

# Luciano Milanesi

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

225  
papers

4,046  
citations

32  
h-index

51  
g-index

273  
ext. papers

4,957  
ext. citations

4.8  
avg. IF

5.09  
L-index

#	Paper	IF	Citations
225	Classification and Personalized Prognostic Assessment on the Basis of Clinical and Genomic Features in Myelodysplastic Syndromes. <i>Journal of Clinical Oncology</i> , <b>2021</b> , 39, 1223-1233	2.2	25
224	Characterization and comparison of gene-centered human interactomes. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	1
223	A Standards Organization for Open and FAIR Neuroscience: the International Neuroinformatics Coordinating Facility. <i>Neuroinformatics</i> , <b>2021</b> , 1	3.2	9
222	Assessment of haptoglobin alleles in autism spectrum disorders. <i>Scientific Reports</i> , <b>2020</b> , 10, 7758	4.9	1
221	Network Diffusion Promotes the Integrative Analysis of Multiple Omics. <i>Frontiers in Genetics</i> , <b>2020</b> , 11, 106	4.5	5
220	Frailness and resilience of gene networks predicted by detection of co-occurring mutations via a stochastic perturbative approach. <i>Scientific Reports</i> , <b>2020</b> , 10, 2643	4.9	1
219	Gene relevance based on multiple evidences in complex networks. <i>Bioinformatics</i> , <b>2020</b> , 36, 865-871	7.2	3
218	ETRIS: a graph-algorithm for comprehensive identification of vector genomic insertion sites. <i>Bioinformatics</i> , <b>2020</b> , 36, 1622-1624	7.2	2
217	Blockade of IGF2R improves muscle regeneration and ameliorates Duchenne muscular dystrophy. <i>EMBO Molecular Medicine</i> , <b>2020</b> , 12, e11019	12	7
216	Profiling the Course of Resolving vs. Persistent Inflammation in Human Monocytes: The Role of IL-1 Family Molecules. <i>Frontiers in Immunology</i> , <b>2020</b> , 11, 1426	8.4	8
215	Transcriptomic Analysis of R7 Grown on -Xylene by RNA-Seq. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 1808	5.7	4
214	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> , <b>2019</b> , 301, 127131	8.5	4
213	isma: an R package for the integrative analysis of mutations detected by multiple pipelines. <i>BMC Bioinformatics</i> , <b>2019</b> , 20, 107	3.6	3
212	Durum wheat genome highlights past domestication signatures and future improvement targets. <i>Nature Genetics</i> , <b>2019</b> , 51, 885-895	36.3	289
211	Inhibition of histone methyltransferase DOT1L silences ER $\alpha$ gene and blocks proliferation of antiestrogen-resistant breast cancer cells. <i>Science Advances</i> , <b>2019</b> , 5, eaav5590	14.3	37
210	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> , <b>2019</b> , 492, 29-36	6.2	11
209	Network-Based Integrative Analysis of Genomics, Epigenomics and Transcriptomics in Autism Spectrum Disorders. <i>International Journal of Molecular Sciences</i> , <b>2019</b> , 20,	6.3	3

208	The role of extracellular matrix in mouse and human corneal neovascularization. <i>Scientific Reports</i> , <b>2019</b> , 9, 14272	4.9	10
207	Heparin and heparan sulfate proteoglycans promote HIV-1 p17 matrix protein oligomerization: computational, biochemical and biological implications. <i>Scientific Reports</i> , <b>2019</b> , 9, 15768	4.9	10
206	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> , <b>2018</b> , 23,	4.8	11
205	Genome-based analysis for the identification of genes involved in o-xylene degradation in <i>Rhodococcus opacus</i> R7. <i>BMC Genomics</i> , <b>2018</b> , 19, 587	4.5	10
204	A Scalable Genetic Programming Approach to Integrate miRNA-Target Predictions: Comparing Different Parallel Implementations of M3GP. <i>Complexity</i> , <b>2018</b> , 2018, 1-13	1.6	1
203	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> , <b>2018</b> , 8, 14721	4.9	19
202	An infrastructure for precision medicine through analysis of big data. <i>BMC Bioinformatics</i> , <b>2018</b> , 19, 351	3.6	12
201	Multiclass HCV resistance to direct-acting antiviral failure in real-life patients advocates for tailored second-line therapies. <i>Liver International</i> , <b>2017</b> , 37, 514-528	7.9	71
200	iSmaRT: a toolkit for a comprehensive analysis of small RNA-Seq data. <i>Bioinformatics</i> , <b>2017</b> , 33, 938-940	7.2	14
199	LAV-BPIFB4 isoform modulates eNOS signalling through Ca <sup>2+</sup> /PKC-alpha-dependent mechanism. <i>Cardiovascular Research</i> , <b>2017</b> , 113, 795-804	9.9	20
198	Low-Power Architectures for miRNA-Target Genome Wide Analysis <b>2017</b> ,		1
197	The nuclear receptor ER $\alpha$ engages AGO2 in regulation of gene transcription, RNA splicing and RISC loading. <i>Genome Biology</i> , <b>2017</b> , 18, 189	18.3	35
196	VISPA2: a scalable pipeline for high-throughput identification and annotation of vector integration sites. <i>BMC Bioinformatics</i> , <b>2017</b> , 18, 520	3.6	14
195	A rare genetic variant of BPIFB4 predisposes to high blood pressure via impairment of nitric oxide signaling. <i>Scientific Reports</i> , <b>2017</b> , 7, 9706	4.9	13
194	A single amino acid substitution confers B-cell clonogenic activity to the HIV-1 matrix protein p17. <i>Scientific Reports</i> , <b>2017</b> , 7, 6555	4.9	11
193	NuChart-II: The road to a fast and scalable tool for Hi-C data analysis. <i>International Journal of High Performance Computing Applications</i> , <b>2017</b> , 31, 196-211	1.8	3
192	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> , <b>2017</b> , 118, 570-584	4.7	17
191	RNA-Generated and Gene-Edited Induced Pluripotent Stem Cells for Disease Modeling and Therapy. <i>Journal of Cellular Physiology</i> , <b>2017</b> , 232, 1262-1269	7	11

