

# 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	Sensitive, reliable and robust circRNA detection from RNA-seq with CirComPara2. Briefings in Bioinformatics, 2022, 23, .	6.5	22
2	CRAFT: a bioinformatics software for custom prediction of circular RNA functions. Briefings in Bioinformatics, 2022, 23, .	6.5	12
3	Clinical significance of circulating tumor cells and cell-free DNA in pediatric rhabdomyosarcoma. Molecular Oncology, 2022, 16, 2071-2085.	4.6	7
4	Detecting differentially expressed circular RNAs from multiple quantification methods using a generalized linear mixed model. Computational and Structural Biotechnology Journal, 2022, 20, 2495-2502.	4.1	3
5	Defining TCR <sup>hi</sup> lymphoproliferative disorders by combined immunophenotypic and molecular evaluation. Nature Communications, 2022, 13, .	12.8	7
6	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
7	Bioinformatic Analysis of Circular RNA Expression. Methods in Molecular Biology, 2021, 2348, 343-370.	0.9	4
8	Bioinformatic Pipelines to Analyze lncRNAs RNAseq Data. Methods in Molecular Biology, 2021, 2348, 55-69.	0.9	0
9	Increased Tenascin C, Osteopontin and HSP90 Levels in Plasmatic Small Extracellular Vesicles of Pediatric ALK-Positive Anaplastic Large Cell Lymphoma: New Prognostic Biomarkers?. Diagnostics, 2021, 11, 253.	2.6	4
10	Editorial: Genomics of Lymphoproliferative Disease. Frontiers in Oncology, 2021, 11, 660016.	2.8	0
11	Low miR-214-5p Expression Correlates With Aggressive Subtypes of Pediatric ALCL With Non-Common Histology. Frontiers in Oncology, 2021, 11, 663221.	2.8	2
12	MicroRNA-497/195 is tumor suppressive and cooperates with CDKN2A/B in pediatric acute lymphoblastic leukemia. Blood, 2021, 138, 1953-1965.	1.4	16
13	CircIMPACT: An R Package to Explore Circular RNA Impact on Gene Expression and Pathways. Genes, 2021, 12, 1044.	2.4	3
14	iWhale: a computational pipeline based on Docker and SCons for detection and annotation of somatic variants in cancer WES data. Briefings in Bioinformatics, 2021, 22, .	6.5	8
15	Circular RNA Dysregulation Characterizes Symptomatic T-LGL Leukemia Patients with <i>STAT3</i> Mutation. Blood, 2021, 138, 1134-1134.	1.4	0
16	A novel germline variant in <i>PIK3R1</i> results in <i>SHORT</i> syndrome associated with <i>TAL</i> <i>LMO</i> T-cell acute lymphoblastic leukemia. American Journal of Hematology, 2020, 95, E335-E338.	4.1	11
17	Large-scale circular RNA deregulation in T-ALL: unlocking unique ectopic expression of molecular subtypes. Blood Advances, 2020, 4, 5902-5914.	5.2	39
18	RNY4 in Circulating Exosomes of Patients With Pediatric Anaplastic Large Cell Lymphoma: An Active Player?. Frontiers in Oncology, 2020, 10, 238.	2.8	12

