Ivan Merelli

List of Publications by Year
in descending order

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	DNA damage contributes to neurotoxic inflammation in Aicardi-GoutiÃ¨res syndrome astrocytes. Journal of Experimental Medicine, 2022, 219, .	4.2	35
2	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
3	Targeted inducible delivery of immunoactivating cytokines reprograms glioblastoma microenvironment and inhibits growth in mouse models. Science Translational Medicine, 2022, 14, .	5.8	32
4	StreamFlow: Cross-Breeding Cloud With HPC. IEEE Transactions on Emerging Topics in Computing, 2021, 9, 1723-1737.	3.2	27
5	Modeling, optimization, and comparable efficacy of T cell and hematopoietic stem cell gene editing for treating hyperâ€‹IgM syndrome. EMBO Molecular Medicine, 2021, 13, e13545.	3.3	36
6	Advantages of using graph databases to explore chromatin conformation capture experiments. BMC Bioinformatics, 2021, 22, 43.	1.2	1
7	Integration of Multiple Resolution Data in 3D Chromatin Reconstruction Using ChromStruct. Biology, 2021, 10, 338.	1.3	1
8	BAR-Seq clonal tracking of gene-edited cells. Nature Protocols, 2021, 16, 2991-3025.	5.5	11
9	Hardware and Software Solutions for Energy-Efficient Computing in Scientific Programming. Scientific Programming, 2021, 2021, 1-9.	0.5	2
10	Oncogene-induced maladaptive activation of trained immunity in the pathogenesis and treatment of Erdheim-Chester disease. Blood, 2021, 138, 1554-1569.	0.6	10
11	Î³-TRIS: a graph-algorithm for comprehensive identification of vector genomic insertion sites. Bioinformatics, 2020, 36, 1622-1624.	1.8	7
12	On lowâ€‹power SoCs as storage bricks for Bioinformatics. Concurrency Computation Practice and Experience, 2020, 32, e5415.	1.4	1
13	A secure cloud-edges computing architecture for metagenomics analysis. Future Generation Computer Systems, 2020, 111, 919-930.	4.9	5
14	Efficient gene editing of human long-term hematopoietic stem cells validated by clonal tracking. Nature Biotechnology, 2020, 38, 1298-1308.	9.4	116
15	Latest advances in parallel, distributed, and networkâ€‹based processing. Concurrency Computation Practice and Experience, 2020, 32, e5683.	1.4	2
16	NeoHiC: A Web Application for the Analysis of Hi-C Data. Lecture Notes in Computer Science, 2020, , 98-107.	1.0	1
17	Hematopoietic stem cell function in Î²-thalassemia is impaired and is rescued by targeting the bone marrow niche. Blood, 2020, 136, 610-622.	0.6	23
18	Combining Edge and Cloud computing for low-power, cost-effective metagenomics analysis. Future Generation Computer Systems, 2019, 90, 79-85.	4.9	32

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19	Infrastructure for High-Performance Computing: Grids and Grid Computing. , 2019, , 230-235.		2
20	Parallel Architectures for Bioinformatics. , 2019, , 209-214.		1
21	Integration of Machine Learning Methods to Dissect Genetically Imputed Transcriptomic Profiles in Alzheimerâ€™s Disease. Frontiers in Genetics, 2019, 10, 726.	1.1	18
22	Exploiting Docker containers over Grid computing for a comprehensive study of chromatin conformation in different cell types. Journal of Parallel and Distributed Computing, 2019, 134, 116-127.	2.7	4
23	GenHap: a novel computational method based on genetic algorithms for haplotype assembly. BMC Bioinformatics, 2019, 20, 172.	1.2	26
24	Parallel Computing in Deep Learning: Bioinformatics Case Studiesa. , 2019, , .		1
25	Precise Gene Editing Preserves Hematopoietic Stem Cell Function following Transient p53-Mediated DNA Damage Response. Cell Stem Cell, 2019, 24, 551-565.e8.	5.2	237
26	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
27	High Performance Computing for Haplotyping: Models and Platforms. Lecture Notes in Computer Science, 2019, , 650-661.	1.0	1
28	Advances in distributed computing with modern drug discovery. Expert Opinion on Drug Discovery, 2019, 14, 9-22.	2.5	12
29	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
30	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
31	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
32	A Scalable Genetic Programming Approach to Integrate miRNA-Target Predictions: Comparing Different Parallel Implementations of M3GP. Complexity, 2018, 2018, 1-13.	0.9	1
33	Parallelizable Strategy for the Estimation of the 3D Structure of Biological Macromolecules. , 2018, , .		0
34	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
35	Low-Power Storage Bricks and Bioinformatics on Systems-On-Chip. , 2018, , .		1
36	Computing Empirical P-Values for Estimating Gene-Gene Interactions in Genome-Wide Association Studies: A Parallel Computing Approach. , 2018, , .		0

