Charlotte G Nyvold

List of Publications by Year in descending order

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81 papers	1,155 citations	430442 18 h-index	414034 32 g-index
87 all docs	87 docs citations	87 times ranked	1628 citing authors

#	Article	IF	Citations
1	Precise quantification of minimal residual disease at day 29 allows identification of children with acute lymphoblastic leukemia and an excellent outcome. Blood, 2002, 99, 1253-1258.	0.6	150
2	Harmonization of BCR-ABL mRNA quantification using a uniform multifunctional control plasmid in 37 international laboratories. Leukemia, 2008, 22, 96-102.	3.3	100
3	Relapse prediction in acute myeloid leukaemia patients in complete remission using WT1 as a molecular marker: development of a mathematical model to predict time from molecular to clinical relapse and define optimal sampling intervals. British Journal of Haematology, 2008, 141, 782-791.	1.2	71
4	Minimal residual core binding factor AMLs by real time quantitative PCRâ€"Initial response to chemotherapy predicts event free survival and close monitoring of peripheral blood unravels the kinetics of relapse. Leukemia Research, 2006, 30, 389-395.	0.4	59
5	Chimeric Antigen Receptor T Cells Targeting CD79b Show Efficacy in Lymphoma with or without Cotargeting CD19. Clinical Cancer Research, 2019, 25, 7046-7057.	3.2	56
6	h<scp>MICL</scp> and <scp>CD</scp>123 in combination with a <scp>CD</scp>45/<scp>CD</scp>34/<scp>CD</scp>117 backbone â€" a universal marker combination for the detection of minimal residual disease in acute myeloid leukaemia. British Journal of Haematology, 2014, 164, 212-222.	1.2	48
7	Post-induction residual leukemia in childhood acute lymphoblastic leukemia quantified by PCR correlates with in vitro prednisolone resistance. Leukemia, 2001, 15, 1066-1071.	3.3	43
8	Molecular typing of adult acute myeloid leukaemia: significance of translocations, tandem duplications, methylation, and selective gene expression profiling. British Journal of Haematology, 2005, 131, 457-467.	1.2	34
9	Immunoelectron microscopy and mass spectrometry for classification of amyloid deposits. Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis, 2020, 27, 59-66.	1.4	34
10	The combined expression of HOXA4 and MEIS1 is an independent prognostic factor in patients with AML. European Journal of Haematology, 2009, 83, 439-448.	1.1	33
11	Wilms' tumor 1 mutation accumulated during therapy in acute myeloid leukemia: biological and clinical implications. Leukemia, 2006, 20, 2051-2054.	3.3	28
12	Analysis of aMycoplasma hominismembrane protein, P120. FEMS Microbiology Letters, 1994, 121, 121-127.	0.7	27
13	Interleukin-21 mRNA expression during virus infections. Cytokine, 2006, 33, 41-45.	1.4	27
14	Characterization and prognostic significance of mitochondrial <scp>DNA</scp> variations in acute myeloid leukemia. European Journal of Haematology, 2013, 90, 385-396.	1.1	27
15	Sensitivity of minimal residual disease in acute myeloid leukaemia in first remission â€" methodologies in relation to their clinical situation. British Journal of Haematology, 2012, 158, 569-580.	1.2	26
16	Sensitive ligand-based protein quantification using immuno-PCR: A critical review of single-probe and proximity ligation assays. BioTechniques, 2014, 56, 217-228.	0.8	24
17	A decade with whole exome sequencing in haematology. British Journal of Haematology, 2020, 188, 367-382.	1.2	24
18	Development of standardized approaches to reporting of minimal residual disease data using a reporting software package designed within the European LeukemiaNet. Leukemia, 2011, 25, 1168-1173.	3.3	23