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19	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
20	A high definition picture of somatic mutations in chronic lymphoproliferative disorder of natural killer cells. <i>Blood Cancer Journal</i> , 2020, 10, 42.	6.2	22
21	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
22	CircRNAs Dysregulated in Juvenile Myelomonocytic Leukemia: CircMCTP1 Stands Out. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 613540.	3.7	12
23	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
24	Abstract 2541: MicroRNA-497-195 cluster suppresses acute lymphoblastic leukemia growth by targeting CCND3/CDK4 and inhibiting cell cycle progression. , 2020, , .		0
25	RNA-seq analysis of plasmatic exosomal miRNAs in pediatric Hodgkin Lymphoma. <i>Klinische Padiatrie</i> , 2020, 232, .	0.6	0
26	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
27	Silencing of miR-182 is associated with modulation of tumorigenesis through apoptosis induction in an experimental model of colorectal cancer. <i>BMC Cancer</i> , 2019, 19, 821.	2.6	22
28	CircRNAs Are Here to Stay: A Perspective on the MLL Recombinome. <i>Frontiers in Genetics</i> , 2019, 10, 88.	2.3	19
29	A high definition picture of key genes and pathways mutated in pediatric follicular lymphoma. <i>Haematologica</i> , 2019, 104, e406-e409.	3.5	11
30	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
31	A survey of software tools for microRNA discovery and characterization using RNA-seq. <i>Briefings in Bioinformatics</i> , 2019, 20, 918-930.	6.5	16
32	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
33	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
34	Identification of differentially expressed small RNAs and prediction of target genes in Italian Large White pigs with divergent backfat deposition. <i>Animal Genetics</i> , 2018, 49, 205-214.	1.7	16
35	Somatic mutations activating Wiskott-Aldrich syndrome protein concomitant with RAS pathway mutations in juvenile myelomonocytic leukemia patients. <i>Human Mutation</i> , 2018, 39, 579-587.	2.5	16
36	Rare Risk Variants Identification by Identity-by-Descent Mapping and Whole-Exome Sequencing Implicates Neuronal Development Pathways in Schizophrenia and Bipolar Disorder. <i>Molecular Neurobiology</i> , 2018, 55, 7366-7376.	4.0	17

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37	Somatic mutations in specific and connected subpathways are associated with short neuroblastoma patients' survival and indicate proteins targetable at onset of disease. <i>International Journal of Cancer</i> , 2018, 143, 2525-2536.	5.1	27
38	Genomic landscape characterization of large granular lymphocyte leukemia with a systems genetics approach. <i>Leukemia</i> , 2017, 31, 1243-1246.	7.2	33
39	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
40	Small RNAs in Circulating Exosomes of Cancer Patients: A Minireview. <i>High-Throughput</i> , 2017, 6, 13.	4.4	17
41	Expression and impact of miR-497-195 in pediatric ALL. , 2017, 229, .		1
42	A guilt-by-association mutation network in LGL leukemia. <i>Oncotarget</i> , 2017, 8, 93299-93300.	1.8	3
43	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
44	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
45	A data-driven network model of primary myelofibrosis: transcriptional and post-transcriptional alterations in CD34+ cells. <i>Blood Cancer Journal</i> , 2016, 6, e439-e439.	6.2	16
46	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
47	Activating somatic mutations outside the SH2-domain of STAT3 in LGL leukemia. <i>Leukemia</i> , 2016, 30, 1204-1208.	7.2	62
48	CircRNAs in hematopoiesis and hematological malignancies. <i>Blood Cancer Journal</i> , 2016, 6, e483-e483.	6.2	139
49	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
50	Loss of zfp36 expression in colorectal cancer correlates to wnt/ $\beta$ -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
51	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
52	An integrative approach for the identification of prognostic and predictive biomarkers in rectal cancer. <i>Oncotarget</i> , 2015, 6, 32561-32574.	1.8	45
53	H-Ferritin-Regulated MicroRNAs Modulate Gene Expression in K562 Cells. <i>PLoS ONE</i> , 2015, 10, e0122105.	2.5	30
54	Small RNA Sequencing Uncovers New miRNAs and moRNAs Differentially Expressed in Normal and Primary Myelofibrosis CD34+ Cells. <i>PLoS ONE</i> , 2015, 10, e0140445.	2.5	20