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37	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
38	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
39	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
40	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
41	Low-Power Architectures for miRNA-Target Genome Wide Analysis. , 2017, , .		1
42	HIV-1-mediated insertional activation of STAT5B and BACH2 trigger viral reservoir in T regulatory cells. Nature Communications, 2017, 8, 498.	5.8	78
43	Rank miRNA: a web tool for identifying polymorphisms altering miRNA target sites. Procedia Computer Science, 2017, 108, 1125-1134.	1.2	2
44	Implementing a Space-Aware Stochastic Simulator on Low-Power Architectures: A Systems Biology Case Study. , 2017, , .		3
45	NuChart-II: The road to a fast and scalable tool for Hi-C data analysis. International Journal of High Performance Computing Applications, 2017, 31, 196-211.	2.4	4
46	VISPA2: a scalable pipeline for high-throughput identification and annotation of vector integration sites. BMC Bioinformatics, 2017, 18, 520.	1.2	23
47	Performance and Economic Evaluations in Adopting Low Power Architectures: A Real Case Analysis. Lecture Notes in Computer Science, 2017, , 177-189.	1.0	2
48	Editorial: High Performance Computing in Drug Discovery. Current Drug Targets, 2016, 17, 1578-1579.	1.0	1
49	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
50	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
51	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
52	537. New Graph-Based Algorithm for Comprehensive Identification and Tracking Retroviral Integration Sites. Molecular Therapy, 2016, 24, S214-S215.	3.7	0
53	A Machine Learning Approach for the Integration of miRNA-Target Predictions. , 2016, , .		2
54	MicroRNA-Target Interaction: A Parallel Approach for Computing Pairing Energy. , 2016, , .		1

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55	Clustering Protein Structures with Hadoop. Lecture Notes in Computer Science, 2016, , 141-153.	1.0	2
56	SPIRE, a modular pipeline for eQTL analysis of RNA-Seq data, reveals a regulatory hotspot controlling miRNA expression in C. elegans. Molecular BioSystems, 2016, 12, 3447-3458.	2.9	4
57	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
58	An atomistic view of Hsp70 allosteric crosstalk: from the nucleotide to the substrate binding domain and back. Scientific Reports, 2016, 6, 23474.	1.6	31
59	PWHATSHAP: efficient haplotyping for future generation sequencing. BMC Bioinformatics, 2016, 17, 342.	1.2	11
60	A novel molecular dynamics approach to evaluate the effect of phosphorylation on multimeric protein interface: the αB-Crystallin case study. BMC Bioinformatics, 2016, 17, 57.	1.2	15
61	How computer science can help in understanding the 3D genome architecture. Briefings in Bioinformatics, 2016, 17, 733-744.	3.2	10
62	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
63	Portals and Web-Based Resources for Virtual Screening. Current Drug Targets, 2016, 17, 1649-1660.	1.0	12
64	Combining Bayesian Approaches and Evolutionary Techniques for the Inference of Breast Cancer Networks. , 2016, , .		1
65	DnaK as Antibiotic Target: Hot Spot Residues Analysis for Differential Inhibition of the Bacterial Protein in Comparison with the Human HSP70. PLoS ONE, 2015, 10, e0124563.	1.1	59
66	Parallel Exploration of the Nuclear Chromosome Conformation with NuChart-II. , 2015, , .		3
67	Integrating multi-omic features exploiting Chromosome Conformation Capture data. Frontiers in Genetics, 2015, 6, 40.	1.1	11
68	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
69	Modelling of Protein Surface Using Parallel Heterogeneous Architectures. , 2015, , 189-199.		0
70	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
71	High-Performance Computing and Big Data in Omics-Based Medicine. BioMed Research International, 2014, 2014, 1-2.	0.9	8
72	Parallel Solutions for Voxel-Based Simulations of Reaction-Diffusion Systems. BioMed Research International, 2014, 2014, 1-10.	0.9	8

