

Ivan Merelli

List of Publications by Year in descending order

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Version: 2024-02-01

131
papers

1,888
citations

279487

23
h-index

315357

38
g-index

133
all docs

133
docs citations

133
times ranked

2875
citing authors

#	ARTICLE	IF	CITATIONS
1	Precise Gene Editing Preserves Hematopoietic Stem Cell Function following Transient p53-Mediated DNA Damage Response. <i>Cell Stem Cell</i> , 2019, 24, 551-565.e8.	5.2	237
2	Managing, Analysing, and Integrating Big Data in Medical Bioinformatics: Open Problems and Future Perspectives. <i>BioMed Research International</i> , 2014, 2014, 1-13.	0.9	118
3	Efficient gene editing of human long-term hematopoietic stem cells validated by clonal tracking. <i>Nature Biotechnology</i> , 2020, 38, 1298-1308.	9.4	116
4	A multilevel data integration resource for breast cancer study. <i>BMC Systems Biology</i> , 2010, 4, 76.	3.0	85
5	HIV-1-mediated insertional activation of STAT5B and BACH2 trigger viral reservoir in T regulatory cells. <i>Nature Communications</i> , 2017, 8, 498.	5.8	78
6	RSSsite: a reference database and prediction tool for the identification of cryptic Recombination Signal Sequences in human and murine genomes. <i>Nucleic Acids Research</i> , 2010, 38, W262-W267.	6.5	76
7	DnaK as Antibiotic Target: Hot Spot Residues Analysis for Differential Inhibition of the Bacterial Protein in Comparison with the Human HSP70. <i>PLoS ONE</i> , 2015, 10, e0124563.	1.1	59
8	Molecular Mechanism of Allosteric Communication in Hsp70 Revealed by Molecular Dynamics Simulations. <i>PLoS Computational Biology</i> , 2012, 8, e1002844.	1.5	49
9	NuChart: An R Package to Study Gene Spatial Neighbourhoods with Multi-Omics Annotations. <i>PLoS ONE</i> , 2013, 8, e75146.	1.1	42
10	Modeling, optimization, and comparable efficacy of T cell and hematopoietic stem cell gene editing for treating hyperæmoglobinemia syndrome. <i>EMBO Molecular Medicine</i> , 2021, 13, e13545.	3.3	36
11	Grid-Enabled High-Throughput In Silico Screening Against Influenza A Neuraminidase. <i>IEEE Transactions on Nanobioscience</i> , 2006, 5, 288-295.	2.2	35
12	DNA damage contributes to neurotoxic inflammation in Aicardi-Goutières syndrome astrocytes. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	35
13	Combining Edge and Cloud computing for low-power, cost-effective metagenomics analysis. <i>Future Generation Computer Systems</i> , 2019, 90, 79-85.	4.9	32
14	Targeted inducible delivery of immunoactivating cytokines reprograms glioblastoma microenvironment and inhibits growth in mouse models. <i>Science Translational Medicine</i> , 2022, 14, .	5.8	32
15	An atomistic view of Hsp70 allosteric crosstalk: from the nucleotide to the substrate binding domain and back. <i>Scientific Reports</i> , 2016, 6, 23474.	1.6	31
16	Virtual screening on large scale grids. <i>Parallel Computing</i> , 2007, 33, 289-301.	1.3	27
17	Static and dynamic interactions between GALK enzyme and known inhibitors: Guidelines to design new drugs for galactosemic patients. <i>European Journal of Medicinal Chemistry</i> , 2013, 63, 423-434.	2.6	27
18	StreamFlow: Cross-Breeding Cloud With HPC. <i>IEEE Transactions on Emerging Topics in Computing</i> , 2021, 9, 1723-1737.	3.2	27

