

Stefania Bortoluzzi

List of Publications by Year in descending order

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Version: 2024-02-01

114
papers

4,328
citations

109321

35
h-index

118850

62
g-index

118
all docs

118
docs citations

118
times ranked

7847
citing authors

#	ARTICLE	IF	CITATIONS
1	Clinical effect of driver mutations of JAK2, CALR, or MPL in primary myelofibrosis. <i>Blood</i> , 2014, 124, 1062-1069.	1.4	340
2	IDEG6: a web tool for detection of differentially expressed genes in multiple tag sampling experiments. <i>Physiological Genomics</i> , 2003, 12, 159-162.	2.3	336
3	Identification of microRNA expression patterns and definition of a microRNA/mRNA regulatory network in distinct molecular groups of multiple myeloma. <i>Blood</i> , 2009, 114, e20-e26.	1.4	224
4	MAGIA, a web-based tool for miRNA and Genes Integrated Analysis. <i>Nucleic Acids Research</i> , 2010, 38, W352-W359.	14.5	150
5	Impact of microRNAs on regulatory networks and pathways in human colorectal carcinogenesis and development of metastasis. <i>BMC Genomics</i> , 2013, 14, 589.	2.8	140
6	CircRNAs in hematopoiesis and hematological malignancies. <i>Blood Cancer Journal</i> , 2016, 6, e483-e483.	6.2	139
7	miR-142-3p Prevents Macrophage Differentiation during Cancer-Induced Myelopoiesis. <i>Immunity</i> , 2013, 38, 1236-1249.	14.3	127
8	Transcriptome sequencing and microarray development for the Manila clam, <i>Ruditapes philippinarum</i> : genomic tools for environmental monitoring. <i>BMC Genomics</i> , 2011, 12, 234.	2.8	120
9	Differential expression of genes coding for ribosomal proteins in different human tissues. <i>Bioinformatics</i> , 2001, 17, 1152-1157.	4.1	113
10	Computational reconstruction of the human skeletal muscle secretome. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 776-792.	2.6	111
11	MAGIA2: 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-W21.	14.5	110
12	miRNA-mRNA integrative analysis in primary myelofibrosis CD34+ cells: role of miR-155/JARID2 axis in abnormal megakaryopoiesis. <i>Blood</i> , 2014, 124, e21-e32.	1.4	105
13	Novel definition files for human GeneChips based on GeneAnnot. <i>BMC Bioinformatics</i> , 2007, 8, 446.	2.6	93
14	High incidence of activating STAT5B mutations in CD4-positive T-cell large granular lymphocyte leukemia. <i>Blood</i> , 2016, 128, 2465-2468.	1.4	86
15	Sequencing, de novo annotation and analysis of the first <i>Anguilla anguilla</i> transcriptome: EeelBase opens new perspectives for the study of the critically endangered european eel. <i>BMC Genomics</i> , 2010, 11, 635.	2.8	83
16	Missense polymorphism in the human carboxypeptidase E gene alters enzymatic activity. <i>Human Mutation</i> , 2001, 18, 120-131.	2.5	75
17	A Comprehensive, High-Resolution Genomic Transcript Map of Human Skeletal Muscle. <i>Genome Research</i> , 1998, 8, 817-825.	5.5	69
18	Circular RNA differential expression in blood cell populations and exploration of circRNA deregulation in pediatric acute lymphoblastic leukemia. <i>Scientific Reports</i> , 2019, 9, 14670.	3.3	69