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19	A highly sensitive and specific <scp>qPCR</scp> assay for quantification of the biomarker SOX11 in mantle cell lymphoma. European Journal of Haematology, 2012, 89, 385-394.	1.1	19
20	Measurable residual disease assessment by qPCR in peripheral blood is an informative tool for disease surveillance in childhood acute myeloid leukaemia. British Journal of Haematology, 2020, 190, 198-208.	1.2	19
21	Competitive PCR for quantification of minimal residual disease in acute lymphoblastic leukaemia. Journal of Immunological Methods, 2000, 233, 107-118.	0.6	15
22	Erythropoietin receptor defect: a cause of primary polycythaemia. British Journal of Haematology, 2004, 125, 537-538.	1.2	15
23	Delineation and molecular characterization of acute myeloid leukemia patients with coduplication of FLT3 and MLL. European Journal of Haematology, 2005, 75, 185-192.	1.1	15
24	Promoter hypermethylation of the retinoic acid receptor beta2 gene is frequent in acute myeloid leukaemia and associated with the presence of CBFbeta-MYH11 fusion transcripts. British Journal of Haematology, 2006, 133, 276-283.	1.2	15
25	Germline GATA1s-generating mutations predispose toÂleukemia with acquired trisomy 21 and Down syndrome-like phenotype. Blood, 2022, 139, 3159-3165.	0.6	15
26	Delineation of known and new transcript variants of the SETMAR (Metnase) gene and the expression profile in hematologic neoplasms. Experimental Hematology, 2014, 42, 448-456.e4.	0.2	14
27	Infectious complications after chemotherapy and stem cell transplantation in multiple myeloma: Implications of Fc gamma receptor and myeloperoxidase promoter polymorphisms. Leukemia and Lymphoma, 2008, 49, 1116-1122.	0.6	13
28	Daratumumab for treatment of blastic plasmacytoid dendritic cell neoplasm. A single-case report. Haematologica, 2019, 104, e432-e433.	1.7	13
29	WT1 gene expression in children with Down syndrome and transient myeloproliferative disorder. Leukemia Research, 2006, 30, 543-546.	0.4	12
30	SOX11 as a minimal residual disease marker for Mantle cell lymphoma. Leukemia Research, 2014, 38, 918-924.	0.4	11
31	Harnessing the Immune System to Fight Multiple Myeloma. Cancers, 2021, 13, 4546.	1.7	10
32	Capillary gel electrophoresis: a simple method for identification of mutations and polymorphisms in the CEBPA gene in patients with acute myeloid leukaemia. European Journal of Haematology, 2008, 81, 273-280.	1.1	9
33	SOX11, CCND1, BCL1/IgH and IgH-VDJ: a battle of minimal residual disease markers in mantle cell lymphoma?. Leukemia and Lymphoma, 2015, 56, 2724-2727.	0.6	9
34	Measurable residual disease monitoring using Wilms tumor gene 1 expression in childhood acute myeloid leukemia based on childâ€specific reference values. Pediatric Blood and Cancer, 2019, 66, e27671.	0.8	9
35	Mitochondrial cytochrome c oxidase subunit <scp>II</scp> variations predict adverse prognosis in cytogenetically normal acute myeloid leukaemia. European Journal of Haematology, 2013, 91, 295-303.	1.1	8
36	Perspective: sensitive detection of residual lymphoproliferative disease by NGS and clonal rearrangementsâ€"how low can you go?. Experimental Hematology, 2021, 98, 14-24.	0.2	8

