Alberto Magi

List of Publications by Year
in descending order

72	2,294	257450 24	243625 44
papers	citations	h-index	g-index

78	78	78	5918
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Third-Generation Cytogenetic Analysis. Journal of Molecular Diagnostics, 2022, 24, 711-718.	2.8	4
2	Heterogeneous magnitude of immunological memory to SARSâ€CoVâ€2 in recovered individuals. Clinical and Translational Immunology, 2021, 10, e1281.	3.8	19
3	Nanopore sequencing from liquid biopsy: analysis of copy number variations from cell-free DNA of lung cancer patients. Molecular Cancer, 2021, 20, 32.	19.2	27
4	Effect of space flight on the behavior of human retinal pigment epithelial ARPE-19 cells and evaluation of coenzyme Q10 treatment. Cellular and Molecular Life Sciences, 2021, 78, 7795-7812.	5.4	11
5	Charting differentially methylated regions in cancer with Rocker-meth. Communications Biology, 2021, 4, 1249.	4.4	7
6	Evaluation of Germline Structural Variant Calling Methods for Nanopore Sequencing Data. Frontiers in Genetics, 2021, 12, 761791.	2.3	12
7	VISOR: a versatile haplotype-aware structural variant simulator for short- and long-read sequencing. Bioinformatics, 2020, 36, 1267-1269.	4.1	29
8	AUDACITY: A comprehensive approach for the detection and classification of Runs of Homozygosity in medical and population genomics. Computational and Structural Biotechnology Journal, 2020, 18, 1956-1967.	4.1	3
9	TRiCoLOR: tandem repeat profiling using whole-genome long-read sequencing data. GigaScience, 2020, 9, .	6.4	15
10	TRPA1 mediates damage of the retina induced by ischemia and reperfusion in mice. Cell Death and Disease, 2020, 11, 633.	6.3	28
11	Sanger Validation of High-Throughput Sequencing in Genetic Diagnosis: Still the Best Practice?. Frontiers in Genetics, 2020, 11, 592588.	2.3	20
12	Genetic and nutritional factors determining circulating levels of lipoprotein(a): results of the â€œMontignoso Studyâ€. Internal and Emergency Medicine, 2020, 15, 1239-1245.	2.0	1
13	Versatile Quality Control Methods for Nanopore Sequencing. Evolutionary Bioinformatics, 2019, 15, 117693431986306.	1.2	1
14	Long Reads, Short Time: Feasibility of Prenatal Sample Karyotyping by Nanopore Genome Sequencing. Clinical Chemistry, 2019, 65, 1605-1608.	3.2	4
15	The ion channels and transporters gene expression profile indicates a shift in excitability and metabolisms during malignant progression of Follicular Lymphoma. Scientific Reports, 2019, 9, 8586.	3.3	20
16	NanoR: A user-friendly R package to analyze and compare nanopore sequencing data. PLoS ONE, 2019, 14, e0216471.	2.5	17
17	PyPore: a python toolbox for nanopore sequencing data handling. Bioinformatics, 2019, 35, 4445-4447.	4.1	9
18	A microRNA profile of pediatric glioblastoma: The role of NUCKS1 upregulation. Molecular and Clinical Oncology, 2019, 10, 331-338.	1.0	13

