

Chiara Romualdi

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.

159
papers

6,274
citations

44
h-index

73
g-index

178
ext. papers

7,282
ext. citations

7.2
avg, IF

5.39
L-index

#	Paper	IF	Citations
159	miRNA bioinformatics and pathway analysis 2022 , 141-150		
158	BrewerIX enables allelic expression analysis of imprinted and X-linked genes from bulk and single-cell transcriptomes.. <i>Communications Biology</i> , 2022 , 5, 146	6.7	1
157	NewWave: a scalable R/Bioconductor package for the dimensionality reduction and batch effect removal of single-cell RNA-seq data.. <i>Bioinformatics</i> , 2022 ,	7.2	1
156	Genome-wide Copy-number Alterations in Circulating Tumor DNA as a Novel Biomarker for Patients with High-grade Serous Ovarian Cancer. <i>Clinical Cancer Research</i> , 2021 , 27, 2549-2559	12.9	7
155	Regional and temporal heterogeneity of epithelial ovarian cancer tumor biopsies: implications for therapeutic strategies. <i>Oncotarget</i> , 2021 , 12, 2404-2417	3.3	11
154	A novel prognostic score to assess the risk of progression in relapsing-remitting multiple sclerosis patients. <i>European Journal of Neurology</i> , 2021 , 28, 2503-2512	6	3
153	MicroRNA expression profiling with a droplet digital PCR assay enables molecular diagnosis and prognosis of cancers of unknown primary. <i>Molecular Oncology</i> , 2021 , 15, 2732-2751	7.9	3
152	Comprehensive Profiling of Hypoxia-Related miRNAs Identifies miR-23a-3p Overexpression as a Marker of Platinum Resistance and Poor Prognosis in High-Grade Serous Ovarian Cancer. <i>Cancers</i> , 2021 , 13,	6.6	1
151	MyoData: An expression knowledgebase at single cell/nucleus level for the discovery of coding-noncoding RNA functional interactions in skeletal muscle. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 4142-4155	6.8	1
150	PsiNorm: a scalable normalization for single-cell RNA-seq data. <i>Bioinformatics</i> , 2021 ,	7.2	4
149	Genome-wide study of salivary miRNAs identifies miR-423-5p as promising diagnostic and prognostic biomarker in oral squamous cell carcinoma. <i>Theranostics</i> , 2021 , 11, 2987-2999	12.1	17
148	The CSF Profile Linked to Cortical Damage Predicts Multiple Sclerosis Activity. <i>Annals of Neurology</i> , 2020 , 88, 562-573	9.4	22
147	Microbiota changes induced by microencapsulated sodium butyrate in patients with inflammatory bowel disease. <i>Neurogastroenterology and Motility</i> , 2020 , 32, e13914	4	19
146	Expression profiles of PRKG1, SDF2L1 and PPP1R12A are predictive and prognostic factors for therapy response and survival in high-grade serous ovarian cancer. <i>International Journal of Cancer</i> , 2020 , 147, 565-574	7.5	4
145	Searching for the Source of Difference: A Graphical Model Approach. <i>Lecture Notes in Computer Science</i> , 2020 , 131-138	0.9	
144	Targeting p53 and histone methyltransferases restores exhausted CD8+ T cells in HCV infection. <i>Nature Communications</i> , 2020 , 11, 604	17.4	24
143	A TGF- β associated genetic score to define prognosis and platinum sensitivity in advanced epithelial ovarian cancer. <i>Gynecologic Oncology</i> , 2020 , 156, 233-242	4.9	2

