

Maria Eugenia Figueroa

List of Publications by Citations

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133
papers

15,411
citations

51
h-index

124
g-index

137
ext. papers

17,851
ext. citations

10.2
avg, IF

5.76
L-index

#	Paper	IF	Citations
133	Leukemic IDH1 and IDH2 mutations result in a hypermethylation phenotype, disrupt TET2 function, and impair hematopoietic differentiation. <i>Cancer Cell</i> , 2010 , 18, 553-67	24.3	1933
132	IDH mutation impairs histone demethylation and results in a block to cell differentiation. <i>Nature</i> , 2012 , 483, 474-8	50.4	1393
131	Prognostic relevance of integrated genetic profiling in acute myeloid leukemia. <i>New England Journal of Medicine</i> , 2012 , 366, 1079-89	59.2	1378
130	Cell type of origin influences the molecular and functional properties of mouse induced pluripotent stem cells. <i>Nature Biotechnology</i> , 2010 , 28, 848-55	44.5	949
129	methylKit: a comprehensive R package for the analysis of genome-wide DNA methylation profiles. <i>Genome Biology</i> , 2012 , 13, R87	18.3	893
128	Tet2 loss leads to increased hematopoietic stem cell self-renewal and myeloid transformation. <i>Cancer Cell</i> , 2011 , 20, 11-24	24.3	876
127	DNA methylation signatures identify biologically distinct subtypes in acute myeloid leukemia. <i>Cancer Cell</i> , 2010 , 17, 13-27	24.3	640
126	A molecular roadmap of reprogramming somatic cells into iPS cells. <i>Cell</i> , 2012 , 151, 1617-32	56.2	620
125	Recurrent somatic TET2 mutations in normal elderly individuals with clonal hematopoiesis. <i>Nature Genetics</i> , 2012 , 44, 1179-81	36.3	552
124	Autophagy maintains the metabolism and function of young and old stem cells. <i>Nature</i> , 2017 , 543, 205-210	50.4	438
123	IDH1(R132H) mutation increases murine haematopoietic progenitors and alters epigenetics. <i>Nature</i> , 2012 , 488, 656-9	50.4	395
122	DNMT1-interacting RNAs block gene-specific DNA methylation. <i>Nature</i> , 2013 , 503, 371-6	50.4	379
121	Restoration of TET2 Function Blocks Aberrant Self-Renewal and Leukemia Progression. <i>Cell</i> , 2017 , 170, 1079-1095.e20	56.2	364
120	Comparative isoschizomer profiling of cytosine methylation: the HELP assay. <i>Genome Research</i> , 2006 , 16, 1046-55	9.7	330
119	MDS and secondary AML display unique patterns and abundance of aberrant DNA methylation. <i>Blood</i> , 2009 , 114, 3448-58	2.2	268
118	Base-pair resolution DNA methylation sequencing reveals profoundly divergent epigenetic landscapes in acute myeloid leukemia. <i>PLoS Genetics</i> , 2012 , 8, e1002781	6	223
117	Mutant DNMT3A: a marker of poor prognosis in acute myeloid leukemia. <i>Blood</i> , 2012 , 119, 5824-31	2.2	193

