Jonathan C Strefford

List of Publications by Year
in descending order

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154 papers	5,885 citations	66315 42 h-index	79644 73 g-index
160 all docs	160 docs citations	160 times ranked	7941 citing authors

#	Article	IF	Citations
1	Deregulated expression of cytokine receptor gene, CRLF2, is involved in lymphoid transformation in B-cell precursor acute lymphoblastic leukemia. Blood, 2009, 114, 2688-2698.	0.6	445
2	Recurrent mutations refine prognosis in chronic lymphocytic leukemia. Leukemia, 2015, 29, 329-336.	3.3	253
3	Two main genetic pathways lead to the transformation of chronic lymphocytic leukemia to Richter syndrome. Blood, 2013, 122, 2673-2682.	0.6	208
4	Prognosis of children with acute lymphoblastic leukemia (ALL) and intrachromosomal amplification of chromosome 21 (iAMP21). Blood, 2007, 109, 2327-2330.	0.6	200
5	The clinical significance of NOTCH1 and SF3B1 mutations in the UK LRF CLL4 trial. Blood, 2013, 121, 468-475.	0.6	190
6	Five members of the CEBP transcription factor family are targeted by recurrent IGH translocations in B-cell precursor acute lymphoblastic leukemia (BCP-ALL). Blood, 2007, 109, 3451-3461.	0.6	188
7	A comprehensive analysis of the CDKN2A gene in childhood acute lymphoblastic leukemia reveals genomic deletion, copy number neutral loss of heterozygosity, and association with specific cytogenetic subgroups. Blood, 2009, 113, 100-107.	0.6	167
8	Recurrent mTORC1-activating RRAGC mutations in follicular lymphoma. Nature Genetics, 2016, 48, 183-188.	9.4	160
9	Complex genomic alterations and gene expression in acute lymphoblastic leukemia with intrachromosomal amplification of chromosome 21. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 8167-8172.	3.3	146
10	Interphase molecular cytogenetic screening for chromosomal abnormalities of prognostic significance in childhood acute lymphoblastic leukaemia: a UK Cancer Cytogenetics Group Study. British Journal of Haematology, 2005, 129, 520-530.	1.2	137
11	miR-153 Supports Colorectal Cancer Progression via Pleiotropic Effects That Enhance Invasion and Chemotherapeutic Resistance. Cancer Research, 2013, 73, 6435-6447.	0.4	132
12	Chromatin accessibility maps of chronic lymphocytic leukaemia identify subtype-specific epigenome signatures and transcription regulatory networks. Nature Communications, 2016, 7, 11938.	5.8	131
13	Whole-exome sequencing in relapsing chronic lymphocytic leukemia: clinical impact of recurrent RPS15 mutations. Blood, 2016, 127, 1007-1016.	0.6	130
14	Genetics and Prognostication in Splenic Marginal Zone Lymphoma: Revelations from Deep Sequencing. Clinical Cancer Research, 2015, 21, 4174-4183.	3.2	129
15	Whole-exome sequencing in splenic marginal zone lymphoma reveals mutations in genes involved in marginal zone differentiation. Leukemia, 2014, 28, 1334-1340.	3.3	115
16	Genomic characterization implicates iAMP21 as a likely primary genetic event in childhood B-cell precursor acute lymphoblastic leukemia. Blood, 2011, 117, 6848-6855.	0.6	108
17	13q deletion anatomy and disease progression in patients with chronic lymphocytic leukemia. Leukemia, 2011, 25, 489-497.	3.3	104
18	Genome complexity in acute lymphoblastic leukemia is revealed by array-based comparative genomic hybridization. Oncogene, 2007, 26, 4306-4318.	2.6	95

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19	Distinct patterns of novel gene mutations in poor-prognostic stereotyped subsets of chronic lymphocytic leukemia: the case of SF3B1 and subset #2. Leukemia, 2013, 27, 2196-2199.	3.3	90
20	The SF3B1 inhibitor spliceostatin A (SSA) elicits apoptosis in chronic lymphocytic leukaemia cells through downregulation of Mcl-1. Leukemia, 2016, 30, 351-360.	3.3	88
