

Niccolo Bolli

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2882800/publications.pdf>

Version: 2024-02-01

141
papers

18,581
citations

66234

42
h-index

18606

119
g-index

154
all docs

154
docs citations

154
times ranked

30361
citing authors

#	ARTICLE	IF	CITATIONS
1	Signatures of mutational processes in human cancer. <i>Nature</i> , 2013, 500, 415-421.	13.7	8,060
2	Genomic Classification and Prognosis in Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , 2016, 374, 2209-2221.	13.9	3,067
3	Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. <i>Nature Communications</i> , 2014, 5, 2997.	5.8	741
4	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. <i>Science</i> , 2014, 345, 1251343.	6.0	348
5	Identification of novel mutational drivers reveals oncogene dependencies in multiple myeloma. <i>Blood</i> , 2018, 132, 587-597.	0.6	335
6	Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer. <i>ELife</i> , 2014, 3, .	2.8	318
7	A high-risk, Double-Hit, group of newly diagnosed myeloma identified by genomic analysis. <i>Leukemia</i> , 2019, 33, 159-170.	3.3	313
8	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. <i>Nature Genetics</i> , 2020, 52, 306-319.	9.4	275
9	Association of a germline copy number polymorphism of APOBEC3A and APOBEC3B with burden of putative APOBEC-dependent mutations in breast cancer. <i>Nature Genetics</i> , 2014, 46, 487-491.	9.4	254
10	Both carboxy-terminus NES motif and mutated tryptophan(s) are crucial for aberrant nuclear export of nucleophosmin leukemic mutants in NPMc+ AML. <i>Blood</i> , 2006, 107, 4514-4523.	0.6	238
11	Precision oncology for acute myeloid leukemia using a knowledge bank approach. <i>Nature Genetics</i> , 2017, 49, 332-340.	9.4	229
12	Acute myeloid leukemia with mutated nucleophosmin (NPM1): is it a distinct entity?. <i>Blood</i> , 2011, 117, 1109-1120.	0.6	210
13	Altered nucleophosmin transport in acute myeloid leukaemia with mutated NPM1: molecular basis and clinical implications. <i>Leukemia</i> , 2009, 23, 1731-1743.	3.3	200
14	Translocations and mutations involving the nucleophosmin (NPM1) gene in lymphomas and leukemias. <i>Haematologica</i> , 2007, 92, 519-532.	1.7	183
15	Genomic landscape and chronological reconstruction of driver events in multiple myeloma. <i>Nature Communications</i> , 2019, 10, 3835.	5.8	183
16	Immunohistochemistry predicts nucleophosmin (NPM) mutations in acute myeloid leukemia. <i>Blood</i> , 2006, 108, 1999-2005.	0.6	181
17	Genomic patterns of progression in smoldering multiple myeloma. <i>Nature Communications</i> , 2018, 9, 3363.	5.8	163
18	KLF2 mutation is the most frequent somatic change in splenic marginal zone lymphoma and identifies a subset with distinct genotype. <i>Leukemia</i> , 2015, 29, 1177-1185.	3.3	156

