Luciano Milanesi

List of Publications by Year
in descending order

261 papers	5,724 citations	109321 35 h-index	123424 61 g-index
273 all docs	273 docs citations	273 times ranked	10563 citing authors

#	Article	IF	Citations
1	A Standards Organization for Open and FAIR Neuroscience: the International Neuroinformatics Coordinating Facility. Neuroinformatics, 2022, 20, 25-36.	2.8	26
2	Classification and Personalized Prognostic Assessment on the Basis of Clinical and Genomic Features in Myelodysplastic Syndromes. Journal of Clinical Oncology, 2021, 39, 1223-1233.	1.6	127
3	Genetic Determinants in a Critical Domain of NS5A Correlate with Hepatocellular Carcinoma in Cirrhotic Patients Infected with HCV Genotype 1b. Viruses, 2021, 13, 743.	3.3	2
4	Characterization and comparison of gene-centered human interactomes. Briefings in Bioinformatics, 2021, 22, .	6.5	9
5	A Boron Delivery Antibody (BDA) with Boronated Specific Residues: New Perspectives in Boron Neutron Capture Therapy from an In Silico Investigation. Cells, 2021, 10, 3225.	4.1	5
6	Gene relevance based on multiple evidences in complex networks. Bioinformatics, 2020, 36, 865-871.	4.1	6
7	Î³-TRIS: a graph-algorithm for comprehensive identification of vector genomic insertion sites. Bioinformatics, 2020, 36, 1622-1624.	4.1	7
8	Blockade of IGF2R improves muscle regeneration and ameliorates Duchenne muscular dystrophy. EMBO Molecular Medicine, 2020, 12, e11019.	6.9	18
9	Profiling the Course of Resolving vs. Persistent Inflammation in Human Monocytes: The Role of IL-1 Family Molecules. Frontiers in Immunology, 2020, 11, 1426.	4.8	18
10	Transcriptomic Analysis of Rhodococcus opacus R7 Grown on o-Xylene by RNA-Seq. Frontiers in Microbiology, 2020, 11, 1808.	3.5	10
11	Assessment of haptoglobin alleles in autism spectrum disorders. Scientific Reports, 2020, 10, 7758.	3.3	2
12	Network Diffusion Promotes the Integrative Analysis of Multiple Omics. Frontiers in Genetics, 2020, 11, 106.	2.3	21
13	Frailness and resilience of gene networks predicted by detection of co-occurring mutations via a stochastic perturbative approach. Scientific Reports, 2020, 10, 2643.	3.3	3
14	Network-Based Integrative Analysis of Genomics, Epigenomics and Transcriptomics in Autism Spectrum Disorders. International Journal of Molecular Sciences, 2019, 20, 3363.	4.1	8
15	The role of extracellular matrix in mouse and human corneal neovascularization. Scientific Reports, 2019, 9, 14272.	3.3	20
16	Exploitation of a novel biosensor based on the full-length human F508del-CFTR with computational studies, biochemical and biological assays for the characterization of a new Lumacaftor/Tezacaftor analogue. Sensors and Actuators B: Chemical, 2019, 301, 127131.	7.8	7
17	isma: an R package for the integrative analysis of mutations detected by multiple pipelines. BMC Bioinformatics, 2019, 20, 107.	2.6	5
18	Durum wheat genome highlights past domestication signatures and future improvement targets. Nature Genetics, 2019, 51, 885-895.	21.4	576

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19	Inhibition of histone methyltransferase DOT1L silences ERα gene and blocks proliferation of antiestrogen-resistant breast cancer cells. Science Advances, 2019, 5, eaav5590.	10.3	70
20	A diethylpyrocarbonate-based derivatization method for the LC-MS/MS measurement of plasma arginine and its chemically related metabolites and analogs. Clinica Chimica Acta, 2019, 492, 29-36.	1.1	20
21	Heparin and heparan sulfate proteoglycans promote HIV-1 p17 matrix protein oligomerization: computational, biochemical and biological implications. Scientific Reports, 2019, 9, 15768.	3.3	18
22	A Scalable Genetic Programming Approach to Integrate miRNA-Target Predictions: Comparing Different Parallel Implementations of M3GP. Complexity, 2018, 2018, 1-13.	1.6	1
23	Antarctic marine ciliates under stress: superoxide dismutases from the psychrophilic Euplotes focardii are cold-active yet heat tolerant enzymes. Scientific Reports, 2018, 8, 14721.	3.3	35
24	An infrastructure for precision medicine through analysis of big data. BMC Bioinformatics, 2018, 19, 351.	2.6	23
25	Speeding Up the Identification of Cystic Fibrosis Transmembrane Conductance Regulator-Targeted Drugs: An Approach Based on Bioinformatics Strategies and Surface Plasmon Resonance. Molecules, 2018, 23, 120.	3.8	14
26	Genome-based analysis for the identification of genes involved in o-xylene degradation in Rhodococcus opacus R7. BMC Genomics, 2018, 19, 587.	2.8	23
27	Multiclass <scp>HCV</scp> resistance to direct‐acting antiviral failure in real‐life patients advocates for tailored second‐line therapies. Liver International, 2017, 37, 514-528.	3.9	84
28	iSmaRT: a toolkit for a comprehensive analysis of small RNA-Seq data. Bioinformatics, 2017, 33, 938-940.	4.1	21
29	LAV-BPIFB4 isoform modulates eNOS signalling through Ca2+/PKC-alpha-dependent mechanism. Cardiovascular Research, 2017, 113, 795-804.	3.8	24
30	Low-Power Architectures for miRNA-Target Genome Wide Analysis. , 2017, , .		1
31	A rare genetic variant of BPIFB4 predisposes to high blood pressure via impairment of nitric oxide signaling. Scientific Reports, 2017, 7, 9706.	3.3	17
32	A single amino acid substitution confers B-cell clonogenic activity to the HIV-1 matrix protein p17. Scientific Reports, 2017, 7, 6555.	3.3	15
33	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.	3.7	4
34	FGF2 and EGF Are Required for Self-Renewal and Organoid Formation of Canine Normal and Tumor Breast Stem Cells. Journal of Cellular Biochemistry, 2017, 118, 570-584.	2.6	28
35	RNA‐Generated and Gene‐Edited Induced Pluripotent Stem Cells for Disease Modeling and Therapy. Journal of Cellular Physiology, 2017, 232, 1262-1269.	4.1	11
36	Study on the Association among Mycotoxins and other Variables in Children with Autism. Toxins, 2017, 9, 203.	3.4	36

