Sonia Fabris

List of Publications by Year
in descending order

92 papers	3,561 citations	101384 36 h-index	143772 57 g-index
92 all docs	92 docs citations	92 times ranked	4994 citing authors

#	Article	IF	Citations
1	Demystifying the diagnostic criteria of indolent systemic mastocytosis. Hematological Oncology, 2022, 40, 123-125.	0.8	0
2	LINC00152 expression in normal and Chronic Lymphocytic Leukemia B cells. Hematological Oncology, 2022, 40, 41-48.	0.8	5
3	Impact on thrombotic risk of canonical and atypical CALR mutations in essential thrombocythemia. A single-center cohort study. Thrombosis Research, 2022, 210, 67-69.	0.8	3
4	Clinical, Morphological and Clonal Progression of VEXAS Syndrome in the Context of Myelodysplasia Treated with Azacytidine. Clinical Hematology International, 2022, 4, 52-55.	0.7	7
5	Triple-Negative Essential Thrombocythemia: Clinical-Pathological and Molecular Features. A Single-Center Cohort Study. Frontiers in Oncology, 2021, 11, 637116.	1.3	15
6	Lymphocyte Doubling Time As A Key Prognostic Factor To Predict Time To First Treatment In Early-Stage Chronic Lymphocytic Leukemia. Frontiers in Oncology, 2021, 11, 684621.	1.3	6
7	Case Report: Evolution of KIT D816V-Positive Systemic Mastocytosis to Myeloid Neoplasm With PDGFRA Rearrangement Responsive to Imatinib. Frontiers in Oncology, 2021, 11, 734025.	1.3	0
8	Long non-coding RNA NEAT1 targeting impairs the DNA repair machinery and triggers anti-tumor activity in multiple myeloma. Leukemia, 2020, 34, 234-244.	3.3	80
9	Time to first treatment and P53 dysfunction in chronic lymphocytic leukaemia: results of the O-CLL1 study in early stage patients. Scientific Reports, 2020, 10, 18427.	1.6	13
10	Limits and Applications of Genomic Analysis of Circulating Tumor DNA as a Liquid Biopsy in Asymptomatic Forms of Multiple Myeloma. HemaSphere, 2020, 4, e402.	1.2	15
11	NEAT1 Long Isoform Is Highly Expressed in Chronic Lymphocytic Leukemia Irrespectively of Cytogenetic Groups or Clinical Outcome. Non-coding RNA, 2020, 6, 11.	1.3	11
12	Frequency and clinical relevance of coding and noncoding NOTCH1 mutations in early stage Binet A chronic lymphocytic leukemia patients. Hematological Oncology, 2020, 38, 406-408.	0.8	5
13	Deregulation of miRNAs-cMYC circuits is a key event in refractory celiac disease type-2 lymphomagenesis. Clinical Science, 2020, 134, 1151-1166.	1.8	14
14	Integrating clinical, morphological, and molecular data to assess prognosis in patients with primary myelofibrosis at diagnosis: A practical approach. Hematological Oncology, 2019, 37, 424-433.	0.8	3
15	The Role of New Technologies in Myeloproliferative Neoplasms. Frontiers in Oncology, 2019, 9, 321.	1.3	37
16	Circulating tumor DNA as a liquid biopsy in plasma cell dyscrasias. Haematologica, 2018, 103, e245-e248.	1.7	29
17	Microenvironmental regulation of the IL-23R/IL-23 axis overrides chronic lymphocytic leukemia indolence. Science Translational Medicine, 2018, 10, .	5.8	13
18	Global methylation patterns in primary plasma cell leukemia. Leukemia Research, 2018, 73, 95-102.	0.4	13