142	Pharmacogenetic score predicts overall survival, progression-free survival and platinum sensitivity in ovarian cancer. <i>Pharmacogenomics</i> , 2020 , 21, 995-1010	2.6	
141	Assessment of statistical methods from single cell, bulk RNA-seq, and metagenomics applied to microbiome data. <i>Genome Biology</i> , 2020 , 21, 191	18.3	21
140	Microbiota of the Therapeutic Euganean Thermal Muds with a Focus on the Main Cyanobacteria Species. <i>Microorganisms</i> , 2020 , 8,	4.9	6
139	Simulating gene silencing through intervention analysis. <i>Journal of the Royal Statistical Society Series C: Applied Statistics</i> , 2020 , 69, 887-907	1.5	
138	FXYS5 (Dysadherin) upregulation predicts shorter survival and reveals platinum resistance in high-grade serous ovarian cancer patients. <i>British Journal of Cancer</i> , 2019 , 121, 584-592	8.7	15
137	Paradoxical GH Increase During OGTT Is Associated With First-Generation Somatostatin Analog Responsiveness in Acromegaly. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2019 , 104, 856-862	5.6	10
136	MOSClip: multi-omic and survival pathway analysis for the identification of survival associated gene and modules. <i>Nucleic Acids Research</i> , 2019 , 47, e80	20.1	5
135	rs4143815-, a New Potential Immunogenetic Biomarker of Biochemical Recurrence in Locally Advanced Prostate Cancer after Radiotherapy. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	3
134	Multisite analysis of high-grade serous epithelial ovarian cancers identifies genomic regions of focal and recurrent copy number alteration in 3q26.2 and 8q24.3. <i>International Journal of Cancer</i> , 2019 , 145, 2670-2681	7.5	7
133	Transcriptome Profiles of Human Visceral Adipocytes in Obesity and Colorectal Cancer Unravel the Effects of Body Mass Index and Polyunsaturated Fatty Acids on Genes and Biological Processes Related to Tumorigenesis. <i>Frontiers in Immunology</i> , 2019 , 10, 265	8.4	15
132	Transcriptomic Analysis of Single Isolated Myofibers Identifies miR-27a-3p and miR-142-3p as Regulators of Metabolism in Skeletal Muscle. <i>Cell Reports</i> , 2019 , 26, 3784-3797.e8	10.6	35
131	Increased NK Cell Count in Multiple Sclerosis Patients Treated With Dimethyl Fumarate: A 2-Year Longitudinal Study. <i>Frontiers in Immunology</i> , 2019 , 10, 1666	8.4	10
130	Sex identification from distinctive gene expression patterns in Antarctic krill (<i>Euphausia superba</i>). <i>Polar Biology</i> , 2019 , 42, 2205-2217	2	1
129	SourceSet: A graphical model approach to identify primary genes in perturbed biological pathways. <i>PLoS Computational Biology</i> , 2019 , 15, e1007357	5	3
128	Individual Radiosensitivity in Oncological Patients: Linking Adverse Normal Tissue Reactions and Genetic Features. <i>Frontiers in Oncology</i> , 2019 , 9, 987	5.3	11
127	Transcriptional Characterization of Stage I Epithelial Ovarian Cancer: A Multicentric Study. <i>Cells</i> , 2019 , 8,	7.9	3
126	metaGraphite-a new layer of pathway annotation to get metabolite networks. <i>Bioinformatics</i> , 2019 , 35, 1258-1260	7.2	19
125	Direct generation of human naive induced pluripotent stem cells from somatic cells in microfluidics. <i>Nature Cell Biology</i> , 2019 , 21, 275-286	23.4	38

