Niccolo Bolli

List of Publications by Year in Descending Order

136 papers	12,925 citations	37 h-index	113 g-index
154 ext. papers	16,340 ext. citations	7.3 avg, IF	5.16 L-index

#	Paper	IF	Citations
136	Chemotherapy-Related Mutational Signatures Reveal the Origins of Therapy-Related Myeloid Neoplasms. *Blood*, **2021**, 138, 3271-3271	2.2	1
135	Dissection of Bone Marrow Microenvironment By Single Cell RNA Sequencing in Warm AIHA Patients: A Proof-of-Concept Analysis. *Blood*, **2021**, 138, 931-931	2.2	
134	MGUS and Chip: Two Faces, but Not of the Same Medal. *Blood*, **2021**, 138, 3800-3800	2.2	
133	CDKN2A deletion is a frequent event associated with poor outcome in patients with peripheral T-cell lymphoma not otherwise specified (PTCL-NOS). *Haematologica*, **2021**, 106, 2918-2926	6.6	3
132	Whole-genome sequencing reveals progressive versus stable myeloma precursor conditions as two distinct entities. *Nature Communications*, **2021**, 12, 1861	17.4	16
131	mmsig: a fitting approach to accurately identify somatic mutational signatures in hematological malignancies. *Communications Biology*, **2021**, 4, 424	6.7	5
130	Classification and Personalized Prognostic Assessment on the Basis of Clinical and Genomic Features in Myelodysplastic Syndromes. *Journal of Clinical Oncology*, **2021**, 39, 1223-1233	2.2	25
129	ROBO1 Promotes Homing, Dissemination, and Survival of Multiple Myeloma within the Bone Marrow Microenvironment. *Blood Cancer Discovery*, **2021**, 2, 338-353	7	1
128	DIS3 mutations in multiple myeloma impact the transcriptional signature and clinical outcome. *Haematologica*, **2021**,	6.6	2
127	CD40 Activity on Mesenchymal Cells Negatively Regulates OX40L to Maintain Bone Marrow Immune Homeostasis Under Stress Conditions. *Frontiers in Immunology*, **2021**, 12, 662048	8.4	0
126	Specific targeting of the KRAS mutational landscape in myeloma as a tool to unveil the elicited antitumor activity. *Blood*, **2021**, 138, 1705-1720	2.2	3
125	Clinical relevance of clonal hematopoiesis in persons aged ≥80 years. *Blood*, **2021**, 138, 2093-2105	2.2	6
124	Cereblon enhancer methylation and IMiD resistance in multiple myeloma. *Blood*, **2021**, 138, 1721-1726	2.2	4
123	What Is New in the Treatment of Smoldering Multiple Myeloma?. *Journal of Clinical Medicine*, **2021**, 10,	5.1	2
122	2021 European Myeloma Network review and consensus statement on smoldering multiple myeloma: how to distinguish (and manage) Dr. Jekyll and Mr. Hyde. *Haematologica*, **2021**, 106, 2799-2812	6.6	4
121	Copy number signatures predict chromothripsis and clinical outcomes in newly diagnosed multiple myeloma. *Nature Communications*, **2021**, 12, 5172	17.4	2
120	Functional Impact of Genomic Complexity on the Transcriptome of Multiple Myeloma. *Clinical Cancer Research*, **2021**, 27, 6479-6490	12.9	1

119	Single- and double-hit events in genes encoding immune targets before and after T cell-engaging antibody therapy in MM. *Blood Advances*, **2021**, 5, 3794-3798	7.8	3
118	The 2020 BMT CTN Myeloma Intergroup Workshop on Immune Profiling and Minimal Residual Disease Testing in Multiple Myeloma. *Transplantation and Cellular Therapy*, **2021**, 27, 807-816		1
117	Application of Next-Generation Sequencing for the Genomic Characterization of Patients with Smoldering Myeloma. *Cancers*, **2020**, 12,	6.6	4
116	Next-Generation Sequencing for Clinical Management of Multiple Myeloma: Ready for Prime Time?. *Frontiers in Oncology*, **2020**, 10, 189	5.3	20