21	Functional loss of Î¹BÎµ leads to NF-Î¹B deregulation in aggressive chronic lymphocytic leukemia. Journal of Experimental Medicine, 2015, 212, 833-843.	4.2	85
22	Exome sequence read depth methods for identifying copy number changes. Briefings in Bioinformatics, 2015, 16, 380-392.	3.2	84
23	Frequent NFKBIE deletions are associated with poor outcome in primary mediastinal B-cell lymphoma. Blood, 2016, 128, 2666-2670.	0.6	82
24	FcÎ³ receptors: genetic variation, function, and disease. Immunological Reviews, 2015, 268, 6-24.	2.8	78
25	Variable breakpoints target PAX5 in patients with dicentric chromosomes: A model for the basis of unbalanced translocations in cancer. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 17050-17054.	3.3	77
26	IL-4 enhances expression and function of surface IgM in CLL cells. Blood, 2016, 127, 3015-3025.	0.6	76
27	ATM mutation rather than BIRC3 deletion and/or mutation predicts reduced survival in 11q-deleted chronic lymphocytic leukemia: data from the UK LRF CLL4 trial. Haematologica, 2014, 99, 736-742.	1.7	69
28	Genomic disruption of the histone methyltransferase SETD2 in chronic lymphocytic leukaemia. Leukemia, 2016, 30, 2179-2186.	3.3	69
29	Overexpression of CEBPA resulting from the translocation t(14;19)(q32;q13) of human precursor B acute lymphoblastic leukemia. Blood, 2006, 108, 3560-3563.	0.6	67
30	Molecular cytogenetic characterization ofTCF3 (E2A)/19p13.3 rearrangements in B-cell precursor acute lymphoblastic leukemia. Genes Chromosomes and Cancer, 2007, 46, 478-486.	1.5	67
31	Whole Exome Sequencing Identifies Novel Recurrently Mutated Genes in Patients with Splenic Marginal Zone Lymphoma. PLoS ONE, 2013, 8, e83244.	1.1	66
32	miR-19â€“Mediated Inhibition of Transglutaminase-2 Leads to Enhanced Invasion and Metastasis in Colorectal Cancer. Molecular Cancer Research, 2015, 13, 1095-1105.	1.5	66
33	Intrachromosomal amplification of chromosome 21 (iAMP21) may arise from a breakageâ€“fusionâ€“bridge cycle. Genes Chromosomes and Cancer, 2007, 46, 318-326.	1.5	64
34	t(6;14)(p22;q32): a new recurrent IGH@ translocation involving ID4 in B-cell precursor acute lymphoblastic leukemia (BCP-ALL). Blood, 2008, 111, 387-391.	0.6	59
35	The complex genomic profile of ETV6â€RUNX1 positive acute lymphoblastic leukemia highlights a recurrent deletion of TBL1XR1. Genes Chromosomes and Cancer, 2008, 47, 1118-1125.	1.5	58
36	Amplification of the ABL gene in T-cell acute lymphoblastic leukemia. Leukemia, 2004, 18, 1153-1156.	3.3	57

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37	Different spectra of recurrent gene mutations in subsets of chronic lymphocytic leukemia harboring stereotyped B-cell receptors. Haematologica, 2016, 101, 959-967.	1.7	57
38	Surface IgM expression and function are associated with clinical behavior, genetic abnormalities, and DNA methylation in CLL. Blood, 2016, 128, 816-826.	0.6	54
39	Proteomics Profiling of CLL Versus Healthy B-cells Identifies Putative Therapeutic Targets and a Subtype-independent Signature of Spliceosome Dysregulation. Molecular and Cellular Proteomics, 2018, 17, 776-791.	2.5	54
40	The Dual Syk/JAK Inhibitor Cerdulatinib Antagonizes B-cell Receptor and Microenvironmental Signaling in Chronic Lymphocytic Leukemia. Clinical Cancer Research, 2017, 23, 2313-2324.	3.2	51
41	Upregulation of FcÎ³RIIb on monocytes is necessary to promote the superagonist activity of TGN1412. Blood, 2015, 125, 102-110.	0.6	47
42	EGR2 mutations define a new clinically aggressive subgroup of chronic lymphocytic leukemia. Leukemia, 2017, 31, 1547-1554.	3.3	46
43	Heterogeneous breakpoints in patients with acute lymphoblastic leukemia and the dic(9;20)(p11Â13;q11) show recurrent involvement of genes at 20q11.21. Haematologica, 2009, 94, 1164-1169.	1.7	43