#	ARTICLE	IF	CITATIONS
19	A practical guide for mutational signature analysis in hematological malignancies. <i>Nature Communications</i> , 2019, 10, 2969.	5.8	145
20	Cell line OCI/AML3 bears exon-12 NPM gene mutation-A and cytoplasmic expression of nucleophosmin. <i>Leukemia</i> , 2005, 19, 1760-1767.	3.3	139
21	Analysis of the genomic landscape of multiple myeloma highlights novel prognostic markers and disease subgroups. <i>Leukemia</i> , 2018, 32, 2604-2616.	3.3	137
22	Cytoplasmic mutated nucleophosmin (NPM) defines the molecular status of a significant fraction of myeloid sarcomas. <i>Leukemia</i> , 2007, 21, 1566-1570.	3.3	127
23	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.	0.8	127
24	Hemopoietic-specific Sf3b1-K700E knock-in mice display the splicing defect seen in human MDS but develop anemia without ring sideroblasts. <i>Leukemia</i> , 2017, 31, 720-727.	3.3	105
25	Timing the initiation of multiple myeloma. <i>Nature Communications</i> , 2020, 11, 1917.	5.8	99
26	Born to Be Exported: COOH-Terminal Nuclear Export Signals of Different Strength Ensure Cytoplasmic Accumulation of Nucleophosmin Leukemic Mutants. <i>Cancer Research</i> , 2007, 67, 6230-6237.	0.4	96
27	Multiple myeloma clonal evolution in homogeneously treated patients. <i>Leukemia</i> , 2018, 32, 2636-2647.	3.3	94
28	Mutated nucleophosmin detects clonal multilineage involvement in acute myeloid leukemia: impact on WHO classification. <i>Blood</i> , 2006, 108, 4146-4155.	0.6	92
29	Biological and prognostic impact of APOBEC-induced mutations in the spectrum of plasma cell dyscrasias and multiple myeloma cell lines. <i>Leukemia</i> , 2018, 32, 1043-1047.	3.3	87
30	Processed pseudogenes acquired somatically during cancer development. <i>Nature Communications</i> , 2014, 5, 3644.	5.8	86
31	Revealing the Impact of Structural Variants in Multiple Myeloma. <i>Blood Cancer Discovery</i> , 2020, 1, 258-273.	2.6	81
32	Expression of the cytoplasmic NPM1 mutant (NPMc+) causes the expansion of hematopoietic cells in zebrafish. <i>Blood</i> , 2010, 115, 3329-3340.	0.6	70
33	Whole-genome sequencing reveals progressive versus stable myeloma precursor conditions as two distinct entities. <i>Nature Communications</i> , 2021, 12, 1861.	5.8	68
34	A dose-dependent tug of war involving the NPM1 leukaemic mutant, nucleophosmin, and ARF. <i>Leukemia</i> , 2009, 23, 501-509.	3.3	63
35	Zebrafish microRNA-126 determines hematopoietic cell fate through c-Myb. <i>Leukemia</i> , 2011, 25, 506-514.	3.3	62
36	A DNA target-enrichment approach to detect mutations, copy number changes and immunoglobulin translocations in multiple myeloma. <i>Blood Cancer Journal</i> , 2016, 6, e467-e467.	2.8	59