115	Early Relapse Risk in Patients with Newly Diagnosed Multiple Myeloma Characterized by Next-generation Sequencing. *Clinical Cancer Research*, **2020**, 26, 4832-4841	12.9	22
114	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. *Nature Genetics*, **2020**, 52, 306-319	36.3	122
113	Timing the initiation of multiple myeloma. *Nature Communications*, **2020**, 11, 1917	17.4	36
112	Revealing Transcriptome Deregulation upon Genomic Complexity in Multiple Myeloma. *Blood*, **2020** , 136, 3-4	2.2	
111	Whole-Genome Sequencing Reveals Evidence of Two Biologically and Clinically Distinct Entities: Progressive Versus Stable Myeloma Precursor Disease. *Blood*, **2020**, 136, 47-48	2.2	2
110	The molecular pathogenesis of multiple myeloma. *Hematology Reports*, **2020**, 12, 9054	0.9	2
109	A Journey Through Myeloma Evolution: From the Normal Plasma Cell to Disease Complexity. *HemaSphere*, **2020**, 4, e502	0.3	4
108	Moving From Cancer Burden to Cancer Genomics for Smoldering Myeloma: A Review. *JAMA Oncology*, **2020**, 6, 425-432	13.4	25
107	A new case of myelodysplastic syndrome associated with t(3;3)(q21;q26) and inv(11)(p15q22). *Tumori*, **2020**, 106, NP18-NP22	1.7	
106	Revealing the impact of structural variants in multiple myeloma. *Blood Cancer Discovery*, **2020**, 1, 258-273		28
105	Limits and Applications of Genomic Analysis of Circulating Tumor DNA as a Liquid Biopsy in Asymptomatic Forms of Multiple Myeloma. *HemaSphere*, **2020**, 4, e402	0.3	5
104	Integrative analysis of the genomic and transcriptomic landscape of double-refractory multiple myeloma. *Blood Advances*, **2020**, 4, 830-844	7.8	21
103	Genomic landscape and chronological reconstruction of driver events in multiple myeloma. *Nature Communications*, **2019**, 10, 3835	17.4	94
102	Integration of transcriptional and mutational data simplifies the stratification of peripheral T-cell lymphoma. *American Journal of Hematology*, **2019**, 94, 628-634	7.1	7

101	A high-risk, Double-Hit, group of newly diagnosed myeloma identified by genomic analysis. *Leukemia*, **2019**, 33, 159-170	10.7	176
100	A practical guide for mutational signature analysis in hematological malignancies. *Nature Communications*, **2019**, 10, 2969	17.4	73
99	The Genomic and Transcriptomic Landscape of Double-Refractory Multiple Myeloma. *Blood*, **2019**, 134, 3056-3056	2.2	1
98	Specific Targeting of KRAS Using a Novel High-Affinity KRAS Antisense Oligonucleotide in Multiple Myeloma. *Blood*, **2019**, 134, 3104-3104	2.2	1
97	Lack of Significant Differences in Somatic Alterations between MGUS, SMM and Symptomatic Multiple Myeloma: A Result from Comprehensive Genomic Profiling Study. *Blood*, **2019**, 134, 3089-3089	2.2	
96	Timing the Initiation of Multiple Myeloma. *Blood*, **2019**, 134, 573-573	2.2	
95	PS1345 CIRCULATING TUMOR DNA AS A LIQUID BIOPSY IN SMOLDERING MULTIPLE MYELOMA TO IDENTIFY BIOMARKERS OF PROGRESSION. *HemaSphere*, **2019**, 3, 614-615	0.3	
94	Comprehensive detection of recurring genomic abnormalities: a targeted sequencing approach for multiple myeloma. *Blood Cancer Journal*, **2019**, 9, 101	7	22
93	Recurrent histone mutations in T-cell acute lymphoblastic leukaemia. *British Journal of Haematology*, **2019**, 184, 676-679	4.5	6
92	Genomic patterns of progression in smoldering multiple myeloma. *Nature Communications*, **2018**, 9, 3363	17.4	99
91	Identification of novel mutational drivers reveals oncogene dependencies in multiple myeloma. *Blood*, **2018**, 132, 587-597	2.2	196