44	Genomic arrays identify high-risk chronic lymphocytic leukemia with genomic complexity: a multi-center study. Haematologica, 2020, 106, 87-97.	1.7	43
45	A combination of molecular cytogenetic analyses reveals complex genetic alterations in conventional renal cell carcinoma. Cancer Genetics and Cytogenetics, 2005, 159, 1-9.	1.0	42
46	Telomere length predicts progression and overall survival in chronic lymphocytic leukemia: data from the UK LRF CLL4 trial. Leukemia, 2015, 29, 2411-2414.	3.3	42
47	Tailored approaches grounded on immunogenetic features for refined prognostication in chronic lymphocytic leukemia. Haematologica, 2019, 104, 360-369.	1.7	42
48	Comparative genomic hybridization and BUB1B mutation analyses in childhood cancers associated with mosaic variegated aneuploidy syndrome. Cancer Letters, 2006, 239, 234-238.	3.2	39
49	Longitudinal copy number, whole exome and targeted deep sequencing of 'good risk' IGHV-mutated CLL patients with progressive disease. Leukemia, 2016, 30, 1301-1310.	3.3	37
50	The use of multicolor fluorescence technologies in the characterization of prostate carcinoma cell lines. Cancer Genetics and Cytogenetics, 2001, 124, 112-121.	1.0	36
51	CYP2B6*6 is an independent determinant of inferior response to fludarabine plus cyclophosphamide in chronic lymphocytic leukemia. Blood, 2013, 122, 4253-4258.	0.6	35
52	Additional trisomies amongst patients with chronic lymphocytic leukemia carrying trisomy 12: the accompanying chromosome makes a difference. Haematologica, 2016, 101, e299-e302.	1.7	35
53	The PI3K/mTOR inhibitor PF-04691502 induces apoptosis and inhibits microenvironmental signaling in CLL and the EÂμ-TCL1 mouse model. Blood, 2015, 125, 4032-4041.	0.6	34
54	Clinical significance of TP53, BIRC3, ATM and MAPK-ERK genes in chronic lymphocytic leukaemia: data from the randomised UK LRF CLL4 trial. Leukemia, 2020, 34, 1760-1774.	3.3	34

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55	Derivative chromosome 9 deletions are a significant feature of childhood Philadelphia chromosome positive acute lymphoblastic leukaemia. Leukemia, 2005, 19, 564-571.	3.3	32
56	Non-coding NOTCH1 mutations in chronic lymphocytic leukemia; their clinical impact in the UK CLL4 trial. Leukemia, 2017, 31, 510-514.	3.3	31
57	Analysis of a breakpoint cluster reveals insight into the mechanism of intrachromosomal amplification in a lymphoid malignancy. Human Molecular Genetics, 2011, 20, 2591-2602.	1.4	29
58	The morphology of CLL revisited: the clinical significance of prolymphocytes and correlations with prognostic/molecular markers in the LRF CLL4 trial. British Journal of Haematology, 2016, 174, 767-775.	1.2	29
59	Methylation of tumour suppressor gene promoters in the presence and absence of transcriptional silencing in high hyperdiploid acute lymphoblastic leukaemia. British Journal of Haematology, 2009, 144, 838-847.	1.2	27
60	Transposon Mutagenesis Reveals Fludarabine Resistance Mechanisms in Chronic Lymphocytic Leukemia. Clinical Cancer Research, 2016, 22, 6217-6227.	3.2	26
61	The genomic landscape of chronic lymphocytic leukaemia: biological and clinical implications. British Journal of Haematology, 2015, 169, 14-31.	1.2	25
62	Lamin B1 regulates somatic mutations and progression of B-cell malignancies. Leukemia, 2018, 32, 364-375.	3.3	25
63	Clinical significance of DNA methylation in chronic lymphocytic leukemia patients: results from 3 UK clinical trials. Blood Advances, 2019, 3, 2474-2481.	2.5	25
64	Systematic Review of Somatic Mutations in Splenic Marginal Zone Lymphoma. Scientific Reports, 2019, 9, 10444.	1.6	23