116	Prolonged administration of azacitidine with or without entinostat for myelodysplastic syndrome and acute myeloid leukemia with myelodysplasia-related changes: results of the US Leukemia Intergroup trial E1905. <i>Journal of Clinical Oncology</i> , 2014 , 32, 1242-8	2.2	187
115	DNA hydroxymethylation profiling reveals that WT1 mutations result in loss of TET2 function in acute myeloid leukemia. <i>Cell Reports</i> , 2014 , 9, 1841-1855	10.6	183
114	MethylSig: a whole genome DNA methylation analysis pipeline. <i>Bioinformatics</i> , 2014 , 30, 2414-22	7.2	141
113	Cell of origin determines clinically relevant subtypes of MLL-rearranged AML. <i>Leukemia</i> , 2013 , 27, 852-60	10.7	134
112	High-resolution genome-wide cytosine methylation profiling with simultaneous copy number analysis and optimization for limited cell numbers. <i>Nucleic Acids Research</i> , 2009 , 37, 3829-39	20.1	133
111	Specific molecular signatures predict decitabine response in chronic myelomonocytic leukemia. <i>Journal of Clinical Investigation</i> , 2015 , 125, 1857-72	15.9	129
110	Notch activation inhibits AML growth and survival: a potential therapeutic approach. <i>Journal of Experimental Medicine</i> , 2013 , 210, 321-37	16.6	109
109	DNA methyltransferase 1 and DNA methylation patterning contribute to germinal center B-cell differentiation. <i>Blood</i> , 2011 , 118, 3559-69	2.2	107
108	IDH1-R132H acts as a tumor suppressor in glioma via epigenetic up-regulation of the DNA damage response. <i>Science Translational Medicine</i> , 2019 , 11,	17.5	98
107	Promoter hypermethylation in MLL-r infant acute lymphoblastic leukemia: biology and therapeutic targeting. <i>Blood</i> , 2010 , 115, 4798-809	2.2	94
106	BCL6 repression of EP300 in human diffuse large B cell lymphoma cells provides a basis for rational combinatorial therapy. <i>Journal of Clinical Investigation</i> , 2010 , 120, 4569-82	15.9	88
105	Integrated genetic and epigenetic analysis of childhood acute lymphoblastic leukemia. <i>Journal of Clinical Investigation</i> , 2013 , 123, 3099-111	15.9	88
104	Kaiso contributes to DNA methylation-dependent silencing of tumor suppressor genes in colon cancer cell lines. <i>Cancer Research</i> , 2008 , 68, 7258-63	10.1	83
103	Aberrant DNA hypermethylation signature in acute myeloid leukemia directed by EVI1. <i>Blood</i> , 2011 , 117, 234-41	2.2	82
102	CD25 expression status improves prognostic risk classification in AML independent of established biomarkers: ECOG phase 3 trial, E1900. <i>Blood</i> , 2012 , 120, 2297-306	2.2	78
101	TET2 Deficiency Causes Germinal Center Hyperplasia, Impairs Plasma Cell Differentiation, and Promotes B-cell Lymphomagenesis. <i>Cancer Discovery</i> , 2018 , 8, 1632-1653	24.4	77
100	Genome-wide epigenetic analysis delineates a biologically distinct immature acute leukemia with myeloid/T-lymphoid features. <i>Blood</i> , 2009 , 113, 2795-804	2.2	74
99	An integrative genomic and epigenomic approach for the study of transcriptional regulation. <i>PLoS ONE</i> , 2008 , 3, e1882	3.7	72

98	Epigenetic Identity in AML Depends on Disruption of Nonpromoter Regulatory Elements and Is Affected by Antagonistic Effects of Mutations in Epigenetic Modifiers. <i>Cancer Discovery</i> , 2017 , 7, 868-883	24.4	69
97	Aging Human Hematopoietic Stem Cells Manifest Profound Epigenetic Reprogramming of Enhancers That May Predispose to Leukemia. <i>Cancer Discovery</i> , 2019 , 9, 1080-1101	24.4	69
96	Safety, efficacy and biological predictors of response to sequential azacitidine and lenalidomide for elderly patients with acute myeloid leukemia. <i>Leukemia</i> , 2012 , 26, 893-901	10.7	68
95	Satb1 regulates the self-renewal of hematopoietic stem cells by promoting quiescence and repressing differentiation commitment. <i>Nature Immunology</i> , 2013 , 14, 437-45	19.1	67
94	CG dinucleotide clustering is a species-specific property of the genome. <i>Nucleic Acids Research</i> , 2007 , 35, 6798-807	20.1	67
93	Enhanced reduced representation bisulfite sequencing for assessment of DNA methylation at base pair resolution. <i>Journal of Visualized Experiments</i> , 2015 , e52246	1.6	65
92	Musashi2 sustains the mixed-lineage leukemia-driven stem cell regulatory program. <i>Journal of Clinical Investigation</i> , 2015 , 125, 1286-98	15.9	64
91	Polycomb complexes associate with enhancers and promote oncogenic transcriptional programs in cancer through multiple mechanisms. <i>Nature Communications</i> , 2018 , 9, 3377	17.4	63
90	Epigenetic roles of MLL oncoproteins are dependent on NF- κ B. <i>Cancer Cell</i> , 2013 , 24, 423-37	24.3	63
89	PRMT4 blocks myeloid differentiation by assembling a methyl-RUNX1-dependent repressor complex. <i>Cell Reports</i> , 2013 , 5, 1625-38	10.6	59
88	Smad1 and Smad5 differentially regulate embryonic hematopoiesis. <i>Blood</i> , 2007 , 110, 3881-90	2.2	57
87	Wilms tumor 1 mutations in the pathogenesis of acute myeloid leukemia. <i>Haematologica</i> , 2016 , 101, 672-9	6.6	55
86	C/EBP β is an essential collaborator in Hoxa9/Meis1-mediated leukemogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 9899-904	11.5	53
85	DNMT3A Haploinsufficiency Transforms FLT3ITD Myeloproliferative Disease into a Rapid, Spontaneous, and Fully Penetrant Acute Myeloid Leukemia. <i>Cancer Discovery</i> , 2016 , 6, 501-15	24.4	53
84	Dissecting the role of aberrant DNA methylation in human leukaemia. <i>Nature Communications</i> , 2015 , 6, 7091	17.4	51
83	DNMT3B7, a truncated DNMT3B isoform expressed in human tumors, disrupts embryonic development and accelerates lymphomagenesis. <i>Cancer Research</i> , 2010 , 70, 5840-50	10.1	51
82	Azacitidine with or without Entinostat for the treatment of therapy-related myeloid neoplasm: further results of the E1905 North American Leukemia Intergroup study. <i>British Journal of Haematology</i> , 2016 , 172, 384-91	4.5	49
81	Two splice-factor mutant leukemia subgroups uncovered at the boundaries of MDS and AML using combined gene expression and DNA-methylation profiling. <i>Blood</i> , 2014 , 123, 3327-35	2.2	45

