

Daniel Remondini

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.

122
papers

2,293
citations

26
h-index

45
g-index

143
ext. papers

2,911
ext. citations

4.4
avg, IF

4.74
L-index

#	Paper	IF	Citations
122	Circumventing the curse of dimensionality in magnetic resonance fingerprinting through a deep learning approach.. <i>NMR in Biomedicine</i> , 2022 , e4670	4.4	0
121	Mortality Prediction of COVID-19 Patients Using Radiomic and Neural Network Features Extracted from a Wide Chest X-ray Sample Size: A Robust Approach for Different Medical Imbalanced Scenarios. <i>Applied Sciences (Switzerland)</i> , 2022 , 12, 3903	2.6	1
120	Effectiveness of Biologically Inspired Neural Network Models in Learning and Patterns Memorization. <i>Entropy</i> , 2022 , 24, 682	2.8	
119	Source Attribution of Human Campylobacteriosis Using Whole-Genome Sequencing Data and Network Analysis. <i>Pathogens</i> , 2022 , 11, 645	4.5	0
118	Clusters of science and health related Twitter users become more isolated during the COVID-19 pandemic. <i>Scientific Reports</i> , 2021 , 11, 19655	4.9	7
117	Node Centrality Measures Identify Relevant Structural MRI Features of Subjects with Autism. <i>Brain Sciences</i> , 2021 , 11,	3.4	2
116	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	2.2	25
115	Characterization and comparison of gene-centered human interactomes. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	1
114	Integrated genomic-metabolic classification of acute myeloid leukemia defines a subgroup with NPM1 and cohesin/DNA damage mutations. <i>Leukemia</i> , 2021 , 35, 2813-2826	10.7	3
113	Network-based strategies for protein characterization. <i>Advances in Protein Chemistry and Structural Biology</i> , 2021 , 127, 217-248	5.3	
112	Comparison between 16S rRNA and shotgun sequencing data for the taxonomic characterization of the gut microbiota. <i>Scientific Reports</i> , 2021 , 11, 3030	4.9	41
111	Are We Ready for the Arrival of the New COVID-19 Vaccinations? Great Promises and Unknown Challenges Still to Come. <i>Vaccines</i> , 2021 , 9,	5.3	5
110	Impact of concurrency on the performance of a whole exome sequencing pipeline. <i>BMC Bioinformatics</i> , 2021 , 22, 60	3.6	0
109	Challenges in the Use of Artificial Intelligence for Prostate Cancer Diagnosis from Multiparametric Imaging Data. <i>Cancers</i> , 2021 , 13,	6.6	3
108	A deep learning approach for magnetic resonance fingerprinting: Scaling capabilities and good training practices investigated by simulations. <i>Physica Medica</i> , 2021 , 89, 80-92	2.7	0
107	Mis-tweeting communication: a Vaccine Hesitancy analysis among twitter users in Italy. <i>Acta Biomedica</i> , 2021 , 92, e2021416	3.2	1
106	Network Approach to Source Attribution of Serovar Typhimurium and Its Monophasic Variant. <i>Frontiers in Microbiology</i> , 2020 , 11, 1205	5.7	5