124	Single cell analysis reveals the involvement of the long non-coding RNA Pvt1 in the modulation of muscle atrophy and mitochondrial network. <i>Nucleic Acids Research</i> , 2019 , 47, 1653-1670	20.1	45
123	Inflammatory intrathecal profiles and cortical damage in multiple sclerosis. <i>Annals of Neurology</i> , 2018 , 83, 739-755	9.4	129
122	A systems biology approach to investigate the mechanism of action of trabectedin in a model of myelomonocytic leukemia. <i>Pharmacogenomics Journal</i> , 2018 , 18, 56-63	3.5	6
121	Changes in Accident & Emergency Visits and Return Visits in Relation to the Enforcement of Daylight Saving Time and Photoperiod. <i>Journal of Biological Rhythms</i> , 2018 , 33, 555-564	3.2	7
120	The cortical damage, early relapses, and onset of the progressive phase in multiple sclerosis. <i>Neurology</i> , 2018 , 90, e2107-e2118	6.5	51
119	The effect of fingolimod on focal and diffuse grey matter damage in active MS patients. <i>Journal of Neurology</i> , 2018 , 265, 2154-2161	5.5	7
118	LINE-1 hypomethylation is associated to specific clinico-pathological features in Stage I non-small cell lung cancer. <i>Lung Cancer</i> , 2017 , 108, 83-89	5.9	18
117	Circulating miRNA landscape identifies miR-1246 as promising diagnostic biomarker in high-grade serous ovarian carcinoma: A validation across two independent cohorts. <i>Cancer Letters</i> , 2017 , 388, 320-327	9.9	52
116	Analysis of potential factors affecting allografts contamination at retrieval. <i>Cell and Tissue Banking</i> , 2017 , 18, 539-545	2.2	8
115	simPATHy: a new method for simulating data from perturbed biological PATHways. <i>Bioinformatics</i> , 2017 , 33, 456-457	7.2	3
114	Cognitive impairment predicts disability progression and cortical thinning in MS: An 8-year study. <i>Multiple Sclerosis Journal</i> , 2017 , 23, 848-854	5	59
113	lncRNAs as Novel Indicators of Patients Prognosis in Stage I Epithelial Ovarian Cancer: A Retrospective and Multicentric Study. <i>Clinical Cancer Research</i> , 2017 , 23, 2356-2366	12.9	47
112	Circulating Cell-Free DNA in Dogs with Mammary Tumors: Short and Long Fragments and Integrity Index. <i>PLoS ONE</i> , 2017 , 12, e0169454	3.7	21
111	KrillDB: A de novo transcriptome database for the Antarctic krill (<i>Euphausia superba</i>). <i>PLoS ONE</i> , 2017 , 12, e0171908	3.7	16
110	NELL1, whose high expression correlates with negative outcomes, has different methylation patterns in alveolar and embryonal rhabdomyosarcoma. <i>Oncotarget</i> , 2017 , 8, 33086-33099	3.3	10
109	Global DNA methylation profiling uncovers distinct methylation patterns of protocadherin alpha4 in metastatic and non-metastatic rhabdomyosarcoma. <i>BMC Cancer</i> , 2016 , 16, 886	4.8	10
108	A prognostic regulatory pathway in stage I epithelial ovarian cancer: new hints for the poor prognosis assessment. <i>Annals of Oncology</i> , 2016 , 27, 1511-9	10.3	15
107	Antimicrobial use and microbiological testing in district general hospital ICUs of the Veneto region of north-east Italy. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2016 , 35, 1627-38	5.3	1

106	Identification of high-grade serous ovarian cancer miRNA species associated with survival and drug response in patients receiving neoadjuvant chemotherapy: a retrospective longitudinal analysis using matched tumor biopsies. <i>Annals of Oncology</i> , 2016 , 27, 625-34	10.3	39
105	COLOMBOS v3.0: leveraging gene expression compendia for cross-species analyses. <i>Nucleic Acids Research</i> , 2016 , 44, D620-3	20.1	41
104	Disentangling the microRNA regulatory milieu in multiple myeloma: integrative genomics analysis outlines mixed miRNA-TF circuits and pathway-derived networks modulated in t(4;14) patients. <i>Oncotarget</i> , 2016 , 7, 2367-78	3.3	35
103	Usefulness of the Total Thrombus-Formation Analysis System (T-TAS) in the diagnosis and characterization of von Willebrand disease. <i>Haemophilia</i> , 2016 , 22, 949-956	3.3	13
102	A data-driven network model of primary myelofibrosis: transcriptional and post-transcriptional alterations in CD34+ cells. <i>Blood Cancer Journal</i> , 2016 , 6, e439	7	12
101	Characterizing genomic alterations in cancer by complementary functional associations. <i>Nature Biotechnology</i> , 2016 , 34, 539-46	44.5	57
100	Similarity Measures Based on the Overlap of Ranked Genes Are Effective for Comparison and Classification of Microarray Data. <i>Journal of Computational Biology</i> , 2016 , 23, 603-14	1.7	2
99	Profiling cancer gene mutations in longitudinal epithelial ovarian cancer biopsies by targeted next-generation sequencing: a retrospective study. <i>Annals of Oncology</i> , 2015 , 26, 1363-71	10.3	28
98	The self-morningness/eveningness (Self-ME): An extremely concise and totally subjective assessment of diurnal preference. <i>Chronobiology International</i> , 2015 , 32, 1192-200	3.6	21
97	Pyrosequencing and de novo assembly of Antarctic krill (<i>Euphausia superba</i>) transcriptome to study the adaptability of krill to climate-induced environmental changes. <i>Molecular Ecology Resources</i> , 2015 , 15, 1460-71	8.4	23
96	Aberrant DNA methylation profiles of inherited and sporadic colorectal cancer. <i>Clinical Epigenetics</i> , 2015 , 7, 131	7.7	39
95	Graphical modeling for gene set analysis: A critical appraisal. <i>Biometrical Journal</i> , 2015 , 57, 852-66	1.5	3
94	Beneficial Bacteria Isolated from Grapevine Inner Tissues Shape <i>Arabidopsis thaliana</i> Roots. <i>PLoS ONE</i> , 2015 , 10, e0140252	3.7	30
93	A founder MYBPC3 mutation results in HCM with a high risk of sudden death after the fourth decade of life. <i>Journal of Medical Genetics</i> , 2015 , 52, 338-47	5.8	30
92	Microsatellite unstable gastrointestinal neuroendocrine carcinomas: a new clinicopathologic entity. <i>Endocrine-Related Cancer</i> , 2015 , 22, 35-45	5.7	94
91	Regional Distribution and Evolution of Gray Matter Damage in Different Populations of Multiple Sclerosis Patients. <i>PLoS ONE</i> , 2015 , 10, e0135428	3.7	39
90	timeClip: pathway analysis for time course data without replicates. <i>BMC Bioinformatics</i> , 2014 , 15 Suppl 5, S3	3.6	10
89	Tissue-specific expression and regulatory networks of pig microRNAome. <i>PLoS ONE</i> , 2014 , 9, e89755	3.7	18