#	Article	IF	Citations
19	Acquired CYP19A1 amplification is an early specific mechanism of aromatase inhibitor resistance in ERÎ± metastatic breast cancer. Nature Genetics, 2017, 49, 444-450.	9.4	77
20	Clonal reticulohistiocytosis of the skin and bone marrow associated with systemic mastocytosis and acute myeloid leukaemia. Histopathology, 2017, 70, 1000-1008.	1.6	8
21	An unusual type of myeloid sarcoma localization following myelofibrosis: A case report and literature review. Leukemia Research Reports, 2017, 8, 7-10.	0.2	6
22	Primary Soft Tissue Lymphomas: Description of Seven Cases and Review of the Literature. Pathology and Oncology Research, 2017, 23, 281-286.	0.9	2
23	Biological and molecular characterization of a rare case of cutaneous Richter syndrome. Hematological Oncology, 2017, 35, 869-874.	0.8	4
24	Anagrelide and Mutational Status in Essential Thrombocythemia. BioDrugs, 2016, 30, 219-223.	2.2	7
25	Compendium of <scp>FAM</scp>46C gene mutations in plasma cell dyscrasias. British Journal of Haematology, 2016, 174, 642-645.	1.2	34
26	Prospective validation of predictive value of abdominal computed tomography scan on time to first treatment in Rai 0 chronic lymphocytic leukemia patients: results of the multicenter Oâ€<scp>CLL</scp>1â€<scp>GISL</scp> study. European Journal of Haematology, 2016, 96, 36-45.	1.1	7
27	Molecular spectrum of TP53 mutations in plasma cell dyscrasias by next generation sequencing: an Italian cohort study and overview of the literature. Oncotarget, 2016, 7, 21353-21361.	0.8	40
28	Whole-exome sequencing of primary plasma cell leukemia discloses heterogeneous mutational patterns. Oncotarget, 2015, 6, 17543-17558.	0.8	55
29	Association between gene and miRNA expression profiles and stereotyped subset #4 B-cell receptor in chronic lymphocytic leukemia. Leukemia and Lymphoma, 2015, 56, 3150-3158.	0.6	23
30	Is ZAP70 still a key prognostic factor in early stage chronic lymphocytic leukaemia? Results of the analysis from a prospective multicentre observational study. British Journal of Haematology, 2015, 168, 455-459.	1.2	9
31	Insulin Growth Factor 1 Receptor Expression Is Associated with NOTCH1 Mutation, Trisomy 12 and Aggressive Clinical Course in Chronic Lymphocytic Leukaemia. PLoS ONE, 2015, 10, e0118801.	1.1	15
32	Molecular spectrum of BRAF, NRAS and KRAS gene mutations in plasma cell dyscrasias: implication for MEK-ERK pathway activation. Oncotarget, 2015, 6, 24205-24217.	0.8	65
33	A compendium of DIS3 mutations and associated transcriptional signatures in plasma cell dyscrasias. Oncotarget, 2015, 6, 26129-26141.	0.8	40
34	Prospective validation of a risk score based on biological markers for predicting progression free survival in Binet stage A chronic lymphocytic leukemia patients: Results of the multicenter Oâ€CLL1â€GISL study. American Journal of Hematology, 2014, 89, 743-750.	2.0	14
35	Molecular events underlying interleukinâ€6 independence in a subclone of the CMAâ€03 multiple myeloma cell line. Genes Chromosomes and Cancer, 2014, 53, 154-167.	1.5	6
36	Distinct patterns of global promoter methylation in early stage chronic lymphocytic leukemia. Genes Chromosomes and Cancer, 2014, 53, 264-273.	1.5	10

#	Article	IF	Citations
37	Highâ€throughput sequencing for the identification of <scp>NOTCH</scp>1 mutations in early stage chronic lymphocytic leukaemia: biological and clinical implications. British Journal of Haematology, 2014, 165, 629-639.	1.2	52
38	Relevance of telomere/telomerase system impairment in early stage chronic lymphocytic leukemia. Genes Chromosomes and Cancer, 2014, 53, 612-621.	1.5	38
39	microRNAome Expression in Chronic Lymphocytic Leukemia: Comparison with Normal B-cell Subsets and Correlations with Prognostic and Clinical Parameters. Clinical Cancer Research, 2014, 20, 4141-4153.	3.2	52
40	Small nucleolar RNAs as new biomarkers in chronic lymphocytic leukemia. BMC Medical Genomics, 2013, 6, 27.	0.7	73
41	Total body computed tomography scan in the initial workâ€up of Binet stage A chronic lymphocytic leukemia patients: Results of the prospective, multicenter Oâ€CLL1â€GISL study. American Journal of Hematology, 2013, 88, 539-544.	2.0	10
42	Genomeâ€wide analysis of primary plasma cell leukemia identifies recurrent imbalances associated with changes in transcriptional profiles. American Journal of Hematology, 2013, 88, 16-23.	2.0	60
43	Chromosome 2p gain in monoclonal Bâ€cell lymphocytosis and in early stage chronic lymphocytic leukemia. American Journal of Hematology, 2013, 88, 24-31.	2.0	27
44	Bâ€cell receptor configuration and adverse cytogenetics are associated with autoimmune hemolytic anemia in chronic lymphocytic leukemia. American Journal of Hematology, 2013, 88, 32-36.	2.0	36
45	EGFR through STAT3 modulates Î”N63Î± expression to sustain tumorâ€initiating cell proliferation in squamous cell carcinomas. Journal of Cellular Physiology, 2013, 228, 871-878.	2.0	24
46	Clinical Monoclonal B Lymphocytosis versus Rai 0 Chronic Lymphocytic Leukemia: A Comparison of Cellular, Cytogenetic, Molecular, and Clinical Features. Clinical Cancer Research, 2013, 19, 5890-5900.	3.2	60
47	Transcriptional Characterization of a Prospective Series of Primary Plasma Cell Leukemia Revealed Signatures Associated with Tumor Progression and Poorer Outcome. Clinical Cancer Research, 2013, 19, 3247-3258.	3.2	50
48	Biological and Clinical Relevance of miRNA Expression Signatures in Primary Plasma Cell Leukemia. Clinical Cancer Research, 2013, 19, 3130-3142.	3.2	86
49	Report from the European Myeloma Network on interphase FISH in multiple myeloma and related disorders. Haematologica, 2012, 97, 1272-1277.	1.7	254
50	Immune Thrombocytopenia in Patients with Chronic Lymphocytic Leukemia Is Associated with Stereotyped B-cell Receptors. Clinical Cancer Research, 2012, 18, 1870-1878.	3.2	33
51	B-Cell Receptor Configuration and Adverse Cytogenetics Are Associated with Autoimmune Hemolytic Anemia in Chronic Lymphocytic Leukemia. Blood, 2012, 120, 1780-1780.	0.6	0
52	Intraclonal Cell Expansion and Selection Driven by B Cell Receptor in Chronic Lymphocytic Leukemia. Molecular Medicine, 2011, 17, 834-839.	1.9	9
53	Relevance of Stereotyped B-Cell Receptors in the Context of the Molecular, Cytogenetic and Clinical Features of Chronic Lymphocytic Leukemia. PLoS ONE, 2011, 6, e24313.	1.1	36
54	Multiplex ligationâ€dependent probe amplification and fluorescence in situ hybridization to detect chromosomal abnormalities in Chronic lymphocytic leukemia: A comparative study. Genes Chromosomes and Cancer, 2011, 50, 726-734.	1.5	24