190	Study on the Association among Mycotoxins and other Variables in Children with Autism. <i>Toxins</i> , <b>2017</b> , 9,	4.9	27
189	Network Diffusion-Based Prioritization of Autism Risk Genes Identifies Significantly Connected Gene Modules. <i>Frontiers in Genetics</i> , <b>2017</b> , 8, 129	4.5	17
188	Ochratoxin A as possible factor triggering autism and its male prevalence via epigenetic mechanism. <i>Nutritional Neuroscience</i> , <b>2016</b> , 19, 43-6	3.6	16
187	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> , <b>2016</b> , 124, 82-102	6.8	27
186	NuchaRt: Embedding High-Level Parallel Computing in R for Augmented Hi-C Data Analysis. <i>Lecture Notes in Computer Science</i> , <b>2016</b> , 259-272	0.9	2
185	An atomistic view of Hsp70 allosteric crosstalk: from the nucleotide to the substrate binding domain and back. <i>Scientific Reports</i> , <b>2016</b> , 6, 23474	4.9	24
184	Removing duplicate reads using graphics processing units. <i>BMC Bioinformatics</i> , <b>2016</b> , 17, 346	3.6	6
183	A novel molecular dynamics approach to evaluate the effect of phosphorylation on multimeric protein interface: the B-Crystallin case study. <i>BMC Bioinformatics</i> , <b>2016</b> , 17 Suppl 4, 57	3.6	13
182	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> , <b>2016</b> , 71, 739-50	5.1	12
181	Methods for the integration of multi-omics data: mathematical aspects. <i>BMC Bioinformatics</i> , <b>2016</b> , 17 Suppl 2, 15	3.6	208
180	Stochastic neutral modelling of the Gut Microbiota's relative species abundance from next generation sequencing data. <i>BMC Bioinformatics</i> , <b>2016</b> , 17 Suppl 2, 16	3.6	14
179	Systems medicine of inflammaging. <i>Briefings in Bioinformatics</i> , <b>2016</b> , 17, 527-40	13.4	27
178	How computer science can help in understanding the 3D genome architecture. <i>Briefings in Bioinformatics</i> , <b>2016</b> , 17, 733-44	13.4	10
177	Specific patterns of PIWI-interacting small noncoding RNA expression in dysplastic liver nodules and hepatocellular carcinoma. <i>Oncotarget</i> , <b>2016</b> , 7, 54650-54661	3.3	51
176	HPC Analysis of Multiple Binding Sites Communication and Allosteric Modulations in Drug Design: The HSP Case Study. <i>Current Drug Targets</i> , <b>2016</b> , 17, 1610-1625	3	2
175	Large-scale profiling of signalling pathways reveals an asthma specific signature in bronchial smooth muscle cells. <i>Oncotarget</i> , <b>2016</b> , 7, 25150-61	3.3	19
174	The Genome Conformation As an Integrator of Multi-Omic Data: The Example of Damage Spreading in Cancer. <i>Frontiers in Genetics</i> , <b>2016</b> , 7, 194	4.5	15
173	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> , <b>2016</b> , 17,	6.3	15

