Samuli Eldfors

List of Publications by Year
in descending order

74 papers	2,938 citations	304743 22 h-index	265206 42 g-index
77 all docs	77 docs citations	77 times ranked	5539 citing authors

#	Article	IF	Citations
1	Somatic *STAT3* Mutations in Large Granular Lymphocytic Leukemia. New England Journal of Medicine, 2012, 366, 1905-1913.	27.0	681
2	Individualized Systems Medicine Strategy to Tailor Treatments for Patients with Chemorefractory Acute Myeloid Leukemia. Cancer Discovery, 2013, 3, 1416-1429.	9.4	334
3	Discovery of somatic STAT5b mutations in large granular lymphocytic leukemia. Blood, 2013, 121, 4541-4550.	1.4	252
4	Comparison of solution-based exome capture methods for next generation sequencing. Genome Biology, 2011, 12, R94.	9.6	237
5	Autoimmunity, hypogammaglobulinemia, lymphoproliferation, and mycobacterial disease in patients with activating mutations in STAT3. Blood, 2015, 125, 639-648.	1.4	229
6	Aggressive natural killer-cell leukemiaÂmutational landscape and drug profiling highlight JAK-STAT signaling as therapeutic target. Nature Communications, 2018, 9, 1567.	12.8	107
7	Novel activating STAT5B mutations as putative drivers of T-cell acute lymphoblastic leukemia. Leukemia, 2014, 28, 1738-1742.	7.2	90
8	High incidence of activating STAT5B mutations in CD4-positive T-cell large granular lymphocyte leukemia. Blood, 2016, 128, 2465-2468.	1.4	86
9	Somatic mutations in clonally expanded cytotoxic T lymphocytes in patients with newly diagnosed rheumatoid arthritis. Nature Communications, 2017, 8, 15869.	12.8	83
10	Discovery of novel drug sensitivities in T-PLL by high-throughput ex vivo drug testing and mutation profiling. Leukemia, 2018, 32, 774-787.	7.2	75
11	Comprehensive Drug Testing of Patient-derived Conditionally Reprogrammed Cells from Castration-resistant Prostate Cancer. European Urology, 2017, 71, 319-327.	1.9	74
12	Implementing a Functional Precision Medicine Tumor Board for Acute Myeloid Leukemia. Cancer Discovery, 2022, 12, 388-401.	9.4	73
13	Activating somatic mutations outside the SH2-domain of STAT3 in LGL leukemia. Leukemia, 2016, 30, 1204-1208.	7.2	62
14	HOX gene expression predicts response to BCL-2 inhibition in acute myeloid leukemia. Leukemia, 2017, 31, 301-309.	7.2	61
15	Novel somatic mutations in large granular lymphocytic leukemia affecting the STAT-pathway and T-cell activation. Blood Cancer Journal, 2013, 3, e168-e168.	6.2	56
16	Enhanced sensitivity to glucocorticoids in cytarabine-resistant AML. Leukemia, 2017, 31, 1187-1195.	7.2	44
17	Idelalisib sensitivity and mechanisms of disease progression in relapsed TCF3-PBX1 acute lymphoblastic leukemia. Leukemia, 2017, 31, 51-57.	7.2	42
18	Dasatinib and navitoclax act synergistically to target NUP98-NSD1+/FLT3-ITD+ acute myeloid leukemia. Leukemia, 2019, 33, 1360-1372.	7.2	40

