47	Clinical Relevance of Clonal Hematopoiesis in the Oldest-Old Population. SSRN Electronic Journal, 0, , .	0.4	0