88	Prognostic relevance of aberrant DNA methylation in g1 and g2 pancreatic neuroendocrine tumors. <i>Neuroendocrinology</i> , 2014 , 100, 26-34	5.6	38
87	Liver transcriptome analysis in gilthead sea bream upon exposure to low temperature. <i>BMC Genomics</i> , 2014 , 15, 765	4.5	58
86	Integration analysis of microRNA and mRNA expression profiles in human peripheral blood lymphocytes cultured in modeled microgravity. <i>BioMed Research International</i> , 2014 , 2014, 296747	3	30
85	Analysis of differential miRNA expression in primary tumor and stroma of colorectal cancer patients. <i>BioMed Research International</i> , 2014 , 2014, 840921	3	46
84	An aberrant microRNA signature in childhood T-cell lymphoblastic lymphoma affecting CDKN1B expression, NOTCH1 and growth factor signaling pathways. <i>Leukemia</i> , 2014 , 28, 1909-12	10.7	11
83	microRNA-181a has a critical role in ovarian cancer progression through the regulation of the epithelial-mesenchymal transition. <i>Nature Communications</i> , 2014 , 5, 2977	17.4	183
82	Wiring miRNAs to pathways: a topological approach to integrate miRNA and mRNA expression profiles. <i>Nucleic Acids Research</i> , 2014 , 42, e96	20.1	34
81	Headrace tunnel of the El Alto hydropower project in Panama / Druckstollen des Wasserkraftprojekts El Alto in Panama. <i>Geomechanik Und Tunnelbau</i> , 2013 , 6, 301-311	0.6	1
80	Low degree of cortical pathology is associated with benign course of multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2013 , 19, 904-11	5	30
79	Resistance to platinum-based chemotherapy is associated with epithelial to mesenchymal transition in epithelial ovarian cancer. <i>European Journal of Cancer</i> , 2013 , 49, 520-30	7.5	121
78	miR148b is a major coordinator of breast cancer progression in a relapse-associated microRNA signature by targeting ITGA5, ROCK1, PIK3CA, NRAS, and CSF1. <i>FASEB Journal</i> , 2013 , 27, 1223-35	0.9	109
77	MiRNA landscape in stage I epithelial ovarian cancer defines the histotype specificities. <i>Clinical Cancer Research</i> , 2013 , 19, 4114-23	12.9	50
76	Systems biology approach to the dissection of the complexity of regulatory networks in the S. scrofa cardiocirculatory system. <i>International Journal of Molecular Sciences</i> , 2013 , 14, 23160-87	6.3	7
75	Graphite Web: Web tool for gene set analysis exploiting pathway topology. <i>Nucleic Acids Research</i> , 2013 , 41, W89-97	20.1	38
74	Along signal paths: an empirical gene set approach exploiting pathway topology. <i>Nucleic Acids Research</i> , 2013 , 41, e19	20.1	88
73	Anticoagulant therapy for venous thromboembolism during pregnancy: a systematic review and a meta-analysis of the literature: a reply to a rebuttal. <i>Journal of Thrombosis and Haemostasis</i> , 2013 , 11, 788-9	15.4	5
72	The changing clinical course of multiple sclerosis: a matter of gray matter. <i>Annals of Neurology</i> , 2013 , 74, 76-83	9.4	55
71	Synthesis of mitochondrial DNA precursors during myogenesis, an analysis in purified C2C12 myotubes. <i>Journal of Biological Chemistry</i> , 2013 , 288, 5624-35	5.4	17