172	Osteogenic Differentiation of MSC through Calcium Signaling Activation: Transcriptomics and Functional Analysis. <i>PLoS ONE</i> , <b>2016</b> , 11, e0148173	3.7	56
171	Further Insights in the Binding Mode of Selective Inhibitors to Human PDE4D Enzyme Combining Docking and Molecular Dynamics. <i>Molecular Informatics</i> , <b>2016</b> , 35, 369-81	3.8	8
170	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> , <b>2016</b> , 167, 766-773	4.7	28
169	Network diffusion-based analysis of high-throughput data for the detection of differentially enriched modules. <i>Scientific Reports</i> , <b>2016</b> , 6, 34841	4.9	24
168	CUDA-quicksort: an improved GPU-based implementation of quicksort. <i>Concurrency Computation Practice and Experience</i> , <b>2016</b> , 28, 21-43	1.4	11
167	A Machine Learning Approach for the Integration of miRNA-Target Predictions <b>2016</b> ,		1
166	MicroRNA-Target Interaction: A Parallel Approach for Computing Pairing Energy <b>2016</b> ,		1
165	Using web-based observations to identify thresholds of a person's stability in a flow. <i>Water Resources Research</i> , <b>2016</b> , 52, 7793-7805	5.4	20
164	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> , <b>2016</b> , 12, 3447-3458		4
163	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> , <b>2016</b> , 37, 101-15	3.5	17
162	Integrating multi-omic features exploiting Chromosome Conformation Capture data. <i>Frontiers in Genetics</i> , <b>2015</b> , 6, 40	4.5	8
161	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> , <b>2015</b> , 33, 85-92	3.6	4
160	Serum BPIFB4 levels classify health status in long-living individuals. <i>Immunity and Ageing</i> , <b>2015</b> , 12, 27	9.7	27
159	G-CNV: A GPU-Based Tool for Preparing Data to Detect CNVs with Read-Depth Methods. <i>Frontiers in Bioengineering and Biotechnology</i> , <b>2015</b> , 3, 28	5.8	6
158	Transposable Element Insertions in Long Intergenic Non-Coding RNA Genes. <i>Frontiers in Bioengineering and Biotechnology</i> , <b>2015</b> , 3, 71	5.8	36
157	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> , <b>2015</b> , 10, e0124563	3.7	24
156	Segmenting the Human Genome into Isochores. <i>Evolutionary Bioinformatics</i> , <b>2015</b> , 11, 253-61	1.9	13
155	Parallel Exploration of the Nuclear Chromosome Conformation with NuChart-II <b>2015</b> ,		3

154	Environment, dysbiosis, immunity and sex-specific susceptibility: a translational hypothesis for regressive autism pathogenesis. <i>Nutritional Neuroscience</i> , <b>2015</b> , 18, 145-61	3.6	44
153	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> , <b>2015</b> , 10, e0139467	3.7	34
152	NuChart-II: A Graph-Based Approach for Analysis and Interpretation of Hi-C Data. <i>Lecture Notes in Computer Science</i> , <b>2015</b> , 298-311	0.9	
151	The WNoDeS Cloud Virtualization Framework: A Macromolecular Surface Analysis Application Case Study <b>2014</b> ,		1
150	P.2.a.006 Agomelatine and fluoxetine induce different and time-dependent modulation of rat hippocampal miRNome. <i>European Neuropsychopharmacology</i> , <b>2014</b> , 24, S364	1.2	1
149	Parallel solutions for voxel-based simulations of reaction-diffusion systems. <i>BioMed Research International</i> , <b>2014</b> , 2014, 980501	3	7
148	Genome Sequence of <i>Rhodococcus opacus</i> Strain R7, a Biodegrader of Mono- and Polycyclic Aromatic Hydrocarbons. <i>Genome Announcements</i> , <b>2014</b> , 2,		8
147	CUDA accelerated molecular surface generation. <i>Concurrency Computation Practice and Experience</i> , <b>2014</b> , 26, 1819-1831	1.4	3
146	Guidelines for managing data and processes in bone and cartilage tissue engineering. <i>BMC Bioinformatics</i> , <b>2014</b> , 15 Suppl 1, S14	3.6	4
145	A tool for mapping Single Nucleotide Polymorphisms using Graphics Processing Units. <i>BMC Bioinformatics</i> , <b>2014</b> , 15 Suppl 1, S10	3.6	3
144	GPU-BSM: a GPU-based tool to map bisulfite-treated reads. <i>PLoS ONE</i> , <b>2014</b> , 9, e97277	3.7	3
143	Diffusion of information throughout the host interactome reveals gene expression variations in network proximity to target proteins of hepatitis C virus. <i>PLoS ONE</i> , <b>2014</b> , 9, e113660	3.7	8
142	SNPranker 2.0: a gene-centric data mining tool for diseases associated SNP prioritization in GWAS. <i>BMC Bioinformatics</i> , <b>2013</b> , 14 Suppl 1, S9	3.6	20
141	Decreased transcriptional activity of calcium-sensing receptor gene promoter 1 is associated with calcium nephrolithiasis. <i>Journal of Clinical Endocrinology and Metabolism</i> , <b>2013</b> , 98, 3839-47	5.6	42
140	Tubulin folding: the special case of a beta-tubulin isotype from the Antarctic psychrophilic ciliate <i>Euplotes focardii</i> . <i>Polar Biology</i> , <b>2013</b> , 36, 1833-1838	2	4
139	Network-based analysis of omics with multi-objective optimization. <i>Molecular BioSystems</i> , <b>2013</b> , 9, 2971-80		14
138	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> , <b>2013</b> , 63, 423-34	6.8	23
137	Myosin-binding protein C DNA variants in domestic cats (A31P, A74T, R820W) and their association with hypertrophic cardiomyopathy. <i>Journal of Veterinary Internal Medicine</i> , <b>2013</b> , 27, 275-85	3.1	35

