Elli Papaemmanuil

List of Publications by Year
in descending order

128 papers	31,030 citations	26630 56 h-index	17592 121 g-index
141 all docs	141 docs citations	141 times ranked	40566 citing authors

#	Article	IF	Citations
1	Prognostic impact of chromosomal abnormalities and copy number alterations in adult B-cell precursor acute lymphoblastic leukaemia: a UKALL14 study. Leukemia, 2022, 36, 625-636.	7.2	25
2	DNA Methylation Profiles of Ovarian Clear Cell Carcinoma. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 132-141.	2.5	12
3	Patient-specific MDS-RS iPSCs define the mis-spliced transcript repertoire and chromatin landscape of SF3B1-mutant HSPCs. Blood Advances, 2022, 6, 2992-3005.	5.2	7
4	Bone Marrow Surveillance of Pediatric Cancer Survivors Identifies Clones that Predict Therapy-Related Leukemia. Clinical Cancer Research, 2022, 28, 1614-1627.	7.0	4
5	â€œRandomized phase II study of azacitidine Â± lenalidomide in higher-risk myelodysplastic syndromes and acute myeloid leukemia with a karyotype including Del(5q)â€• Leukemia, 2022, 36, 1436-1439.	7.2	6
6	Capture Rate of V(D)J Sequencing for Minimal Residual Disease Detection in Multiple Myeloma. Clinical Cancer Research, 2022, 28, 2160-2166.	7.0	2
7	Feasibility of whole genome and transcriptome profiling in pediatric and young adult cancers. Nature Communications, 2022, 13, 2485.	12.8	31
8	Molecular International Prognostic Scoring System for Myelodysplastic Syndromes. , 2022, 1, .		259
9	The clinical implications of clonal hematopoiesis in hematopoietic cell transplantation. Blood Reviews, 2021, 46, 100744.	5.7	16
10	Modulation of IL-6/STAT3 signaling axis in CD4+FOXP3â^' T cells represents a potential antitumor mechanism of azacitidine. Blood Advances, 2021, 5, 129-142.	5.2	7
11	Initial Whole-Genome Sequencing of Plasma Cell Neoplasms in First Responders and Recovery Workers Exposed to the World Trade Center Attack of September 11, 2001. Clinical Cancer Research, 2021, 27, 2111-2118.	7.0	5
12	Interplay between chromosomal alterations and gene mutations shapes the evolutionary trajectory of clonal hematopoiesis. Nature Communications, 2021, 12, 338.	12.8	64
13	Comprehensive Molecular Profiling of Desmoplastic Small Round Cell Tumor. Molecular Cancer Research, 2021, 19, 1146-1155.	3.4	14
14	Recurrent Mutations in Cyclin D3 Confer Clinical Resistance to FLT3 Inhibitors in Acute Myeloid Leukemia. Clinical Cancer Research, 2021, 27, 4003-4011.	7.0	7
15	ZBTB33 Is Mutated in Clonal Hematopoiesis and Myelodysplastic Syndromes and Impacts RNA Splicing. Blood Cancer Discovery, 2021, 2, 500-517.	5.0	17
16	Association of BRAF V600E mutations with vasoactive intestinal peptide syndrome in MYCNâ€amplified neuroblastoma. Pediatric Blood and Cancer, 2021, 68, e29265.	1.5	7
17	PATZ1 fusions define a novel molecularly distinct neuroepithelial tumor entity with a broad histological spectrum. Acta Neuropathologica, 2021, 142, 841-857.	7.7	36
18	Allogeneic Hematopoietic Stem Cell Transplantation for Chronic Myelomonocytic Leukemia: Clinical and Molecular Genetic Prognostic Factors in a Nordic Population. Transplantation and Cellular Therapy, 2021, 27, 991.e1-991.e9.	1.2	6

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19	IKZF1 alterations are not associated with outcome in 498 adults with B-precursor ALL enrolled in the UKALL14 trial. Blood Advances, 2021, 5, 3322-3332.	5.2	7
20	Clonal hematopoiesis is associated with risk of severe Covid-19. Nature Communications, 2021, 12, 5975.	12.8	81
21	Isogenic MDS-RS Patient-Derived iPSCs Define the Mis-Spliced Transcript Repertoire and Chromatin Landscape of SF3B1-Mutant Hematopoietic Stem/Progenitor Cells. Blood, 2021, 138, 147-147.	1.4	0
22	Whole Transcriptome Analysis Identifies Distinct Gene Expression Profiles between SF3B1mut and SF3B1 wt Myelodysplastic Syndrome with Ring Sideroblasts. Blood, 2021, 138, 3695-3695.	1.4	0
23	Role of AID in the temporal pattern of acquisition of driver mutations in multiple myeloma. Leukemia, 2020, 34, 1476-1480.	7.2	39
24	Accelerated single cell seeding in relapsed multiple myeloma. Nature Communications, 2020, 11, 3617.	12.8	41
25	Baseline VDJ clonotype detection using a targeted sequencing NGS assay: allowing for subsequent MRD assessment. Blood Cancer Journal, 2020, 10, 76.	6.2	9
26	Implications of TP53 allelic state for genome stability, clinical presentation and outcomes in myelodysplastic syndromes. Nature Medicine, 2020, 26, 1549-1556.	30.7	372
27	Cancer therapy shapes the fitness landscape of clonal hematopoiesis. Nature Genetics, 2020, 52, 1219-1226.	21.4	367
28	Revealing the Impact of Structural Variants in Multiple Myeloma. Blood Cancer Discovery, 2020, 1, 258-273.	5.0	81
29	Isabl Platform, a digital biobank for processing multimodal patient data. BMC Bioinformatics, 2020, 21, 549.	2.6	26
30	RUNX1-mutated families show phenotype heterogeneity and a somatic mutation profile unique to germline predisposed AML. Blood Advances, 2020, 4, 1131-1144.	5.2	102
31	SF3B1-mutant MDS as a distinct disease subtype: a proposal from the International Working Group for the Prognosis of MDS. Blood, 2020, 136, 157-170.	1.4	195
32	The Clinical Management of Clonal Hematopoiesis. Hematology/Oncology Clinics of North America, 2020, 34, 357-367.	2.2	42
33	11p15.5 epimutations in children with Wilms tumor and hepatoblastoma detected in peripheral blood. Cancer, 2020, 126, 3114-3121.	4.1	23
34	Timing the initiation of multiple myeloma. Nature Communications, 2020, 11, 1917.	12.8	99
35	Clonal Hematopoiesis and COVID-19 Severity in Cancer Patients. Blood, 2020, 136, 37-38.	1.4	1
36	Post-Treatment Clone Size Predicts Survival Independently of IPSS-R and Response after Azacitidine Therapy for MDS.. Blood, 2020, 136, 12-13.	1.4	0