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37	Network Diffusion-Based Prioritization of Autism Risk Genes Identifies Significantly Connected Gene Modules. Frontiers in Genetics, 2017, 8, 129.	2.3	20
38	The nuclear receptor ERÎ² engages AGO2 in regulation of gene transcription, RNA splicing and RISC loading. Genome Biology, 2017, 18, 189.	8.8	63
39	VISPA2: a scalable pipeline for high-throughput identification and annotation of vector integration sites. BMC Bioinformatics, 2017, 18, 520.	2.6	23
40	Large-scale profiling of signalling pathways reveals an asthma specific signature in bronchial smooth muscle cells. Oncotarget, 2016, 7, 25150-25161.	1.8	32
41	The Genome Conformation As an Integrator of Multi-Omic Data: The Example of Damage Spreading in Cancer. Frontiers in Genetics, 2016, 7, 194.	2.3	22
42	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.	4.1	16
43	Osteogenic Differentiation of MSC through Calcium Signaling Activation: Transcriptomics and Functional Analysis. PLoS ONE, 2016, 11, e0148173.	2.5	99
44	Further Insights in the Binding Mode of Selective Inhibitors to Human PDE4D Enzyme Combining Docking and Molecular Dynamics. Molecular Informatics, 2016, 35, 369-381.	2.5	17
45	Phenotype microarray analysis may unravel genetic determinants of the stress response by Rhodococcus aetherivorans BCP1 and Rhodococcus opacus R7. Research in Microbiology, 2016, 167, 766-773.	2.1	43
46	Network diffusion-based analysis of high-throughput data for the detection of differentially enriched modules. Scientific Reports, 2016, 6, 34841.	3.3	31
47	529. Lentiviral Vectors with a Reduced Splicing Interference Potential Have a Significantly Improved Safety Profile In Vivo. Molecular Therapy, 2016, 24, S211-S212.	8.2	0
48	CUDAâ€quicksort: an improved GPUâ€based implementation of quicksort. Concurrency Computation Practice and Experience, 2016, 28, 21-43.	2.2	16
49	A Machine Learning Approach for the Integration of miRNA-Target Predictions. , 2016, , .		2
50	MicroRNA-Target Interaction: A Parallel Approach for Computing Pairing Energy. , 2016, , .		1
51	Using web-based observations to identify thresholds of a person's stability in a flow. Water Resources Research, 2016, 52, 7793-7805.	4.2	29
52	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
53	Exome sequencing identifies variants in two genes encoding the LIM-proteins NRAP and FHL1 in an Italian patient with BAG3 myofibrillar myopathy. Journal of Muscle Research and Cell Motility, 2016, 37, 101-115.	2.0	23
54	New insights into selective PDE4D inhibitors: 3-(Cyclopentyloxy)-4-methoxybenzaldehyde O-(2-(2,6-dimethylmorpholino)-2-oxoethyl) oxime (GEBR-7b) structural development and promising activities to restore memory impairment. European Journal of Medicinal Chemistry, 2016, 124, 82-102.	5.5	31

