

Luciano Milanesi

List of Publications by Year in descending order

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261
papers

5,724
citations

109321

35
h-index

123424

61
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273
all docs

273
docs citations

273
times ranked

10563
citing authors

#	ARTICLE	IF	CITATIONS
1	Durum wheat genome highlights past domestication signatures and future improvement targets. <i>Nature Genetics</i> , 2019, 51, 885-895.	21.4	576
2	Methods for the integration of multi-omics data: mathematical aspects. <i>BMC Bioinformatics</i> , 2016, 17, 15.	2.6	316
3	Blood microRNA changes in depressed patients during antidepressant treatment. <i>European Neuropsychopharmacology</i> , 2013, 23, 602-611.	0.7	197
4	Analysis of donor splice sites in different eukaryotic organisms. <i>Journal of Molecular Evolution</i> , 1997, 45, 50-59.	1.8	148
5	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
6	Presence of ATG triplets in 5' untranslated regions of eukaryotic cDNAs correlates with a weak' context of the start codon. <i>Bioinformatics</i> , 2001, 17, 890-900.	4.1	126
7	Evaluation of BioCreAtIvE assessment of task 2. <i>BMC Bioinformatics</i> , 2005, 6, S16.	2.6	108
8	Osteogenic Differentiation of MSC through Calcium Signaling Activation: Transcriptomics and Functional Analysis. <i>PLoS ONE</i> , 2016, 11, e0148173.	2.5	99
9	A multilevel data integration resource for breast cancer study. <i>BMC Systems Biology</i> , 2010, 4, 76.	3.0	85
10	Multiclass HCV resistance to direct-acting antiviral failure in real-life patients advocates for tailored second-line therapies. <i>Liver International</i> , 2017, 37, 514-528.	3.9	84
11	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.	14.5	76
12	Association Study on Long-Living Individuals from Southern Italy Identifies rs10491334 in the <i>CAMKIV</i> Gene That Regulates Survival Proteins. <i>Rejuvenation Research</i> , 2011, 14, 283-291.	1.8	72
13	Inhibition of histone methyltransferase DOT1L silences ER α gene and blocks proliferation of antiestrogen-resistant breast cancer cells. <i>Science Advances</i> , 2019, 5, eaav5590.	10.3	70
14	Systematic analysis of human kinase genes: a large number of genes and alternative splicing events result in functional and structural diversity. <i>BMC Bioinformatics</i> , 2005, 6, S20.	2.6	65
15	The nuclear receptor ER α engages AGO2 in regulation of gene transcription, RNA splicing and RISC loading. <i>Genome Biology</i> , 2017, 18, 189.	8.8	63
16	Specific patterns of PIWI-interacting small noncoding RNA expression in dysplastic liver nodules and hepatocellular carcinoma. <i>Oncotarget</i> , 2016, 7, 54650-54661.	1.8	63
17	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.	2.5	59
18	GeneBuilder: interactive in silico prediction of gene structure. <i>Bioinformatics</i> , 1999, 15, 612-621.	4.1	58