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19	Surviving in a toxic world: transcriptomics and gene expression profiling in response to environmental pollution in the critically endangered European eel. <i>BMC Genomics</i> , 2012, 13, 507.	2.8	68
20	Activating somatic mutations outside the SH2-domain of STAT3 in LGL leukemia. <i>Leukemia</i> , 2016, 30, 1204-1208.	7.2	62
21	Genome Evolution in the Cold: Antarctic Icefish Muscle Transcriptome Reveals Selective Duplications Increasing Mitochondrial Function. <i>Genome Biology and Evolution</i> , 2013, 5, 45-60.	2.5	56
22	Detecting differentially expressed genes in multiple tag sampling experiments: comparative evaluation of statistical tests. <i>Human Molecular Genetics</i> , 2001, 10, 2133-2141.	2.9	54
23	Loss of zfp36 expression in colorectal cancer correlates to wnt/ β -catenin activity and enhances epithelial-to-mesenchymal transition through upregulation of zeb1, sox9 and macc1. <i>Oncotarget</i> , 2016, 7, 59144-59157.	1.8	53
24	Circulating miR-182 is a biomarker of colorectal adenocarcinoma progression. <i>Oncotarget</i> , 2014, 5, 6611-6619.	1.8	53
25	Characterization of C14orf4, a Novel Intronless Human Gene Containing a Polyglutamine Repeat, Mapped to the ARVD1 Critical Region. <i>Biochemical and Biophysical Research Communications</i> , 2000, 278, 766-774.	2.1	49
26	The Human Adult Skeletal Muscle Transcriptional Profile Reconstructed by a Novel Computational Approach. <i>Genome Research</i> , 2000, 10, 344-349.	5.5	47
27	Transcriptional profiling of subcutaneous adipose tissue in Italian Large White pigs divergent for backfat thickness. <i>Animal Genetics</i> , 2016, 47, 306-323.	1.7	47
28	TRAM (Transcriptome Mapper): database-driven creation and analysis of transcriptome maps from multiple sources. <i>BMC Genomics</i> , 2011, 12, 121.	2.8	45
29	An integrative approach for the identification of prognostic and predictive biomarkers in rectal cancer. <i>Oncotarget</i> , 2015, 6, 32561-32574.	1.8	45
30	An integrative framework identifies alternative splicing events in colorectal cancer development. <i>Molecular Oncology</i> , 2014, 8, 129-141.	4.6	43
31	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, 2367-2378.	1.8	41
32	CirComPara: A Multi-Method Comparative Bioinformatics Pipeline to Detect and Study circRNAs from RNA-seq Data. <i>Non-coding RNA</i> , 2017, 3, 8.	2.6	41
33	mRNA-Seq and microarray development for the Grooved carpet shell clam, <i>Ruditapes decussatus</i> : a functional approach to unravel host-parasite interaction. <i>BMC Genomics</i> , 2013, 14, 741.	2.8	39
34	Large-scale circular RNA deregulation in T-ALL: unlocking unique ectopic expression of molecular subtypes. <i>Blood Advances</i> , 2020, 4, 5902-5914.	5.2	39
35	A-MADMAN: Annotation-based microarray data meta-analysis tool. <i>BMC Bioinformatics</i> , 2009, 10, 201.	2.6	38
36	Defining the gene expression signature of rhabdomyosarcoma by meta-analysis. <i>BMC Genomics</i> , 2006, 7, 287.	2.8	37

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37	Impact of Host Genes and Strand Selection on miRNA and miRNA* Expression. PLoS ONE, 2011, 6, e23854.	2.5	37
38	MicroRNA“offset RNAs (moRNAs): by-product spectators or functional players?. Trends in Molecular Medicine, 2011, 17, 473-474.	6.7	34
39	Characterization and discovery of novel miRNAs and moRNAs in JAK2V617F-mutated SET2 cells. Blood, 2012, 119, e120-e130.	1.4	34
40	Genomic landscape characterization of large granular lymphocyte leukemia with a systems genetics approach. Leukemia, 2017, 31, 1243-1246.	7.2	33
41	REEF: searching REgionally Enriched Features in genomes. BMC Bioinformatics, 2006, 7, 453.	2.6	32
42	Genomic expression during human myelopoiesis. BMC Genomics, 2007, 8, 264.	2.8	31
43	H-Ferritin-Regulated MicroRNAs Modulate Gene Expression in K562 Cells. PLoS ONE, 2015, 10, e0122105.	2.5	30
44	Somatic mutations in specific and connected subpathways are associated with short neuroblastoma patients“ survival and indicate proteins targetable at onset of disease. International Journal of Cancer, 2018, 143, 2525-2536.	5.1	27
45	The human SLC8A3 gene and the tissue-specific Na ⁺ /Ca ²⁺ exchanger 3 isoforms. Gene, 2002, 298, 1-7.	2.2	26
46	DHPLC analysis of the MECP2 gene in Italian Rett patients. Human Mutation, 2001, 18, 132-140.	2.5	25
47	Control of the Na ⁺ /Ca ²⁺ exchanger 3 promoter by cyclic adenosine monophosphate and Ca ²⁺ in differentiating neurons. Journal of Neurochemistry, 2003, 84, 282-293.	3.9	23
48	Sequencing and Characterization of Striped Venus Transcriptome Expand Resources for Clam Fishery Genetics. PLoS ONE, 2012, 7, e44185.	2.5	23
49	A constitutive active MAPK/ERK pathway due to BRAFV600E positively regulates AHR pathway in PTC. Oncotarget, 2015, 6, 32104-32114.	1.8	23
50	Towards an in silico analysis of transcription patterns. Trends in Genetics, 1999, 15, 118-119.	6.7	22
51	Silencing of miR-182 is associated with modulation of tumorigenesis through apoptosis induction in an experimental model of colorectal cancer. BMC Cancer, 2019, 19, 821.	2.6	22
52	A high definition picture of somatic mutations in chronic lymphoproliferative disorder of natural killer cells. Blood Cancer Journal, 2020, 10, 42.	6.2	22
53	Sensitive, reliable and robust circRNA detection from RNA-seq with CirComPara2. Briefings in Bioinformatics, 2022, 23, .	6.5	22
54	MiR-26a-5p as a Reference to Normalize MicroRNA qRT-PCR Levels in Plasma Exosomes of Pediatric Hematological Malignancies. Cells, 2021, 10, 101.	4.1	21