#	ARTICLE	IF	CITATIONS
37	Identification and functional characterization of a cytoplasmic nucleophosmin leukaemic mutant generated by a novel exon-11 NPM1 mutation. <i>Leukemia</i> , 2007, 21, 1099-1103.	3.3	57
38	Differential and limited expression of mutant alleles in multiple myeloma. <i>Blood</i> , 2014, 124, 3110-3117.	0.6	54
39	Integrative analysis of the genomic and transcriptomic landscape of double-refractory multiple myeloma. <i>Blood Advances</i> , 2020, 4, 830-844.	2.5	54
40	Development and validation of a comprehensive genomic diagnostic tool for myeloid malignancies. <i>Blood</i> , 2016, 128, e1-e9.	0.6	49
41	In human genome, generation of a nuclear export signal through duplication appears unique to nucleophosmin (NPM1) mutations and is restricted to AML. <i>Leukemia</i> , 2008, 22, 1285-1289.	3.3	46
42	Cytoplasmic mutated nucleophosmin is stable in primary leukemic cells and in a xenotransplant model of NPMc+ acute myeloid leukemia in SCID mice. <i>Haematologica</i> , 2008, 93, 775-779.	1.7	45
43	Aberrant subcellular expression of nucleophosmin and NPM-MLF1 fusion protein in acute myeloid leukaemia carrying t(3;5): A comparison with NPMc+ AML. <i>Leukemia</i> , 2006, 20, 368-371.	3.3	43
44	Ddx18 is essential for cell-cycle progression in zebrafish hematopoietic cells and is mutated in human AML. <i>Blood</i> , 2011, 118, 903-915.	0.6	43
45	Characterization of gene mutations and copy number changes in acute myeloid leukemia using a rapid target enrichment protocol. <i>Haematologica</i> , 2015, 100, 214-222.	1.7	43
46	Tumor protein D52 (TPD52): a novel B-cell/plasma-cell molecule with unique expression pattern and Ca ²⁺ -dependent association with annexin VI. <i>Blood</i> , 2005, 105, 2812-2820.	0.6	41
47	Moving From Cancer Burden to Cancer Genomics for Smoldering Myeloma. <i>JAMA Oncology</i> , 2020, 6, 425.	3.4	41
48	Comprehensive detection of recurring genomic abnormalities: a targeted sequencing approach for multiple myeloma. <i>Blood Cancer Journal</i> , 2019, 9, 101.	2.8	40
49	Clinical relevance of clonal hematopoiesis in persons aged ≥80 years. <i>Blood</i> , 2021, 138, 2093-2105.	0.6	37
50	Angioimmunoblastic T cell lymphoma: novel molecular insights by mutation profiling. <i>Oncotarget</i> , 2017, 8, 17763-17770.	0.8	37
51	Aberrant cytoplasmic expression of C-terminal-truncated NPM leukaemic mutant is dictated by tryptophans loss and a new NES motif. <i>Leukemia</i> , 2007, 21, 2052-2054.	3.3	36
52	Next-Generation Sequencing for Clinical Management of Multiple Myeloma: Ready for Prime Time?. <i>Frontiers in Oncology</i> , 2020, 10, 189.	1.3	33
53	Early Relapse Risk in Patients with Newly Diagnosed Multiple Myeloma Characterized by Next-generation Sequencing. <i>Clinical Cancer Research</i> , 2020, 26, 4832-4841.	3.2	33
54	Single- and double-hit events in genes encoding immune targets before and after T cell-engaging antibody therapy in MM. <i>Blood Advances</i> , 2021, 5, 3794-3798.	2.5	30

#	ARTICLE	IF	CITATIONS
55	cpsf1 is required for definitive HSC survival in zebrafish. <i>Blood</i> , 2011, 117, 3996-4007.	0.6	29
56	Detailed molecular characterisation of acute myeloid leukaemia with a normal karyotype using targeted DNA capture. <i>Leukemia</i> , 2013, 27, 1820-1825.	3.3	29
57	The human NPM1 mutation A perturbs megakaryopoiesis in a conditional mouse model. <i>Blood</i> , 2013, 121, 3447-3458.	0.6	29
58	Cytoplasmic nucleophosmin in myeloid sarcoma occurring 20 years after diagnosis of acute myeloid leukaemia. <i>Lancet Oncology</i> , 2006, 7, 350-352.	5.1	28
59	Copy number signatures predict chromothripsis and clinical outcomes in newly diagnosed multiple myeloma. <i>Nature Communications</i> , 2021, 12, 5172.	5.8	27
60	Cereblon enhancer methylation and IMiD resistance in multiple myeloma. <i>Blood</i> , 2021, 138, 1721-1726.	0.6	25
61	A western blot assay for detecting mutant nucleophosmin (NPM1) proteins in acute myeloid leukaemia. <i>Leukemia</i> , 2008, 22, 2285-2288.	3.3	24
62	A one-mutation mathematical model can explain the age incidence of acute myeloid leukemia with mutated nucleophosmin (NPM1). <i>Haematologica</i> , 2008, 93, 1219-1226.	1.7	23
63	Prognostic impact of genetic characterization in the GIMEMA LAM99P multicenter study for newly diagnosed acute myeloid leukemia. <i>Haematologica</i> , 2008, 93, 1017-1024.	1.7	22
64	2021 European Myeloma Network review and consensus statement on smoldering multiple myeloma: how to distinguish (and manage) Dr. Jekyll and Mr. Hyde. <i>Haematologica</i> , 2021, 106, 2799-2812.	1.7	22
65	Absence of nucleophosmin leukaemic mutants in B and T cells from AML with NPM1 mutations: implications for the cell of origin of NPMc+ AML. <i>Leukemia</i> , 2008, 22, 195-198.	3.3	21
66	mmsig: a fitting approach to accurately identify somatic mutational signatures in hematological malignancies. <i>Communications Biology</i> , 2021, 4, 424.	2.0	21
67	<i>CDKN2A</i> deletion is a frequent event associated with poor outcome in patients with peripheral T-cell lymphoma not otherwise specified (PTCL-NOS). <i>Haematologica</i> , 2021, 106, 2918-2926.	1.7	18
68	Integration of transcriptional and mutational data simplifies the stratification of peripheral T cell lymphoma. <i>American Journal of Hematology</i> , 2019, 94, 628-634.	2.0	16
69	Limits and Applications of Genomic Analysis of Circulating Tumor DNA as a Liquid Biopsy in Asymptomatic Forms of Multiple Myeloma. <i>HemaSphere</i> , 2020, 4, e402.	1.2	15
70	Sustained ventricular tachycardia in a thalidomide-treated patient with primary plasma-cell leukemia. <i>Nature Clinical Practice Oncology</i> , 2007, 4, 722-725.	4.3	14
71	DIS3 mutations in multiple myeloma impact the transcriptional signature and clinical outcome. <i>Haematologica</i> , 2022, 107, 921-932.	1.7	14
72	Biology of peripheral T cell lymphomas “ Not otherwise specified: Is something finally happening?. <i>Pathogenesis</i> , 2016, 3, 9-18.	0.8	12