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55	NuchaRt: Embedding High-Level Parallel Computing in R for Augmented Hi-C Data Analysis. Lecture Notes in Computer Science, 2016, , 259-272.	1.3	2
56	An atomistic view of Hsp70 allosteric crosstalk: from the nucleotide to the substrate binding domain and back. Scientific Reports, 2016, 6, 23474.	3.3	31
57	BITS 2015: the annual meeting of the Italian Society of Bioinformatics. BMC Bioinformatics, 2016, 17, 396.	2.6	0
58	Removing duplicate reads using graphics processing units. BMC Bioinformatics, 2016, 17, 346.	2.6	12
59	A novel molecular dynamics approach to evaluate the effect of phosphorylation on multimeric protein interface: the Î±B-Crystallin case study. BMC Bioinformatics, 2016, 17, 57.	2.6	15
60	HCV NS3 sequencing as a reliable and clinically useful tool for the assessment of genotype and resistance mutations for clinical samples with different HCV-RNA levels. Journal of Antimicrobial Chemotherapy, 2016, 71, 739-750.	3.0	13
61	Methods for the integration of multi-omics data: mathematical aspects. BMC Bioinformatics, 2016, 17, 15.	2.6	316
62	Stochastic neutral modelling of the Gut Microbiotaâ€™s relative species abundance from next generation sequencing data. BMC Bioinformatics, 2016, 17, 16.	2.6	19
63	Systems medicine of inflammaging. Briefings in Bioinformatics, 2016, 17, 527-540.	6.5	35
64	How computer science can help in understanding the 3D genome architecture. Briefings in Bioinformatics, 2016, 17, 733-744.	6.5	10
65	Ochratoxin A as possible factor trigging autism and its male prevalence <i>via</i> epigenetic mechanism. Nutritional Neuroscience, 2016, 19, 43-46.	3.1	19
66	Specific patterns of PIWI-interacting small noncoding RNA expression in dysplastic liver nodules and hepatocellular carcinoma. Oncotarget, 2016, 7, 54650-54661.	1.8	63
67	HPC Analysis of Multiple Binding Sites Communication and Allosteric Modulations in Drug Design: The HSP Case Study. Current Drug Targets, 2016, 17, 1610-1625.	2.1	2
68	Serum BPIFB4 levels classify health status in long-living individuals. Immunity and Ageing, 2015, 12, 27.	4.2	39
69	G-CNV: A GPU-Based Tool for Preparing Data to Detect CNVs with Read-Depth Methods. Frontiers in Bioengineering and Biotechnology, 2015, 3, 28.	4.1	8
70	Transposable Element Insertions in Long Intergenic Non-Coding RNA Genes. Frontiers in Bioengineering and Biotechnology, 2015, 3, 71.	4.1	45
71	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.	2.5	59
72	Segmenting the Human Genome into Isochores. Evolutionary Bioinformatics, 2015, 11, EBO.S27693.	1.2	18

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73	Parallel Exploration of the Nuclear Chromosome Conformation with NuChart-II. , 2015, , .		3
74	Environment, dysbiosis, immunity and sex-specific susceptibility: A translational hypothesis for regressive autism pathogenesis. Nutritional Neuroscience, 2015, 18, 145-161.	3.1	57
75	Integrating multi-omic features exploiting Chromosome Conformation Capture data. Frontiers in Genetics, 2015, 6, 40.	2.3	11
76	Molecular dynamics and docking simulation of a natural variant of Activated Protein C with impaired protease activity: implications for integrin-mediated antiseptic function. Journal of Biomolecular Structure and Dynamics, 2015, 33, 85-92.	3.5	6
77	Genome and Phenotype Microarray Analyses of Rhodococcus sp. BCP1 and Rhodococcus opacus R7: Genetic Determinants and Metabolic Abilities with Environmental Relevance. PLoS ONE, 2015, 10, e0139467.	2.5	53
78	NuChart-II: A Graph-Based Approach for Analysis and Interpretation of Hi-C Data. Lecture Notes in Computer Science, 2015, , 298-311.	1.3	1
79	Parallel Solutions for Voxel-Based Simulations of Reaction-Diffusion Systems. BioMed Research International, 2014, 2014, 1-10.	1.9	8
80	Genome Sequence of Rhodococcus opacus Strain R7, a Biodegrader of Mono- and Polycyclic Aromatic Hydrocarbons. Genome Announcements, 2014, 2, .	0.8	15
81	CUDA accelerated molecular surface generation. Concurrency Computation Practice and Experience, 2014, 26, 1819-1831.	2.2	4
82	Guidelines for managing data and processes in bone and cartilage tissue engineering. BMC Bioinformatics, 2014, 15, S14.	2.6	8
83	A tool for mapping Single Nucleotide Polymorphisms using Graphics Processing Units. BMC Bioinformatics, 2014, 15, S10.	2.6	5
84	The WNoDeS Cloud Virtualization Framework: A Macromolecular Surface Analysis Application Case Study. , 2014, , .		2
85	A CUDA Implementation of the Spatial TAU-Leaping in Crowded Compartments (STAUCC) Simulator. , 2014, , .		0
86	P.2.a.006 Agomelatine and fluoxetine induce different and time-dependent modulation of rat hippocampal miRNome. European Neuropsychopharmacology, 2014, 24, S364.	0.7	1
87	GPU-BSM: A GPU-Based Tool to Map Bisulfite-Treated Reads. PLoS ONE, 2014, 9, e97277.	2.5	6
88	Diffusion of Information throughout the Host Interactome Reveals Gene Expression Variations in Network Proximity to Target Proteins of Hepatitis C Virus. PLoS ONE, 2014, 9, e113660.	2.5	11
89	SNPranker 2.0: a gene-centric data mining tool for diseases associated SNP prioritization in GWAS. BMC Bioinformatics, 2013, 14, S9.	2.6	23
90	Decreased Transcriptional Activity of *Calcium-sensing receptor* Gene Promoter 1 Is Associated With Calcium Nephrolithiasis. Journal of Clinical Endocrinology and Metabolism, 2013, 98, 3839-3847.	3.6	49