70	Revertant fibers in the mdx murine model of Duchenne muscular dystrophy: an age- and muscle-related reappraisal. <i>PLoS ONE</i> , 2013 , 8, e72147	3.7	22
69	Consequences of heat shock protein 72 (Hsp72) expression and activity on stress-induced apoptosis in CD30+ NPM-ALK+ anaplastic large-cell lymphomas. <i>Leukemia</i> , 2012 , 26, 1375-82	10.7	6
68	Cortical lesion load associates with progression of disability in multiple sclerosis. <i>Brain</i> , 2012 , 135, 2952-61.2	61.2	191
67	graphite - a Bioconductor package to convert pathway topology to gene network. <i>BMC Bioinformatics</i> , 2012 , 13, 20	3.6	131
66	Genotype-specific mutations in the polymerase gene of hepatitis B virus potentially associated with resistance to oral antiviral therapy. <i>Antiviral Research</i> , 2012 , 96, 422-9	10.8	20
65	A systems biology approach to characterize the regulatory networks leading to trabectedin resistance in an in vitro model of myxoid liposarcoma. <i>PLoS ONE</i> , 2012 , 7, e35423	3.7	17
64	Cortical pathology in multiple sclerosis patients with epilepsy: a 3 year longitudinal study. <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2012 , 83, 49-54	5.5	54
63	Gray matter pathology in MS: a 3-year longitudinal study in a pediatric population. <i>American Journal of Neuroradiology</i> , 2012 , 33, 1507-11	4.4	19
62	MAGIA ² from miRNA and genes expression data integrative analysis to microRNA-transcription factor mixed regulatory circuits (2012 update). <i>Nucleic Acids Research</i> , 2012 , 40, W13-21	20.1	101
61	High IGFBP2 expression correlates with tumor severity in pediatric rhabdomyosarcoma. <i>American Journal of Pathology</i> , 2011 , 179, 2611-24	5.8	17
60	Association between miR-200c and the survival of patients with stage I epithelial ovarian cancer: a retrospective study of two independent tumour tissue collections. <i>Lancet Oncology, The</i> , 2011 , 12, 273-85	21.7	163
59	Statistical Test of Expression Pattern (STEPath): a new strategy to integrate gene expression data with genomic information in individual and meta-analysis studies. <i>BMC Bioinformatics</i> , 2011 , 12, 92	3.6	4
58	Global analysis of gene expression in mineralizing fish vertebra-derived cell lines: new insights into anti-mineralogenic effect of vanadate. <i>BMC Genomics</i> , 2011 , 12, 310	4.5	11
57	parmigene--a parallel R package for mutual information estimation and gene network reconstruction. <i>Bioinformatics</i> , 2011 , 27, 1876-7	7.2	61
56	The Biological Connection Markup Language: a SBGN-compliant format for visualization, filtering and analysis of biological pathways. <i>Bioinformatics</i> , 2011 , 27, 2127-33	7.2	20
55	Impact of host genes and strand selection on miRNA and miRNA* expression. <i>PLoS ONE</i> , 2011 , 6, e23854	3.7	33
54	Impact of probe annotation on the integration of miRNA-mRNA expression profiles for miRNA target detection. <i>Nucleic Acids Research</i> , 2010 , 38, e97	20.1	7
53	MAGIA, a web-based tool for miRNA and Genes Integrated Analysis. <i>Nucleic Acids Research</i> , 2010 , 38, W352-9	20.1	135