90	Multiple myeloma clonal evolution in homogeneously treated patients. *Leukemia*, **2018**, 32, 2636-2647	10.7	51
89	The Landscape of Structural Variant Signatures in Multiple Myeloma Identifies Distinct Disease Subgroups with Implications for Pathogenesis. *Blood*, **2018**, 132, 109-109	2.2	
88	Mytype: A Capture Based Sequencing Approach to Detect Somatic Mutations, Copy Number Changes and IGH Translocations in Multiple Myeloma. *Blood*, **2018**, 132, 5588-5588	2.2	
87	Whole Genome Sequencing Reveals Recurrent Structural Driver Events in Peripheral T-Cell Lymphomas Not Otherwise Specified. *Blood*, **2018**, 132, 4115-4115	2.2	
86	Clinical Relevance of Clonal Hematopoiesis in the Oldest-Old Population: Analysis of the "Health and Anemia" Study. *Blood*, **2018**, 132, 750-750	2.2	
85	Biological and prognostic impact of APOBEC-induced mutations in the spectrum of plasma cell dyscrasias and multiple myeloma cell lines. *Leukemia*, **2018**, 32, 1044-1048	10.7	52
84	Analysis of the genomic landscape of multiple myeloma highlights novel prognostic markers and disease subgroups. *Leukemia*, **2018**, 32, 2604-2616	10.7	90

83	Precision oncology for acute myeloid leukemia using a knowledge bank approach. *Nature Genetics*, **2017**, 49, 332-340	36.3	155
82	Next-generation sequencing of a family with a high penetrance of monoclonal gammopathies for the identification of candidate risk alleles. *Cancer*, **2017**, 123, 3701-3708	6.4	8
81	Analysis of the genomic landscape of multiple myeloma highlights novel prognostic markers and disease subgroups. *Leukemia*, **2017**,	10.7	9
80	Rapid parallel acquisition of somatic mutations after NPM1 in acute myeloid leukaemia evolution. *British Journal of Haematology*, **2017**, 176, 825-829	4.5	3
79	Hemopoietic-specific Sf3b1-K700E knock-in mice display the splicing defect seen in human MDS but develop anemia without ring sideroblasts. *Leukemia*, **2017**, 31, 720-727	10.7	76
78	Angioimmunoblastic T cell lymphoma: novel molecular insights by mutation profiling. *Oncotarget*, **2017**, 8, 17763-17770	3.3	29
77	A rare case of atypical chronic lymphocytic leukaemia presenting as nephrotic syndrome. *BMJ Case Reports*, **2017**, 2017,	0.9	1
76	Bowel perforation from occult ileal involvement after diagnosis in a case of primary mediastinal large B-cell lymphoma. *BMJ Case Reports*, **2016**, 2016,	0.9	1
75	High-dose chemotherapy followed by autologous transplantation may overcome the poor prognosis of diffuse large B-cell lymphoma patients with MYC/BCL2 co-expression. *Blood Cancer Journal*, **2016**, 6, e491	7	4
74	Genomic Classification and Prognosis in Acute Myeloid Leukemia. *New England Journal of Medicine*, **2016**, 374, 2209-2221	59.2	1999
73	Analysis of Mutational Signatures Suggest That Aid Has an Early and Driver Role in Multiple Myeloma. *Blood*, **2016**, 128, 116-116	2.2	2
72	Whole Genome Sequencing of Unique Paired SMM/MGUS Progressing to MM Samples Reveals a Genomic Landscape with Diverse Evolutionary Pattern. *Blood*, **2016**, 128, 2088-2088	2.2	0
71	Peripheral T-Cell Lymphomas Not Otherwise Specified: Potential Novel Molecular Entities Based on Both Tumor and Microenvironment Cellular Components. *Blood*, **2016**, 128, 4098-4098	2.2	2
70	The Complex Landscape of Rearrangements in Smoldering and Symptomatic Multiple Myeloma Revealed By Whole-Genome Sequencing. *Blood*, **2016**, 128, 236-236	2.2	