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91	Tubulin folding: the special case of a beta-tubulin isotype from the Antarctic psychrophilic ciliate Euplotes focardii. Polar Biology, 2013, 36, 1833-1838.	1.2	8
92	Network-based analysis of omics with multi-objective optimization. Molecular BioSystems, 2013, 9, 2971.	2.9	16
93	Molecular Mechanism of Allosteric Communication in Hsp70 Revealed by Molecular Dynamics Simulations. Biophysical Journal, 2013, 104, 571a.	0.5	0
94	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.	5.5	27
95	*Myosin–Binding Protein C* DNA Variants in Domestic Cats (A31P, A74T, R820W) and their Association with Hypertrophic Cardiomyopathy. Journal of Veterinary Internal Medicine, 2013, 27, 275-285.	1.6	51
96	Blood microRNA changes in depressed patients during antidepressant treatment. European Neuropsychopharmacology, 2013, 23, 602-611.	0.7	197
97	Molecular Interaction Studies of HIV-1 Matrix Protein p17 and Heparin. Journal of Biological Chemistry, 2013, 288, 1150-1161.	3.4	30
98	Genome Sequence of *Rhodococcus* sp. Strain BCP1, a Biodegrader of Alkanes and Chlorinated Compounds. Genome Announcements, 2013, 1, .	0.8	9
99	Cloud Infrastructures for *In Silico* Drug Discovery: Economic and Practical Aspects. BioMed Research International, 2013, 2013, 1-19.	1.9	25
100	A Parallel Implementation of the Stau-DPP Stochastic Simulator for the Modelling of Biological Systems. , 2013, , .		2
101	Homology Modeling, Docking Studies and Molecular Dynamic Simulations Using Graphical Processing Unit Architecture to Probe the Type–11 Phosphodiesterase Catalytic Site: A Computational Approach for the Rational Design of Selective Inhibitors. Chemical Biology and Drug Design, 2013, 82, 718-731.	3.2	33
102	SENSITIVITY ANALYSIS FOR STUDYING THE RELATION BETWEEN BIOCHEMICAL REACTIONS AND METABOLIC PHENOTYPES. Journal of Bioinformatics and Computational Biology, 2013, 11, 1340002.	0.8	2
103	NuChart: An R Package to Study Gene Spatial Neighbourhoods with Multi-Omics Annotations. PLoS ONE, 2013, 8, e75146.	2.5	42
104	Mathematical Model, Model Theory. , 2013, , 1181-1181.		0
105	High-Throughput Computing, Asynchronous Communication. , 2013, , 892-892.		0
106	Evolutionary Algorithms. , 2013, , 695-695.		0
107	Parallel Computing, Data Parallelism. , 2013, , 1624-1624.		0
108	Complex System. , 2013, , 456-456.		0

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109	Grid Computing, Parameter Estimation for Ordinary Differential Equations. , 2013, , 870-871.		0
110	Mathematical Programming, Constraint. , 2013, , 1186-1187.		0
111	Cell Cycle Database. , 2013, , 260-263.		0
112	Data Integration. , 2013, , 519-519.		0
113	Mathematics, Nonlinear Programming. , 2013, , 1188-1188.		0
114	Cell Cycle, Biology. , 2013, , 336-337.		0
115	Data Integration, Breast Cancer Database. , 2013, , 523-524.		0
116	Describing the genes social networks relying on chromosome conformation capture data. EMBnet Journal, 2013, 19, 73.	0.6	0
117	Molecular Mechanism of Allosteric Communication in Hsp70 Revealed by Molecular Dynamics Simulations. PLoS Computational Biology, 2012, 8, e1002844.	3.2	49
118	Computational Modeling of the Metabolic States Regulated by the Kinase Akt. Frontiers in Physiology, 2012, 3, 418.	2.8	20
119	A CUDA-based Implementation of the SSAKE Genomics Application. , 2012, , .		0
120	IBDsite: a Galaxy-interacting, integrative database for supporting inflammatory bowel disease high throughput data analysis. BMC Bioinformatics, 2012, 13, S5.	2.6	12
121	Literature Retrieval and Mining in Bioinformatics: State of the Art and Challenges. Advances in Bioinformatics, 2012, 2012, 1-10.	5.7	16
122	Structural thermal adaptation of Î²â€‘tubulins from the Antarctic psychrophilic protozoan <i>Euplotes focardii</i>. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1154-1166.	2.6	25
123	Correlation assessment among clinical phenotypes, expression analysis and molecular modeling of 14 novel variations in the human galactose-1-phosphate uridylyltransferase gene. Human Mutation, 2012, 33, 1107-1115.	2.5	25
124	Nanoinformatics: developing new computing applications for nanomedicine. Computing (Vienna/New) Tj ETQq0 0 0 rgBT /Overlock 10 T	4.8	15
125	Systems biology of the metabolic network regulated by the Akt pathway. Biotechnology Advances, 2012, 30, 131-141.	11.7	37
126	Solving Biclustering with a GRASP-Like Metaheuristic: Two Case-Studies on Gene Expression Analysis. Lecture Notes in Computer Science, 2012, , 253-267.	1.3	1