80	C/EBPβ deregulation results in differentiation arrest in acute myeloid leukemia. <i>Journal of Clinical Investigation</i> , 2012 , 122, 4490-504	15.9	43
79	A phase II, multicentre trial of decitabine in higher-risk chronic myelomonocytic leukemia. <i>Leukemia</i> , 2018 , 32, 413-418	10.7	42
78	Aberrant epigenetic and genetic marks are seen in myelodysplastic leukocytes and reveal Dock4 as a candidate pathogenic gene on chromosome 7q. <i>Journal of Biological Chemistry</i> , 2011 , 286, 25211-23	5.4	38
77	Development of acute megakaryoblastic leukemia in Down syndrome is associated with sequential epigenetic changes. <i>Blood</i> , 2013 , 122, e33-43	2.2	36
76	CD2-positive B-cell precursor acute lymphoblastic leukemia with an early switch to the monocytic lineage. <i>Leukemia</i> , 2014 , 28, 609-20	10.7	35
75	Dnmt3a regulates T-cell development and suppresses T-ALL transformation. <i>Leukemia</i> , 2017 , 31, 2479-2489	10.9	31
74	H2.0-like homeobox regulates early hematopoiesis and promotes acute myeloid leukemia. <i>Cancer Cell</i> , 2012 , 22, 194-208	24.3	31
73	Genome-wide determination of DNA methylation by Hpa II tiny fragment enrichment by ligation-mediated PCR (HELP) for the study of acute leukemias. <i>Methods in Molecular Biology</i> , 2009 , 538, 395-407	1.4	31
72	Inhibition of DNA methyltransferase activates tumor necrosis factor alpha-induced monocytic differentiation in acute myeloid leukemia cells. <i>Cancer Research</i> , 2009 , 69, 55-64	10.1	24
71	HELP (HpaII tiny fragment enrichment by ligation-mediated PCR) assay for DNA methylation profiling of primary normal and malignant B lymphocytes. <i>Methods in Molecular Biology</i> , 2010 , 632, 191-201	1.4	23
70	Interpreting new molecular genetics in myelodysplastic syndromes. <i>Hematology American Society of Hematology Education Program</i> , 2012 , 2012, 56-64	3.1	22
69	Integrative Model-based clustering of microarray methylation and expression data. <i>Annals of Applied Statistics</i> , 2012 , 6,	2.1	19
68	Cancer-specific CTCF binding facilitates oncogenic transcriptional dysregulation. <i>Genome Biology</i> , 2020 , 21, 247	18.3	18
67	Plasticity of DNA methylation in a nerve injury model of pain. <i>Epigenetics</i> , 2015 , 10, 200-12	5.7	17
66	A clinical measure of DNA methylation predicts outcome in de novo acute myeloid leukemia. <i>JCI Insight</i> , 2016 , 1,	9.9	14
65	Transcription and methylation analyses of preleukemic promyelocytes indicate a dual role for PML/RARA in leukemia initiation. <i>Haematologica</i> , 2015 , 100, 1064-75	6.6	12
64	Cytosine modifications in myeloid malignancies. <i>Pharmacology & Therapeutics</i> , 2015 , 152, 42-53	13.9	11
63	Microsphere-based multiplex analysis of DNA methylation in acute myeloid leukemia. <i>Journal of Molecular Diagnostics</i> , 2014 , 16, 207-15	5.1	9