69	RNA-Seq De Novo Assembly of Clonal Immunoglobulin Rearrangements Identifies Interesting Biology and Uncovers Prognostic Features in Multiple Myeloma. *Blood*, **2016**, 128, 195-195	2.2	
68	Development and validation of a comprehensive genomic diagnostic tool for myeloid malignancies. *Blood*, **2016**, 128, e1-9	2.2	36
67	A DNA target-enrichment approach to detect mutations, copy number changes and immunoglobulin translocations in multiple myeloma. *Blood Cancer Journal*, **2016**, 6, e467	7	47
66	Biology of peripheral T cell lymphomas Not otherwise specified: Is something finally happening? **2016**, 3, 9-18		9

65	KLF2 mutation is the most frequent somatic change in splenic marginal zone lymphoma and identifies a subset with distinct genotype. *Leukemia*, **2015**, 29, 1177-85	10.7	118
64	Characterization of gene mutations and copy number changes in acute myeloid leukemia using a rapid target enrichment protocol. *Haematologica*, **2015**, 100, 214-22	6.6	38
63	The Molecular Basis of Haematological Malignancies **2015**, 314-331		
62	Sf3b1 K700E Mutation Impairs Pre-mRNA Splicing and Definitive Hematopoiesis in a Conditional Knock-in Mouse Model. *Blood*, **2015**, 126, 140-140	2.2	4
61	Genomic Landscape and Its Prognostic Implications in Multiple Myeloma Using a Targeted Sequencing Approach. *Blood*, **2015**, 126, 370-370	2.2	1
60	GATA-3 Expression in Peripheral T-Cell Lymphomas (PTCL): Identification of a Cut-Off and Prognostic Value in PTCL-NOS Versus Others Hystotypes. *Blood*, **2015**, 126, 3889-3889	2.2	1
59	Dissecting Genetic and Phenotypic Heterogeneity to Map Molecular Phylogenies and Deliver Personalized Outcome and Treatment Predictions in AML. *Blood*, **2015**, 126, 803-803	2.2	2
58	Redefining Mutational Profiling Using RNA-Seq: Insight into the Functional Mutational Landscape of Multiple Myeloma. *Blood*, **2015**, 126, 837-837	2.2	0
57	Personally Tailored Risk Prediction of AML Based on Comprehensive Genomic and Clinical Data. *Blood*, **2015**, 126, 85-85	2.2	1
56	Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. *Nature Communications*, **2014**, 5, 2997	17.4	564
55	Mobile DNA in cancer. Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. *Science*, **2014**, 345, 1251343	33.3	250
54	Association of a germline copy number polymorphism of APOBEC3A and APOBEC3B with burden of putative APOBEC-dependent mutations in breast cancer. *Nature Genetics*, **2014**, 46, 487-91	36.3	208
53	Differential and limited expression of mutant alleles in multiple myeloma. *Blood*, **2014**, 124, 3110-7	2.2	42
52	Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer. *ELife*, **2014**, 3,	8.9	229
51	Processed pseudogenes acquired somatically during cancer development. *Nature Communications*, **2014**, 5, 3644	17.4	68
50	A Next Generation Sequencing-Based Approach to Detect Gene Mutations, Copy Number Changes and IGH Translocations in Multiple Myeloma. *Blood*, **2014**, 124, 3364-3364	2.2	2
49	Differential and Limited Expression of Mutant Alleles in Multiple Myeloma. *Blood*, **2014**, 124, 2007-2007	2.2	
48	Signatures of mutational processes in human cancer. *Nature*, **2013**, 500, 415-21	50.4	5895

47	Detailed molecular characterisation of acute myeloid leukaemia with a normal karyotype using targeted DNA capture. *Leukemia*, **2013**, 27, 1820-5	10.7	26
46	The human NPM1 mutation A perturbs megakaryopoiesis in a conditional mouse model. *Blood*, **2013**, 121, 3447-58	2.2	25
45	Whole Exome Sequencing Of Multiple Myeloma Reveals An Heterogeneous Clonal Architecture and Genomic Evolution. *Blood*, **2013**, 122, 399-399	2.2	