52	Widespread cortical thinning characterizes patients with MS with mild cognitive impairment. <i>Neurology</i> , 2010 , 74, 321-8	6.5	118
51	Microsatellite (GT) _n is part of the von Willebrand factor (VWF) promoter region that influences the glucocorticoid-induced increase in VWF in Cushing's syndrome. <i>Thrombosis Research</i> , 2010 , 125, e275-80	8.2	9
50	Magnetic resonance evidence of cerebellar cortical pathology in multiple sclerosis. <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2010 , 81, 401-4	5.5	51
49	Gene set analysis exploiting the topology of a pathway. <i>BMC Systems Biology</i> , 2010 , 4, 121	3.5	50
48	Evidence for relative cortical sparing in benign multiple sclerosis: a longitudinal magnetic resonance imaging study. <i>Multiple Sclerosis Journal</i> , 2009 , 15, 36-41	5	64
47	A modified LOESS normalization applied to microRNA arrays: a comparative evaluation. <i>Bioinformatics</i> , 2009 , 25, 2685-91	7.2	40
46	Cortical lesions in primary progressive multiple sclerosis: a 2-year longitudinal MR study. <i>Neurology</i> , 2009 , 72, 1330-6	6.5	108
45	Expression profiling of skeletal muscle in young bulls treated with steroidal growth promoters. <i>Physiological Genomics</i> , 2009 , 38, 138-48	3.6	33
44	A-MADMAN: annotation-based microarray data meta-analysis tool. <i>BMC Bioinformatics</i> , 2009 , 10, 201	3.6	23
43	A comparison on effects of normalisations in the detection of differentially expressed genes. <i>BMC Bioinformatics</i> , 2009 , 10, 61	3.6	14
42	Filling gaps in PPAR-alpha signaling through comparative nutrigenomics analysis. <i>BMC Genomics</i> , 2009 , 10, 596	4.5	8
41	Selection of multipotent cells and enhanced muscle reconstruction by myogenic macrophage-secreted factors. <i>Experimental Cell Research</i> , 2009 , 315, 915-27	4.2	18
40	Correlation between gene expression and clinical data through linear and nonlinear principal components analyses: muscular dystrophies as case studies. <i>OMICS A Journal of Integrative Biology</i> , 2009 , 13, 173-84	3.8	7
39	Statistical Tools for Gene Expression Analysis and Systems Biology and Related Web Resources 2009 , 181-205		1
38	Development and validation of a gene expression oligo microarray for the gilthead sea bream (<i>Sparus aurata</i>). <i>BMC Genomics</i> , 2008 , 9, 580	4.5	53
37	Meta-analysis of expression signatures of muscle atrophy: gene interaction networks in early and late stages. <i>BMC Genomics</i> , 2008 , 9, 630	4.5	46
36	Morphology and evolution of cortical lesions in multiple sclerosis. A longitudinal MRI study. <i>NeuroImage</i> , 2008 , 42, 1324-8	7.9	51
35	Ripening and genotype control stilbene accumulation in healthy grapes. <i>Journal of Agricultural and Food Chemistry</i> , 2008 , 56, 11773-85	5.7	150

34	Polymorphisms in von Willebrand factor gene promoter influence the glucocorticoid-induced increase in von Willebrand factor: the lesson learned from Cushing syndrome. <i>British Journal of Haematology</i> , 2008 , 140, 230-5	4.5	24
33	A global gene evolution analysis on Vibrionaceae family using phylogenetic profile. <i>BMC Bioinformatics</i> , 2007 , 8 Suppl 1, S23	3.6	9
32	Smokers and passive smokers gene expression profiles: correlation with the DNA oxidation damage. <i>Free Radical Biology and Medicine</i> , 2007 , 43, 415-22	7.8	24
31	Cortical atrophy is relevant in multiple sclerosis at clinical onset. <i>Journal of Neurology</i> , 2007 , 254, 1212-29.5	29.5	182
30	Detection of cortical inflammatory lesions by double inversion recovery magnetic resonance imaging in patients with multiple sclerosis. <i>Archives of Neurology</i> , 2007 , 64, 1416-22		249
29	Development of mussel mRNA profiling: Can gene expression trends reveal coastal water pollution?. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2006 , 602, 121-34.3	34.3	96
28	Defining the gene expression signature of rhabdomyosarcoma by meta-analysis. <i>BMC Genomics</i> , 2006 , 7, 287	4.5	34
27	Gene expression profiling identifies potential relevant genes in alveolar rhabdomyosarcoma pathogenesis and discriminates PAX3-FKHR positive and negative tumors. <i>International Journal of Cancer</i> , 2006 , 118, 2772-81	7.5	44
26	Longitudinal analysis of immune cell phenotypes in early stage multiple sclerosis: distinctive patterns characterize MRI-active patients. <i>Brain</i> , 2006 , 129, 1993-2007	11.2	34
25	Expression profiling characterization of laminin alpha-2 positive MDC. <i>Biochemical and Biophysical Research Communications</i> , 2006 , 350, 345-51	3.4	4
24	Expression analysis of androgen-responsive genes in the prostate of veal calves treated with anabolic hormones. <i>Domestic Animal Endocrinology</i> , 2006 , 30, 38-55	2.3	39
23	Differential gene expression profiling in genetic and multifactorial cardiovascular diseases. <i>Journal of Molecular and Cellular Cardiology</i> , 2006 , 41, 934-48	5.8	55
22	Denervation in murine fast-twitch muscle: short-term physiological changes and temporal expression profiling. <i>Physiological Genomics</i> , 2006 , 25, 60-74	3.6	64
21	Parallel protein and transcript profiles of FSHD patient muscles correlate to the D4Z4 arrangement and reveal a common impairment of slow to fast fibre differentiation and a general deregulation of MyoD-dependent genes. <i>Proteomics</i> , 2006 , 6, 5303-21	4.8	89
20	Novel genes, possibly relevant for molecular diagnosis or therapy of human rhabdomyosarcoma, detected by genomic expression profiling. <i>Gene</i> , 2005 , 348, 65-71	3.8	14
19	Life at depth: Photobacterium profundum genome sequence and expression analysis. <i>Science</i> , 2005 , 307, 1459-61	33.3	230
18	RAP: a new computer program for de novo identification of repeated sequences in whole genomes. <i>Bioinformatics</i> , 2005 , 21, 582-8	7.2	32
17	Territorial male gobies respond aggressively to sneakers but do not adjust their sperm expenditure. <i>Behavioral Ecology</i> , 2005 , 16, 1001-1007	2.3	31