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55	A constitutive active MAPK/ERK pathway due to BRAFV600E positively regulates AHR pathway in PTC. <i>Oncotarget</i> , 2015, 6, 32104-32114.	1.8	23
56	Clinical effect of driver mutations of JAK2, CALR, or MPL in primary myelofibrosis. <i>Blood</i> , 2014, 124, 1062-1069.	1.4	340
57	miRNome of Italian Large White pig subcutaneous fat tissue: new miRNAs, isomiRNAs and moRNAs. <i>Animal Genetics</i> , 2014, 45, 685-698.	1.7	17
58	Human miRNome profiling in colorectal cancer and liver metastasis development. <i>Genomics Data</i> , 2014, 2, 184-188.	1.3	7
59	An integrative framework identifies alternative splicing events in colorectal cancer development. <i>Molecular Oncology</i> , 2014, 8, 129-141.	4.6	43
60	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
61	Circulating miR-182 is a biomarker of colorectal adenocarcinoma progression. <i>Oncotarget</i> , 2014, 5, 6611-6619.	1.8	53
62	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
63	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
64	miR-142-3p Prevents Macrophage Differentiation during Cancer-Induced Myelopoiesis. <i>Immunity</i> , 2013, 38, 1236-1249.	14.3	127
65	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
66	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
67	Sequencing and Characterization of Striped Venus Transcriptome Expand Resources for Clam Fishery Genetics. <i>PLoS ONE</i> , 2012, 7, e44185.	2.5	23
68	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
69	Characterization and discovery of novel miRNAs and moRNAs in JAK2V617F-mutated SET2 cells. <i>Blood</i> , 2012, 119, e120-e130.	1.4	34
70	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
71	Regulatory Mrna/Microna Networks in CD34+ Cells From Primary Myelofibrosis.. <i>Blood</i> , 2012, 120, 2854-2854.	1.4	0
72	MicroRNA "offset RNAs (moRNAs): by-product spectators or functional players?. <i>Trends in Molecular Medicine</i> , 2011, 17, 473-474.	6.7	34

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73	MicroRNA expression in HTLV-1 infection and pathogenesis. <i>Retrovirology</i> , 2011, 8, .	2.0	0
74	TRAM (Transcriptome Mapper): database-driven creation and analysis of transcriptome maps from multiple sources. <i>BMC Genomics</i> , 2011, 12, 121.	2.8	45
75	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
76	Impact of Host Genes and Strand Selection on miRNA and miRNA* Expression. <i>PLoS ONE</i> , 2011, 6, e23854.	2.5	37
77	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
78	Age estimation in subadult Egyptian remains. <i>HOMO- Journal of Comparative Human Biology</i> , 2010, 61, 337-358.	0.7	20
79	Impact of probe annotation on the integration of miRNA and mRNA expression profiles for miRNA target detection. <i>Nucleic Acids Research</i> , 2010, 38, e97-e97.	14.5	7
80	MAGIA, a web-based tool for miRNA and Genes Integrated Analysis. <i>Nucleic Acids Research</i> , 2010, 38, W352-W359.	14.5	150
81	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
82	Characterization of Targets of Plitidepsin In JAK2V617F-Mutated Cells From Myeloproliferative Neoplasms. <i>Blood</i> , 2010, 116, 4093-4093.	1.4	0
83	Motif discovery in promoters of genes co-localized and co-expressed during myeloid cells differentiation. <i>Nucleic Acids Research</i> , 2009, 37, 533-549.	14.5	15
84	A-MADMAN: Annotation-based microarray data meta-analysis tool. <i>BMC Bioinformatics</i> , 2009, 10, 201.	2.6	38
85	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
86	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
87	CRITICAL ANALYSIS OF TRANSCRIPTIONAL AND POST-TRANSCRIPTIONAL REGULATORY NETWORKS IN MULTIPLE MYELOMA. , 2009, , 397-408.		5
88	Analysis of LGI1 promoter sequence, PDYN and GABBR1 polymorphisms in sporadic and familial lateral temporal lobe epilepsy. <i>Neuroscience Letters</i> , 2008, 436, 23-26.	2.1	17
89	Novel definition files for human GeneChips based on GeneAnnot. <i>BMC Bioinformatics</i> , 2007, 8, 446.	2.6	93
90	Genomic expression during human myelopoiesis. <i>BMC Genomics</i> , 2007, 8, 264.	2.8	31