136	Blood microRNA changes in depressed patients during antidepressant treatment. <i>European Neuropsychopharmacology</i> , <b>2013</b> , 23, 602-11	1.2	163
135	Molecular interaction studies of HIV-1 matrix protein p17 and heparin: identification of the heparin-binding motif of p17 as a target for the development of multitarget antagonists. <i>Journal of Biological Chemistry</i> , <b>2013</b> , 288, 1150-61	5.4	24
134	Genome Sequence of Rhodococcus sp. Strain BCP1, a Biodegrader of Alkanes and Chlorinated Compounds. <i>Genome Announcements</i> , <b>2013</b> , 1,		7
133	Cloud infrastructures for in silico drug discovery: economic and practical aspects. <i>BioMed Research International</i> , <b>2013</b> , 2013, 138012	3	18
132	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. <i>Chemical Biology and Drug Design</i> , <b>2013</b> , 82, 718-31	2.9	24
131	Sensitivity analysis for studying the relation between biochemical reactions and metabolic phenotypes. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2013</b> , 11, 1340002	1	1
130	NuChart: an R package to study gene spatial neighbourhoods with multi-omics annotations. <i>PLoS ONE</i> , <b>2013</b> , 8, e75146	3.7	26
129	Complex System <b>2013</b> , 456-456		
128	Systems biology of the metabolic network regulated by the Akt pathway. <i>Biotechnology Advances</i> , <b>2012</b> , 30, 131-41	17.8	34
127	IBDsite: a Galaxy-interacting, integrative database for supporting inflammatory bowel disease high throughput data analysis. <i>BMC Bioinformatics</i> , <b>2012</b> , 13 Suppl 14, S5	3.6	12
126	Literature retrieval and mining in bioinformatics: state of the art and challenges. <i>Advances in Bioinformatics</i> , <b>2012</b> , 2012, 573846	5.5	14
125	Structural thermal adaptation of $\beta$ tubulins from the Antarctic psychrophilic protozoan <i>Euplotes focardii</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2012</b> , 80, 1154-66	4.2	20
124	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> , <b>2012</b> , 33, 1107-15	4.7	17
123	Nanoinformatics: developing new computing applications for nanomedicine. <i>Computing (Vienna/New York)</i> , <b>2012</b> , 94, 521-539	2.2	12
122	Molecular mechanism of allosteric communication in Hsp70 revealed by molecular dynamics simulations. <i>PLoS Computational Biology</i> , <b>2012</b> , 8, e1002844	5	43
121	Computational modeling of the metabolic States regulated by the kinase akt. <i>Frontiers in Physiology</i> , <b>2012</b> , 3, 418	4.6	17
120	Bioinformatics approach for data management about bone cells grown on substitute materials. <i>EMBnet Journal</i> , <b>2012</b> , 18, 148	2.3	2
119	Solving Biclustering with a GRASP-Like Metaheuristic: Two Case-Studies on Gene Expression Analysis. <i>Lecture Notes in Computer Science</i> , <b>2012</b> , 253-267	0.9	1