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19	GenHap: a novel computational method based on genetic algorithms for haplotype assembly. BMC Bioinformatics, 2019, 20, 172.	1.2	26
20	Structural thermal adaptation of β -tubulins from the Antarctic psychrophilic protozoan <i>Euplotes focardii</i> . Proteins: Structure, Function and Bioinformatics, 2012, 80, 1154-1166.	1.5	25
21	Cloud Infrastructures for In Silico Drug Discovery: Economic and Practical Aspects. BioMed Research International, 2013, 2013, 1-19.	0.9	25
22	Low-power portable devices for metagenomics analysis: Fog computing makes bioinformatics ready for the Internet of Things. Future Generation Computer Systems, 2018, 88, 467-478.	4.9	25
23	In silico saturation mutagenesis and docking screening for the analysis of protein-ligand interaction: the Endothelial Protein C Receptor case study. BMC Bioinformatics, 2009, 10, S3.	1.2	24
24	A data integration approach for cell cycle analysis oriented to model simulation in systems biology. BMC Systems Biology, 2007, 1, 35.	3.0	23
25	myMIR: a genome-wide microRNA targets identification and annotation tool. Briefings in Bioinformatics, 2011, 12, 588-600.	3.2	23
26	SNPranker 2.0: a gene-centric data mining tool for diseases associated SNP prioritization in GWAS. BMC Bioinformatics, 2013, 14, S9.	1.2	23
27	VISPA2: a scalable pipeline for high-throughput identification and annotation of vector integration sites. BMC Bioinformatics, 2017, 18, 520.	1.2	23
28	Hematopoietic stem cell function in β -thalassemia is impaired and is rescued by targeting the bone marrow niche. Blood, 2020, 136, 610-622.	0.6	23
29	Version VI of the ESTree db: an improved tool for peach transcriptome analysis. BMC Bioinformatics, 2008, 9, S9.	1.2	22
30	Image-Based Surface Matching Algorithm Oriented to Structural Biology. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 1004-1016.	1.9	22
31	The Genome Conformation As an Integrator of Multi-Omic Data: The Example of Damage Spreading in Cancer. Frontiers in Genetics, 2016, 7, 194.	1.1	22
32	A sentence sliding window approach to extract protein annotations from biomedical articles. BMC Bioinformatics, 2005, 6, S19.	1.2	18
33	Integration of Machine Learning Methods to Dissect Genetically Imputed Transcriptomic Profiles in Alzheimer's Disease. Frontiers in Genetics, 2019, 10, 726.	1.1	18
34	Virtual screening pipeline and ligand modelling for H5N1 neuraminidase. Biochemical and Biophysical Research Communications, 2009, 383, 445-449.	1.0	17
35	Association Analysis of Noncoding Variants in Neuroligins 3 and 4X Genes with Autism Spectrum Disorder in an Italian Cohort. International Journal of Molecular Sciences, 2016, 17, 1765.	1.8	16
36	A novel molecular dynamics approach to evaluate the effect of phosphorylation on multimeric protein interface: the β -Crystallin case study. BMC Bioinformatics, 2016, 17, 57.	1.2	15

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37	Ontology-based, Tissue MicroArray oriented, image centered tissue bank. BMC Bioinformatics, 2008, 9, S4.	1.2	13
38	The cell cycle DB: a systems biology approach to cell cycle analysis. Nucleic Acids Research, 2007, 36, D641-D645.	6.5	12
39	IBDsite: a Galaxy-interacting, integrative database for supporting inflammatory bowel disease high throughput data analysis. BMC Bioinformatics, 2012, 13, S5.	1.2	12
40	High parathyroid hormone concentration in tenofovir-treated patients are due to inhibition of calcium-sensing receptor activity. Biomedicine and Pharmacotherapy, 2018, 97, 969-974.	2.5	12
41	SoC-based computing infrastructures for scientific applications and commercial services: Performance and economic evaluations. Future Generation Computer Systems, 2019, 96, 11-22.	4.9	12
42	Advances in distributed computing with modern drug discovery. Expert Opinion on Drug Discovery, 2019, 14, 9-22.	2.5	12
43	Portals and Web-Based Resources for Virtual Screening. Current Drug Targets, 2016, 17, 1649-1660.	1.0	12
44	Exploring the role of the phospholipid ligand in endothelial protein C receptor: A molecular dynamics study. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2679-2690.	1.5	11
45	Integrating multi-omic features exploiting Chromosome Conformation Capture data. Frontiers in Genetics, 2015, 6, 40.	1.1	11
46	PWHATSHAP: efficient haplotyping for future generation sequencing. BMC Bioinformatics, 2016, 17, 342.	1.2	11
47	BAR-Seq clonal tracking of gene-edited cells. Nature Protocols, 2021, 16, 2991-3025.	5.5	11
48	How computer science can help in understanding the 3D genome architecture. Briefings in Bioinformatics, 2016, 17, 733-744.	3.2	10
49	Oncogene-induced maladaptive activation of trained immunity in the pathogenesis and treatment of Erdheim-Chester disease. Blood, 2021, 138, 1554-1569.	0.6	10
50	ChromStruct 4: A Python Code to Estimate the Chromatin Structure from Hi-C Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, , 1-1.	1.9	9
51	Follicular helper T cell signature of replicative exhaustion, apoptosis, and senescence in common variable immunodeficiency. European Journal of Immunology, 2022, 52, 1171-1189.	1.6	9
52	GoSh: a web-based database for goat and sheep EST sequences. Bioinformatics, 2007, 23, 1043-1045.	1.8	8
53	Ontology-oriented retrieval of putative microRNAs in Vitis vinifera via GrapeMiRNA: a web database of de novo predicted grape microRNAs. BMC Plant Biology, 2009, 9, 82.	1.6	8
54	High-Performance Computing and Big Data in Omics-Based Medicine. BioMed Research International, 2014, 2014, 1-2.	0.9	8