#	Article	IF	Citations
55	Biological and clinical relevance of quantitative global methylation of repetitive DNA sequences in chronic lymphocytic leukemia. Epigenetics, 2011, 6, 188-194.	1.3	58
56	Prognostic Significance of Telomere Length in Chronic Lymphocytic Leukemia Patients in Early Stage Disease,. Blood, 2011, 118, 3890-3890.	0.6	7
57	Immune Thrombocytopenia in Patients with Chronic Lymphocytic Leukemia Is Associated with Stereotyped B-Cell Receptors. Blood, 2011, 118, 2847-2847.	0.6	0
58	The clinical and biological features of a series of immunophenotypic variant of Bâ€CLL. European Journal of Haematology, 2010, 85, 120-129.	1.1	13
59	Clinical categories identified by a new prognostic index reflect biological characteristics of patients in early chronic lymphocytic leukemia: The Gruppo Italiano Studio Linfomi (GISL) experience. Leukemia Research, 2010, 34, e217-e218.	0.4	3
60	Integrative Genomics Analyses Reveal Molecularly Distinct Subgroups of B-Cell Chronic Lymphocytic Leukemia Patients with 13q14 Deletion. Clinical Cancer Research, 2010, 16, 5641-5653.	3.2	52
61	Differential repetitive DNA methylation in multiple myeloma molecular subgroups. Carcinogenesis, 2009, 30, 1330-1335.	1.3	99
62	CD26 expression in mature Bâ€cell neoplasia: its possible role as a new prognostic marker in Bâ€CLL. Hematological Oncology, 2009, 27, 140-147.	0.8	46
63	Integrative highâ€resolution microarray analysis of human myeloma cell lines reveals deregulated miRNA expression associated with allelic imbalances and gene expression profiles. Genes Chromosomes and Cancer, 2009, 48, 521-531.	1.5	60
64	A SNP microarray and FISHâ€based procedure to detect allelic imbalances in multiple myeloma: An integrated genomics approach reveals a wide gene dosage effect. Genes Chromosomes and Cancer, 2009, 48, 603-614.	1.5	134
65	Definition of progression risk based on combinations of cellular and molecular markers in patients with Binet stage A chronic lymphocytic leukaemia. British Journal of Haematology, 2009, 146, 44-53.	1.2	50
66	Identification of microRNA expression patterns and definition of a microRNA/mRNA regulatory network in distinct molecular groups of multiple myeloma. Blood, 2009, 114, e20-e26.	0.6	224
67	An integrative genomic approach reveals coordinated expression of intronic miR-335, miR-342, and miR-561 with deregulated host genes in multiple myeloma. BMC Medical Genomics, 2008, 1, 37.	0.7	104
68	Molecular and transcriptional characterization of 17p loss in Bâ€cell chronic lymphocytic leukemia. Genes Chromosomes and Cancer, 2008, 47, 781-793.	1.5	59
69	Immunoreactivity for cyclin D1 is a reliable marker of gene aberration in plasma cell myeloma but does not specify patients prognosis. Leukemia Research, 2008, 32, 1628-1632.	0.4	1
70	Repetitive DNA Hypomethylation in Multiple Myeloma. Blood, 2008, 112, 2703-2703.	0.6	16
71	Integrative genomic analysis reveals distinct transcriptional and genetic features associated with chromosome 13 deletion in multiple myeloma. Haematologica, 2007, 92, 56-65.	1.7	34
72	Relevance ofRas gene mutations in the context of the molecular heterogeneity of multiple myeloma. Hematological Oncology, 2007, 25, 6-10.	0.8	8