105	Gut microbiota ecology: Biodiversity estimated from hybrid neutral-niche model increases with health status and aging. <i>PLoS ONE</i> , 2020 , 15, e0237207	3.7	1
104	rFBP: Replicated Focusing Belief Propagation algorithm. <i>Journal of Open Source Software</i> , 2020 , 5, 2663	5.2	
103	Merging 1D and 3D genomic information: Challenges in modelling and validation. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020 , 1863, 194415	6	2
102	Water exchange between intra and extracellular compartments studied by nuclear magnetic resonance relaxometry and optical microscopy. <i>Journal Physics D: Applied Physics</i> , 2020 , 53, 085401	3	0
101	Understanding and predicting ciprofloxacin minimum inhibitory concentration in Escherichia coli with machine learning. <i>Scientific Reports</i> , 2020 , 10, 15026	4.9	13
100	Galvanotactic Phenomenon Induced by Non-Contact Electrostatic Field: Investigation in a Scratch Assay. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2020 , 2020, 2520-2523	0.9	
99	Prediction of vascular aging based on smartphone acquired PPG signals. <i>Scientific Reports</i> , 2020 , 10, 19746	4.6	13
98	WISDoM: Characterizing Neurological Time Series With the Wishart Distribution. <i>Frontiers in Neuroinformatics</i> , 2020 , 14, 611762	3.9	
97	Systems Biology approaches to cancer: towards new therapeutical strategies and personalized approaches. <i>Molecular and Cellular Oncology</i> , 2019 , 6, 1561118	1.2	1
96	Linking aberrant chromatin features in chronic lymphocytic leukemia to transcription factor networks. <i>Molecular Systems Biology</i> , 2019 , 15, e8339	12.2	20
95	Molecular Aging of Human Liver: An Epigenetic/Transcriptomic Signature. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2019 , 74, 1-8	6.4	17
94	The Hippo pathway modulates resistance to BET proteins inhibitors in lung cancer cells. <i>Oncogene</i> , 2019 , 38, 6801-6817	9.2	34
93	Cognitive Decline and Alzheimer's Disease in Old Age: A Sex-Specific Cytokine Signature. <i>Journal of Alzheimer's Disease</i> , 2019 , 72, 911-918	4.3	7
92	Application of different DNA extraction procedures, library preparation protocols and sequencing platforms: impact on sequencing results. <i>Heliyon</i> , 2019 , 5, e02745	3.6	6
91	Aneuploid acute myeloid leukemia exhibits a signature of genomic alterations in the cell cycle and protein degradation machinery. <i>Cancer</i> , 2019 , 125, 712-725	6.4	33
90	Quantifying the contribution of four resistance mechanisms to ciprofloxacin MIC in Escherichia coli: a systematic review. <i>Journal of Antimicrobial Chemotherapy</i> , 2019 , 74, 298-310	5.1	14
89	On the multiplicity of Laplacian eigenvalues and Fiedler partitions. <i>Linear Algebra and Its Applications</i> , 2018 , 544, 206-222	0.9	4
88	Brain functional connectivity in sleep-related hypermotor epilepsy. <i>NeuroImage: Clinical</i> , 2018 , 17, 873-883	3.5	10