65	Overexpression of genes on 16q associated with cisplatin resistance of testicular germ cell tumor cell lines. Genes Chromosomes and Cancer, 2005, 43, 211-216.	1.5	22
66	Episomal amplification of NUP214-ABL1 fusion gene in B-cell acute lymphoblastic leukemia. Blood, 2012, 120, 4441-4443.	0.6	21
67	Low frequency mutations independently predict poor treatment-free survival in early stage chronic lymphocytic leukemia and monoclonal B-cell lymphocytosis. Haematologica, 2015, 100, e237-e239.	1.7	21
68	The characterisation of the lymphoma cell line U937, using comparative genomic hybridisation and multi-plex FISH. Cytogenetic and Genome Research, 2001, 94, 9-14.	0.6	20
69	Spontaneous and induced aneuploidy, considerations which may influence chromosome malsegregation. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2002, 504, 119-129.	0.4	20
70	Authentication and characterisation of a new oesophageal adenocarcinoma cell line: MFD-1. Scientific Reports, 2016, 6, 32417.	1.6	20
71	The outcome of Chronic lymphocytic leukaemia patients with 97% <scp>IGHV</scp> gene identity to germline is distinct from cases with <97% identity and similar to those with 98% identity. British Journal of Haematology, 2016, 173, 127-136.	1.2	19
72	Impact of Human FcÎ³R Gene Polymorphisms on IgG-Triggered Cytokine Release: Critical Importance of Cell Assay Format. Frontiers in Immunology, 2019, 10, 390.	2.2	19

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73	Variant IRF4/MUM1 associates with CD38 status and treatment-free survival in chronic lymphocytic leukaemia. Leukemia, 2010, 24, 877-881.	3.3	18
74	Chromosome banding analysis and genomic microarrays are both useful but not equivalent methods for genomic complexity risk stratification in chronic lymphocytic leukemia patients. Haematologica, 2022, 107, 593-603.	1.7	18
75	T-cell dysfunction in chronic lymphocytic leukemia from an epigenetic perspective. Haematologica, 2021, 106, 1234-1243.	1.7	18
76	Evaluation of High-Throughput Genomic Assays for the Fc Gamma Receptor Locus. PLoS ONE, 2015, 10, e0142379.	1.1	17
77	ATM mutations in major stereotyped subsets of chronic lymphocytic leukemia: enrichment in subset #2 is associated with markedly short telomeres. Haematologica, 2016, 101, e369-e373.	1.7	16
78	Disruption of ETV6 in intron 2 results in upregulatory and insertional events in childhood acute lymphoblastic leukaemia. Leukemia, 2008, 22, 114-123.	3.3	15
79	Modeling the molecular consequences of unbalanced translocations in cancer: Lessons from acute lymphoblastic leukemia. Cell Cycle, 2009, 8, 2175-2184.	1.3	13
80	A novel scoring system combining expression of CD23, CD20, and CD38 with platelet count predicts for the presence of the t(11;14) translocation of mantle cell lymphoma. Cytometry Part B - Clinical Cytometry, 2011, 80B, 230-237.	0.7	13
81	BCR signaling contributes to autophagy regulation in chronic lymphocytic leukemia. Leukemia, 2020, 34, 640-644.	3.3	12
82	Novel chromosome findings in bladder cancer cell lines detected with multiplex fluorescence in situ hybridization. Cancer Genetics and Cytogenetics, 2002, 135, 139-146.	1.0	11
83	A new minimal deleted region at 11q22.3 reveals the importance of interpretation of diminished FISH signals and the choice of probe for ATM deletion screening in chronic lymphocytic leukemia. Leukemia Research, 2012, 36, 307-310.	0.4	11
84	Splenic marginal-zone lymphoma: ontogeny and genetics. Leukemia and Lymphoma, 2015, 56, 301-310.	0.6	11
85	Molecular characterisation of the t(1;15)(p22;q22) translocation in the prostate cancer cell line LNCaP. Cytogenetic and Genome Research, 2006, 112, 45-52.	0.6	10
86	Comparative analysis of targeted next-generation sequencing panels for the detection of gene mutations in chronic lymphocytic leukemia: an ERIC multi-center study. Haematologica, 2021, 106, 682-691.	1.7	10