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19	Environment, dysbiosis, immunity and sex-specific susceptibility: A translational hypothesis for regressive autism pathogenesis. <i>Nutritional Neuroscience</i> , 2015, 18, 145-161.	3.1	57
20	Genome and Phenotype Microarray Analyses of <i>Rhodococcus</i> sp. BCP1 and <i>Rhodococcus opacus</i> R7: Genetic Determinants and Metabolic Abilities with Environmental Relevance. <i>PLoS ONE</i> , 2015, 10, e0139467.	2.5	53
21	<i>Myosin-binding Protein C</i> DNA Variants in Domestic Cats (<i>CCAG31CCAGP</i> , <i>CCAG74CT</i> , <i>CCAG820CW</i>) and their Association with Hypertrophic Cardiomyopathy. <i>Journal of Veterinary Internal Medicine</i> , 2013, 27, 275-285.	1.6	51
22	Molecular Mechanism of Allosteric Communication in Hsp70 Revealed by Molecular Dynamics Simulations. <i>PLoS Computational Biology</i> , 2012, 8, e1002844.	3.2	49
23	Decreased Transcriptional Activity of <i>Calcium-sensing receptor</i> Gene Promoter 1 Is Associated With Calcium Nephrolithiasis. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2013, 98, 3839-3847.	3.6	49
24	Calcium kidney stones are associated with a haplotype of the calcium-sensing receptor gene regulatory region. <i>Nephrology Dialysis Transplantation</i> , 2010, 25, 2245-2252.	0.7	47
25	Transposable Element Insertions in Long Intergenic Non-Coding RNA Genes. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 71.	4.1	45
26	Methylation and sequence analysis around Eagi sites: identification of 28 new CpG islands in XQ24-XQ28. <i>Nucleic Acids Research</i> , 1992, 20, 727-733.	14.5	44
27	Phenotype microarray analysis may unravel genetic determinants of the stress response by <i>Rhodococcus aetherivorans</i> BCP1 and <i>Rhodococcus opacus</i> R7. <i>Research in Microbiology</i> , 2016, 167, 766-773.	2.1	43
28	NuChart: An R Package to Study Gene Spatial Neighbourhoods with Multi-Omics Annotations. <i>PLoS ONE</i> , 2013, 8, e75146.	2.5	42
29	Strategies for comparing gene expression profiles from different microarray platforms: Application to a case-control experiment. <i>Analytical Biochemistry</i> , 2006, 353, 43-56.	2.4	40
30	Fine mapping of <i>AHL1</i> as a schizophrenia susceptibility gene: from association to evolutionary evidence. <i>FASEB Journal</i> , 2010, 24, 3066-3082.	0.5	39
31	Serum BPIFB4 levels classify health status in long-living individuals. <i>Immunity and Ageing</i> , 2015, 12, 27.	4.2	39
32	ESTree db: a Tool for Peach Functional Genomics. <i>BMC Bioinformatics</i> , 2005, 6, S16.	2.6	38
33	The Subclass Approach for Mutational Spectrum Analysis: Application of the SEM Algorithm. <i>Journal of Theoretical Biology</i> , 1998, 192, 475-487.	1.7	37
34	Towards a systems biology approach to mammalian cell cycle: modeling the entrance into S phase of quiescent fibroblasts after serum stimulation. <i>BMC Bioinformatics</i> , 2009, 10, S16.	2.6	37
35	Systems biology of the metabolic network regulated by the Akt pathway. <i>Biotechnology Advances</i> , 2012, 30, 131-141.	11.7	37
36	Eukaryotic promoter recognition by binding sites for transcription factors. <i>Bioinformatics</i> , 1995, 11, 477-488.	4.1	36

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37	Biowep: a workflow enactment portal for bioinformatics applications. <i>BMC Bioinformatics</i> , 2007, 8, S19.	2.6	36
38	Homology modeling in tandem with 3D-QSAR analyses: A computational approach to depict the agonist binding site of the human CB2 receptor. <i>European Journal of Medicinal Chemistry</i> , 2011, 46, 4489-4505.	5.5	36
39	Study on the Association among Mycotoxins and other Variables in Children with Autism. <i>Toxins</i> , 2017, 9, 203.	3.4	36
40	Grid-Enabled High-Throughput In Silico Screening Against Influenza A Neuraminidase. <i>IEEE Transactions on Nanobioscience</i> , 2006, 5, 288-295.	3.3	35
41	Systems medicine of inflammaging. <i>Briefings in Bioinformatics</i> , 2016, 17, 527-540.	6.5	35
42	Antarctic marine ciliates under stress: superoxide dismutases from the psychrophilic <i>Euplotes focardii</i> are cold-active yet heat tolerant enzymes. <i>Scientific Reports</i> , 2018, 8, 14721.	3.3	35
43	Assessment and comparison of three scatter correction techniques in single photon emission computed tomography. <i>Journal of Nuclear Medicine</i> , 1988, 29, 1971-9.	5.0	34
44	Homology Modeling, Docking Studies and Molecular Dynamic Simulations Using Graphical Processing Unit Architecture to Probe the Type I Phosphodiesterase Catalytic Site: A Computational Approach for the Rational Design of Selective Inhibitors. <i>Chemical Biology and Drug Design</i> , 2013, 82, 718-731.	3.2	33
45	Large-scale profiling of signalling pathways reveals an asthma specific signature in bronchial smooth muscle cells. <i>Oncotarget</i> , 2016, 7, 25150-25161.	1.8	32
46	Protein annotation as term categorization in the gene ontology using word proximity networks. <i>BMC Bioinformatics</i> , 2005, 6, S20.	2.6	31
47	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
48	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. <i>European Journal of Medicinal Chemistry</i> , 2016, 124, 82-102.	5.5	31
49	An atomistic view of Hsp70 allosteric crosstalk: from the nucleotide to the substrate binding domain and back. <i>Scientific Reports</i> , 2016, 6, 23474.	3.3	31
50	Molecular Interaction Studies of HIV-1 Matrix Protein p17 and Heparin. <i>Journal of Biological Chemistry</i> , 2013, 288, 1150-1161.	3.4	30
51	The Exon-Intron Organization of the Human X-Linked Gene (FLN1) Encoding Actin-Binding Protein 280. <i>Genomics</i> , 1994, 21, 71-76.	2.9	29
52	ASPD (Artificially Selected Proteins/Peptides Database): a database of proteins and peptides evolved in vitro. <i>Nucleic Acids Research</i> , 2002, 30, 200-202.	14.5	29
53	Using web-based observations to identify thresholds of a person's stability in a flow. <i>Water Resources Research</i> , 2016, 52, 7793-7805.	4.2	29
54	FGF2 and EGF Are Required for Self-Renewal and Organoid Formation of Canine Normal and Tumor Breast Stem Cells. <i>Journal of Cellular Biochemistry</i> , 2017, 118, 570-584.	2.6	28