87	Integrated Molecular Characterization of Gastrointestinal Stromal Tumors (GIST) Harboring the Rare D842V Mutation in PDGFRA Gene. <i>International Journal of Molecular Sciences</i> , 2018 , 19,	6.3	19
86	Altered modulation of lamin A/C-HDAC2 interaction and p21 expression during oxidative stress response in HGPS. <i>Aging Cell</i> , 2018 , 17, e12824	9.9	21
85	Toward the Authentication of European Sea Bass Origin through a Combination of Biometric Measurements and Multiple Analytical Techniques. <i>Journal of Agricultural and Food Chemistry</i> , 2018 , 66, 6822-6831	5.7	6
84	BK channel overexpression on plasma membrane of fibroblasts from Hutchinson-Gilford progeria syndrome. <i>Aging</i> , 2018 , 10, 3148-3160	5.6	3
83	A New Gene Expression Profile Signature CRLF2 Overexpression Based Identifies Novel Adult "Triple Negative" Acute Lymphoblastic Leukemia Subgroups. <i>Blood</i> , 2018 , 132, 5284-5284	2.2	
82	Network integration of multi-tumour omics data suggests novel targeting strategies. <i>Nature Communications</i> , 2018 , 9, 4514	17.4	21
81	Identification of miR-31-5p, miR-141-3p, miR-200c-3p, and GLT1 as human liver aging markers sensitive to donor-recipient age-mismatch in transplants. <i>Aging Cell</i> , 2017 , 16, 262-272	9.9	36
80	Identification of a T cell gene expression clock obtained by exploiting a MZ twin design. <i>Scientific Reports</i> , 2017 , 7, 6005	4.9	1
79	RUNX2 expression in thyroid and breast cancer requires the cooperation of three non-redundant enhancers under the control of BRD4 and c-JUN. <i>Nucleic Acids Research</i> , 2017 , 45, 11249-11267	20.1	42
78	Entropy-Based Network Representation of the Individual Metabolic Phenotype. <i>Journal of Proteome Research</i> , 2016 , 15, 3298-307	5.6	20
77	Methods for the integration of multi-omics data: mathematical aspects. <i>BMC Bioinformatics</i> , 2016 , 17 Suppl 2, 15	3.6	208
76	Characterization of DNA methylation as a function of biological complexity via dinucleotide inter-distances. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2016 , 374,	3	6
75	Stochastic neutral modelling of the Gut Microbiota's relative species abundance from next generation sequencing data. <i>BMC Bioinformatics</i> , 2016 , 17 Suppl 2, 16	3.6	14
74	Systems medicine of inflammaging. <i>Briefings in Bioinformatics</i> , 2016 , 17, 527-40	13.4	27
73	Aggressive Aneuploid Acute Myeloid Leukemia Is Dependent on Alterations of P53, Gain of APC and PLK1 and Loss of RAD50. <i>Blood</i> , 2016 , 128, 1702-1702	2.2	1
72	Alterations of BRCA1 and PALB2 Define a Novel Class of Complex-Karyotype AML with a Very Bad Prognosis. <i>Blood</i> , 2016 , 128, 1677-1677	2.2	
71	Quality Matters: Systematic Analysis of Endpoints Related to "Cellular Life" in Vitro Data of Radiofrequency Electromagnetic Field Exposure. <i>International Journal of Environmental Research and Public Health</i> , 2016 , 13,	4.6	23
70	The genetic and genomic background of multiple myeloma patients achieving complete response after induction therapy with bortezomib, thalidomide and dexamethasone (VTD). <i>Oncotarget</i> , 2016 , 7, 9666-79	3.3	16