44	Acute myeloid leukemia with mutated nucleophosmin (NPM1): is it a distinct entity?. *Blood*, **2011**, 117, 1109-20	2.2	178
43	cpsf1 is required for definitive HSC survival in zebrafish. *Blood*, **2011**, 117, 3996-4007	2.2	25
42	Ddx18 is essential for cell-cycle progression in zebrafish hematopoietic cells and is mutated in human AML. *Blood*, **2011**, 118, 903-15	2.2	29
41	Zebrafish microRNA-126 determines hematopoietic cell fate through c-Myb. *Leukemia*, **2011**, 25, 506-14	10.7	49
40	Upregulation of eIF4E in Nucleophosmin 1 (NPM1) Haploinsufficient Cells Alters CCAAT Enhancer Binding Protein Alpha (C/EBP□Activity: Implications for MDS and AML. *Blood*, **2011**, 118, 2432-2432	2.2	
39	Expression of the cytoplasmic NPM1 mutant (NPMc+) causes the expansion of hematopoietic cells in zebrafish. *Blood*, **2010**, 115, 3329-40	2.2	61
38	Cleavage and Polyadenylation Specificity Factor 1 Is Required for Definitive Hematopoietic Stem Cell Survival In Zebrafish.. *Blood*, **2010**, 116, 1606-1606	2.2	
37	A dose-dependent tug of war involving the NPM1 leukaemic mutant, nucleophosmin, and ARF. *Leukemia*, **2009**, 23, 501-9	10.7	59
36	Altered nucleophosmin transport in acute myeloid leukaemia with mutated NPM1: molecular basis and clinical implications. *Leukemia*, **2009**, 23, 1731-43	10.7	156
35	A western blot assay for detecting mutant nucleophosmin (NPM1) proteins in acute myeloid leukaemia. *Leukemia*, **2008**, 22, 2285-8	10.7	20
34	Absence of nucleophosmin leukaemic mutants in B and T cells from AML with NPM1 mutations: implications for the cell of origin of NPMc+ AML. *Leukemia*, **2008**, 22, 195-8	10.7	21
33	In human genome, generation of a nuclear export signal through duplication appears unique to nucleophosmin (NPM1) mutations and is restricted to AML. *Leukemia*, **2008**, 22, 1285-9	10.7	36
32	A one-mutation mathematical model can explain the age incidence of acute myeloid leukemia with mutated nucleophosmin (NPM1). *Haematologica*, **2008**, 93, 1219-26	6.6	20
31	Cytoplasmic mutated nucleophosmin is stable in primary leukemic cells and in a xenotransplant model of NPMc+ acute myeloid leukemia in SCID mice. *Haematologica*, **2008**, 93, 775-9	6.6	42
30	Prognostic impact of genetic characterization in the GIMEMA LAM99P multicenter study for newly diagnosed acute myeloid leukemia. *Haematologica*, **2008**, 93, 1017-24	6.6	16

29	The Role of RNA Helicase Dead Box 18 in Zebrafish Hematopoiesis and Human MDS. *Blood*, **2008**, 112, 500-500	2.2	
28	Identification and functional characterization of a cytoplasmic nucleophosmin leukaemic mutant generated by a novel exon-11 NPM1 mutation. *Leukemia*, **2007**, 21, 1099-103	10.7	46
27	Cytoplasmic mutated nucleophosmin (NPM) defines the molecular status of a significant fraction of myeloid sarcomas. *Leukemia*, **2007**, 21, 1566-70	10.7	97
26	Aberrant cytoplasmic expression of C-terminal-truncated NPM leukaemic mutant is dictated by tryptophans loss and a new NES motif. *Leukemia*, **2007**, 21, 2052-4; author reply 2054; discussion 2055-6	10.7	32
25	Reply to "Aberrant cytoplasmic expression of C-terminal truncated NPM leukaemic mutant is dictated by tryptophans loss and a new NES motif" by Falini et al.. *Leukemia*, **2007**, 21, 2054-2054	10.7	1
24	Reply to Pitiot et al.. *Leukemia*, **2007**, 21, 2055-2056	10.7	2
23	Translocations and mutations involving the nucleophosmin (NPM1) gene in lymphomas and leukemias. *Haematologica*, **2007**, 92, 519-32	6.6	156