#	Article	IF	Citations
73	Molecular characterization of human multiple myeloma cell lines by integrative genomics: Insights into the biology of the disease. Genes Chromosomes and Cancer, 2007, 46, 226-238.	1.5	62
74	Molecular and transcriptional characterization of the novel 17p11.2â€p12 amplicon in multiple myeloma. Genes Chromosomes and Cancer, 2007, 46, 1109-1118.	1.5	20
75	Upregulation of translational machinery and distinct genetic subgroups characterise hyperdiploidy in multiple myeloma. British Journal of Haematology, 2007, 136, 565-573.	1.2	66
76	Gene expression profiling of plasma cell dyscrasias reveals molecular patterns associated with distinct IGH translocations in multiple myeloma. Oncogene, 2005, 24, 2461-2473.	2.6	118
77	Characterization of oncogene dysregulation in multiple myeloma by combined FISH and DNA microarray analyses. Genes Chromosomes and Cancer, 2005, 42, 117-127.	1.5	49
78	The transactivating isoforms of p63 are overexpressed in high-grade follicular lymphomas independent of the occurrence ofp63 gene amplification. Journal of Pathology, 2005, 206, 337-345.	2.1	39
79	Molecular Classification of Multiple Myeloma: A Distinct Transcriptional Profile Characterizes Patients Expressing CCND1 and Negative for 14q32 Translocations. Journal of Clinical Oncology, 2005, 23, 7296-7306.	0.8	123
80	Molecular and biological characterization of three novel interleukin-6-dependent human myeloma cell lines. Haematologica, 2005, 90, 1541-8.	1.7	11
81	Identification of a novel IGH-MMSET fusion transcript in a human myeloma cell line with the t(4;14)(p16Â·3;q32) chromosomal translocation. British Journal of Haematology, 2004, 126, 437-439.	1.2	5
82	IgV gene intraclonal diversification and clonal evolution in B-cell chronic lymphocytic leukaemia. British Journal of Haematology, 2004, 133, 060118040555003.	1.2	20
83	Cyclin D3 immunoreactivity in follicular lymphoma is independent of the t(6;14)(p21.1;q32.3) translocation orcyclin D3 gene amplification and is correlated with histologic grade and Ki-67 labeling index. International Journal of Cancer, 2004, 112, 71-77.	2.3	16
84	Heterogeneous pattern of chromosomal breakpoints involving theMYC locus in multiple myeloma. Genes Chromosomes and Cancer, 2003, 37, 261-269.	1.5	31
85	Immunoreactivity for cyclin D3 is frequently detectable in high-grade primary gastric lymphomas in the absence of the t(6;14)(p21.1;q32.3) chromosomal translocation. Journal of Pathology, 2003, 200, 596-601.	2.1	8
86	Cyclin D3 Immunoreactivity in Gastrointestinal Stromal Tumors Is Independent of Cyclin D3 Gene Amplification and Is Associated with Nuclear p27 Accumulation. Modern Pathology, 2003, 16, 886-892.	2.9	22
87	Cyclin D1 overexpression is a favorable prognostic variable for newly diagnosed multiple myeloma patients treated with high-dose chemotherapy and single or double autologous transplantation. Blood, 2003, 102, 1588-1594.	0.6	113
88	Analysis of FGFR3 gene mutations in multiple myeloma patients with t(4;14). British Journal of Haematology, 2001, 114, 362-364.	1.2	59
89	Immunohistochemical Analysis of Cyclin D1 Shows Deregulated Expression in Multiple Myeloma with the t(11;14). American Journal of Pathology, 2000, 156, 1505-1513.	1.9	72
90	Detection of t(4;14)(p16.3;q32) Chromosomal Translocation in Multiple Myeloma by Double-Color Fluorescent In Situ Hybridization. Blood, 1999, 94, 724-732.	0.6	58

#	Article	IF	Citations
91	Molecular Analysis of 11q13 Breakpoints in Multiple Myeloma. Blood, 1999, 93, 1330-1337.	0.6	80
92	Molecular Analysis of 11q13 Breakpoints in Multiple Myeloma. Blood, 1999, 93, 1330-1337.	0.6	6