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55	Virtual screening on large scale grids. <i>Parallel Computing</i> , 2007, 33, 289-301.	2.1	27
56	ProCMD: a database and 3D web resource for protein C mutants. <i>BMC Bioinformatics</i> , 2007, 8, S11.	2.6	27
57	Medical Informatics and Bioinformatics: A Bibliometric Study. <i>IEEE Transactions on Information Technology in Biomedicine</i> , 2007, 11, 237-243.	3.2	27
58	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.	5.5	27
59	A Standards Organization for Open and FAIR Neuroscience: the International Neuroinformatics Coordinating Facility. <i>Neuroinformatics</i> , 2022, 20, 25-36.	2.8	26
60	Modelling the interaction of steroid receptors with endocrine disrupting chemicals. <i>BMC Bioinformatics</i> , 2005, 6, S10.	2.6	25
61	Reconstructing networks of pathways via significance analysis of their intersections. <i>BMC Bioinformatics</i> , 2008, 9, S9.	2.6	25
62	Trends in modeling Biomedical Complex Systems. <i>BMC Bioinformatics</i> , 2009, 10, I1.	2.6	25
63	Structural thermal adaptation of β -tubulins from the Antarctic psychrophilic protozoan <i>Euplotes focardii</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 1154-1166.	2.6	25
64	Correlation assessment among clinical phenotypes, expression analysis and molecular modeling of 14 novel variations in the human galactose-1-phosphate uridylyltransferase gene. <i>Human Mutation</i> , 2012, 33, 1107-1115.	2.5	25
65	Cloud Infrastructures for <i>In Silico</i> Drug Discovery: Economic and Practical Aspects. <i>BioMed Research International</i> , 2013, 2013, 1-19.	1.9	25
66	A novel polymorphism in SEL1L confers susceptibility to Alzheimer's disease. <i>Neuroscience Letters</i> , 2006, 398, 53-58.	2.1	24
67	In silico saturation mutagenesis and docking screening for the analysis of protein-ligand interaction: the Endothelial Protein C Receptor case study. <i>BMC Bioinformatics</i> , 2009, 10, S3.	2.6	24
68	LAV-BPIFB4 isoform modulates eNOS signalling through Ca ²⁺ /PKC-alpha-dependent mechanism. <i>Cardiovascular Research</i> , 2017, 113, 795-804.	3.8	24
69	Hamming-Clustering method for signals prediction in 5' and 3' regions of eukaryotic genes. <i>Bioinformatics</i> , 1996, 12, 399-404.	4.1	23
70	A data integration approach for cell cycle analysis oriented to model simulation in systems biology. <i>BMC Systems Biology</i> , 2007, 1, 35.	3.0	23
71	myMIR: a genome-wide microRNA targets identification and annotation tool. <i>Briefings in Bioinformatics</i> , 2011, 12, 588-600.	6.5	23
72	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