118	Functional Genomics Applications in GRID <b>2012</b> , 899-917		1
117	Human aryl-hydrocarbon receptor and its interaction with dioxin and physiological ligands investigated by molecular modelling and docking simulations. <i>Biochemical and Biophysical Research Communications</i> , <b>2011</b> , 413, 176-81	3.4	12
116	Ontology-based resources for bioinformatics analysis. <i>International Journal of Metadata, Semantics and Ontologies</i> , <b>2011</b> , 6, 35	0.6	2
115	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> , <b>2011</b> , 46, 4489-505	6.8	32
114	A grid portal with robot certificates for bioinformatics phylogenetic analyses. <i>Concurrency Computation Practice and Experience</i> , <b>2011</b> , 23, 246-255	1.4	9
113	Image-based surface matching algorithm oriented to structural biology. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2011</b> , 8, 1004-16	3	17
112	Modeling the cell cycle: from deterministic models to hybrid systems. <i>BioSystems</i> , <b>2011</b> , 105, 34-40	1.9	8
111	Modeling Biochemical Pathways <b>2011</b> , 111-126		
110	myMIR: a genome-wide microRNA targets identification and annotation tool. <i>Briefings in Bioinformatics</i> , <b>2011</b> , 12, 588-600	13.4	21
109	Association study on long-living individuals from Southern Italy identifies rs10491334 in the CAMKIV gene that regulates survival proteins. <i>Rejuvenation Research</i> , <b>2011</b> , 14, 283-91	2.6	68
108	Parallelization of the SSAKE Genomics Application <b>2011</b> ,		1
107	Grid Computing for Sensitivity Analysis of Stochastic Biological Models. <i>Lecture Notes in Computer Science</i> , <b>2011</b> , 62-73	0.9	3
106	Population Stratification Analysis in Genome-Wide Association Studies <b>2011</b> , 177-196		
105	Complex Search, Ranks, and Biological Discovery: A User's Perspective. <i>Lecture Notes in Computer Science</i> , <b>2011</b> , 226-235	0.9	1
104	Fine mapping of AHI1 as a schizophrenia susceptibility gene: from association to evolutionary evidence. <i>FASEB Journal</i> , <b>2010</b> , 24, 3066-82	0.9	32
103	A Dynamic Parallel Approach to Recognize Tubular Breast Cancer for TMA Image Building <b>2010</b> ,		1
102	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> , <b>2010</b> , 38, W262-7	20.1	42
101	Calcium kidney stones are associated with a haplotype of the calcium-sensing receptor gene regulatory region. <i>Nephrology Dialysis Transplantation</i> , <b>2010</b> , 25, 2245-52	4.3	43



100	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 <b>2010</b> , 119-130		
99	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> , <b>2010</b> , 10, 207-21	2	6
98	SNPRanker: a tool for identification and scoring of SNPs associated to target genes. <i>Journal of Integrative Bioinformatics</i> , <b>2010</b> , 7, 331-345	3.8	3
97	Grid Based Genome Wide Studies on Atrial Flutter. <i>Journal of Grid Computing</i> , <b>2010</b> , 8, 511-527	4.2	2
96	Molecular remodeling of potassium channels in fibroblasts from centenarians: a marker of longevity?. <i>Mechanisms of Ageing and Development</i> , <b>2010</b> , 131, 674-81	5.6	5
95	Semi-automatic identification of punching areas for tissue microarray building: the tubular breast cancer pilot study. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 566	3.6	2
94	A multilevel data integration resource for breast cancer study. <i>BMC Systems Biology</i> , <b>2010</b> , 4, 76	3.5	67
93	Exploring the role of the phospholipid ligand in endothelial protein C receptor: a molecular dynamics study. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2010</b> , 78, 2679-90	4.2	10
92	A Novel Variant of P Systems for the Modelling and Simulation of Biochemical Systems. <i>Lecture Notes in Computer Science</i> , <b>2010</b> , 210-226	0.9	2
91	Modelling Spatial Heterogeneity and Macromolecular Crowding with Membrane Systems. <i>Lecture Notes in Computer Science</i> , <b>2010</b> , 285-304	0.9	3
90	SNPRanker: a tool for identification and scoring of SNPs associated to target genes. <i>Journal of Integrative Bioinformatics</i> , <b>2010</b> , 7,	3.8	2
89	Trends in modeling Biomedical Complex Systems. <i>BMC Bioinformatics</i> , <b>2009</b> , 10 Suppl 12, I1	3.6	18
88	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> , <b>2009</b> , 10 Suppl 12, S16	3.6	35
87	The Human EST Ontology Explorer: a tissue-oriented visualization system for ontologies distribution in human EST collections. <i>BMC Bioinformatics</i> , <b>2009</b> , 10 Suppl 12, S2	3.6	1
86	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> , <b>2009</b> , 10 Suppl 12, S3	3.6	19
85	Identification of functionally related genes using data mining and data integration: a breast cancer case study. <i>BMC Bioinformatics</i> , <b>2009</b> , 10 Suppl 12, S8	3.6	16
84	The GENIUS Grid Portal and robot certificates: a new tool for e-Science. <i>BMC Bioinformatics</i> , <b>2009</b> , 10 Suppl 6, S21	3.6	8
83	Ontology-oriented retrieval of putative microRNAs in <i>Vitis vinifera</i> via GrapeMiRNA: a web database of de novo predicted grape microRNAs. <i>BMC Plant Biology</i> , <b>2009</b> , 9, 82	5.3	6