69	Network diffusion-based analysis of high-throughput data for the detection of differentially enriched modules. <i>Scientific Reports</i> , 2016 , 6, 34841	4.9	24
68	Optimized pipeline of MuTect and GATK tools to improve the detection of somatic single nucleotide polymorphisms in whole-exome sequencing data. <i>BMC Bioinformatics</i> , 2016 , 17, 341	3.6	60
67	Network measures for protein folding state discrimination. <i>Scientific Reports</i> , 2016 , 6, 30367	4.9	3
66	Opposite activation of the Hedgehog pathway in CD138+ plasma cells and CD138-CD19+ B cells identifies two subgroups of patients with multiple myeloma and different prognosis. <i>Leukemia</i> , 2016 , 30, 1869-76	10.7	6
65	Statistical strategies and stochastic predictive models for the MARK-AGE data. <i>Mechanisms of Ageing and Development</i> , 2015 , 151, 45-53	5.6	3
64	NETWORK APPROACHES FOR ANALYSIS AND MODELING OF THE HUMAN METABOLISM. <i>Journal of Mechanics in Medicine and Biology</i> , 2015 , 15, 1540026	0.7	
63	Multiscale characterization of ageing and cancer progression by a novel network entropy measure. <i>Molecular BioSystems</i> , 2015 , 11, 1824-31		14
62	MODELING GLIOBLASTOMA RESPONSE TO RADIOTHERAPY BY COMBINING A TWO-COMPARTMENT KINETIC MODEL AND MULTIPARAMETRIC NMR DATA. <i>Journal of Mechanics in Medicine and Biology</i> , 2015 , 15, 1540017	0.7	
61	Water compartmentalization, cell viability and morphology changes monitored under stress by ¹ H-NMR relaxometry and phase contrast optical microscopy. <i>Journal Physics D: Applied Physics</i> , 2015 , 48, 415401	3	2
60	Active Degradation Explains the Distribution of Nuclear Proteins during Cellular Senescence. <i>PLoS ONE</i> , 2015 , 10, e0118442	3.7	2
59	Identification of a DNA methylation signature in blood cells from persons with Down Syndrome. <i>Aging</i> , 2015 , 7, 82-96	5.6	68
58	Genome-Wide Molecular Portrait of Aggressive Systemic Mastocytosis and Mast Cell Leukemia Depicted By Whole Exome Sequencing and Copy Number Variation Analysis. <i>Blood</i> , 2015 , 126, 4085-4085	2.2	1
57	A meta-analysis on age-associated changes in blood DNA methylation: results from an original analysis pipeline for Infinium 450k data. <i>Aging</i> , 2015 , 7, 97-109	5.6	40
56	Genomic-Wide Analysis By High Resolution SNP Array Identifies Novel Genomic Alteration in Acute Myeloid Leukemia. <i>Blood</i> , 2015 , 126, 2600-2600	2.2	
55	Novel Genomic Patterns of Metabolic Remodeling in Acute Myeloid Leukemia. <i>Blood</i> , 2015 , 126, 3837-3837		
54	Clustering Adult ACUTE Lymphoblastic Leukemia (ALL) Philadelphia Negative (Ph-) By Whole Exome Sequencing (WES) Analysis. <i>Blood</i> , 2015 , 126, 2623-2623	2.2	
53	The Alternate Activation of Hedgehog Pathway, Either in CD138+ or in CD138-CD19+ Multiple Myeloma Primary Cells, Impacts on Disease Outcome. <i>Blood</i> , 2015 , 126, 2961-2961	2.2	
52	A Specific Pattern of Somatic Mutations Associates with Poor Prognosis Aneuploid Acute Myeloid Leukemia: Results from the European NGS-PTL Consortium. <i>Blood</i> , 2015 , 126, 3840-3840	2.2	

51	Changes in IgG and total plasma protein glycomes in acute systemic inflammation. <i>Scientific Reports</i> , 2014 , 4, 4347	4.9	91
50	Weighted multiplex networks. <i>PLoS ONE</i> , 2014 , 9, e97857	3.7	135
49	Correlations between weights and overlap in ensembles of weighted multiplex networks. <i>Physical Review E</i> , 2014 , 90, 062817	2.4	24
48	Systems biology and brain activity in neuronal pathways by smart device and advanced signal processing. <i>Frontiers in Genetics</i> , 2014 , 5, 253	4.5	10
47	Lifelong maintenance of composition, function and cellular/subcellular distribution of proteasomes in human liver. <i>Mechanisms of Ageing and Development</i> , 2014 , 141-142, 26-34	5.6	17
46	Dissecting the Molecular Mechanisms of Aneuploidy in Acute Myeloid Leukemia By Next Generation Sequencing. <i>Blood</i> , 2014 , 124, 1028-1028	2.2	1
45	High-Throughput Molecular Profiling of Multiple Myeloma (MM) Clonotypic CD19+ B Cells Highlights Pathways Potentially Involved in the Disease Endurance. <i>Blood</i> , 2014 , 124, 2054-2054	2.2	
44	Cow's milk allergy (CMA) in children: identification of allergologic tests predictive of food allergy. <i>European Annals of Allergy and Clinical Immunology</i> , 2014 , 46, 100-5	1.3	5
43	Correlation between eight-gene expression profiling and response to therapy of newly diagnosed multiple myeloma patients treated with thalidomide-dexamethasone incorporated into double autologous transplantation. <i>Annals of Hematology</i> , 2013 , 92, 1271-80	3	3
42	Analysis of noise-induced bimodality in a Michaelis-Menten single-step enzymatic cycle. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2013 , 392, 336-342	3.3	6
41	Role of epigenetics in human aging and longevity: genome-wide DNA methylation profile in centenarians and centenarians' offspring. <i>Age</i> , 2013 , 35, 1961-73		146
40	The posterior iliac crest outperforms the anterior iliac crest when obtaining mesenchymal stem cells from bone marrow. <i>Journal of Bone and Joint Surgery - Series A</i> , 2013 , 95, 1101-7	5.6	74
39	ELF magnetic fields tuned to ion parametric resonance conditions do not affect TEA-sensitive voltage-dependent outward K(+) currents in a human neural cell line. <i>Bioelectromagnetics</i> , 2013 , 34, 579-88	1.6	4
38	Survival features of EBV-stabilized cells from centenarians: morpho-functional and transcriptomic analyses. <i>Age</i> , 2012 , 34, 1341-59		6
37	Efficient isolation and enrichment of mesenchymal stem cells from bone marrow. <i>Cytotherapy</i> , 2012 , 14, 686-93	4.8	23
36	Bistability in the chemical master equation for dual phosphorylation cycles. <i>Journal of Chemical Physics</i> , 2012 , 136, 235102	3.9	10
35	Measures of centrality based on the spectrum of the Laplacian. <i>Physical Review E</i> , 2012 , 85, 066127	2.4	10
34	Stochastic analysis of a miRNA-protein toggle switch. <i>Molecular BioSystems</i> , 2011 , 7, 2796-803		14