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73	Exome sequencing identifies variants in two genes encoding the LIM-proteins NRAP and FHL1 in an Italian patient with BAG3 myofibrillar myopathy. <i>Journal of Muscle Research and Cell Motility</i> , 2016, 37, 101-115.	2.0	23
74	VISPA2: a scalable pipeline for high-throughput identification and annotation of vector integration sites. <i>BMC Bioinformatics</i> , 2017, 18, 520.	2.6	23
75	An infrastructure for precision medicine through analysis of big data. <i>BMC Bioinformatics</i> , 2018, 19, 351.	2.6	23
76	Genome-based analysis for the identification of genes involved in o-xylene degradation in <i>Rhodococcus opacus</i> R7. <i>BMC Genomics</i> , 2018, 19, 587.	2.8	23
77	Data handling strategies for high throughput pyrosequencers. <i>BMC Bioinformatics</i> , 2007, 8, S22.	2.6	22
78	Version VI of the ESTree db: an improved tool for peach transcriptome analysis. <i>BMC Bioinformatics</i> , 2008, 9, S9.	2.6	22
79	Image-Based Surface Matching Algorithm Oriented to Structural Biology. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 1004-1016.	3.0	22
80	The Genome Conformation As an Integrator of Multi-Omic Data: The Example of Damage Spreading in Cancer. <i>Frontiers in Genetics</i> , 2016, 7, 194.	2.3	22
81	Integrated databases and computer systems for studying eukaryotic gene expression. <i>Bioinformatics</i> , 1999, 15, 669-686.	4.1	21
82	iSMART: a toolkit for a comprehensive analysis of small RNA-Seq data. <i>Bioinformatics</i> , 2017, 33, 938-940.	4.1	21
83	Network Diffusion Promotes the Integrative Analysis of Multiple Omics. <i>Frontiers in Genetics</i> , 2020, 11, 106.	2.3	21
84	Identification of functionally related genes using data mining and data integration: a breast cancer case study. <i>BMC Bioinformatics</i> , 2009, 10, S8.	2.6	20
85	Computational Modeling of the Metabolic States Regulated by the Kinase Akt. <i>Frontiers in Physiology</i> , 2012, 3, 418.	2.8	20
86	Network Diffusion-Based Prioritization of Autism Risk Genes Identifies Significantly Connected Gene Modules. <i>Frontiers in Genetics</i> , 2017, 8, 129.	2.3	20
87	The role of extracellular matrix in mouse and human corneal neovascularization. <i>Scientific Reports</i> , 2019, 9, 14272.	3.3	20
88	A diethylpyrocarbonate-based derivatization method for the LC-MS/MS measurement of plasma arginine and its chemically related metabolites and analogs. <i>Clinica Chimica Acta</i> , 2019, 492, 29-36.	1.1	20
89	A Hybrid Genetic-Neural System for Predicting Protein Secondary Structure. <i>BMC Bioinformatics</i> , 2005, 6, S3.	2.6	19
90	SNPLims: a data management system for genome wide association studies. <i>BMC Bioinformatics</i> , 2008, 9, S13.	2.6	19

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91	Stochastic neutral modelling of the Gut Microbiota's relative species abundance from next generation sequencing data. BMC Bioinformatics, 2016, 17, 16.	2.6	19
92	Ochratoxin A as possible factor triggering autism and its male prevalence <i>via</i> epigenetic mechanism. Nutritional Neuroscience, 2016, 19, 43-46.	3.1	19
93	Protein-coding regions prediction combining similarity searches and conservative evolutionary properties of protein-coding sequences. Gene, 1999, 226, 129-137.	2.2	18
94	A sentence sliding window approach to extract protein annotations from biomedical articles. BMC Bioinformatics, 2005, 6, S19.	2.6	18
95	SYMBIOmatics: Synergies in Medical Informatics and Bioinformatics " exploring current scientific literature for emerging topics. BMC Bioinformatics, 2007, 8, S18.	2.6	18
96	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
97	Segmenting the Human Genome into Isochores. Evolutionary Bioinformatics, 2015, 11, EBO.S27693.	1.2	18
98	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
99	Blockade of IGF2R improves muscle regeneration and ameliorates Duchenne muscular dystrophy. EMBO Molecular Medicine, 2020, 12, e11019.	6.9	18
100	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
101	Virtual screening pipeline and ligand modelling for H5N1 neuraminidase. Biochemical and Biophysical Research Communications, 2009, 383, 445-449.	2.1	17
102	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
103	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
104	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
105	Computational analysis of mutation spectra. Briefings in Bioinformatics, 2003, 4, 210-227.	6.5	16
106	Web services and workflow management for biological resources. BMC Bioinformatics, 2005, 6, S24.	2.6	16
107	CYCLONET--an integrated database on cell cycle regulation and carcinogenesis. Nucleic Acids Research, 2007, 35, D550-D556.	14.5	16
108	Literature Retrieval and Mining in Bioinformatics: State of the Art and Challenges. Advances in Bioinformatics, 2012, 2012, 1-10.	5.7	16