#	ARTICLE	IF	CITATIONS
73	Next-generation sequencing of a family with a high penetrance of monoclonal gammopathies for the identification of candidate risk alleles. <i>Cancer</i> , 2017, 123, 3701-3708.	2.0	12
74	Treating two concurrent B-cell and T-cell lymphoid neoplasms with alemtuzumab monotherapy. <i>Lancet Oncology</i> , The, 2004, 5, 64-65.	5.1	10
75	Specific targeting of the KRAS mutational landscape in myeloma as a tool to unveil the elicited antitumor activity. <i>Blood</i> , 2021, 138, 1705-1720.	0.6	10
76	A Journey Through Myeloma Evolution: From the Normal Plasma Cell to Disease Complexity. <i>HemaSphere</i> , 2020, 4, e502.	1.2	10
77	RNA-Seq De Novo Assembly of Clonal Immunoglobulin Rearrangements Identifies Interesting Biology and Uncovers Prognostic Features in Multiple Myeloma. <i>Blood</i> , 2016, 128, 195-195.	0.6	10
78	Analysis of the genomic landscape of multiple myeloma highlights novel prognostic markers and disease subgroups. <i>Leukemia</i> , 2017, , .	3.3	9
79	Functional Impact of Genomic Complexity on the Transcriptome of Multiple Myeloma. <i>Clinical Cancer Research</i> , 2021, 27, 6479-6490.	3.2	9
80	The Molecular Pathogenesis of Multiple Myeloma. <i>Hematology Reports</i> , 2020, 12, 9054.	0.3	9
81	ROBO1 Promotes Homing, Dissemination, and Survival of Multiple Myeloma within the Bone Marrow Microenvironment. <i>Blood Cancer Discovery</i> , 2021, 2, 338-353.	2.6	8
82	Transcriptomic Analysis in Multiple Myeloma and Primary Plasma Cell Leukemia with t(11;14) Reveals Different Expression Patterns with Biological Implications in Venetoclax Sensitivity. <i>Cancers</i> , 2021, 13, 4898.	1.7	8
83	Recurrent histone mutations in T-cell acute lymphoblastic leukaemia. <i>British Journal of Haematology</i> , 2019, 184, 676-679.	1.2	7
84	Application of Next-Generation Sequencing for the Genomic Characterization of Patients with Smoldering Myeloma. <i>Cancers</i> , 2020, 12, 1332.	1.7	7
85	What Is New in the Treatment of Smoldering Multiple Myeloma?. <i>Journal of Clinical Medicine</i> , 2021, 10, 421.	1.0	7
86	Clinical, Morphological and Clonal Progression of VEXAS Syndrome in the Context of Myelodysplasia Treated with Azacytidine. <i>Clinical Hematology International</i> , 2022, 4, 52-55.	0.7	7
87	The Route of the Malignant Plasma Cell in Its Survival Niche: Exploring "Multiple Myelomas". <i>Cancers</i> , 2022, 14, 3271.	1.7	5
88	High-dose chemotherapy followed by autologous transplantation may overcome the poor prognosis of diffuse large B-cell lymphoma patients with MYC/BCL2 co-expression. <i>Blood Cancer Journal</i> , 2016, 6, e491-e491.	2.8	4
89	Sf3b1 K700E Mutation Impairs Pre-mRNA Splicing and Definitive Hematopoiesis in a Conditional Knock-in Mouse Model. <i>Blood</i> , 2015, 126, 140-140.	0.6	4
90	Analysis of Mutational Signatures Suggest That Aid Has an Early and Driver Role in Multiple Myeloma. <i>Blood</i> , 2016, 128, 116-116.	0.6	4