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55	Parallel Solutions for Voxel-Based Simulations of Reaction-Diffusion Systems. <i>BioMed Research International</i> , 2014, 2014, 1-10.	0.9	8
56	Î³-TRIS: a graph-algorithm for comprehensive identification of vector genomic insertion sites. <i>Bioinformatics</i> , 2020, 36, 1622-1624.	1.8	7
57	Evaluation of a Grid Based Molecular Dynamics Approach for Polypeptide Simulations. <i>IEEE Transactions on Nanobioscience</i> , 2007, 6, 229-234.	2.2	6
58	High performance cDNA sequence analysis using grid technology. <i>Journal of Parallel and Distributed Computing</i> , 2006, 66, 1482-1488.	2.7	5
59	Stochastic Simulations on a Grid Framework for Parameter Sweep Applications in Biological Models. , 2009, , .		5
60	Latest advances in distributed, parallel, and graphic processing unit accelerated approaches to computational biology. <i>Concurrency Computation Practice and Experience</i> , 2014, 26, 1699-1704.	1.4	5
61	A secure cloud-edges computing architecture for metagenomics analysis. <i>Future Generation Computer Systems</i> , 2020, 111, 919-930.	4.9	5
62	High performance workflow implementation for protein surface characterization using grid technology. <i>BMC Bioinformatics</i> , 2005, 6, S19.	1.2	4
63	Using Parallel Isosurface Extraction in Superficial Molecular Modeling. , 0, , .		4
64	Images Based System for Surface Matching in Macromolecular Screening. , 2008, , .		4
65	A parallel protein surface reconstruction system. <i>International Journal of Bioinformatics Research and Applications</i> , 2008, 4, 221.	0.1	4
66	SNPRanker: a tool for identification and scoring of SNPs associated to target genes. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, 331-345.	1.0	4
67	CUDA accelerated molecular surface generation. <i>Concurrency Computation Practice and Experience</i> , 2014, 26, 1819-1831.	1.4	4
68	SPIRE, a modular pipeline for eQTL analysis of RNA-Seq data, reveals a regulatory hotspot controlling miRNA expression in <i>C. elegans</i> . <i>Molecular BioSystems</i> , 2016, 12, 3447-3458.	2.9	4
69	NuChart-II: The road to a fast and scalable tool for Hi-C data analysis. <i>International Journal of High Performance Computing Applications</i> , 2017, 31, 196-211.	2.4	4
70	Exploiting Docker containers over Grid computing for a comprehensive study of chromatin conformation in different cell types. <i>Journal of Parallel and Distributed Computing</i> , 2019, 134, 116-127.	2.7	4
71	SNPRanker: a tool for identification and scoring of SNPs associated to target genes. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.0	4
72	Representation and Modeling of Protein Surface Determinants. <i>IEEE Transactions on Nanobioscience</i> , 2005, 4, 301-305.	2.2	3