33	Pooled genome-wide analysis to identify novel risk loci for pediatric allergic asthma. <i>PLoS ONE</i> , 2011 , 6, e16912	3.7	15
32	Multiscale Network Reconstruction from Gene Expression Measurements: Correlations, Perturbations, and A Priori Biological Knowledge 2011 , 105-131		
31	A 41-Gene Signature Predicts Complete Response (CR) to Bortezomib-Thalidomide-Dexamethasone (VTD) As Induction Therapy Prior to Autologous Stem-Cell Transplantation (ASCT) in Multiple Myeloma (MM). <i>Blood</i> , 2011 , 118, 805-805	2.2	
30	Complex patterns of gene expression in human T cells during in vivo aging. <i>Molecular BioSystems</i> , 2010 , 6, 1983-92		23
29	Molecular remodeling of potassium channels in fibroblasts from centenarians: a marker of longevity?. <i>Mechanisms of Ageing and Development</i> , 2010 , 131, 674-81	5.6	5
28	Network, degeneracy and bow tie. Integrating paradigms and architectures to grasp the complexity of the immune system. <i>Theoretical Biology and Medical Modelling</i> , 2010 , 7, 32	2.3	57
27	Overcoming resistance to conventional drugs in Ewing sarcoma and identification of molecular predictors of outcome. <i>Journal of Clinical Oncology</i> , 2009 , 27, 2209-16	2.2	93
26	Trends in modeling Biomedical Complex Systems. <i>BMC Bioinformatics</i> , 2009 , 10 Suppl 12, I1	3.6	18
25	Mechanisms of gene amplification and evidence of coamplification in drug-resistant human osteosarcoma cell lines. <i>Genes Chromosomes and Cancer</i> , 2009 , 48, 289-309	5	41
24	Functional models for large-scale gene regulation networks: realism and fiction. <i>Molecular BioSystems</i> , 2009 , 5, 335-44		19
23	Complete Response to First-Line Bortezomib-Thalidomide-Dexamethasone Therapy in Multiple Myeloma Patients with t(4;14): Analysis of Gene Expression Profile.. <i>Blood</i> , 2009 , 114, 2811-2811	2.2	
22	Reconstructing networks of pathways via significance analysis of their intersections. <i>BMC Bioinformatics</i> , 2008 , 9 Suppl 4, S9	3.6	22
21	P53 oncosuppressor influences selection of genomic imbalances in response to ionizing radiations in human osteosarcoma cell line SAOS-2. <i>International Journal of Radiation Biology</i> , 2008 , 84, 591-601	2.9	6
20	A novel gene signature for molecular diagnosis of human prostate cancer by RT-qPCR. <i>PLoS ONE</i> , 2008 , 3, e3617	3.7	38
19	Effects of 50 Hz sinusoidal magnetic fields on Hsp27, Hsp70, Hsp90 expression in porcine aortic endothelial cells (PAEC). <i>Bioelectromagnetics</i> , 2007 , 28, 231-7	1.6	28
18	Correlation analysis reveals the emergence of coherence in the gene expression dynamics following system perturbation. <i>BMC Bioinformatics</i> , 2007 , 8 Suppl 1, S16	3.6	4
17	Effects of exogenous electromagnetic fields on a simplified ion channel model. <i>Journal of Biological Physics</i> , 2007 , 33, 183-94	1.6	5
16	NETWORKS FROM GENE EXPRESSION TIME SERIES: CHARACTERIZATION OF CORRELATION PATTERNS. <i>International Journal of Bifurcation and Chaos in Applied Sciences and Engineering</i> , 2007 , 17, 2477-2483	2	5