82	Virtual screening pipeline and ligand modelling for H5N1 neuraminidase. <i>Biochemical and Biophysical Research Communications</i> , <b>2009</b> , 383, 445-9	3.4	17
81	Stochastic Simulations on a Grid Framework for Parameter Sweep Applications in Biological Models <b>2009</b> ,		4
80	Parallel Decomposition of 3D Surfaces in Images of Local Descriptors for Molecular Screening <b>2009</b> ,		1
79	Multi-Level Data Integration and Data Mining in Systems Biology <b>2009</b> , 476-496		1
78	Ontological Enrichment of the Genes-to-Systems Breast Cancer Database. <i>Communications in Computer and Information Science</i> , <b>2009</b> , 171-182	0.3	1
77	A Visualization ToolKit Based Application for Representing Macromolecular Surfaces. <i>Lecture Notes in Computer Science</i> , <b>2009</b> , 284-292	0.9	
76	SNPLims: a data management system for genome wide association studies. <i>BMC Bioinformatics</i> , <b>2008</b> , 9 Suppl 2, S13	3.6	14
75	Version VI of the ESTree db: an improved tool for peach transcriptome analysis. <i>BMC Bioinformatics</i> , <b>2008</b> , 9 Suppl 2, S9	3.6	21
74	Ontology-based, Tissue MicroArray oriented, image centered tissue bank. <i>BMC Bioinformatics</i> , <b>2008</b> , 9 Suppl 4, S4	3.6	10
73	Reconstructing networks of pathways via significance analysis of their intersections. <i>BMC Bioinformatics</i> , <b>2008</b> , 9 Suppl 4, S9	3.6	22
72	Images Based System for Surface Matching in Macromolecular Screening <b>2008</b> ,		4
71	TMAinspect, an EGEE Framework for Tissue MicroArray Image Handling <b>2008</b> ,		2
70	Mining the bovine genome with the "Bovine SNP Retriever". <i>Journal of Heredity</i> , <b>2008</b> , 99, 696-8	2.4	
69	<b>2008</b> ,		1
68	A parallel protein surface reconstruction system. <i>International Journal of Bioinformatics Research and Applications</i> , <b>2008</b> , 4, 221-39	0.9	3
67	The cell cycle DB: a systems biology approach to cell cycle analysis. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D641-51	1.5	10
66	Bayesian Phylogeny on Grid. <i>Communications in Computer and Information Science</i> , <b>2008</b> , 404-416	0.3	6
65	Grid methodology for identifying co-regulated genes and transcription factor binding sites. <i>IEEE Transactions on Nanobioscience</i> , <b>2007</b> , 6, 162-7	3.4	2

64	An agent-based multilayer architecture for bioinformatics grids. <i>IEEE Transactions on Nanobioscience</i> , <b>2007</b> , 6, 142-8	3.4	12
63	A fast job scheduling system for a wide range of bioinformatic applications. <i>IEEE Transactions on Nanobioscience</i> , <b>2007</b> , 6, 149-54	3.4	3
62	Evaluation of a grid based molecular dynamics approach for polypeptide simulations. <i>IEEE Transactions on Nanobioscience</i> , <b>2007</b> , 6, 229-34	3.4	5
61	Virtual screening on large scale grids. <i>Parallel Computing</i> , <b>2007</b> , 33, 289-301	1	16
60	A data integration approach for cell cycle analysis oriented to model simulation in systems biology. <i>BMC Systems Biology</i> , <b>2007</b> , 1, 35	3.5	22
59	ProCMD: a database and 3D web resource for protein C mutants. <i>BMC Bioinformatics</i> , <b>2007</b> , 8 Suppl 1, S11	3.6	24
58	ESTuber db: an online database for Tuber borchii EST sequences. <i>BMC Bioinformatics</i> , <b>2007</b> , 8 Suppl 1, S13	3.6	8
57	SYMBIOmatics: synergies in Medical Informatics and Bioinformatics--exploring current scientific literature for emerging topics. <i>BMC Bioinformatics</i> , <b>2007</b> , 8 Suppl 1, S18	3.6	15
56	Biowep: a workflow enactment portal for bioinformatics applications. <i>BMC Bioinformatics</i> , <b>2007</b> , 8 Suppl 1, S19	3.6	24
55	Data handling strategies for high throughput pyrosequencers. <i>BMC Bioinformatics</i> , <b>2007</b> , 8 Suppl 1, S22	3.6	20
54	Medical informatics and bioinformatics: a bibliometric study. <i>IEEE Transactions on Information Technology in Biomedicine</i> , <b>2007</b> , 11, 237-43		24
53	NETWORKS FROM GENE EXPRESSION TIME SERIES: CHARACTERIZATION OF CORRELATION PATTERNS. <i>International Journal of Bifurcation and Chaos in Applied Sciences and Engineering</i> , <b>2007</b> , 17, 2477-2483	2	5
52	CYCLONET--an integrated database on cell cycle regulation and carcinogenesis. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D550-6	20.1	13
51	Grid-Enabled High Throughput Virtual Screening <b>2007</b> , 45-59		1
50	BGBlast: a BLAST grid implementation with database self-updating and adaptive replication. <i>Studies in Health Technology and Informatics</i> , <b>2007</b> , 126, 23-30	0.5	3
49	Parameter estimation for cell cycle ordinary differential equation (ODE) models using a grid approach. <i>Studies in Health Technology and Informatics</i> , <b>2007</b> , 126, 93-102	0.5	1
48	Tissue MicroArray: a distributed Grid approach for image analysis. <i>Studies in Health Technology and Informatics</i> , <b>2007</b> , 126, 291-8	0.5	2
47	Grid-enabled high-throughput in silico screening against influenza A neuraminidase. <i>IEEE Transactions on Nanobioscience</i> , <b>2006</b> , 5, 288-95	3.4	23