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55	Age estimation in subadult Egyptian remains. HOMO- Journal of Comparative Human Biology, 2010, 61, 337-358.	0.7	20
56	Small RNA Sequencing Uncovers New miRNAs and moRNAs Differentially Expressed in Normal and Primary Myelofibrosis CD34+ Cells. PLoS ONE, 2015, 10, e0140445.	2.5	20
57	Disease genes and intracellular protein networks. Physiological Genomics, 2003, 15, 223-227.	2.3	19
58	CircRNAs Are Here to Stay: A Perspective on the MLL Recombinome. Frontiers in Genetics, 2019, 10, 88.	2.3	19
59	A multistep bioinformatic approach detects putative regulatory elements in gene promoters. BMC Bioinformatics, 2005, 6, 121.	2.6	18
60	A novel resource for the study of genes expressed in the adult human retina. Investigative Ophthalmology and Visual Science, 2000, 41, 3305-8.	3.3	18
61	Analysis of LGI1 promoter sequence, PDYN and GABBR1 polymorphisms in sporadic and familial lateral temporal lobe epilepsy. Neuroscience Letters, 2008, 436, 23-26.	2.1	17
62	miRNAome of Italian Large White pig subcutaneous fat tissue: new miRNAs, isomiRs and moRNAs. Animal Genetics, 2014, 45, 685-698.	1.7	17
63	Small RNAs in Circulating Exosomes of Cancer Patients: A Minireview. High-Throughput, 2017, 6, 13.	4.4	17
64	Rare Risk Variants Identification by Identity-by-Descent Mapping and Whole-Exome Sequencing Implicates Neuronal Development Pathways in Schizophrenia and Bipolar Disorder. Molecular Neurobiology, 2018, 55, 7366-7376.	4.0	17
65	A data-driven network model of primary myelofibrosis: transcriptional and post-transcriptional alterations in CD34+ cells. Blood Cancer Journal, 2016, 6, e439-e439.	6.2	16
66	Identification of differentially expressed small RNAs and prediction of target genes in Italian Large White pigs with divergent backfat deposition. Animal Genetics, 2018, 49, 205-214.	1.7	16
67	Somatic mutations activating Wiskott-Aldrich syndrome protein concomitant with RAS pathway mutations in juvenile myelomonocytic leukemia patients. Human Mutation, 2018, 39, 579-587.	2.5	16
68	A survey of software tools for microRNA discovery and characterization using RNA-seq. Briefings in Bioinformatics, 2019, 20, 918-930.	6.5	16
69	MicroRNA-497/195 is tumor suppressive and cooperates with CDKN2A/B in pediatric acute lymphoblastic leukemia. Blood, 2021, 138, 1953-1965.	1.4	16
70	Novel genes, possibly relevant for molecular diagnosis or therapy of human rhabdomyosarcoma, detected by genomic expression profiling. Gene, 2005, 348, 65-71.	2.2	15
71	Motif discovery in promoters of genes co-localized and co-expressed during myeloid cells differentiation. Nucleic Acids Research, 2009, 37, 533-549.	14.5	15
72	The preliminary transcript map of a human skeletal muscle. Human Molecular Genetics, 1997, 6, 1445-1450.	2.9	14