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127	G-SNPM - A GPU-based SNP mapping tool. EMBnet Journal, 2012, 18, 138.	0.6	1
128	Bioinformatics approach for data management about bone cells grown on substitute materials. EMBnet Journal, 2012, 18, 148.	0.6	2
129	Functional Genomics Applications in GRID. , 2012, , 899-917.		2
130	OsteoChondroDB: a database about biomolecular chondral- bone development in physiological and diseased conditions. EMBnet Journal, 2012, 18, 80.	0.6	0
131	Image-Based Surface Matching Algorithm Oriented to Structural Biology. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 1004-1016.	3.0	22
132	Human aryl-hydrocarbon receptor and its interaction with dioxin and physiological ligands investigated by molecular modelling and docking simulations. Biochemical and Biophysical Research Communications, 2011, 413, 176-181.	2.1	18
133	Ontology-based resources for bioinformatics analysis. International Journal of Metadata, Semantics and Ontologies, 2011, 6, 35.	0.2	3
134	Homology modeling in tandem with 3D-QSAR analyses: A computational approach to depict the agonist binding site of the human CB2 receptor. European Journal of Medicinal Chemistry, 2011, 46, 4489-4505.	5.5	36
135	A grid portal with robot certificates for bioinformatics phylogenetic analyses. Concurrency Computation Practice and Experience, 2011, 23, 246-255.	2.2	14
136	Modeling the cell cycle: From deterministic models to hybrid systems. BioSystems, 2011, 105, 34-40.	2.0	14
137	Modeling Biochemical Pathways. , 2011, , 111-126.		0
138	myMIR: a genome-wide microRNA targets identification and annotation tool. Briefings in Bioinformatics, 2011, 12, 588-600.	6.5	23
139	Association Study on Long-Living Individuals from Southern Italy Identifies rs10491334 in the <i>CAMKIV</i> Gene That Regulates Survival Proteins. Rejuvenation Research, 2011, 14, 283-291.	1.8	72
140	Parallelization of the SSAKE Genomics Application. , 2011, , .		2
141	Population Stratification Analysis in Genome-Wide Association Studies. , 2011, , 177-196.		0
142	Complex Search, Ranks, and Biological Discovery: A User's Perspective. Lecture Notes in Computer Science, 2011, , 226-235.	1.3	1
143	Overlapping Genes May Control Reprogramming of Mouse Somatic Cells into Induced Pluripotent Stem Cells (iPSCs) and Breast Cancer Stem Cells. In Silico Biology, 2010, 10, 207-221.	0.9	6
144	SNPRanker: a tool for identification and scoring of SNPs associated to target genes. Journal of Integrative Bioinformatics, 2010, 7, 331-345.	1.5	4

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145	Grid Based Genome Wide Studies on Atrial Flutter. Journal of Grid Computing, 2010, 8, 511-527.	3.9	2
146	Molecular remodeling of potassium channels in fibroblasts from centenarians: A marker of longevity?. Mechanisms of Ageing and Development, 2010, 131, 674-681.	4.6	8
147	Semi-automatic identification of punching areas for tissue microarray building: the tubular breast cancer pilot study. BMC Bioinformatics, 2010, 11, 566.	2.6	2
148	A multilevel data integration resource for breast cancer study. BMC Systems Biology, 2010, 4, 76.	3.0	85
149	A systems biology approach for the identification of glycolysis key regulators in cancer cells. Journal of Biotechnology, 2010, 150, 545-546.	3.8	0
150	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.	2.6	11
151	Fine mapping of *AHI1* as a schizophrenia susceptibility gene: from association to evolutionary evidence. FASEB Journal, 2010, 24, 3066-3082.	0.5	39
152	A Dynamic Parallel Approach to Recognize Tubular Breast Cancer for TMA Image Building. , 2010, , .		1
153	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.	14.5	76
154	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
155	INFN, IT the GENIUS grid portal and the robot certificates to perform phylogenetic analysis on large scale: a success story from the International LIBI project. , 2010, , 119-130.		0
156	A Parallel Algorithm for Molecular Surface Matching Through Image Representation. , 2010, , .		0
157	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
158	Modelling Spatial Heterogeneity and Macromolecular Crowding with Membrane Systems. Lecture Notes in Computer Science, 2010, , 285-304.	1.3	6
159	SNPRanker: a tool for identification and scoring of SNPs associated to target genes. Journal of Integrative Bioinformatics, 2010, 7, .	1.5	4
160	Trends in modeling Biomedical Complex Systems. BMC Bioinformatics, 2009, 10, I1.	2.6	25
161	Towards a systems biology approach to mammalian cell cycle: modeling the entrance into S phase of quiescent fibroblasts after serum stimulation. BMC Bioinformatics, 2009, 10, S16.	2.6	37
162	The Human EST Ontology Explorer: a tissue-oriented visualization system for ontologies distribution in human EST collections. BMC Bioinformatics, 2009, 10, S2.	2.6	1