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37	A novel <scp>RT</scp>â€q<scp>PCR</scp> assay for quantification of the <scp>MLL</scp>â€<scp>MLLT</scp>3 fusion transcript in acute myeloid leukaemia. European Journal of Haematology, 2013, 91, 394-398.	1.1	7
38	Common consensus LNA probe for quantitative PCR assays in cancer: Vehicles for minimal residual disease detection in t(11;14) and t(14;18) positive malignant lymphomas. Journal of Immunological Methods, 2014, 406, 131-136.	0.6	7
39	Chronic lymphocytic leukemia patients with heterogeneously or fully methylated LPL promotor display longer time to treatment. Epigenomics, 2018, 10, 1155-1166.	1.0	7
40	Molecular characterization of sorted malignant B cells from patients clinically identified with mantle cell lymphoma. Experimental Hematology, 2020, 84, 7-18.e12.	0.2	7
41	A patient with a 20-year lag phase between JAK2-V617F+ myeloproliferation and NPM1-mutated AML arguing against a common origin of disease. European Journal of Haematology, 2011, 87, 461-463.	1.1	6
42	Differential expression levels and methylation status of ROBO1 in mantle cell lymphoma and chronic lymphocytic leukaemia. International Journal of Laboratory Hematology, 2017, 39, e70-e73.	0.7	6
43	Measurable Residual Disease Assessment By qPCR in Peripheral Blood Is an Informative Tool for Disease Surveillance in Childhood Acute Myeloid Leukemia. Blood, 2018, 132, 2754-2754.	0.6	6
44	Novel scripts for improved annotation and selection of variants from whole exome sequencing in cancer research. MethodsX, 2015, 2, 145-153.	0.7	5
45	IGHV-associated methylation signatures more accurately predict clinical outcomes of chronic lymphocytic leukemia patients than IGHV mutation load. Haematologica, 2022, 107, 877-886.	1.7	5
46	Nature and nurture: a case of transcending haematological preâ€malignancies in a pair of monozygotic twins adding possible clues on the pathogenesis of Bâ€cell proliferations. British Journal of Haematology, 2015, 169, 391-400.	1.2	4
47	Rapid detection of FLT3 exon 20 tyrosine kinase domain mutations in patients with acute myeloid leukemia by high-resolution melting analysis. Leukemia and Lymphoma, 2012, 53, 1225-1229.	0.6	3
48	Chronic myeloid leukaemia presenting with isolated thrombocythaemia, a case revealing its stem cell biology. British Journal of Haematology, 2013, 162, 141-144.	1.2	3
49	Cell sorting enables interphase fluorescence in situ hybridization detection of low <scp>BCRâ€ABL</scp>1 producing stem cells in chronic myeloid leukaemia patients beyond deep molecular remission. British Journal of Haematology, 2014, 164, 53-60.	1.2	3
50	Detailed characterization of the transcriptome of single B cells in mantle cell lymphoma suggesting a potential use for SOX4. Scientific Reports, 2021, 11, 19092.	1.6	3
51	Multiplex PCR for the detection ofBCL-1/IGHandBCL-2/IGHgene rearrangements â€“ clinical validation in a prospective study of blood and bone marrow in 258 patients with or suspected of non-Hodgkin's lymphoma.. Acta OncolÃ³gica, 2007, 46, 21-30.	0.8	2
52	Critical methodological factors in diagnosing minimal residual disease in hematological malignancies using quantitative PCR. Expert Review of Molecular Diagnostics, 2015, 15, 581-584.	1.5	2
53	CNAplot â€" Software for visual inspection of chromosomal copy number alteration in cancer using juxtaposed sequencing read depth ratios and variant allele frequencies. SoftwareX, 2020, 11, 100503.	1.2	2
54	Distal chromosome 1q aberrations and initial response to ibrutinib in central nervous system relapsed mantle cell lymphoma. Leukemia Research Reports, 2021, 15, 100255.	0.2	2