62	Oncogenic N-Ras and Tet2 haploinsufficiency collaborate to dysregulate hematopoietic stem and progenitor cells. <i>Blood Advances</i> , 2018 , 2, 1259-1271	7.8	9
61	Validation of DNA methylation to predict outcome in acute myeloid leukemia by use of xMELP. <i>Clinical Chemistry</i> , 2015 , 61, 249-58	5.5	8
60	levels in human hematopoietic progenitors are regulated by aging and dictate erythroid-myeloid balance. <i>Haematologica</i> , 2020 , 105, 905-913	6.6	8
59	Multilayer intraclonal heterogeneity in chronic myelomonocytic leukemia. <i>Haematologica</i> , 2020 , 105, 112-123	6.6	8
58	Cytokine-like protein 1-induced survival of monocytes suggests a combined strategy targeting MCL1 and MAPK in CMML. <i>Blood</i> , 2021 , 137, 3390-3402	2.2	7
57	SLC5A3-dependent myo-inositol auxotrophy in acute myeloid leukemia. <i>Cancer Discovery</i> , 2021 ,	24.4	6
56	Epigenetic deregulation in myeloid malignancies. <i>Translational Research</i> , 2015 , 165, 102-14	11	5
55	The Lysine-Specific Demethylase 1 (LSD1) Inhibitor Tranylcypromine (TCP) in Combination with ATRA Is Tolerable and Has Anti-Leukemic Activity in Adult Patients with Relapsed/Refractory AML and MDS. <i>Blood</i> , 2018 , 132, 2721-2721	2.2	5
54	Transcriptional Silencing of Confers a Dependency on Fanconi Anemia Proteins in Acute Myeloid Leukemia. <i>Cancer Discovery</i> , 2021 , 11, 2300-2315	24.4	5
53	Risk of disease progression in low-risk MDS is linked to distinct epigenetic subtypes. <i>Leukemia</i> , 2019 , 33, 2753-2757	10.7	4
52	A distinct epigenetic program underlies the 1;7 translocation in myelodysplastic syndromes. <i>Leukemia</i> , 2019 , 33, 2481-2494	10.7	3
51	TNFAIP3 Plays a Role in Aging of the Hematopoietic System. <i>Frontiers in Immunology</i> , 2020 , 11, 536442	8.4	3
50	Integrative Genomic Analysis Reveals Aberrant Epigenetic Marks in MDS That Can Be Seen in Peripheral Blood Leucocytes. <i>Blood</i> , 2008 , 112, 595-595	2.2	3
49	Two Different EVI1 Expressing Poor-Risk AML Subgroups with Distinct Epigenetic Signatures Uncovered by Genome Wide DNA Methylation Profiling. <i>Blood</i> , 2008 , 112, 757-757	2.2	3
48	In vivogenetic screen identifies a SLC5A3-dependent myo-inositol auxotrophy in acute myeloid leukemia		3
47	5-Hydroxymethylation highlights the heterogeneity in keratinization and cell junctions in head and neck cancers. <i>Clinical Epigenetics</i> , 2020 , 12, 175	7.7	3
46	Human hematopoiesis: aging and leukemogenic risk. <i>Current Opinion in Hematology</i> , 2021 , 28, 57-63	3.3	3
45	Epigenetic Signatures Identify New Clinically Relevant Subtypes and Define Gene Regulatory Patterns in Patients with Acute Myeloid Leukemia (AML). <i>Blood</i> , 2008 , 112, 756-756	2.2	2