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19	Mutation accumulation in cancer genes relates to nonoptimal outcome in chronic myeloid leukemia. Blood Advances, 2020, 4, 546-559.	5.2	36
20	Identification of precision treatment strategies for relapsed/refractory multiple myeloma by functional drug sensitivity testing. Oncotarget, 2017, 8, 56338-56350.	1.8	35
21	Converging endometrial and ovarian tumorigenesis in Lynch syndrome: Shared origin of synchronous carcinomas. Gynecologic Oncology, 2018, 150, 92-98.	1.4	29
22	Clonal heterogeneity influences drug responsiveness in renal cancer assessed by *ex vivo* drug testing of multiple patient–derived cancer cells. International Journal of Cancer, 2019, 144, 1356-1366.	5.1	29
23	Epidemiological, clinical and molecular characterization of Lynch–like syndrome: A population–based study. International Journal of Cancer, 2019, 145, 87-98.	5.1	28
24	Somatic mTOR mutation in clonally expanded T lymphocytes associated with chronic graft versus host disease. Nature Communications, 2020, 11, 2246.	12.8	20
25	Sequencing of Lynch syndrome tumors reveals the importance of epigenetic alterations. Oncotarget, 2017, 8, 108020-108030.	1.8	18
26	Somatic mutations and T-cell clonality in patients with immunodeficiency. Haematologica, 2020, 105, 2757-2768.	3.5	18
27	Novel TBL1XR1, EPHA7 and SLFN12 mutations in a Sezary syndrome patient discovered by whole exome sequencing. Experimental Dermatology, 2014, 23, 366-368.	2.9	12
28	Systematic drug screening reveals specific vulnerabilities and co-resistance patterns in endocrine-resistant breast cancer. BMC Cancer, 2016, 16, 378.	2.6	11
29	Monitoring therapy responses at the leukemic subclone level by ultra-deep amplicon resequencing in acute myeloid leukemia. Leukemia, 2017, 31, 1048-1058.	7.2	11
30	Adult-Onset Anti-Citrullinated Peptide Antibody-Negative Destructive Rheumatoid Arthritis Is Characterized by a Disease-Specific CD8+ T Lymphocyte Signature. Frontiers in Immunology, 2020, 11, 578848.	4.8	11
31	Does breast carcinoma belong to the Lynch syndrome tumor spectrum? – Somatic mutational profiles vs. ovarian and colorectal carcinomas. Oncotarget, 2020, 11, 1244-1256.	1.8	11
32	Molecular Basis of Mismatch Repair Protein Deficiency in Tumors from Lynch Suspected Cases with Negative Germline Test Results. Cancers, 2020, 12, 1853.	3.7	8
33	Recurrent Missense Mutations in the STAT3 Gene in LGL Leukemia Provide Insights to Pathogenetic Mechanisms and Suggest Potential Diagnostic and Therapeutic Applications. Blood, 2011, 118, 936-936.	1.4	6
34	Rad51c- and Trp53-double-mutant mouse model reveals common features of homologous recombination-deficient breast cancers. Oncogene, 2016, 35, 4601-4610.	5.9	5
35	Novel Activating STAT5B Mutations As Drivers Of T-ALL. Blood, 2013, 122, 3863-3863.	1.4	5
36	Abstract 3175: Genomic and transcriptomic data integration in chronic myelomonocytic leukemia reveals a novel fusion gene involving onco-miR-125b-2. , 2012, , .		3

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37	Integration of Ex Vivo Drug Testing and in-Depth Molecular Profiling Reveals Oncogenic Signaling Pathways and Novel Therapeutic Strategies for Multiple Myeloma. Blood, 2014, 124, 2046-2046.	1.4	3
38	Predictive Response Biomarkers for BET Inhibitors in AML. Blood, 2018, 132, 2749-2749.	1.4	2
39	Discovery of STAT5b Mutations and Small Subclones of STAT3 Mutations in Large Granular Lymphocytic (LGL) Leukemia. Blood, 2012, 120, 871-871.	1.4	2
40	Abstract 4580: Personalized treatment selection for therapy-resistant AML by integrating ex-vivo drug sensitivity and resistance testing (DSRT) as well as serial genomic, transcriptomic and phosphoproteomic profiling. , 2012, , .		1
41	Abstract 5067: Exome sequencing reveals both DNA sequence and copy number changes in AML: Potential driver changes and mechanisms of drug resistance revealed from serial samples from the same patients. , 2012, , .		1
42	Somatic Mutations in T Cells As Possible Regulators of Immunodeficiency. Blood, 2018, 132, 515-515.	1.4	1
43	Landscape of Mutations in Relapsed Acute Myeloid Leukemia. Blood, 2014, 124, 2367-2367.	1.4	1
44	Identification and Clinical Exploration of Individualized Targeted Therapeutic Approaches in Acute Myeloid Leukemia Patients By Integrating Drug Response and Deep Molecular Profiles. Blood, 2017, 130, 854-854.	1.4	1
45	High-Throughput Ex Vivo Drug Sensitivity and Resistance Testing (DSRT) Integrated with Deep Genomic and Molecular Profiling Reveal New Therapy Options with Targeted Drugs in Subgroups of Relapsed Chemorefractory AML. Blood, 2012, 120, 288-288.	1.4	1
46	Abstract 608: Comprehensive drug testing of patient-derived conditionally reprogrammed cells from castration-resistant prostate cancer. , 2016, , .		1
47	Abstract 2378: Responses of AML patients to tailored drug regimens: monitoring cancer subclones by ultra-deep resequencing. , 2016, , .		1
48	Somatic Mutations in CD8+ T Cells in Patients with Chronic Immune Thrombocytopenia Are Associated with Increased Clonality and Cytotoxic Phenotype of CD8+ T Cells. Blood, 2018, 132, 131-131.	1.4	1
49	825 Exome Sequencing of T-LGL Leukemia Patient Revealed ANGPT2 as a Possible Mutational Target. European Journal of Cancer, 2012, 48, S198.	2.8	0
50	A6.02â€¦Somatic mutations in clonally expanded CD8$^+$T cells in patients with newly diagnosed rheumatoid arthritis. Annals of the Rheumatic Diseases, 2016, 75, A47.2-A48.	0.9	0
51	Development of a Cancer Pharmacopeia-Wide Ex-Vivo Drug Sensitivity and Resistance Testing (DSRT) Platform: Identification of MEK and mTOR As Patient-Specific Molecular Drivers of Adult AML and Potent Therapeutic Combinations with Dasatinib. Blood, 2011, 118, 2487-2487.	1.4	0
52	Abstract 895: Quantitative drug sensitivity and resistance testing (DSRT) of primary ex vivo AML blasts highlights mTOR and MEK as potential key molecular driver signals of therapeutic significance. , 2012, , .		0
53	Abstract 3188: Development of a cancer pharmacopeia-wideex-vivodrug sensitivity and resistance testing (DSRT) platform for AML: Towards individually optimized therapy and improved understanding of drug resistance patterns. , 2012, , .		0
54	Somatic PTPRT and ANGPT2 Mutations in Large Granulocyte Leukemia. Blood, 2012, 120, 1302-1302.	1.4	0