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19	RNA sequencing reveals PNN and KCNQ1OT1 as predictive biomarkers of clinical outcome in stage III colorectal cancer patients treated with adjuvant chemotherapy. International Journal of Cancer, 2019, 145, 2580-2593.	5.1	26
20	Nano-GLADIATOR: real-time detection of copy number alterations from nanopore sequencing data. Bioinformatics, 2019, 35, 4213-4221.	4.1	15
21	Involvement of RUNX1 Pathway Is a Common Event in the Leukemic Transformation of Chronic Myeloproliferative Neoplasms (MPNs). Blood, 2019, 134, 2968-2968.	1.4	4
22	Nanopore sequencing data analysis: state of the art, applications and challenges. Briefings in Bioinformatics, 2018, 19, 1256-1272.	6.5	91
23	A new hybrid approach for MHC genotyping: high-throughput NGS and long read MinION nanopore sequencing, with application to the non-model vertebrate Alpine chamois (Rupicapra rupicapra). Heredity, 2018, 121, 293-303.	2.6	25
24	Precision Trial Drawer, a Computational Tool to Assist Planning of Genomics-Driven Trials in Oncology. JCO Precision Oncology, 2018, 2, 1-16.	3.0	2
25	Bicuspid Aortic Valve: Role of Multiple Gene Variants in Influencing the Clinical Phenotype. BioMed Research International, 2018, 2018, 1-9.	1.9	6
26	The Coenzyme Q10 (CoQ10) as Countermeasure for Retinal Damage Onboard the International Space Station: the CORM Project. Microgravity Science and Technology, 2018, 30, 925-931.	1.4	3
27	Xome-Blender: A novel cancer genome simulator. PLoS ONE, 2018, 13, e0194472.	2.5	14
28	Using XCAVATOR and EXCAVATOR2 to Identify CNVs from WGS, WES, and TS Data. Current Protocols in Human Genetics, 2018, 98, e65.	3.5	7
29	Comparative Genomic and Expression Analysis of Chronic and Blast-Phase Cells in Patients with Myeloproliferative Neoplasms. Blood, 2018, 132, 1777-1777.	1.4	0
30	Large Genomic Alterations Occurring in the Transition from Chronic to Blast Phase of Chronic Myeloproliferative Neoplasms. Blood, 2018, 132, 3028-3028.	1.4	0
31	Characterization of MinION nanopore data for resequencing analyses. Briefings in Bioinformatics, 2017, 18, bbw077.	6.5	55
32	Exome sequencing of two Italian pedigrees with non-isolated Chiari malformation type I reveals candidate genes for cranio-facial development. European Journal of Human Genetics, 2017, 25, 952-959.	2.8	18
33	SLMSuite: a suite of algorithms for segmenting genomic profiles. BMC Bioinformatics, 2017, 18, 321.	2.6	3
34	A novel founder MYO15A frameshift duplication is the major cause of genetic hearing loss in Oman. Journal of Human Genetics, 2017, 62, 259-264.	2.3	21
35	GENE-03. MICRORNAS PROFILE IN PAEDIATRIC GBMS. Neuro-Oncology, 2017, 19, iv18-iv18.	1.2	1
36	Genetic Bases of Bicuspid Aortic Valve: The Contribution of Traditional and High-Throughput Sequencing Approaches on Research and Diagnosis. Frontiers in Physiology, 2017, 8, 612.	2.8	57

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37	XCAVATOR: accurate detection and genotyping of copy number variants from second and third generation whole-genome sequencing experiments. BMC Genomics, 2017, 18, 747.	2.8	29
38	Editorial: Repetitive Structures in Biological Sequences: Algorithms and Applications. Frontiers in Bioengineering and Biotechnology, 2016, 4, 66.	4.1	0
39	Apolipoprotein(a) Kringle-IV Type 2 Copy Number Variation Is Associated with Venous Thromboembolism. PLoS ONE, 2016, 11, e0149427.	2.5	24
40	Enhanced copy number variants detection from whole-exome sequencing data using EXCAVATOR2. Nucleic Acids Research, 2016, 44, gkw695.	14.5	75
41	Epilepsy with auditory features. Neurology: Genetics, 2015, 1, e5.	1.9	55
42	Detection of Genomic Structural Variants from Next-Generation Sequencing Data. Frontiers in Bioengineering and Biotechnology, 2015, 3, 92.	4.1	212
43	Characterization and identification of hidden rare variants in the human genome. BMC Genomics, 2015, 16, 340.	2.8	24
44	Detection of Runs of Homozygosity from Whole Exome Sequencing Data: State of the Art and Perspectives for Clinical, Population and Epidemiological Studies. Human Heredity, 2014, 77, 63-72.	0.8	21
45	H Â3 ÂM Â2 : detection of runs of homozygosity from whole-exome sequencing data. Bioinformatics, 2014, 30, 2852-2859.	4.1	88
46	Genome-wide copy number analysis in pediatric glioblastoma multiforme. American Journal of Cancer Research, 2014, 4, 293-303.	1.4	10
47	A systematic analysis of bone marrow cells by flow cytometry defines a specific phenotypic profile beyond GPI deficiency in paroxysmal nocturnal hemoglobinuria. Cytometry Part B - Clinical Cytometry, 2013, 84B, 71-81.	1.5	7
48	Moment estimation in discrete shifting level model applied to fast arrayâ€CGH segmentation. Statistica Neerlandica, 2013, 67, 227-262.	1.6	0
49	EXCAVATOR: detecting copy number variants from whole-exome sequencing data. Genome Biology, 2013, 14, R120.	9.6	213
50	Desmoglein-2-Integrin Beta-8 Interaction Regulates Actin Assembly in Endothelial Cells: Deregulation in Systemic Sclerosis. PLoS ONE, 2013, 8, e68117.	2.5	27
51	Discovering chimeric transcripts in paired-end RNA-seq data by using EricScript. Bioinformatics, 2012, 28, 3232-3239.	4.1	154
52	Clinical Significance of Rare Copy Number Variations in Epilepsy. Archives of Neurology, 2012, 69, 322.	4.5	61
53	Genetic polymorphisms of antioxidant enzymes as risk factors for oxidative stress-associated complications in preterm infants. Free Radical Research, 2012, 46, 1130-1139.	3.3	43
54	372Âkb microdeletion in 18q12.3 causing SETBP1 haploinsufficiency associated with mild mental retardation and expressive speech impairment. European Journal of Medical Genetics, 2012, 55, 216-221.	1.3	55