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73	Ontology-based resources for bioinformatics analysis. International Journal of Metadata, Semantics and Ontologies, 2011, 6, 35.	0.2	3
74	Parallel Exploration of the Nuclear Chromosome Conformation with NuChart-II. , 2015, , .		3
75	Implementing a Space-Aware Stochastic Simulator on Low-Power Architectures: A Systems Biology Case Study. , 2017, , .		3
76	Improving eQTL Analysis Using a Machine Learning Approach for Data Integration: A Logistic Model Tree Solution. Journal of Computational Biology, 2018, 25, 1091-1105.	0.8	3
77	BGBlast: a BLAST grid implementation with database self-updating and adaptive replication. Studies in Health Technology and Informatics, 2007, 126, 23-30.	0.2	3
78	TMAinspect, an EGEE Framework for Tissue MicroArray Image Handling. , 2008, , .		2
79	Parallel Decomposition of 3D Surfaces in Images of Local Descriptors for Molecular Screening. , 2009, , .		2
80	Semi-automatic identification of punching areas for tissue microarray building: the tubular breast cancer pilot study. BMC Bioinformatics, 2010, 11, 566.	1.2	2
81	Parallelization of the SSAKE Genomics Application. , 2011, , .		2
82	A Parallel Implementation of the Stau-DPP Stochastic Simulator for the Modelling of Biological Systems. , 2013, , .		2
83	SENSITIVITY ANALYSIS FOR STUDYING THE RELATION BETWEEN BIOCHEMICAL REACTIONS AND METABOLIC PHENOTYPES. Journal of Bioinformatics and Computational Biology, 2013, 11, 1340002.	0.3	2
84	The WNoDeS Cloud Virtualization Framework: A Macromolecular Surface Analysis Application Case Study. , 2014, , .		2
85	A Machine Learning Approach for the Integration of miRNA-Target Predictions. , 2016, , .		2
86	Clustering Protein Structures with Hadoop. Lecture Notes in Computer Science, 2016, , 141-153.	1.0	2
87	NuchaRt: Embedding High-Level Parallel Computing in R for Augmented Hi-C Data Analysis. Lecture Notes in Computer Science, 2016, , 259-272.	1.0	2
88	Porting bioinformatics applications from grid to cloud: A macromolecular surface analysis application case study. International Journal of High Performance Computing Applications, 2017, 31, 182-195.	2.4	2
89	Rank miRNA: a web tool for identifying polymorphisms altering miRNA target sites. Procedia Computer Science, 2017, 108, 1125-1134.	1.2	2
90	Infrastructure for High-Performance Computing: Grids and Grid Computing. , 2019, , 230-235.		2

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91	Latest advances in parallel, distributed, and network-based processing. Concurrency Computation Practice and Experience, 2020, 32, e5683.	1.4	2
92	Hardware and Software Solutions for Energy-Efficient Computing in Scientific Programming. Scientific Programming, 2021, 2021, 1-9.	0.5	2
93	Performance and Economic Evaluations in Adopting Low Power Architectures: A Real Case Analysis. Lecture Notes in Computer Science, 2017, , 177-189.	1.0	2
94	Grid-Enabled High Throughput Virtual Screening. , 2007, , 45-59.		2
95	HPC Analysis of Multiple Binding Sites Communication and Allosteric Modulations in Drug Design: The HSP Case Study. Current Drug Targets, 2016, 17, 1610-1625.	1.0	2
96	Functional Genomics Applications in GRID. , 2012, , 899-917.		2
97	Mining the Bovine Genome with the "Bovine SNP Retriever". Journal of Heredity, 2008, 99, 696-698.	1.0	1
98	Enabling Parallel TMA Image Analysis in a Grid Environment. , 2008, , .		1
99	The Human EST Ontology Explorer: a tissue-oriented visualization system for ontologies distribution in human EST collections. BMC Bioinformatics, 2009, 10, S2.	1.2	1
100	Editorial: High Performance Computing in Drug Discovery. Current Drug Targets, 2016, 17, 1578-1579.	1.0	1
101	MicroRNA-Target Interaction: A Parallel Approach for Computing Pairing Energy. , 2016, , .		1
102	Low-Power Architectures for miRNA-Target Genome Wide Analysis. , 2017, , .		1
103	A Scalable Genetic Programming Approach to Integrate miRNA-Target Predictions: Comparing Different Parallel Implementations of M3GP. Complexity, 2018, 2018, 1-13.	0.9	1
104	Low-Power Storage Bricks and Bioinformatics on Systems-On-Chip. , 2018, , .		1
105	Parallel Architectures for Bioinformatics. , 2019, , 209-214.		1
106	Parallel Computing in Deep Learning: Bioinformatics Case Studiesa. , 2019, , .		1
107	High Performance Computing for Haplotyping: Models and Platforms. Lecture Notes in Computer Science, 2019, , 650-661.	1.0	1
108	On low-power SoCs as storage bricks for Bioinformatics. Concurrency Computation Practice and Experience, 2020, 32, e5415.	1.4	1