87	Single-nucleotide FcÎ³ receptor polymorphisms do not impact obinutuzumab/rituximab outcome in patients with lymphoma. Blood Advances, 2021, 5, 2935-2944.	2.5	10
88	Insertion of atypical glycans into the tumor antigen-binding site identifies DLBCLs with distinct origin and behavior. Blood, 2021, 138, 1570-1582.	0.6	9
89	The Genomics of Hairy Cell Leukaemia and Splenic Diffuse Red Pulp Lymphoma. Cancers, 2022, 14, 697.	1.7	9
90	HIF activation enhances FcÎ³RIIb expression on mononuclear phagocytes impeding tumor targeting antibody immunotherapy. Journal of Experimental and Clinical Cancer Research, 2022, 41, 131.	3.5	9

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91	The association between deaths from infection and mutations of the BRAF, FBXW7, NRAS and XPO1 genes: a report from the LRF CLL4 trial. Leukemia, 2021, 35, 2563-2569.	3.3	8
92	Role of obinutuzumab exposure on clinical outcome of follicular lymphoma treated with firstâ€line immunochemotherapy. British Journal of Clinical Pharmacology, 2019, 85, 1495-1506.	1.1	7
93	Dissecting the role of TP53 alterations in del(11q) chronic lymphocytic leukemia. Clinical and Translational Medicine, 2021, 11, e304.	1.7	7
94	Prognostic significance of FCGR2B expression for the response of DLBCL patients to rituximab or obinutuzumab treatment. Blood Advances, 2021, 5, 2945-2957.	2.5	7
95	CBL-MZ is not a single biological entity: evidence from genomic analysis and prolonged clinical follow-up. Blood Advances, 2018, 2, 1116-1119.	2.5	6
96	Subset-Specific Spectra of Recurrent Gene Mutations in Chronic Lymphocytic Leukemia with Stereotyped B-Cell Receptors. Blood, 2014, 124, 3320-3320.	0.6	6
97	Identification of a Recurrent t(4;6) Chromosomal Translocation in Prostate Cancer. Journal of Urology, 2007, 177, 1907-1912.	0.2	5
98	Different time-dependent changes of risk for evolution in chronic lymphocytic leukemia with mutated or unmutated antigen B cell receptors. Leukemia, 2019, 33, 1801-1805.	3.3	5
99	The mutational signature of chronic lymphocytic leukemia. Biochemical Journal, 2016, 473, 3725-3740.	1.7	4
100	DC-SIGN binding to mannosylated B-cell receptors in follicular lymphoma down-modulates receptor signaling capacity. Scientific Reports, 2021, 11, 11676.	1.6	4
101	Array-Based Comparative Genomic Hybridization as a Tool for Analyzing the Leukemia Genome. Methods in Molecular Biology, 2009, 538, 151-177.	0.4	4
102	High Surface IgM Levels Associate with Shorter Response Duration and Bypass of the BTK Blockade during Ibrutinib Therapy in CLL Patients. Blood, 2019, 134, 1752-1752.	0.6	4
103	Haploinsufficiency of the MLL and TOB2 genes in lymphoid malignancy. Leukemia, 2010, 24, 649-652.	3.3	3
104	Prognostic Impact of Germ-Line FCGR2A (H131R), FCGR3A (F158V), and FCGR2B (I232T) Single Nucleotide Polymorphisms in Lymphoma Patients Treated with Obinutuzumab or Rituximab in Combination with Chemotherapy: Results from the Phase III GALLIUM and GOYA Clinical Trials. Blood, 2018, 132, 4109-4109.	0.6	3
105	13q Deletion Size Predicts Disease Progression and Response to Treatment in Patients with Chronic Lymphocytic Leukaemia.. Blood, 2009, 114, 671-671.	0.6	3
106	The SykJak Inhibitor Cerdulatinib (PRT062070) Shows Promising Preclinical Activity in Chronic Lymphocytic Leukemia By Antagonising B Cell Receptor and Microenvironmental Signalling. Blood, 2015, 126, 1716-1716.	0.6	3
107	High surface IgM levels associate with shorter response to ibrutinib and BTK bypass in patients with CLL. Blood Advances, 2022, 6, 5494-5504.	2.5	3
108	The (epi)genomic landscape of splenic marginal zone lymphoma, biological implications, clinical utility, and future questions. , 0, , .		2