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91	REEF: searching REgionally Enriched Features in genomes. BMC Bioinformatics, 2006, 7, 453.	2.6	32
92	Defining the gene expression signature of rhabdomyosarcoma by meta-analysis. BMC Genomics, 2006, 7, 287.	2.8	37
93	A multistep bioinformatic approach detects putative regulatory elements in gene promoters. BMC Bioinformatics, 2005, 6, 121.	2.6	18
94	Computational reconstruction of the human skeletal muscle secretome. Proteins: Structure, Function and Bioinformatics, 2005, 62, 776-792.	2.6	111
95	Detecting seeded motifs in DNA sequences. Nucleic Acids Research, 2005, 33, e135-e135.	14.5	11
96	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
97	Detection of chromosomal regions showing differential gene expression in human skeletal muscle and in alveolar rhabdomyosarcoma. BMC Bioinformatics, 2004, 5, 68.	2.6	5
98	Control of the Na <sup>+</sup> /Ca <sup>2+</sup> exchanger 3 promoter by cyclic adenosine monophosphate and Ca <sup>2+</sup> in differentiating neurons. Journal of Neurochemistry, 2003, 84, 282-293.	3.9	23
99	IDE6: a web tool for detection of differentially expressed genes in multiple tag sampling experiments. Physiological Genomics, 2003, 12, 159-162.	2.3	336
100	Disease genes and intracellular protein networks. Physiological Genomics, 2003, 15, 223-227.	2.3	19
101	The human SLC8A3 gene and the tissue-specific Na <sup>+</sup> /Ca <sup>2+</sup> exchanger 3 isoforms. Gene, 2002, 298, 1-7.	2.2	26
102	The Gene Promoter of Human Na <sup>+</sup> /Ca <sup>2+</sup> Exchanger Isoform 3 (SLC8A3) Is Controlled by cAMP and Calcium. Annals of the New York Academy of Sciences, 2002, 976, 282-284.	3.8	6
103	Missense polymorphism in the human carboxypeptidase E gene alters enzymatic activity. Human Mutation, 2001, 18, 120-131.	2.5	75
104	DHPLC analysis of the MECP2 gene in Italian Rett patients. Human Mutation, 2001, 18, 132-140.	2.5	25
105	Detecting differentially expressed genes in multiple tag sampling experiments: comparative evaluation of statistical tests. Human Molecular Genetics, 2001, 10, 2133-2141.	2.9	54
106	Differential expression of genes coding for ribosomal proteins in different human tissues. Bioinformatics, 2001, 17, 1152-1157.	4.1	113
107	The Human Adult Skeletal Muscle Transcriptional Profile Reconstructed by a Novel Computational Approach. Genome Research, 2000, 10, 344-349.	5.5	47
108	Characterization of C14orf4, a Novel Intronless Human Gene Containing a Polyglutamine Repeat, Mapped to the ARVD1 Critical Region. Biochemical and Biophysical Research Communications, 2000, 278, 766-774.	2.1	49

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109	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
110	A novel resource for the study of genes expressed in the adult human retina. <i>Investigative Ophthalmology and Visual Science</i> , 2000, 41, 3305-8.	3.3	18
111	Towards an in silico analysis of transcription patterns. <i>Trends in Genetics</i> , 1999, 15, 118-119.	6.7	22
112	A Comprehensive, High-Resolution Genomic Transcript Map of Human Skeletal Muscle. <i>Genome Research</i> , 1998, 8, 817-825.	5.5	69
113	Chromosomal localization of four MAPK signaling cascade genes: MEK1, MEK3, MEK4 and MEKK5. <i>Cytogenetic and Genome Research</i> , 1997, 78, 301-303.	1.1	5
114	The preliminary transcript map of a human skeletal muscle. <i>Human Molecular Genetics</i> , 1997, 6, 1445-1450.	2.9	14