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109	Advantages of using graph databases to explore chromatin conformation capture experiments. BMC Bioinformatics, 2021, 22, 43.	1.2	1
110	Integration of Multiple Resolution Data in 3D Chromatin Reconstruction Using ChromStruct. Biology, 2021, 10, 338.	1.3	1
111	NeoHiC: A Web Application for the Analysis of Hi-C Data. Lecture Notes in Computer Science, 2020, , 98-107.	1.0	1
112	Functional Genomics Applications in GRID. , 2009, , 149-167.		1
113	Combining Bayesian Approaches and Evolutionary Techniques for the Inference of Breast Cancer Networks. , 2016, , .		1
114	Ontological Enrichment of the Genes-to-Systems Breast Cancer Database. Communications in Computer and Information Science, 2009, , 171-182.	0.4	1
115	NuChart-II: A Graph-Based Approach for Analysis and Interpretation of Hi-C Data. Lecture Notes in Computer Science, 2015, , 298-311.	1.0	1
116	Dissecting Ex Vivo Expansion of Mobilized Peripheral Blood Hematopoietic Stem and Progenitor Cells By Single Cell RNA Sequencing. Blood, 2018, 132, 3343-3343.	0.6	1
117	Integrated Epigenetic Profiling Identifies EZH2 As a Therapeutic Target to Re-Establish Immune Recognition of Leukemia Relapses with Loss of HLA Class II Expression. Blood, 2019, 134, 514-514.	0.6	1
118	A Grid Service based Parallel Molecular Surface Reconstruction System. , 2008, , .		0
119	A Parallel Algorithm for Molecular Surface Matching Through Image Representation. , 2010, , .		0
120	A CUDA-based Implementation of the SSAKE Genomics Application. , 2012, , .		0
121	Molecular Mechanism of Allosteric Communication in Hsp70 Revealed by Molecular Dynamics Simulations. Biophysical Journal, 2013, 104, 571a.	0.2	0
122	A CUDA Implementation of the Spatial TAU-Leaping in Crowded Compartments (STAUCC) Simulator. , 2014, , .		0
123	529. Lentiviral Vectors with a Reduced Splicing Interference Potential Have a Significantly Improved Safety Profile In Vivo. Molecular Therapy, 2016, 24, S211-S212.	3.7	0
124	537. New Graph-Based Algorithm for Comprehensive Identification and Tracking Retroviral Integration Sites. Molecular Therapy, 2016, 24, S214-S215.	3.7	0
125	Parallelizable Strategy for the Estimation of the 3D Structure of Biological Macromolecules. , 2018, , .		0
126	Computing Empirical P-Values for Estimating Gene-Gene Interactions in Genome-Wide Association Studies: A Parallel Computing Approach. , 2018, , .		0

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127	A Visualization ToolKit Based Application for Representing Macromolecular Surfaces. Lecture Notes in Computer Science, 2009, , 284-292.	1.0	0
128	Data Integration, Breast Cancer Database. , 2013, , 523-524.		0
129	A Fine-Grained CUDA Implementation of the Multi-objective Evolutionary Approach NSGA-II: Potential Impact for Computational and Systems Biology Applications. Lecture Notes in Computer Science, 2015, , 273-284.	1.0	0
130	Modelling of Protein Surface Using Parallel Heterogeneous Architectures. , 2015, , 189-199.		0
131	Longitudinal Tracking of Acute Myeloid Leukemia Stem Cells in Xenografts and Patients By microRNA Reporters and Single Cell RNA Sequencing. Blood, 2019, 134, 916-916.	0.6	0