#	ARTICLE	IF	CITATIONS
91	Timing the Initiation of Multiple Myeloma. SSRN Electronic Journal, 0, , .	0.4	4
92	â€Reply to Pitiot et al.â€™. Leukemia, 2007, 21, 2055-2056.	3.3	3
93	Rapid parallel acquisition of somatic mutations after <i><sc>NPM</sc>1</i> in acute myeloid leukaemia evolution. British Journal of Haematology, 2017, 176, 825-829.	1.2	3
94	CD40 Activity on Mesenchymal Cells Negatively Regulates OX40L to Maintain Bone Marrow Immune Homeostasis Under Stress Conditions. Frontiers in Immunology, 2021, 12, 662048.	2.2	3
95	Pathogenetic and Prognostic Implications of Increased Mitochondrial Content in Multiple Myeloma. Cancers, 2021, 13, 3189.	1.7	3
96	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.	0.6	3
97	MGUS and clonal hematopoiesis show unrelated clinical and biological trajectories in an older population cohort. Blood Advances, 2022, 6, 5702-5706.	2.5	3
98	Genomics of Smoldering Multiple Myeloma: Time for Clinical Translation of Findings?. Cancers, 2021, 13, 3319.	1.7	2
99	Specific Targeting of KRAS Using a Novel High-Affinity KRAS Antisense Oligonucleotide in Multiple Myeloma. Blood, 2019, 134, 3104-3104.	0.6	2
100	Whole-Genome Sequencing Reveals Evidence of Two Biologically and Clinically Distinct Entities: Progressive <i>Versus</i> Stable Myeloma Precursor Disease. Blood, 2020, 136, 47-48.	0.6	2
101	A Next Generation Sequencing-Based Approach to Detect Gene Mutations, Copy Number Changes and IGH Translocations in Multiple Myeloma. Blood, 2014, 124, 3364-3364.	0.6	2
102	Dissecting Genetic and Phenotypic Heterogeneity to Map Molecular Phylogenies and Deliver Personalized Outcome and Treatment Predictions in AML. Blood, 2015, 126, 803-803.	0.6	2
103	Redefining Mutational Profiling Using RNA-Seq: Insight into the Functional Mutational Landscape of Multiple Myeloma. Blood, 2015, 126, 837-837.	0.6	2
104	Peripheral T-Cell Lymphomas Not Otherwise Specified: Potential Novel Molecular Entities Based on Both Tumor and Microenvironment Cellular Components. Blood, 2016, 128, 4098-4098.	0.6	2
105	A rare case of atypical chronic lymphocytic leukaemia presenting as nephrotic syndrome. BMJ Case Reports, 2017, 2017, bcr-2016-218850.	0.2	2
106	Clinical Relevance of Clonal Hematopoiesis in the Oldest-Old Population: Analysis of the "Health and Anemia" Study. Blood, 2018, 132, 750-750.	0.6	2
107	Reply to â€Aberrant cytoplasmic expression of C-terminal truncated NPM leukaemic mutant is dictated by tryptophans loss and a new NES motifâ€™ by Falini et al.. Leukemia, 2007, 21, 2054-2054.	3.3	1
108	Next Generation Sequencing in Multiple Myeloma. Clinical Lymphoma, Myeloma and Leukemia, 2015, 15, e2-e3.	0.2	1