22	Sustained ventricular tachycardia in a thalidomide-treated patient with primary plasma-cell leukemia. *Nature Clinical Practice Oncology*, **2007**, 4, 722-5		11
21	Born to be exported: COOH-terminal nuclear export signals of different strength ensure cytoplasmic accumulation of nucleophosmin leukemic mutants. *Cancer Research*, **2007**, 67, 6230-7	10.1	81
20	Function of Nucleophosmin in Zebrafish Hematopoiesis.. *Blood*, **2007**, 110, 2644-2644	2.2	
19	Cytoplasmic nucleophosmin in myeloid sarcoma occurring 20 years after diagnosis of acute myeloid leukaemia. *Lancet Oncology, The*, **2006**, 7, 350-2	21.7	24
18	Both carboxy-terminus NES motif and mutated tryptophan(s) are crucial for aberrant nuclear export of nucleophosmin leukemic mutants in NPMc+ AML. *Blood*, **2006**, 107, 4514-23	2.2	201
17	Immunohistochemistry predicts nucleophosmin (NPM) mutations in acute myeloid leukemia. *Blood*, **2006**, 108, 1999-2005	2.2	146
16	Mutated nucleophosmin detects clonal multilineage involvement in acute myeloid leukemia: Impact on WHO classification. *Blood*, **2006**, 108, 4146-55	2.2	82
15	Aberrant subcellular expression of nucleophosmin and NPM-MLF1 fusion protein in acute myeloid leukaemia carrying t(3;5): a comparison with NPMc+ AML. *Leukemia*, **2006**, 20, 368-71	10.7	37
14	Reciprocal Interaction between NPM Leukemic Mutants and Arf: Structural Basis and Functional Consequences.. *Blood*, **2006**, 108, 1939-1939	2.2	
13	Tumor protein D52 (TPD52): a novel B-cell/plasma-cell molecule with unique expression pattern and Ca(2+)-dependent association with annexin VI. *Blood*, **2005**, 105, 2812-20	2.2	34
12	Cell line OCI/AML3 bears exon-12 NPM gene mutation-A and cytoplasmic expression of nucleophosmin. *Leukemia*, **2005**, 19, 1760-7	10.7	124

11	Exon-12 Nucleophosmin (NPM) Mutation and Aberrant Cytoplasmic Expression of NPM Protein in Leukemia Cell Line OCI-AML3.. *Blood*, **2005**, 106, 2376-2376	2.2	
10	Prognostic Impact of Genetic Characterization in the GIMEMA LAM99P Study for Newly Diagnosed Adult AML. Relevance of Combined Analysis of Conventional Karyotyping, FLT3 and NPM Mutational Status.. *Blood*, **2005**, 106, 226-226	2.2	
9	Mechanism of Altered Nucleo-Cytoplasmic Traffic of Nucleophosmin in Acute Myelogenous Leukemia Carrying Exon-12 NPM Mutations (NPMc+ AML).. *Blood*, **2005**, 106, 4396-4396	2.2	
8	Treating two concurrent B-cell and T-cell lymphoid neoplasms with alemtuzumab monotherapy. *Lancet Oncology, The*, **2004**, 5, 64-5	21.7	9
7	Tumor Protein D52 (TPD52): A Novel B Cell/Plasma Cell Molecule Identified through a Proteomic Approach and Characterized by Unique Expression Pattern and Ca2+-Dependent Association with Annexin VI.. *Blood*, **2004**, 104, 3652-3652	2.2	
6	Timing the Initiation of Multiple Myeloma. *SSRN Electronic Journal*,	1	3
5	Pan-cancer analysis of whole genomes reveals driver rearrangements promoted by LINE-1 retrotransposition in human tumours		10
4	Revealing the impact of recurrent and rare structural variants in multiple myeloma		1
3	Whole genome sequencing provides evidence of two biologically and clinically distinct entities of asymptomatic monoclonal gammopathies: progressive versus stable myeloma precursor condition		1
2	Genomic landscape and chronological reconstruction of driver events in multiple myeloma		6
1	Clinical, Morphological and Clonal Progression of VEXAS Syndrome in the Context of Myelodysplasia Treated with Azacytidine. *Clinical Hematology International*,1	1.8	0