46	A novel polymorphism in SEL1L confers susceptibility to Alzheimer's disease. <i>Neuroscience Letters</i> , <b>2006</b> , 398, 53-8	3.3	22
45	Network integration of data and analysis of oncology interest. <i>Journal of Integrative Bioinformatics</i> , <b>2006</b> , 3, 45-55	3.8	1
44	Strategies for comparing gene expression profiles from different microarray platforms: application to a case-control experiment. <i>Analytical Biochemistry</i> , <b>2006</b> , 353, 43-56	3.1	37
43	High performance cDNA sequence analysis using grid technology. <i>Journal of Parallel and Distributed Computing</i> , <b>2006</b> , 66, 1482-1488	4.4	3
42	High performance GRID based implementation for genomics and protein analysis. <i>Studies in Health Technology and Informatics</i> , <b>2006</b> , 120, 374-80	0.5	2
41	Representation and modeling of protein surface determinants. <i>IEEE Transactions on Nanobioscience</i> , <b>2005</b> , 4, 301-5	3.4	1
40	Multiple alignment through protein secondary-structure information. <i>IEEE Transactions on Nanobioscience</i> , <b>2005</b> , 4, 207-11	3.4	1
39	Evaluation of BioCreAtivE assessment of task 2. <i>BMC Bioinformatics</i> , <b>2005</b> , 6 Suppl 1, S16	3.6	82
38	A sentence sliding window approach to extract protein annotations from biomedical articles. <i>BMC Bioinformatics</i> , <b>2005</b> , 6 Suppl 1, S19	3.6	13
37	Protein annotation as term categorization in the gene ontology using word proximity networks. <i>BMC Bioinformatics</i> , <b>2005</b> , 6 Suppl 1, S20	3.6	20
36	Overview of BITS2005, the Second Annual Meeting of the Italian Bioinformatics Society. <i>BMC Bioinformatics</i> , <b>2005</b> , 6, S1	3.6	3
35	Modelling the interaction of steroid receptors with endocrine disrupting chemicals. <i>BMC Bioinformatics</i> , <b>2005</b> , 6 Suppl 4, S10	3.6	19
34	ESTree db: a tool for peach functional genomics. <i>BMC Bioinformatics</i> , <b>2005</b> , 6 Suppl 4, S16	3.6	28
33	High performance workflow implementation for protein surface characterization using grid technology. <i>BMC Bioinformatics</i> , <b>2005</b> , 6 Suppl 4, S19	3.6	3
32	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> , <b>2005</b> , 6 Suppl 4, S20	3.6	56
31	Web services and workflow management for biological resources. <i>BMC Bioinformatics</i> , <b>2005</b> , 6 Suppl 4, S24	3.6	13
30	A hybrid genetic-neural system for predicting protein secondary structure. <i>BMC Bioinformatics</i> , <b>2005</b> , 6 Suppl 4, S3	3.6	14
29	Using Secondary Structure Information to Perform Multiple Alignment. <i>Lecture Notes in Computer Science</i> , <b>2005</b> , 78-88	0.9	