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73	A Computational Reconstruction of the Adult Human Heart Transcriptional Profile. <i>Journal of Molecular and Cellular Cardiology</i> , 2000, 32, 1931-1938.	1.9	13
74	RNY4 in Circulating Exosomes of Patients With Pediatric Anaplastic Large Cell Lymphoma: An Active Player?. <i>Frontiers in Oncology</i> , 2020, 10, 238.	2.8	12
75	CircRNAs Dysregulated in Juvenile Myelomonocytic Leukemia: CircMCTP1 Stands Out. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 613540.	3.7	12
76	CRAFT: a bioinformatics software for custom prediction of circular RNA functions. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	12
77	Detecting seeded motifs in DNA sequences. <i>Nucleic Acids Research</i> , 2005, 33, e135-e135.	14.5	11
78	A high definition picture of key genes and pathways mutated in pediatric follicular lymphoma. <i>Haematologica</i> , 2019, 104, e406-e409.	3.5	11
79	A novel germline variant in <i>PIK3R1</i> results in <i>SHORT</i> syndrome associated with <i>TAL</i> <i>T</i> cell acute lymphoblastic leukemia. <i>American Journal of Hematology</i> , 2020, 95, E335-E338.	4.1	11
80	Expanding the repertoire of miRNAs and miRNA-offset RNAs expressed in multiple myeloma by small RNA deep sequencing. <i>Blood Cancer Journal</i> , 2019, 9, 21.	6.2	10
81	MiR&moRe2: A Bioinformatics Tool to Characterize microRNAs and microRNA-Offset RNAs from Small RNA-Seq Data. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1754.	4.1	10
82	iWhale: a computational pipeline based on Docker and SCons for detection and annotation of somatic variants in cancer WES data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	8
83	Impact of probe annotation on the integration of miRNA mRNA expression profiles for miRNA target detection. <i>Nucleic Acids Research</i> , 2010, 38, e97-e97.	14.5	7
84	Human miRNome profiling in colorectal cancer and liver metastasis development. <i>Genomics Data</i> , 2014, 2, 184-188.	1.3	7
85	Clinical significance of circulating tumor cells and cell-free DNA in pediatric rhabdomyosarcoma. <i>Molecular Oncology</i> , 2022, 16, 2071-2085.	4.6	7
86	Defining TCR lymphoproliferative disorders by combined immunophenotypic and molecular evaluation. <i>Nature Communications</i> , 2022, 13, .	12.8	7
87	The Gene Promoter of Human Na ⁺ /Ca ²⁺ Exchanger Isoform 3 (SLC8A3) Is Controlled by cAMP and Calcium. <i>Annals of the New York Academy of Sciences</i> , 2002, 976, 282-284.	3.8	6
88	Chromosomal localization of four MAPK signaling cascade genes: MEK1, MEK3, MEK4 and MEK5. <i>Cytogenetic and Genome Research</i> , 1997, 78, 301-303.	1.1	5
89	Detection of chromosomal regions showing differential gene expression in human skeletal muscle and in alveolar rhabdomyosarcoma. <i>BMC Bioinformatics</i> , 2004, 5, 68.	2.6	5
90	CRITICAL ANALYSIS OF TRANSCRIPTIONAL AND POST-TRANSCRIPTIONAL REGULATORY NETWORKS IN MULTIPLE MYELOMA. , 2009, , 397-408.		5