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73	Managing, Analysing, and Integrating Big Data in Medical Bioinformatics: Open Problems and Future Perspectives. BioMed Research International, 2014, 2014, 1-13.	0.9	118
74	CUDA accelerated molecular surface generation. Concurrency Computation Practice and Experience, 2014, 26, 1819-1831.	1.4	4
75	The WNoDeS Cloud Virtualization Framework: A Macromolecular Surface Analysis Application Case Study. , 2014, , .		2
76	A CUDA Implementation of the Spatial TAU-Leaping in Crowded Compartments (STAUCC) Simulator. , 2014, , .		0
77	Latest advances in distributed, parallel, and graphic processing unit accelerated approaches to computational biology. Concurrency Computation Practice and Experience, 2014, 26, 1699-1704.	1.4	5
78	SNPranker 2.0: a gene-centric data mining tool for diseases associated SNP prioritization in GWAS. BMC Bioinformatics, 2013, 14, S9.	1.2	23
79	Molecular Mechanism of Allosteric Communication in Hsp70 Revealed by Molecular Dynamics Simulations. Biophysical Journal, 2013, 104, 571a.	0.2	0
80	Static and dynamic interactions between GALK enzyme and known inhibitors: Guidelines to design new drugs for galactosemic patients. European Journal of Medicinal Chemistry, 2013, 63, 423-434.	2.6	27
81	Cloud Infrastructures for *In Silico* Drug Discovery: Economic and Practical Aspects. BioMed Research International, 2013, 2013, 1-19.	0.9	25
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	NuChart: An R Package to Study Gene Spatial Neighbourhoods with Multi-Omics Annotations. PLoS ONE, 2013, 8, e75146.	1.1	42
85	Data Integration, Breast Cancer Database. , 2013, , 523-524.		0
86	Molecular Mechanism of Allosteric Communication in Hsp70 Revealed by Molecular Dynamics Simulations. PLoS Computational Biology, 2012, 8, e1002844.	1.5	49
87	A CUDA-based Implementation of the SSAKE Genomics Application. , 2012, , .		0
88	IBDsite: a Galaxy-interacting, integrative database for supporting inflammatory bowel disease high throughput data analysis. BMC Bioinformatics, 2012, 13, S5.	1.2	12
89	Structural thermal adaptation of Î²â€‘tubulins from the Antarctic psychrophilic protozoan *Euplotes focardii*. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1154-1166.	1.5	25
90	Functional Genomics Applications in GRID. , 2012, , 899-917.		2