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109	Network-based analysis of omics with multi-objective optimization. <i>Molecular BioSystems</i> , 2013, 9, 2971.	2.9	16
110	Association Analysis of Noncoding Variants in Neuroligins 3 and 4X Genes with Autism Spectrum Disorder in an Italian Cohort. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1765.	4.1	16
111	CUDA's quicksort: an improved GPU-based implementation of quicksort. <i>Concurrency Computation Practice and Experience</i> , 2016, 28, 21-43.	2.2	16
112	Prediction of Human Gene Structure. , 1998, , 215-259.		16
113	Gene structure prediction using information on homologous protein sequence. <i>Bioinformatics</i> , 1996, 12, 161-170.	4.1	15
114	An Agent-Based Multilayer Architecture for Bioinformatics Grids. <i>IEEE Transactions on Nanobioscience</i> , 2007, 6, 142-148.	3.3	15
115	Nanoinformatics: developing new computing applications for nanomedicine. <i>Computing (Vienna/New)</i> Tj ETQq1 1 0.784314 15 BT /Over 4.8	4.8	15
116	Genome Sequence of <i>Rhodococcus opacus</i> Strain R7, a Biodegrader of Mono- and Polycyclic Aromatic Hydrocarbons. <i>Genome Announcements</i> , 2014, 2, .	0.8	15
117	A novel molecular dynamics approach to evaluate the effect of phosphorylation on multimeric protein interface: the β -Crystallin case study. <i>BMC Bioinformatics</i> , 2016, 17, 57.	2.6	15
118	A single amino acid substitution confers B-cell clonogenic activity to the HIV-1 matrix protein p17. <i>Scientific Reports</i> , 2017, 7, 6555.	3.3	15
119	GENVIEWER: A COMPUTING TOOL FOR PROTEIN-CODING REGIONS PREDICTION IN NUCLEOTIDE SEQUENCES. , 1993, , .		14
120	A grid portal with robot certificates for bioinformatics phylogenetic analyses. <i>Concurrency Computation Practice and Experience</i> , 2011, 23, 246-255.	2.2	14
121	Modeling the cell cycle: From deterministic models to hybrid systems. <i>BioSystems</i> , 2011, 105, 34-40.	2.0	14
122	Speeding Up the Identification of Cystic Fibrosis Transmembrane Conductance Regulator-Targeted Drugs: An Approach Based on Bioinformatics Strategies and Surface Plasmon Resonance. <i>Molecules</i> , 2018, 23, 120.	3.8	14
123	Ontology-based, Tissue MicroArray oriented, image centered tissue bank. <i>BMC Bioinformatics</i> , 2008, 9, S4.	2.6	13
124	The GENIUS Grid Portal and robot certificates: a new tool for e-Science. <i>BMC Bioinformatics</i> , 2009, 10, S21.	2.6	13
125	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. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 739-750.	3.0	13
126	The cell cycle DB: a systems biology approach to cell cycle analysis. <i>Nucleic Acids Research</i> , 2007, 36, D641-D645.	14.5	12