15	Capturing Degeneracy in the Immune System 2007 , 109-118		2
14	Genomic imbalances associated with secondary acute leukemias in Hodgkin lymphoma. <i>Oncology Reports</i> , 2007 , 18, 1427-34	3.5	4
13	Gene expression analysis of ELF-MF exposed human monocytes indicating the involvement of the alternative activation pathway. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2006 , 1763, 402-129	4.9	43
12	Molecular classification of green tea catechin-sensitive and green tea catechin-resistant prostate cancer in the TRAMP mice model by quantitative real-time PCR gene profiling. <i>Carcinogenesis</i> , 2006 , 27, 1047-53	4.6	26
11	Gene expression changes in human cells after exposure to mobile phone microwaves. <i>Proteomics</i> , 2006 , 6, 4745-54	4.8	63
10	Age-dependent effects of in vitro radiofrequency exposure (mobile phone) on CD95+ T helper human lymphocytes. <i>Annals of the New York Academy of Sciences</i> , 2006 , 1067, 493-9	6.5	8
9	Induced metastable memory in heat shock response. <i>Journal of Biological Physics</i> , 2006 , 32, 49-59	1.6	3
8	Turning on stem cell cardiogenesis with extremely low frequency magnetic fields. <i>FASEB Journal</i> , 2005 , 19, 155-7	0.9	71
7	Targeting c-Myc-activated genes with a correlation method: detection of global changes in large gene expression network dynamics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 6902-6	11.5	42
6	50 Hz sinusoidal magnetic fields do not affect human lymphocyte activation and proliferation in vitro. <i>Physical Biology</i> , 2004 , 1, 211-9	3	10
5	1800 MHz radiofrequency (mobile phones, different Global System for Mobile communication modulations) does not affect apoptosis and heat shock protein 70 level in peripheral blood mononuclear cells from young and old donors. <i>International Journal of Radiation Biology</i> , 2004 , 80, 389-97	2.9	56
4	The effect of noise on a class of energy-based learning rules. <i>Neural Computation</i> , 2003 , 15, 1621-40	2.9	6
3	Genomic imbalances associated with methotrexate resistance in human osteosarcoma cell lines detected by comparative genomic hybridization-based techniques. <i>European Journal of Cell Biology</i> , 2003 , 82, 483-93	6.1	34
2	Quantifying the contribution of four resistance mechanisms to ciprofloxacin minimum inhibitory concentration in <i>Escherichia coli</i> : a systematic review		2
1	Understanding and predicting ciprofloxacin minimum inhibitory concentration in <i>Escherichia coli</i> with machine learning		4