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91	Image-Based Surface Matching Algorithm Oriented to Structural Biology. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 1004-1016.	1.9	22
92	Ontology-based resources for bioinformatics analysis. International Journal of Metadata, Semantics and Ontologies, 2011, 6, 35.	0.2	3
93	myMIR: a genome-wide microRNA targets identification and annotation tool. Briefings in Bioinformatics, 2011, 12, 588-600.	3.2	23
94	Parallelization of the SSAKE Genomics Application. , 2011, , .		2
95	SNPRanker: a tool for identification and scoring of SNPs associated to target genes. Journal of Integrative Bioinformatics, 2010, 7, 331-345.	1.0	4
96	Semi-automatic identification of punching areas for tissue microarray building: the tubular breast cancer pilot study. BMC Bioinformatics, 2010, 11, 566.	1.2	2
97	A multilevel data integration resource for breast cancer study. BMC Systems Biology, 2010, 4, 76.	3.0	85
98	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
99	RSSsite: a reference database and prediction tool for the identification of cryptic Recombination Signal Sequences in human and murine genomes. Nucleic Acids Research, 2010, 38, W262-W267.	6.5	76
100	A Parallel Algorithm for Molecular Surface Matching Through Image Representation. , 2010, , .		0
101	SNPRanker: a tool for identification and scoring of SNPs associated to target genes. Journal of Integrative Bioinformatics, 2010, 7, .	1.0	4
102	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
103	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
104	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
105	Virtual screening pipeline and ligand modelling for H5N1 neuraminidase. Biochemical and Biophysical Research Communications, 2009, 383, 445-449.	1.0	17
106	Stochastic Simulations on a Grid Framework for Parameter Sweep Applications in Biological Models. , 2009, , .		5
107	Parallel Decomposition of 3D Surfaces in Images of Local Descriptors for Molecular Screening. , 2009, , .		2
108	Functional Genomics Applications in GRID. , 2009, , 149-167.		1

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109	Ontological Enrichment of the Genes-to-Systems Breast Cancer Database. Communications in Computer and Information Science, 2009, , 171-182.	0.4	1
110	A Visualization ToolKit Based Application for Representing Macromolecular Surfaces. Lecture Notes in Computer Science, 2009, , 284-292.	1.0	0
111	Version VI of the ESTree db: an improved tool for peach transcriptome analysis. BMC Bioinformatics, 2008, 9, S9.	1.2	22
112	Ontology-based, Tissue MicroArray oriented, image centered tissue bank. BMC Bioinformatics, 2008, 9, S4.	1.2	13
113	Images Based System for Surface Matching in Macromolecular Screening. , 2008, , .		4
114	TMAinspect, an EGEE Framework for Tissue MicroArray Image Handling. , 2008, , .		2
115	A Grid Service based Parallel Molecular Surface Reconstruction System. , 2008, , .		0
116	Mining the Bovine Genome with the â€œBovine SNP Retrieverâ€. Journal of Heredity, 2008, 99, 696-698.	1.0	1
117	Enabling Parallel TMA Image Analysis in a Grid Environment. , 2008, , .		1
118	A parallel protein surface reconstruction system. International Journal of Bioinformatics Research and Applications, 2008, 4, 221.	0.1	4
119	GoSh: a web-based database for goat and sheep EST sequences. Bioinformatics, 2007, 23, 1043-1045.	1.8	8
120	The cell cycle DB: a systems biology approach to cell cycle analysis. Nucleic Acids Research, 2007, 36, D641-D645.	6.5	12
121	Evaluation of a Grid Based Molecular Dynamics Approach for Polypeptide Simulations. IEEE Transactions on Nanobioscience, 2007, 6, 229-234.	2.2	6
122	Virtual screening on large scale grids. Parallel Computing, 2007, 33, 289-301.	1.3	27
123	A data integration approach for cell cycle analysis oriented to model simulation in systems biology. BMC Systems Biology, 2007, 1, 35.	3.0	23
124	Grid-Enabled High Throughput Virtual Screening. , 2007, , 45-59.		2
125	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
126	Grid-Enabled High-Throughput In Silico Screening Against Influenza A Neuraminidase. IEEE Transactions on Nanobioscience, 2006, 5, 288-295.	2.2	35

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127	High performance cDNA sequence analysis using grid technology. Journal of Parallel and Distributed Computing, 2006, 66, 1482-1488.	2.7	5
128	A sentence sliding window approach to extract protein annotations from biomedical articles. BMC Bioinformatics, 2005, 6, S19.	1.2	18
129	High performance workflow implementation for protein surface characterization using grid technology. BMC Bioinformatics, 2005, 6, S19.	1.2	4
130	Representation and Modeling of Protein Surface Determinants. IEEE Transactions on Nanobioscience, 2005, 4, 301-305.	2.2	3
131	Using Parallel Isosurface Extraction in Superficial Molecular Modeling. , 0, , .		4