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127	IBDsite: a Galaxy-interacting, integrative database for supporting inflammatory bowel disease high throughput data analysis. BMC Bioinformatics, 2012, 13, S5.	2.6	12
128	Removing duplicate reads using graphics processing units. BMC Bioinformatics, 2016, 17, 346.	2.6	12
129	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
130	Integrating multi-omic features exploiting Chromosome Conformation Capture data. Frontiers in Genetics, 2015, 6, 40.	2.3	11
131	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
132	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
133	SITEVIDEO: a computer system for functional site analysis and recognition. Investigation of the human splice sites. Bioinformatics, 1993, 9, 617-627.	4.1	10
134	Prediction and phylogenetic analysis of mammalian short interspersed elements (SINEs). Briefings in Bioinformatics, 2000, 1, 260-274.	6.5	10
135	How computer science can help in understanding the 3D genome architecture. Briefings in Bioinformatics, 2016, 17, 733-744.	6.5	10
136	Transcriptomic Analysis of Rhodococcus opacus R7 Grown on o-Xylene by RNA-Seq. Frontiers in Microbiology, 2020, 11, 1808.	3.5	10
137	FROM CONTEXT-DEPENDENCE OF MUTATIONS TO MOLECULAR MECHANISMS OF MUTAGENESIS. , 2004, , .		10
138	ESTuber db: an online database for Tuber borchii EST sequences. BMC Bioinformatics, 2007, 8, S13.	2.6	9
139	Genome Sequence of <i>Rhodococcus</i> sp. Strain BCP1, a Biodegrader of Alkanes and Chlorinated Compounds. Genome Announcements, 2013, 1, .	0.8	9
140	Characterization and comparison of gene-centered human interactomes. Briefings in Bioinformatics, 2021, 22, .	6.5	9
141	Bayesian Phylogeny on Grid. Communications in Computer and Information Science, 2008, , 404-416.	0.5	9
142	Overview of BITS2005, the Second Annual Meeting of the Italian Bioinformatics Society. BMC Bioinformatics, 2005, 6, S1.	2.6	8
143	Ontology-oriented retrieval of putative microRNAs in <i>Vitis vinifera</i> via GrapeMiRNA: a web database of de novo predicted grape microRNAs. BMC Plant Biology, 2009, 9, 82.	3.6	8
144	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

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145	Tubulin folding: the special case of a beta-tubulin isotype from the Antarctic psychrophilic ciliate <i>Euplotes focardii</i> . <i>Polar Biology</i> , 2013, 36, 1833-1838.	1.2	8
146	Parallel Solutions for Voxel-Based Simulations of Reaction-Diffusion Systems. <i>BioMed Research International</i> , 2014, 2014, 1-10.	1.9	8
147	Guidelines for managing data and processes in bone and cartilage tissue engineering. <i>BMC Bioinformatics</i> , 2014, 15, S14.	2.6	8
148	G-CNV: A GPU-Based Tool for Preparing Data to Detect CNVs with Read-Depth Methods. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 28.	4.1	8
149	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
150	Biomedical applications of cyclotrons and review of commercially available models. <i>Journal of Medical Engineering and Technology</i> , 1987, 11, 166-176.	1.4	7
151	Sequence and Gene Content in 35 kb Genomic Clone Mapping in the Human Xq27.1 Region. <i>DNA Sequence</i> , 1997, 8, 1-15.	0.7	7
152	Î ³ -TRIS: a graph-algorithm for comprehensive identification of vector genomic insertion sites. <i>Bioinformatics</i> , 2020, 36, 1622-1624.	4.1	7
153	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. <i>Sensors and Actuators B: Chemical</i> , 2019, 301, 127131.	7.8	7
154	Evaluation of a Grid Based Molecular Dynamics Approach for Polypeptide Simulations. <i>IEEE Transactions on Nanobioscience</i> , 2007, 6, 229-234.	3.3	6
155	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
156	Molecular dynamics and docking simulation of a natural variant of Activated Protein C with impaired protease activity: implications for integrin-mediated antiseptic function. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 85-92.	3.5	6
157	Gene relevance based on multiple evidences in complex networks. <i>Bioinformatics</i> , 2020, 36, 865-871.	4.1	6
158	Modelling Spatial Heterogeneity and Macromolecular Crowding with Membrane Systems. <i>Lecture Notes in Computer Science</i> , 2010, , 285-304.	1.3	6
159	GPU-BSM: A GPU-Based Tool to Map Bisulfite-Treated Reads. <i>PLoS ONE</i> , 2014, 9, e97277.	2.5	6
160	Quantitative radionuclide angiocardigraphy using gold-195m. <i>American Journal of Cardiology</i> , 1984, 53, 1442-1446.	1.6	5
161	High performance cDNA sequence analysis using grid technology. <i>Journal of Parallel and Distributed Computing</i> , 2006, 66, 1482-1488.	4.1	5
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