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163	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.	2.6	24
164	Identification of functionally related genes using data mining and data integration: a breast cancer case study. BMC Bioinformatics, 2009, 10, S8.	2.6	20
165	The GENIUS Grid Portal and robot certificates: a new tool for e-Science. BMC Bioinformatics, 2009, 10, S21.	2.6	13
166	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.	3.6	8
167	Virtual screening pipeline and ligand modelling for H5N1 neuraminidase. Biochemical and Biophysical Research Communications, 2009, 383, 445-449.	2.1	17
168	Stochastic Simulations on a Grid Framework for Parameter Sweep Applications in Biological Models. , 2009, , .		5
169	Parallel Decomposition of 3D Surfaces in Images of Local Descriptors for Molecular Screening. , 2009, , .		2
170	Multi-Level Data Integration and Data Mining in Systems Biology. , 2009, , 476-496.		1
171	Ontological Enrichment of the Genes-to-Systems Breast Cancer Database. Communications in Computer and Information Science, 2009, , 171-182.	0.5	1
172	A Visualization ToolKit Based Application for Representing Macromolecular Surfaces. Lecture Notes in Computer Science, 2009, , 284-292.	1.3	0
173	SNPLims: a data management system for genome wide association studies. BMC Bioinformatics, 2008, 9, S13.	2.6	19
174	Version VI of the ESTree db: an improved tool for peach transcriptome analysis. BMC Bioinformatics, 2008, 9, S9.	2.6	22
175	Ontology-based, Tissue MicroArray oriented, image centered tissue bank. BMC Bioinformatics, 2008, 9, S4.	2.6	13
176	Reconstructing networks of pathways via significance analysis of their intersections. BMC Bioinformatics, 2008, 9, S9.	2.6	25
177	Images Based System for Surface Matching in Macromolecular Screening. , 2008, , .		4
178	TMAinspect, an EGEE Framework for Tissue MicroArray Image Handling. , 2008, , .		2
179	A Grid Service based Parallel Molecular Surface Reconstruction System. , 2008, , .		0
180	Mining the Bovine Genome with the â€œBovine SNP Retrieverâ€. Journal of Heredity, 2008, 99, 696-698.	2.4	1

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181	Enabling Parallel TMA Image Analysis in a Grid Environment. , 2008, , .		1
182	A parallel protein surface reconstruction system. International Journal of Bioinformatics Research and Applications, 2008, 4, 221.	0.2	4
183	Bayesian Phylogeny on Grid. Communications in Computer and Information Science, 2008, , 404-416.	0.5	9
184	An unusal distribution of 6-nt sequences near the transcription start site. Journal of Integrative Bioinformatics, 2008, 5, .	1.5	0
185	NETWORKS FROM GENE EXPRESSION TIME SERIES: CHARACTERIZATION OF CORRELATION PATTERNS. International Journal of Bifurcation and Chaos in Applied Sciences and Engineering, 2007, 17, 2477-2483.	1.7	5
186	The cell cycle DB: a systems biology approach to cell cycle analysis. Nucleic Acids Research, 2007, 36, D641-D645.	14.5	12
187	Guest Editorial: Special Section on Grid, Web Services, Software Agents, and Ontology Applications for Life Sciences. IEEE Transactions on Nanobioscience, 2007, 6, 101-103.	3.3	5
188	CYCLONET--an integrated database on cell cycle regulation and carcinogenesis. Nucleic Acids Research, 2007, 35, D550-D556.	14.5	16
189	Grid Methodology for Identifying Co-Regulated Genes and Transcription Factor Binding Sites. IEEE Transactions on Nanobioscience, 2007, 6, 162-167.	3.3	4
190	An Agent-Based Multilayer Architecture for Bioinformatics Grids. IEEE Transactions on Nanobioscience, 2007, 6, 142-148.	3.3	15
191	A Fast Job Scheduling System for a Wide Range of Bioinformatic Applications. IEEE Transactions on Nanobioscience, 2007, 6, 149-154.	3.3	4
192	Evaluation of a Grid Based Molecular Dynamics Approach for Polypeptide Simulations. IEEE Transactions on Nanobioscience, 2007, 6, 229-234.	3.3	6
193	Virtual screening on large scale grids. Parallel Computing, 2007, 33, 289-301.	2.1	27
194	A data integration approach for cell cycle analysis oriented to model simulation in systems biology. BMC Systems Biology, 2007, 1, 35.	3.0	23
195	ProCMD: a database and 3D web resource for protein C mutants. BMC Bioinformatics, 2007, 8, S11.	2.6	27
196	ESTuber db: an online database for Tuber borchii EST sequences. BMC Bioinformatics, 2007, 8, S13.	2.6	9
197	SYMBIOmatics: Synergies in Medical Informatics and Bioinformatics â€" exploring current scientific literature for emerging topics. BMC Bioinformatics, 2007, 8, S18.	2.6	18
198	Biowep: a workflow enactment portal for bioinformatics applications. BMC Bioinformatics, 2007, 8, S19.	2.6	36