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55	Primary T-Prolymphocytic Leukemia (T-PLL) Cells Are Sensitive To BCL-2 and HDAC Inhibitors: Results From High-Throughput Ex Vivo Drug Testing. Blood, 2013, 122, 3828-3828.	1.4	0
56	Identification Of AML Subtype-Selective Drugs By Functional Ex Vivo Drug Sensitivity and Resistance Testing and Genomic Profiling. Blood, 2013, 122, 482-482.	1.4	0
57	Abstract 982: Analysis of clonal evolution of leukemia in vivo following novel targeted treatments. , 2014, , .		0
58	Identification of Dual PI3K/mTOR and BCL2 Inhibitors for the Treatment of High Risk Multiple Myeloma. Blood, 2014, 124, 646-646.	1.4	0
59	Landscape of Driver Lesions in Multiple Myeloma and Consequences for Targeted Drug Response. Blood, 2014, 124, 3351-3351.	1.4	0
60	Abstract 606: Novel somatic mutations in the DNA-binding and coiled-coil domain of the STAT3 gene in LGL-leukemia. , 2015, , .		0
61	Stratification of Multiple Myeloma Patients Based on Ex Vivo Drug Sensitivity and Identification of New Treatments for Patients with High-Risk Relapsed/Refractory Disease. Blood, 2015, 126, 3006-3006.	1.4	0
62	BCL2-Inhibitors Target a Major Group of Newly-Diagnosed and Relapsed/Refractory Acute Myeloid Leukemia Ex Vivo. Blood, 2015, 126, 2462-2462.	1.4	0
63	Exome Sequencing of Aggressive Natural Killer Cell Leukemia and Drug Profiling Highlight Candidate Driver Pathways in Malignant Natural Killer Cells. Blood, 2015, 126, 700-700.	1.4	0
64	Abstract 4679: Acquisition of cytarabine resistance leads to increased glucocorticoid sensitivity in AML. , 2016, , .		0
65	Mutational Landscape of Aggressive Natural Killer Cell Leukemia and Drug Sensitivity Profiling Reveal Therapeutic Options in Natural Killer Cell Malignancies. Blood, 2016, 128, 2921-2921.	1.4	0
66	Novel Mutations in Patients with Blast Crisis or Accelerated Phase Chronic Myeloid Leukemia. Blood, 2016, 128, 1924-1924.	1.4	0
67	Transcriptional Regulatory Landscape of TCF3-PBX1-Positive Leukemia and Novel Targeted Treatments. Blood, 2016, 128, 4077-4077.	1.4	0
68	DNA Damage Repair Pathway Alterations in Multiple Myeloma Predict Poor Prognosis, but Correlate with Sensitivity to IGF1R-PI3K-mTOR and HDAC Inhibitors. Blood, 2016, 128, 198-198.	1.4	0
69	Abstract 424: Landscape of somatic mutations in drug-resistant acute myeloid leukemia. , 2017, , .		0
70	Abstract 410: Identifying ovarian cancer specific targeted drugs using high-throughput drug sensitivity profiles of primary cancer cells. , 2017, , .		0
71	Abstract 5369: Tumorigenesis in Lynch syndrome: Somatic mutation profiles compared to sporadic counterparts. , 2018, , .		0
72	Abstract 3277: Identification of internal tandem duplication within theFLT3gene from AML patient next-generation sequence data. , 2018, , .		0

#	Article	IF	Citations
73	Abstract 2199: Establishment and high-throughput drug testing of multiple patient-derived cells from each renal cancer; intratumor heterogeneity of drug response and implications for precision medicine. , 2018, , .		0
74	Abstract 3899: Discovery and clinical implementation of individualized therapies in acute myeloid leukemia based onex vivodrug sensitivity testing and multi-omics profiling. , 2018, , .		0