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91	Bioinformatic Analysis of Circular RNA Expression. <i>Methods in Molecular Biology</i> , 2021, 2348, 343-370.	0.9	4
92	Increased Tenascin C, Osteopontin and HSP90 Levels in Plasmatic Small Extracellular Vesicles of Pediatric ALK-Positive Anaplastic Large Cell Lymphoma: New Prognostic Biomarkers?. <i>Diagnostics</i> , 2021, 11, 253.	2.6	4
93	Lack of Viral Load Within Chronic Lymphoproliferative Disorder of Natural Killer Cells: What Is Outside the Leukemic Clone?. <i>Frontiers in Oncology</i> , 2020, 10, 613570.	2.8	3
94	CircIMPACT: An R Package to Explore Circular RNA Impact on Gene Expression and Pathways. <i>Genes</i> , 2021, 12, 1044.	2.4	3
95	A guilt-by-association mutation network in LGL leukemia. <i>Oncotarget</i> , 2017, 8, 93299-93300.	1.8	3
96	Detecting differentially expressed circular RNAs from multiple quantification methods using a generalized linear mixed model. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2495-2502.	4.1	3
97	Low miR-214-5p Expression Correlates With Aggressive Subtypes of Pediatric ALCL With Non-Common Histology. <i>Frontiers in Oncology</i> , 2021, 11, 663221.	2.8	2
98	Expression and impact of miR-497 in pediatric ALL. , 2017, 229, .		1
99	Identification of MicroRNA Expression Patterns and Definition of a MicroRNAs/mRNA Regulatory Network in Distinct Molecular Groups of Multiple Myeloma.. <i>Blood</i> , 2009, 114, 2824-2824.	1.4	1
100	PF362 A FIRST HIGH-DEFINITION LANDSCAPE OF SOMATIC MUTATIONS IN CHRONIC LYMPHOPROLIFERATIVE DISORDER OF NK CELLS. <i>HemaSphere</i> , 2019, 3, 132-133.	2.7	1
101	817 Integration of gene and miRNA expression profiles in clear cell renal carcinoma cell lines and relationship with VHL gene status. <i>European Journal of Cancer, Supplement</i> , 2010, 8, 206.	2.2	0
102	MicroRNA expression in HTLV-1 infection and pathogenesis. <i>Retrovirology</i> , 2011, 8, .	2.0	0
103	P3043 Study of differentially expressed short-RNAs in swine backfat between fat and lean animals and target prediction of genes regulating fat traits. <i>Journal of Animal Science</i> , 2016, 94, 74-74.	0.5	0
104	Bioinformatic Pipelines to Analyze lncRNAs RNAseq Data. <i>Methods in Molecular Biology</i> , 2021, 2348, 55-69.	0.9	0
105	Editorial: Genomics of Lymphoproliferative Disease. <i>Frontiers in Oncology</i> , 2021, 11, 660016.	2.8	0
106	Characterization of Targets of Plitidepsin In JAK2V617F-Mutated Cells From Myeloproliferative Neoplasms. <i>Blood</i> , 2010, 116, 4093-4093.	1.4	0
107	Regulatory Mrna/Microrna Networks in CD34+ Cells From Primary Myelofibrosis.. <i>Blood</i> , 2012, 120, 2854-2854.	1.4	0
108	Integrative Analysis Of mRNA/miRNA Expression Profiles Identified JARID2 As a Shared Target Of Deregulated Mirnas In Primary Myelofibrosis. <i>Blood</i> , 2013, 122, 1600-1600.	1.4	0

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109	Subset-Specific Recurrence of Mutations and Identification of Functional Modules Provides New Clues about the Pathogenesis of Large Granular Lymphocyte Leukemia. <i>Blood</i> , 2016, 128, 4117-4117.	1.4	0
110	Whole Exome Sequencing Analysis in Chronic Lymphoproliferative Disorder of NK Cells (CLPD-NK) Patients Fails to Detect Significant Viral Load. <i>Blood</i> , 2019, 134, 5214-5214.	1.4	0
111	MicroRNA-497-195 cluster suppresses cell cycle progression by targeting CCND3/CDK4 in acute lymphoblastic leukemia. <i>Klinische Padiatrie</i> , 2020, 232, .	0.6	0
112	Abstract 2541: MicroRNA-497-195 cluster suppresses acute lymphoblastic leukemia growth by targeting CCND3/CDK4 and inhibiting cell cycle progression. , 2020, , .		0
113	RNA-seq analysis of plasmatic exosomal miRNAs in pediatric Hodgkin Lymphoma. <i>Klinische Padiatrie</i> , 2020, 232, .	0.6	0
114	Circular RNA Dysregulation Characterizes Symptomatic T-LGL Leukemia Patients with <i>STAT3</i> Mutation. <i>Blood</i> , 2021, 138, 1134-1134.	1.4	0