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55	WNP: A Novel Algorithm for Gene Products Annotation from Weighted Functional Networks. PLoS ONE, 2012, 7, e38767.	2.5	5
56	Read count approach for DNA copy number variants detection. Bioinformatics, 2012, 28, 470-478.	4.1	67
57	EX-HOM (EXome HOMozygosity): A Proof of Principle. Human Heredity, 2011, 72, 45-53.	0.8	27
58	Sphingosine 1-Phosphate Induces Differentiation of Mesoangioblasts towards Smooth Muscle. A Role for GATA6. PLoS ONE, 2011, 6, e20389.	2.5	23
59	Detecting common copy number variants in high-throughput sequencing data by using JointSLM algorithm. Nucleic Acids Research, 2011, 39, e65-e65.	14.5	63
60	Carotid Artery Disease: Novel Pathophysiological Mechanisms Identified by Gene-expression Profiling of Peripheral Blood. European Journal of Vascular and Endovascular Surgery, 2010, 40, 549-558.	1.5	2
61	A very fast and accurate method for calling aberrations in array-CGH data. Biostatistics, 2010, 11, 515-518.	1.5	16
62	Early-onset ischaemic stroke: Analysis of 58 polymorphisms in 17 genes involved in methionine metabolism. Thrombosis and Haemostasis, 2010, 104, 231-242.	3.4	35
63	A shifting level model algorithm that identifies aberrations in array-CGH data. Biostatistics, 2010, 11, 265-280.	1.5	26
64	Assessment of Fibrinolytic Activity by Measuring the Lysis Time of a Tissue Factor-induced Clot: A Feasibility Evaluation. Clinical and Applied Thrombosis/Hemostasis, 2010, 16, 337-344.	1.7	12
65	Bioinformatics for Next Generation Sequencing Data. Genes, 2010, 1, 294-307.	2.4	65
66	Gene expression profile of rat left ventricles reveals persisting changes following chronic mild exercise protocol: implications for cardioprotection. BMC Genomics, 2009, 10, 342.	2.8	22
67	Gene Expression Profiling of Peripheral Blood in Patients with Abdominal Aortic Aneurysm. European Journal of Vascular and Endovascular Surgery, 2009, 38, 104-112.	1.5	42
68	High-Throughput Multiplex Single-Nucleotide Polymorphism (SNP) Analysis in Genes Involved in Methionine Metabolism. Biochemical Genetics, 2008, 46, 406-423.	1.7	7
69	Genetic analysis of 56 polymorphisms in 17 genes involved in methionine metabolism in patients with abdominal aortic aneurysm. Journal of Medical Genetics, 2008, 45, 721-730.	3.2	63
70	A model of anti-angiogenesis: differential transcriptosome profiling of microvascular endothelial cells from diffuse systemic sclerosis patients. Arthritis Research and Therapy, 2006, 8, R115.	3.5	56
71	Using a calibration experiment to assess gene-specific information: full Bayesian and empirical Bayesian models for two-channel microarray data. Bioinformatics, 2006, 22, 50-57.	4.1	8
72	The antiangiogenic tissue kallikrein pattern of endothelial cells in systemic sclerosis. Arthritis and Rheumatism, 2005, 52, 3618-3628.	6.7	55