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109	The Spectrum and Prognostic Relevance of Additional Abnormalities, Involving 12p and 21q, in Children with ETV6-RUNX1 Positive Acute Lymphoblastic Leukaemia (ALL). Blood, 2008, 112, 430-430.	0.6	2
110	Global and MYC-Specific Translation Is Enhanced in Activated Chronic Lymphocytic Leukemia Cells Carrying NOTCH1 C.7541_7542delct Mutations. Blood, 2016, 128, 970-970.	0.6	2
111	IGH@ Translocations Involving the Pseudoautosomal Region 1 (PAR1) of Both Sex Chromosomes Deregulate the Cytokine Receptor-Like Factor 2 (CRLF2) Gene in B Cell Precursor Acute Lymphoblastic Leukemia (BCP-ALL). Blood, 2008, 112, 787-787.	0.6	2
112	Genomic Dissection of the FcÎ³ Receptor Region in the Context of Monoclonal Antibody Therapy. Blood, 2014, 124, 2996-2996.	0.6	2
113	B-cell receptor dependent phagocytosis and presentation of particulate antigen by chronic lymphocytic leukemia cells. Exploration of Targeted Anti-tumor Therapy, 2022, 3, 37-49.	0.5	2
114	Advances in Molecular Cytogenetics to Study the Leukemia Genome. Laboratory Medicine, 2007, 38, 527-535.	0.8	1
115	A unique genome in EBV-positive BL. Blood, 2019, 133, 1269-1270.	0.6	1
116	Characterization of Somatically-Acquired Copy Number Alterations in Chronic Lymphocytic Leukaemia Using Shallow Whole Genome Sequencing. Methods in Molecular Biology, 2019, 1881, 327-353.	0.4	1
117	Deletion Size Influences Clinical Outcome In Patients with Chronic Lymphocytic Leukemia; 13q Deletion Anatomy, Cooperating Lesions and Cancer Pathogenesis. Blood, 2010, 116, 757-757.	0.6	1
118	Differential Distribution Of Recurrent Gene Mutations In Subsets Of Chronic Lymphocytic Leukemia Patients With Stereotyped B-Cell Receptors: Results From A Multicenter Project Of The European Research Initiative On CLL In A Series Of 2482 Cases. Blood, 2013, 122, 4113-4113.	0.6	1
119	SNP-Arrays Provide New Insights Into the Pathogenesis of Richter Syndrome (RS). Blood, 2011, 118, 263-263.	0.6	1
120	The Correlation Between Deletion Architecture, ATM Mutational Status and BIRC3 Disruption in 11q-Deleted CLL. Blood, 2012, 120, 658-658.	0.6	1
121	Deep-Sequencing Reveals the Molecular Landscape of Splenic Marginal Zone Lymphoma: Biological and Clinical Implications. Blood, 2014, 124, 76-76.	0.6	1
122	Different Prognostic Impact of Recurrent Gene Mutations in IGHV-Mutated and IGHV-Unmutated Chronic Lymphocytic Leukemia: A Retrospective, Multi-Center Cohort Study By Eric, the European Research Initiative on CLL, in Harmony. Blood, 2021, 138, 2617-2617.	0.6	1
123	Characteristising recurrent chromosomal translocations in prostate cancer â€" The search for novel fusion genes. European Urology Supplements, 2003, 2, 155.	0.1	0
124	High-density and targeted array-based comparative genomic hybridisation (CGH) provides for a genomic fingerprint of prostate cancer. European Urology Supplements, 2003, 2, 154.	0.1	0
125	Solving Problems in Multiplex FISH. , 2003, 220, 235-244.		0
126	Cytogenetic and genomic characterization of cell line ARH77. Cancer Genetics and Cytogenetics, 2008, 181, 40-45.	1.0	0

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127	THE T(4;6) CHROMOSOMAL TRANSLOCATION IS A RECURRENT EVENT IN PROSTATE CANCER. European Urology Supplements, 2008, 7, 272.	0.1	0
128	A novel tumour-based test to identify breast cancer due to BRCA1 and BRCA2 mutations. Breast Cancer Research, 2010, 12, .	2.2	0
129	Molecular Biology and Cytogenetics of Chronic Lymphocytic Leukemia. , 2013, , 91-101.		0
130	Single cell genetic analysis of Trisomy12-NOTCH1 mutated chronic lymphocytic leukaemia: Hidden sub-clones. Clinical Lymphoma, Myeloma and Leukemia, 2015, 15, S23-S24.	0.2	0