44	Transcriptional silencing of ALDH2 in acute myeloid leukemia confers a dependency on Fanconi anemia proteins		2
43	IDH1R132H acts as a tumor suppressor in glioma via epigenetic upregulation of the DNA damage response		2
42	Epigenetic dysregulation in myeloid malignancies. <i>Blood</i> , 2021 ,	2.2	2
41	Combination of azacitidine and enasidenib enhances leukemic cell differentiation and cooperatively hypomethylates DNA. <i>Experimental Hematology</i> , 2021 , 98, 47-52.e6	3.1	2
40	Genetic vs. Epigenetic Disruption of the CEBPA Locus Yields Epigenomically and Biologically Distinct Leukemia Phenotypes.. <i>Blood</i> , 2007 , 110, 2117-2117	2.2	1
39	DNA Methyltransferase 1 Contributes to Epigenetic Signatures and Biological Phenotype during Normal B-Cell Differentiation and Lymphomagenesis.. <i>Blood</i> , 2007 , 110, 685-685	2.2	1
38	Epigenetic Determinants of Pathogenesis and Resistance to Proteasome Inhibition in Mantle Cell Lymphoma.. <i>Blood</i> , 2008 , 112, 3373-3373	2.2	1
37	High-Throughput Mutational Profiling In AML: Mutational Analysis of the ECOG E1900 Trial. <i>Blood</i> , 2010 , 116, 851-851	2.2	1
36	Epigenetic Effects of IDH1/IDH2 Mutations. <i>Blood</i> , 2011 , 118, SCI-33-SCI-33	2.2	1
35	Connectivity Mapping of BCL6 Targeted Therapy Guides Rational Design of Potent and Specific Non-Chemotherapy Combinatorial Regimens in DLBCL.. <i>Blood</i> , 2007 , 110, 523-523	2.2	1
34	Development of Acute Megakaryoblastic Leukemia in Down Syndrome Is Associated with Sequential Epigenetic Changes That Target the Down Syndrome Critical Region on Chromosome 21,. <i>Blood</i> , 2011 , 118, 3451-3451	2.2	1
33	Dynamic Changes Of DNA Methylation and a Functional Role For TET2 DNA Dioxygenase In Human Erythroid Differentiation. <i>Blood</i> , 2013 , 122, 3415-3415	2.2	1
32	Macrophage migration inhibitory factor is overproduced through EGR1 in TET2 resting monocytes.. <i>Communications Biology</i> , 2022 , 5, 110	6.7	0
31	Vitamin C Enhances PARPi Efficacy for the Treatment of AML. <i>Blood</i> , 2021 , 138, 1168-1168	2.2	0
30	EP300 Suppresses Leukemia Development in Myelodysplastic Syndrome through Myb Repression. <i>Blood</i> , 2019 , 134, 561-561	2.2	0
29	Ultra-Deep Sequencing of Bisulfite-Modified DNA 2016 , 47-72		
28	Analysis of the Global Methylation Profile of Accelerated and Blast Phase Myeloproliferative Neoplasms and Its Association with Response to Decitabine-Based Therapy. <i>Blood</i> , 2020 , 136, 18-20	2.2	
27	Development of a Fast and Reproducible Assay for the Clinical Implementation of Epigenetic Biomarkers to Predict Decitabine Response in Patients with Chronic Myelomonocytic Leukemia. <i>Blood</i> , 2021 , 138, 1515-1515	2.2	