#	Article	IF	Citations
199	Data handling strategies for high throughput pyrosequencers. BMC Bioinformatics, 2007, 8, S22.	2.6	22
200	Medical Informatics and Bioinformatics: A Bibliometric Study. IEEE Transactions on Information Technology in Biomedicine, 2007, 11, 237-243.	3.2	27
201	Grid-Enabled High Throughput Virtual Screening. , 2007, , 45-59.		2
202	BIOINFOGRID: BIOINFORMATICS SIMULATION AND MODELING BASED ON GRID. , 2007, , .		0
203	BGBlast: a BLAST grid implementation with database self-updating and adaptive replication. Studies in Health Technology and Informatics, 2007, 126, 23-30.	0.3	3
204	Parameter estimation for cell cycle ordinary differential equation (ODE) models using a grid approach. Studies in Health Technology and Informatics, 2007, 126, 93-102.	0.3	1
205	Tissue MicroArray: a distributed Grid approach for image analysis. Studies in Health Technology and Informatics, 2007, 126, 291-8.	0.3	2
206	Amino Acids Surface Patterns in Protein Domain Functionality Analysis. , 2006, , 225-233.		0
207	Grid-Enabled High-Throughput In Silico Screening Against Influenza A Neuraminidase. IEEE Transactions on Nanobioscience, 2006, 5, 288-295.	3.3	35
208	A novel polymorphism in SEL1L confers susceptibility to Alzheimer's disease. Neuroscience Letters, 2006, 398, 53-58.	2.1	24
209	Network integration of data and analysis of oncology interest. Journal of Integrative Bioinformatics, 2006, 3, 45-55.	1.5	1
210	Strategies for comparing gene expression profiles from different microarray platforms: Application to a case–control experiment. Analytical Biochemistry, 2006, 353, 43-56.	2.4	40
211	High performance cDNA sequence analysis using grid technology. Journal of Parallel and Distributed Computing, 2006, 66, 1482-1488.	4.1	5
212	High performance GRID based implementation for genomics and protein analysis. Studies in Health Technology and Informatics, 2006, 120, 374-80.	0.3	3
213	Evaluation of BioCreAtIvE assessment of task 2. BMC Bioinformatics, 2005, 6, S16.	2.6	108
214	A sentence sliding window approach to extract protein annotations from biomedical articles. BMC Bioinformatics, 2005, 6, S19.	2.6	18
215	Protein annotation as term categorization in the gene ontology using word proximity networks. BMC Bioinformatics, 2005, 6, S20.	2.6	31
216	Overview of BITS2005, the Second Annual Meeting of the Italian Bioinformatics Society. BMC Bioinformatics, 2005, 6, S1.	2.6	8

#	Article	IF	Citations
217	Modelling the interaction of steroid receptors with endocrine disrupting chemicals. BMC Bioinformatics, 2005, 6, S10.	2.6	25
218	ESTree db: a Tool for Peach Functional Genomics. BMC Bioinformatics, 2005, 6, S16.	2.6	38
219	High performance workflow implementation for protein surface characterization using grid technology. BMC Bioinformatics, 2005, 6, S19.	2.6	4
220	Systematic analysis of human kinase genes: a large number of genes and alternative splicing events result in functional and structural diversity. BMC Bioinformatics, 2005, 6, S20.	2.6	65
221	Web services and workflow management for biological resources. BMC Bioinformatics, 2005, 6, S24.	2.6	16
222	A Hybrid Genetic-Neural System for Predicting Protein Secondary Structure. BMC Bioinformatics, 2005, 6, S3.	2.6	19
223	Representation and Modeling of Protein Surface Determinants. IEEE Transactions on Nanobioscience, 2005, 4, 301-305.	3.3	3
224	Multiple Alignment Through Protein Secondary-Structure Information. IEEE Transactions on Nanobioscience, 2005, 4, 207-211.	3.3	1
225	Using Secondary Structure Information to Perform Multiple Alignment. Lecture Notes in Computer Science, 2005, , 78-88.	1.3	0
226	FROM CONTEXT-DEPENDENCE OF MUTATIONS TO MOLECULAR MECHANISMS OF MUTAGENESIS. , 2004, , .		10
227	Computational analysis of mutation spectra. Briefings in Bioinformatics, 2003, 4, 210-227.	6.5	16
228	ESTMAP: a system for expressed sequence tags mapping on genomic sequences. IEEE Transactions on Nanobioscience, 2003, 2, 75-78.	3.3	4
229	ASPD (Artificially Selected Proteins/Peptides Database): a database of proteins and peptides evolved in vitro. Nucleic Acids Research, 2002, 30, 200-202.	14.5	29
230	Presence of ATG triplets in 5' untranslated regions of eukaryotic cDNAs correlates with a weak' context of the start codon. Bioinformatics, 2001, 17, 890-900.	4.1	126
231	Prediction and phylogenetic analysis of mammalian short interspersed elements (SINEs). Briefings in Bioinformatics, 2000, 1, 260-274.	6.5	10
232	GeneBuilder: interactive in silico prediction of gene structure. Bioinformatics, 1999, 15, 612-621.	4.1	58
233	Integrated databases and computer systems for studying eukaryotic gene expression. Bioinformatics, 1999, 15, 669-686.	4.1	21
234	Protein-coding regions prediction combining similarity searches and conservative evolutionary properties of protein-coding sequences. Gene, 1999, 226, 129-137.	2.2	18