#	ARTICLE	IF	CITATIONS
109	Bowel perforation from occult ileal involvement after diagnosis in a case of primary mediastinal large B-cell lymphoma. <i>BMJ Case Reports</i> , 2016, 2016, bcr2016216317.	0.2	1
110	The Genomic and Transcriptomic Landscape of Double-Refractory Multiple Myeloma. <i>Blood</i> , 2019, 134, 3056-3056.	0.6	1
111	Genomic Landscape and Its Prognostic Implications in Multiple Myeloma Using a Targeted Sequencing Approach. <i>Blood</i> , 2015, 126, 370-370.	0.6	1
112	GATA-3 Expression in Peripheral T-Cell Lymphomas (PTCL): Identification of a Cut-Off and Prognostic Value in PTCL-NOS Versus Others Hystotypes. <i>Blood</i> , 2015, 126, 3889-3889.	0.6	1
113	Personally Tailored Risk Prediction of AML Based on Comprehensive Genomic and Clinical Data. <i>Blood</i> , 2015, 126, 85-85.	0.6	1
114	Whole Genome Sequencing of Unique Paired SMM/MGUS Progressing to MM Samples Reveals a Genomic Landscape with Diverse Evolutionary Pattern. <i>Blood</i> , 2016, 128, 2088-2088.	0.6	1
115	Chemotherapy-Related Mutational Signatures Reveal the Origins of Therapy-Related Myeloid Neoplasms. <i>Blood</i> , 2021, 138, 3271-3271.	0.6	1
116	MGUS and Chip: Two Faces, but Not of the Same Medal. <i>Blood</i> , 2021, 138, 3800-3800.	0.6	1
117	OAB-041: Epithelial-mesenchymal-transition regulated by Junctional Adhesion Molecule-A (JAM-A) associates with aggressive extramedullary multiple myeloma disease. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2021, 21, S26-S27.	0.2	1
118	Analysis of the genomic and transcriptomic landscape of chemoresistant multiple myeloma. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2019, 19, e58-e59.	0.2	0
119	PS1345 CIRCULATING TUMOR DNA AS A LIQUID BIOPSY IN SMOLDERING MULTIPLE MYELOMA TO IDENTIFY BIOMARKERS OF PROGRESSION. <i>HemaSphere</i> , 2019, 3, 614-615.	1.2	0
120	A new case of myelodysplastic syndrome associated with t(3;3)(q21;q26) and inv(11)(p15q22). <i>Tumori</i> , 2020, 106, NP18-NP22.	0.6	0
121	Tumor Protein D52 (TPD52): A Novel B Cell/Plasma Cell Molecule Identified through a Proteomic Approach and Characterized by Unique Expression Pattern and Ca ²⁺ -Dependent Association with Annexin VI.. <i>Blood</i> , 2004, 104, 3652-3652.	0.6	0
122	Exon-12 Nucleophosmin (NPM) Mutation and Aberrant Cytoplasmic Expression of NPM Protein in Leukemia Cell Line OCI-AML3.. <i>Blood</i> , 2005, 106, 2376-2376.	0.6	0
123	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.. <i>Blood</i> , 2005, 106, 226-226.	0.6	0
124	Mechanism of Altered Nucleo-Cytoplasmic Traffic of Nucleophosmin in Acute Myelogenous Leukemia Carrying Exon-12 NPM Mutations (NPMc+ AML).. <i>Blood</i> , 2005, 106, 4396-4396.	0.6	0
125	Reciprocal Interaction between NPM Leukemic Mutants and Arf: Structural Basis and Functional Consequences.. <i>Blood</i> , 2006, 108, 1939-1939.	0.6	0
126	Function of Nucleophosmin in Zebrafish Hematopoiesis.. <i>Blood</i> , 2007, 110, 2644-2644.	0.6	0