28	Computational analysis of mutation spectra. <i>Briefings in Bioinformatics</i> , <b>2003</b> , 4, 210-27	13.4	12
27	ESTMAP: a system for expressed sequence tags mapping on genomic sequences. <i>IEEE Transactions on Nanobioscience</i> , <b>2003</b> , 2, 75-8	3.4	3
26	ASPD (Artificially Selected Proteins/Peptides Database): a database of proteins and peptides evolved in vitro. <i>Nucleic Acids Research</i> , <b>2002</b> , 30, 200-2	20.1	21
25	Presence of ATG triplets in 5' untranslated regions of eukaryotic cDNAs correlates with a 'weak' context of the start codon. <i>Bioinformatics</i> , <b>2001</b> , 17, 890-900	7.2	118
24	Prediction and phylogenetic analysis of mammalian short interspersed elements (SINEs). <i>Briefings in Bioinformatics</i> , <b>2000</b> , 1, 260-74	13.4	10
23	GeneBuilder: interactive in silico prediction of gene structure. <i>Bioinformatics</i> , <b>1999</b> , 15, 612-21	7.2	52
22	Integrated databases and computer systems for studying eukaryotic gene expression. <i>Bioinformatics</i> , <b>1999</b> , 15, 669-86	7.2	19
21	Protein-coding regions prediction combining similarity searches and conservative evolutionary properties of protein-coding sequences. <i>Gene</i> , <b>1999</b> , 226, 129-37	3.8	16
20	The subclass approach for mutational spectrum analysis: application of the SEM algorithm. <i>Journal of Theoretical Biology</i> , <b>1998</b> , 192, 475-87	2.3	35
19	Molecular Probe Data Base (MPDB). <i>Nucleic Acids Research</i> , <b>1998</b> , 26, 145-7	20.1	2
18	Prediction of Human Gene Structure <b>1998</b> , 215-259		10
17	Sequence and gene content in 35 kb genomic clone mapping in the human Xq27.1 region. <i>DNA Sequence</i> , <b>1997</b> , 8, 1-15		4
16	Identification of a U7snRNA homologue mapping to the human Xq27.1 region, between the DXS1232 and DXS119 loci. <i>Gene</i> , <b>1997</b> , 187, 221-4	3.8	2
15	Analysis of donor splice sites in different eukaryotic organisms. <i>Journal of Molecular Evolution</i> , <b>1997</b> , 45, 50-9	3.1	135
14	Characterization and fine localization of two new genes in Xq28 using the genomic sequence/EST database screening approach. <i>Genomics</i> , <b>1996</b> , 34, 323-7	4.3	14
13	Gene structure prediction using information on homologous protein sequence. <i>Bioinformatics</i> , <b>1996</b> , 12, 161-70	7.2	8
12	Hamming-Clustering method for signals prediction in 5' and 3' regions of eukaryotic genes. <i>Bioinformatics</i> , <b>1996</b> , 12, 399-404	7.2	15
11	Eukaryotic promoter recognition by binding sites for transcription factors. <i>Bioinformatics</i> , <b>1995</b> , 11, 477-88	7.2	18

10	Data bank homology search algorithm with linear computation complexity. <i>Bioinformatics</i> , <b>1994</b> , 10, 319-22	7.2	1
9	The exon-intron organization of the human X-linked gene (FLN1) encoding actin-binding protein 280. <i>Genomics</i> , <b>1994</b> , 21, 71-6	4.3	25
8	Concept-based indexing and retrieval of multimedia documents. <i>Journal of Information Science</i> , <b>1994</b> , 20, 185-196	2	1
7	SITEVIDEO: a computer system for functional site analysis and recognition. Investigation of the human splice sites. <i>Bioinformatics</i> , <b>1993</b> , 9, 617-27	7.2	6
6	GENVIEWER: A COMPUTING TOOL FOR PROTEIN-CODING REGIONS PREDICTION IN NUCLEOTIDE SEQUENCES <b>1993</b> ,		7
5	Methylation and sequence analysis around EagI sites: identification of 28 new CpG islands in XQ24-XQ28. <i>Nucleic Acids Research</i> , <b>1992</b> , 20, 727-33	20.1	42
4	Fast, statistically based alignment of amino acid sequences on the base of diagonal fragments of DOT-matrices. <i>Bioinformatics</i> , <b>1992</b> , 8, 529-34	7.2	1
3	Assessment and comparison of three scatter correction techniques in single photon emission computed tomography. <i>Journal of Nuclear Medicine</i> , <b>1988</b> , 29, 1971-9	8.9	33
2	Biomedical applications of cyclotrons and review of commercially available models. <i>Journal of Medical Engineering and Technology</i> , <b>1987</b> , 11, 166-76	1.8	7
1	Quantitative radionuclide angiocardiology using gold-195m. <i>American Journal of Cardiology</i> , <b>1984</b> , 53, 1442-6	3	5