16	MIDAW: a web tool for statistical analysis of microarray data. <i>Nucleic Acids Research</i> , 2005 , 33, W644-9	20.1	40
15	A leukemia-enriched cDNA microarray platform identifies new transcripts with relevance to the biology of pediatric acute lymphoblastic leukemia. <i>Haematologica</i> , 2005 , 90, 890-8	6.6	22
14	Altered glucose metabolism and proteolysis in pancreatic cancer cell conditioned myoblasts: searching for a gene expression pattern with a microarray analysis of 5000 skeletal muscle genes. <i>Gut</i> , 2004 , 53, 1159-66	19.2	41
13	Improved detection of differentially expressed genes in microarray experiments through multiple scanning and image integration. <i>Nucleic Acids Research</i> , 2003 , 31, e149	20.1	21
12	IDE6: a web tool for detection of differentially expressed genes in multiple tag sampling experiments. <i>Physiological Genomics</i> , 2003 , 12, 159-62	3.6	310
11	Disease genes and intracellular protein networks. <i>Physiological Genomics</i> , 2003 , 15, 223-7	3.6	18
10	Pattern recognition in gene expression profiling using DNA array: a comparative study of different statistical methods applied to cancer classification. <i>Human Molecular Genetics</i> , 2003 , 12, 823-36	5.6	38
9	TRAIT (TRANscript Integrated Table): a knowledgebase of human skeletal muscle transcripts. <i>Bioinformatics</i> , 2003 , 19, 661-2	7.2	4
8	Patterns of human diversity, within and among continents, inferred from biallelic DNA polymorphisms. <i>Genome Research</i> , 2002 , 12, 602-12	9.7	153
7	Simplifying amino acid alphabets by means of a branch and bound algorithm and substitution matrices. <i>Bioinformatics</i> , 2002 , 18, 1102-8	7.2	30
6	Gene expression profiling in dysferlinopathies using a dedicated muscle microarray. <i>Human Molecular Genetics</i> , 2002 , 11, 3283-98	5.6	63
5	Detecting differentially expressed genes in multiple tag sampling experiments: comparative evaluation of statistical tests. <i>Human Molecular Genetics</i> , 2001 , 10, 2133-41	5.6	49
4	Gene flow and genetic diversity: a comparison of freshwater bryozoan populations in Europe and North America. <i>Heredity</i> , 2000 , 85 Pt 5, 498-508	3.6	29
3	The human adult skeletal muscle transcriptional profile reconstructed by a novel computational approach. <i>Genome Research</i> , 2000 , 10, 344-9	9.7	37
2	Probability of conception on different days of the menstrual cycle: an ongoing exercise. <i>Advances in Contraception: the Official Journal of the Society for the Advancement of Contraception</i> , 1997 , 13, 105-15		22
1	Assessment of statistical methods from single cell, bulk RNA-seq and metagenomics applied to microbiome data		1