#	ARTICLE	IF	CITATIONS
127	The Role of RNA Helicase Dead Box 18 in Zebrafish Hematopoiesis and Human MDS. <i>Blood</i> , 2008, 112, 500-500.	0.6	0
128	Cleavage and Polyadenylation Specificity Factor 1 Is Required for Definitive Hematopoietic Stem Cell Survival In Zebrafish.. <i>Blood</i> , 2010, 116, 1606-1606.	0.6	0
129	Upregulation of eIF4E in Nucleophosmin 1 (NPM1) Haploinsufficient Cells Alters CCAAT Enhancer Binding Protein Alpha (C/EBP α) Activity: Implications for MDS and AML. <i>Blood</i> , 2011, 118, 2432-2432.	0.6	0
130	Whole Exome Sequencing Of Multiple Myeloma Reveals An Heterogeneous Clonal Architecture and Genomic Evolution. <i>Blood</i> , 2013, 122, 399-399.	0.6	0
131	Differential and Limited Expression of Mutant Alleles in Multiple Myeloma. <i>Blood</i> , 2014, 124, 2007-2007.	0.6	0
132	The Complex Landscape of Rearrangements in Smoldering and Symptomatic Multiple Myeloma Revealed By Whole-Genome Sequencing. <i>Blood</i> , 2016, 128, 236-236.	0.6	0
133	The Landscape of Structural Variant Signatures in Multiple Myeloma Identifies Distinct Disease Subgroups with Implications for Pathogenesis. <i>Blood</i> , 2018, 132, 109-109.	0.6	0
134	Mytype: A Capture Based Sequencing Approach to Detect Somatic Mutations, Copy Number Changes and IGH Translocations in Multiple Myeloma. <i>Blood</i> , 2018, 132, 5588-5588.	0.6	0
135	Whole Genome Sequencing Reveals Recurrent Structural Driver Events in Peripheral T-Cell Lymphomas Not Otherwise Specified. <i>Blood</i> , 2018, 132, 4115-4115.	0.6	0
136	Lack of Significant Differences in Somatic Alterations between MGUS, SMM and Symptomatic Multiple Myeloma: A Result from Comprehensive Genomic Profiling Study. <i>Blood</i> , 2019, 134, 3089-3089.	0.6	0
137	Timing the Initiation of Multiple Myeloma. <i>Blood</i> , 2019, 134, 573-573.	0.6	0
138	Dissection of Bone Marrow Microenvironment By Single Cell RNA Sequencing in Warm AIHA Patients: A Proof-of-Concept Analysis. <i>Blood</i> , 2021, 138, 931-931.	0.6	0
139	Revealing Transcriptome Deregulation upon Genomic Complexity in Multiple Myeloma. <i>Blood</i> , 2020, 136, 3-4.	0.6	0
140	P-058: The dynamics of nucleotide variants in the progression from myeloma precursor conditions to multiple myeloma using targeted sequencing of serial bone marrow samples. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2021, 21, S70.	0.2	0
141	The Dynamics of Nucleotide Variants in the Progression from Low-Intermediate Myeloma Precursor Conditions to Multiple Myeloma: Studying Serial Samples with a Targeted Sequencing Approach. <i>Cancers</i> , 2022, 14, 1035.	1.7	0