131	The Genomic and Epigenomic Landscape of Chronic Lymphocytic Leukemia. , 2018, , 99-116.		0
132	Inactivation of CDKN2A in Childhood Acute Lymphoblastic Leukemia (ALL) Occurs Principally by Deletion and Is Strongly Correlated with Cytogenetic Subgroups.. Blood, 2007, 110, 457-457.	0.6	0
133	Variable Breakpoints Target PAX5 in Patients with Dicentric Chromosomes: A Model for the Basis of Unbalanced Translocations in Cancer. Blood, 2008, 112, 790-790.	0.6	0
134	What Is the Initiating Mechanism of iAMP21 in Childhood B Cell Precursor ALL?.. Blood, 2009, 114, 581-581.	0.6	0
135	Sequential SNP6.0 Microarray Analysis In Rai Stage 0 CLL Patients with Either Stable or Progressive Identifies Genomic Evolution In Both Cohorts. Blood, 2010, 116, 1696-1696.	0.6	0
136	dic(9;20)(p11-13;q11). Atlas of Genetics and Cytogenetics in Oncology and Haematology, 2011, , .	0.1	0
137	Phenethyl Isothiocyanate (PEITC) Regulates Autophagy in Chronic Lymphocytic Leukemia.. Blood, 2012, 120, 2906-2906.	0.6	0
138	Novel Gene Mutations In Chronic Lymphocytic Leukemia: Prevalence and Clinical Implications In A Series Of 3185 Cases - Initial Results From The European Research Initiative On CLL. Blood, 2013, 122, 1614-1614.	0.6	0
139	ZAP70 Methylation Is An Independent Prognostic Biomarker For Front Line Therapy Of Chronic Lymphocytic Leukemia : Results From The UK LRF CLL4 Trial. Blood, 2013, 122, 4137-4137.	0.6	0
140	Modulation of B Cell Receptor Signalling By IL-4 In Chronic Lymphocytic Leukaemia. Blood, 2013, 122, 4125-4125.	0.6	0
141	Recurrent Mutations within the Nfkbie gene: A Novel Mechanism for NF-Î¹B Deregulation in Aggressive Chronic Lymphocytic Leukemia. Blood, 2014, 124, 297-297.	0.6	0
142	Splicing Inhibition By Spliceostatin_A Is a Promising Therapeutic Strategy in Chronic Lymphocytic Leukaemia. Blood, 2014, 124, 3301-3301.	0.6	0
143	Surface IgM Levels Independently Influence Clinical Behavior and Associate with Altered Phenotype and Genetics in Chronic Lymphocytic Leukemia. Blood, 2014, 124, 830-830.	0.6	0
144	IL-4 Exerts Opposing Effects on Surface-IgM and CXCR4 Mediated Signalling in Chronic Lymphocytic Leukaemia. Blood, 2014, 124, 3299-3299.	0.6	0

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145	Tracking Subclonal Mutations in IGHV-Mutated CLL with Progressive Disease. Blood, 2014, 124, 1962-1962.	0.6	0
146	The Dual PI3K/mTOR Inhibitor PF-04691502 Induces Substantial Apoptosis in Chronic Lymphocytic Leukemia Cells in Vitro and Prolongs Survival in the EÂµ-TCL1 Mouse Model. Blood, 2014, 124, 832-832.	0.6	0
147	Biological Significance of B Cell Receptor Mediated Regulation of Autophagy in Chronic Lymphocytic Leukemia. Blood, 2015, 126, 4130-4130.	0.6	0
148	ATM Mutations in Major Stereotyped CLL Subsets: Enrichment in Subset #2 is Associated with Unfavourable Outcome. Blood, 2015, 126, 1712-1712.	0.6	0
149	Genomic Disruption of the Histone Methyltransferase SETD2 in Chronic Lymphocytic Leukemia. Blood, 2015, 126, 365-365.	0.6	0
150	EGR2 Mutations in Chronic Lymphocytic Leukemia: A New Bad Player. Blood, 2015, 126, 4126-4126.	0.6	0
151	Regulation of B-Cell Receptor Signalling By the Tumour Microenvironment in Chronic Lymphocytic Leukemia (CLL) and Its Impact on Adhesion and miRNA Expression. Blood, 2016, 128, 351-351.	0.6	0
152	Tailored Approaches for Refined Prognostication in Chronic Lymphocytic Leukemia Patients with Mutated Versus Unmutated Immunoglobulin Receptors. Blood, 2016, 128, 3199-3199.	0.6	0
153	ÎFÎšÎ'Î™Î• Deletions: A Novel Marker of Clinical Aggressiveness in Primary Mediastinal B-Cell Lymphoma. Blood, 2016, 128, 609-609.	0.6	0
154	The Association between Deaths Due to Infection and Mutations of the BRAF, FBXW7, NRAS and XPO1 genes: A Report from the LRF CLL4 Trial. Blood, 2020, 136, 37-38.	0.6	0