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55	Measurable Residual Disease Monitoring of SPAG6, ST18, PRAME, and XAGE1A Expression in Peripheral Blood May Detect Imminent Relapse in Childhood Acute Myeloid Leukemia. Journal of Molecular Diagnostics, 2021, 23, 1787-1799.	1.2	2
56	Unraveling The Leukemic Nature Of hMICL and CD123 Expressing Cells In Acute Myeloid Leukemia. Blood, 2013, 122, 2626-2626.	0.6	2
57	Investigation of circulating DNA integrity after blood collection. BioTechniques, 2021, 71, 550-555.	0.8	2
58	Harmonized Testing for BCR-ABL Kinase Domain Mutations In CML: Results of a Survey and First Control Round within 28 National Reference Laboratories In Europe. Blood, 2010, 116, 894-894.	0.6	1
59	Chronic Myeloid Leukemia Presenting with Isolated Thrombocythemia: A Case Revealing Its Stem Cell Biology. Blood, 2012, 120, 4427-4427.	0.6	1
60	Efficient, Non-Viral and Reproducible Protocol for Stable Knockdown of Genes in Mantle Cell Lymphoma Cell Lines. Blood, 2020, 136, 1-2.	0.6	1
61	Acute myeloid leukemia exhibiting clonal instability during treatment: Implications for measurable residual disease assessments. Experimental Hematology, 2022, 107, 51-59.	0.2	1
62	Mantle cell lymphoma and the evidence of an immature lymphoid component. Leukemia Research, 2022, 115, 106824.	0.4	1
63	Reply to â€˜Wilms' tumour 1 mutations are associated with FLT3-ITD and failure of standard induction chemotherapy in patients with normal karyotype AMLâ€™ by Summers et al.. Leukemia, 2007, 21, 552-552.	3.3	0
64	Sensitive quantification of the intronless SOX11 mRNA from lymph nodes biopsies in mantle cell lymphoma. Leukemia Research, 2019, 78, 1-2.	0.4	0
65	Treatment of Molecular Relapse by Cessation of Immunosuppression After Hematopoietic Stem Cell Transplantation in Pediatric FLT3-ITD AML Monitored by WT1 Expression in Peripheral Blood. Journal of Pediatric Hematology/Oncology, 2019, 41, 417-419.	0.3	0
66	Replicate whole-genome next-generation sequencing data derived from Caucasian donor saliva samples. Data in Brief, 2021, 38, 107349.	0.5	0
67	A Multiplex PCR for Detection of Genetic Aberrations in Non-Hodkinâ€™s Lymphoma.. Blood, 2004, 104, 4554-4554.	0.6	0
68	Clues for Novel Pathways in Leukemogenesis: Global Gene Expression Profiling in Acute Myeloid Leukemia Patients Negative for a Comprehensive Series of Molecular Alterations.. Blood, 2004, 104, 3375-3375.	0.6	0
69	Relapse Prediction in AML Patients in Complete Remission Using WT1 as a Molecular Marker: Development of a Mathematical Model To Predict Time from Molecular to Clinical Relapse and Define Optimal Sampling Intervals.. Blood, 2007, 110, 3495-3495.	0.6	0
70	Mutations in Mitochondrial DNA Is An Adverse Factor for Survival in Patients with Acute Myeloid Leukemia.. Blood, 2008, 112, 1523-1523.	0.6	0
71	Development of Standardized Approaches to Reporting of Minimal Residual Disease Data Using a Reporting Software Package Designed within the European LeukemiaNet (ELN).. Blood, 2009, 114, 1619-1619.	0.6	0
72	Development of a Splenic Marginal Zone Lymphoma Associated with Active Chronic Visceral Leishmaniasis. Blood, 2011, 118, 5202-5202.	0.6	0

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73	Two Hematological Pre-Malignancies In a Pair Of Homozygous Twins Revealing Differences In Their Pre- and Postnatal Development. Blood, 2013, 122, 5262-5262.	0.6	0
74	Human MICL Is An Early Marker In Myeloid Differentiation and Identifies a Subgroup Of CML Patients With Expanded Granulocyte-Macrophage Progenitor Populations At Diagnosis. Blood, 2013, 122, 2704-2704.	0.6	0
75	Cell Sorting Enables iFISH Detection Of Low BCR-ABL Producing Stem Cells In CML Patients Beyond Deep Molecular Remission. Blood, 2013, 122, 1501-1501.	0.6	0
76	Relapse Kinetics in Acute Myeloid Leukemis Cases Encompassing More Than One Common Mutation: Towards a Unified Model. Blood, 2014, 124, 1055-1055.	0.6	0
77	SOX11, CCND1, BCL1/Igh, and Igh-VDJ â€“ a Plethora of Markers for Minimal Residual Disease in Mantle Cell Lymphoma: Which One to Choose?. Blood, 2014, 124, 2957-2957.	0.6	0
78	A New Approach to Identify Pathogenic Mutations and Inherited Variants By Exome Sequencing â€“ Using a Pair of Identical Twins with Monoclonal Lymphosis As Case Model. Blood, 2014, 124, 1979-1979.	0.6	0
79	qPCR MRD Monitoring in Peripheral Blood May Predict Hematological Relapse in Pediatric Acute Myeloid Leukemia. Blood, 2015, 126, 3749-3749.	0.6	0
80	Post-Therapy Measurable Residual Disease Monitoring in Peripheral Blood Using Overexpressed Genes in Childhood Acute Myeloid Leukemia. Blood, 2018, 132, 1480-1480.	0.6	0
81	Quantification of Fusion Transcripts Reveals Slower Treatment Kinetics As Compared with Multiparameter Flow Cytometry during Induction Treatment of Acute Myeloid Leukemia in Children. Blood, 2018, 132, 2814-2814.	0.6	0