#	Article	IF	Citations
235	The Subclass Approach for Mutational Spectrum Analysis: Application of the SEM Algorithm. Journal of Theoretical Biology, 1998, 192, 475-487.	1.7	37
236	Molecular Probe Data Base (MPDB). Nucleic Acids Research, 1998, 26, 145-147.	14.5	2
237	Prediction of Human Gene Structure. , 1998, , 215-259.		16
238	Sequence and Gene Content in 35 kb Genomic Clone Mapping in the Human Xq27.1 Region. DNA Sequence, 1997, 8, 1-15.	0.7	7
239	Identification of a U7snRNA homologue mapping to the human Xq27.1 region, between the DXS1232 and DXS119 loci. Gene, 1997, 187, 221-224.	2.2	2
240	Analysis of donor splice sites in different eukaryotic organisms. Journal of Molecular Evolution, 1997, 45, 50-59.	1.8	148
241	Characterization and Fine Localization of Two New Genes in Xq28 Using the Genomic Sequence/EST Database Screening Approach. Genomics, 1996, 34, 323-327.	2.9	16
242	Gene structure prediction using information on homologous protein sequence. Bioinformatics, 1996, 12, 161-170.	4.1	15
243	Hamming-Clustering method for signals prediction in 5â€² and 3â€² regions of eukaryotic genes. Bioinformatics, 1996, 12, 399-404.	4.1	23
244	Eukaryotic promoter recognition by binding sites for transcription factors. Bioinformatics, 1995, 11, 477-488.	4.1	36
245	Data bank homology search algorithm with linear computation complexity. Bioinformatics, 1994, 10, 319-322.	4.1	1
246	The Exon-Intron Organization of the Human X-Linked Gene (FLN1) Encoding Actin-Binding Protein 280. Genomics, 1994, 21, 71-76.	2.9	29
247	Concept-based indexing and retrieval of multimedia documents. Journal of Information Science, 1994, 20, 185-196.	3.3	5
248	SITEVIDEO: a computer system for functional site analysis and recognition. Investigation of the human splice sites. Bioinformatics, 1993, 9, 617-627.	4.1	10
249	MULTIPLE SEQUENCE ALIGNMENT BASED ON NEW APPROACHES OF TREE CONSTRUCTION AND SEQUENCE COMPARISON. , 1993, , .		0
250	GENVIEWER: A COMPUTING TOOL FOR PROTEIN-CODING REGIONS PREDICTION IN NUCLEOTIDE SEQUENCES. , 1993, , .		14
251	APPLICATION OF FRACTAL REPRESENTATION OF GENETIC TEXTS FOR RECOGNITION OF GENOME FUNCTIONAL AND CODING REGIONS. , 1993, , .		0
252	Methylation and sequence analysis around Eagi sites: identification of 28 new CpG islands in XQ24-XQ28. Nucleic Acids Research, 1992, 20, 727-733.	14.5	44

#	Article	IF	Citations
253	Fast, statistically based alignment of amino acid sequences on the base of diagonal fragments of DOT-matrices. Bioinformatics, 1992, 8, 529-534.	4.1	2
254	Assessment and comparison of three scatter correction techniques in single photon emission computed tomography. Journal of Nuclear Medicine, 1988, 29, 1971-9.	5.0	34
255	Biomedical applications of cyclotrons and review of commercially available models. Journal of Medical Engineering and Technology, 1987, 11, 166-176.	1.4	7
256	Quantitative radionuclide angiocardiography using gold-195m. American Journal of Cardiology, 1984, 53, 1442-1446.	1.6	5
257	Microarray imaging data pre-processing. , 0, , .		0
258	Using Parallel Isosurface Extraction in Superficial Molecular Modeling. , 0, , .		4
259	Nervous System Database (NSD): data integration spanning molecular and system levels. Frontiers in Neuroinformatics, 0, 3, .	2.5	1
260	Bioinformatics molecular dynamics and docking pipeline analysis for high-throughput genome analysis and drug discovery oriented to personalized pain therapy in non-responsive patients.. Frontiers in Neuroinformatics, 0, 7, .	2.5	0
261	Multidisciplinary approach to identify gene-environment interplay triggering autism. Frontiers in Neuroscience, 0, 9, .	2.8	0