- 26 The Autocrine Secreted PDZD2 Functions As a Novel Tumor Suppressor in AML, Inducing Growth Inhibition and Cell Cycle Arrest. *Blood*, **2021**, 138, 3320-3320 2.2
- 25 Age-Acquired Downregulation of Lmna Leads to Epigenetic Deregulation and Altered HSPC Function. *Blood*, **2021**, 138, 3280-3280 2.2
- 24 Intronic Architecture Links DNA Methylation to Gene Expression and Helps Drive Subtype-Specific Transcriptional Landscapes in DNMT3A- and IDH1/2-Mutant Acute Myeloid Leukemias (AML). *Blood*, **2021**, 138, 3290-3290 2.2
- 23 A FLI1-KLF6 Axis Regulates Aging in Human Hematopoietic Stem and Progenitor Cells and Normalization of KLF6 Levels in Aged Cells Leads to Their Rejuvenation. *Blood*, **2021**, 138, 19-19 2.2
- 22 An Integrated Epigenomic Analysis Approach To Determine the Molecular Basis of Acute Leukemias.. *Blood*, **2005**, 106, 3276-3276 2.2
- 21 Sensitivity of Diffuse Large B-Cell Lymphomas to DNA Methyltransferase Inhibitors Is Associated with a Specific Epigenetic Signature.. *Blood*, **2006**, 108, 831-831 2.2
- 20 BCL6 Regulates Diffuse Large B-Cell Lymphoma Cell Cycle and Apoptosis Checkpoints through Direct Repression of the p300 Histone Acetyl-Transferase.. *Blood*, **2006**, 108, 1413-1413 2.2
- 19 Epigenetic Signatures Accurately Distinguish Leukemia Subtypes and Provide a More Comprehensive Representation of Differentially Regulated Genes Than Gene Expression Profiling.. *Blood*, **2006**, 108, 735-735 2.2
- 18 Epigenetic Dysregulation of Candidate Cis-Regulatory Sequences in Hematological Malignancies.. *Blood*, **2006**, 108, 2229-2229 2.2
- 17 Myelodysplastic Syndrome (MDS) Displays Profound and Functionally Significant Epigenetic Deregulation Compared to Acute Myeloid Leukemia (AML) and Normal Bone Marrow Cells.. *Blood*, **2007**, 110, 345-345 2.2
- 16 Integrative Epigenetic and Single-Cell RNA-Seq Profiling of Human Hematopoietic Stem Cells Reveals Epigenetic Reprogramming of Enhancer and Regulatory Elements during Normal Aging. *Blood*, **2017**, 130, 770-770 2.2
- 15 Dysregulation of RUNX3 in Aged Human HSPCs May Contribute to Perturbations in Erythropoiesis and Balanced Lineage Output. *Blood*, **2018**, 132, 2553-2553 2.2
- 14 Loss of KLF6 Recapitulates Molecular and Functional Changes Associated with Aging in Human Hematopoietic Stem and Progenitor Cells. *Blood*, **2019**, 134, 447-447 2.2
- 13 Molecular Background of BCP-ALL Cases with an Early Switch to Monocytic Lineage. *Blood*, **2014**, 124, 3562-3562 2.2
- 12 Aldehyde Dehydrogenase Activity in the Leukemic Stem Cell Compartment Uncovers Opposing Methylation Patterns of Leukemia Stem Cells in AML. *Blood*, **2016**, 128, 3925-3925 2.2
- 11 Hyperactive Nras and Dose Reduction of Tet2 Collaborate to Dys-Regulate Hematopoietic Stem Cells and Promote Leukemogenesis. *Blood*, **2016**, 128, 1204-1204 2.2
- 10 Aging Human Hematopoietic Stem Cells Manifest Massive Epigenetic Reprogramming and Altered Gene Splicing of Key Hematopoietic Gene Sets. *Blood*, **2016**, 128, 885-885 2.2
- 9 RNA Binding Protein Syncrip Regulates the Leukemia Stem Cell Program. *Blood*, **2016**, 128, 739-739 2.2

- 8 DNA Methylation Profiling Predicts Clinical Outcomes and Reveals Unique Insights Into the Molecular Complexity of Acute Myeloid Leukemia.. *Blood*, **2009**, 114, 707-707 2.2
- 7 Promoter Hypermethylation in MLL-r Leukemia: Biology and Therapeutic Targeting.. *Blood*, **2009**, 114, 3472-3472 2.2
- 6 ABC and GCB DLBCLs Display Unique Biologically Distinct and Clinically Relevant Epigenetic Signatures.. *Blood*, **2009**, 114, 619-619 2.2
- 5 Integrated Genetic and Epigenetic Analysis of Childhood Acute Lymphoblastic Leukemia Reveals a Synergistic Role for Structural and Epigenetic Lesions In Determining Disease Phenotype. *Blood*, **2010**, 116, 537-537 2.2
- 4 Differential DNA Methylation of TUBB1 Correlates with Tissue-Specific H β 1 Tubulin Expression. *Blood*, **2011**, 118, 4796-4796 2.2
- 3 H2.0-Like Homeobox (HLX) Induces Unlimited Clonogenicity, Blocks Differentiation, and Cooperates with FLT3-ITD in the Induction of Acute Myeloid Leukemia. *Blood*, **2012**, 120, 651-651 2.2
- 2 Epigenetic Changes in CEBP β Gene and Xenotransplantation Model of B Cell Precursor Acute Lymphoblastic Leukemia Switching to Monocytoid Lineage During the Early Phase of the Treatment. *Blood*, **2012**, 120, 876-876 2.2
- 1 Lineage, Fusion Partner and Age Differences in the Methylome of MLL-r Leukemias. *Blood*, **2012**, 120, 3506-3506 2.2