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37	Interplay between Chromosomal Alterations and Gene Mutations Shapes the Evolutionary Trajectory of Clonal Hematopoiesis. Blood, 2020, 136, 29-30.	1.4	0
38	Germline Contributions to Clonal Hematopoiesis in Solid Cancer Patients. Blood, 2020, 136, 30-31.	1.4	1
39	Initial Whole Genome Sequencing of Plasma Cell Neoplasms in First Responders and Recovery Workers Exposed to the World Trade Center Attack of September 11, 2001. Blood, 2020, 136, 50-51.	1.4	0
40	Multifaceted modes of action of azacytidine: a riddle wrapped up in an enigma. Leukemia and Lymphoma, 2019, 60, 3277-3281.	1.3	2
41	Mechanisms of Progression of Myeloid Preleukemia to Transformed Myeloid Leukemia in Children with Down Syndrome. Cancer Cell, 2019, 36, 123-138.e10.	16.8	93
42	Stability and uniqueness of clonal immunoglobulin CDR3 sequences for MRD tracking in multiple myeloma. American Journal of Hematology, 2019, 94, 1364-1373.	4.1	22
43	Pegylated interferon alfa-2a for polycythemia vera or essential thrombocythemia resistant or intolerant to hydroxyurea. Blood, 2019, 134, 1498-1509.	1.4	123
44	Baseline identification of clonal V(D)J sequences for DNA-based minimal residual disease detection in multiple myeloma. PLoS ONE, 2019, 14, e0211600.	2.5	24
45	Contrasting requirements during disease evolution identify EZH2 as a therapeutic target in AML. Journal of Experimental Medicine, 2019, 216, 966-981.	8.5	91
46	Patient-Driven Discovery, Therapeutic Targeting, and Post-Clinical Validation of a Novel AKT1 Fusionâ€“Driven Cancer. Cancer Discovery, 2019, 9, 605-616.	9.4	11
47	Managing Clonal Hematopoiesis in Patients With Solid Tumors. Journal of Clinical Oncology, 2019, 37, 7-11.	1.6	60
48	Molecular underpinnings of clinical disparity patterns in African American vs. Caucasian American multiple myeloma patients. Blood Cancer Journal, 2019, 9, 15.	6.2	30
49	Cohesin-dependent regulation of gene expression during differentiation is lost in cohesin-mutated myeloid malignancies. Blood, 2019, 134, 2195-2208.	1.4	39
50	Epigenetic therapy of myelodysplastic syndromes connects to cellular differentiation independently of endogenous retroelement derepression. Genome Medicine, 2019, 11, 86.	8.2	20
51	Comprehensive detection of recurring genomic abnormalities: a targeted sequencing approach for multiple myeloma. Blood Cancer Journal, 2019, 9, 101.	6.2	40
52	Single cell analysis of clonal architecture in acute myeloid leukaemia. Leukemia, 2019, 33, 1113-1123.	7.2	65
53	TP53 mutation status divides myelodysplastic syndromes with complex karyotypes into distinct prognostic subgroups. Leukemia, 2019, 33, 1747-1758.	7.2	195
54	Prognostic Impact of Chromosomal Abnormalities and Copy Number Alterations Among Adults with B-Cell Precursor Acute Lymphoblastic Leukaemia Treated on UKALL14. Blood, 2019, 134, 288-288.	1.4	6

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55	Genetic and Genomic Characterisation of Older Adults with Acute Lymphoblastic Leukemia Treated on the UKALL14 and UKALL60+ Clinical Trials. Blood, 2019, 134, 2746-2746.	1.4	1
56	Revealing the Impact of Recurrent and Rare Structural Variations in Multiple Myeloma. Blood, 2019, 134, 576-576.	1.4	5
57	Use of Machine Learning in 2074 Cases of Acute Myeloid Leukemia for Genetic Risk Profiling. Blood, 2019, 134, 1392-1392.	1.4	6
58	Single Cell DNA Sequencing Identifies Combinatorial Mutation Patterns and Clonal Architecture in Myeloid Malignancies. Blood, 2019, 134, 913-913.	1.4	1
59	Abnormal oxidative metabolism in a quiet genomic background underlies clear cell papillary renal cell carcinoma. ELife, 2019, 8, .	6.0	31
60	Timing the Initiation of Multiple Myeloma. Blood, 2019, 134, 573-573.	1.4	0
61	Targeted Sequencing Predicts the Development of Myeloid Malignancies and Clinical Outcome in Patients with Unexplained Cytopenia. Blood, 2019, 134, 1712-1712.	1.4	1
62	Molecular Characteristics That Predict Response to Azacitidine Therapy. Blood, 2019, 134, 4246-4246.	1.4	0
63	Ezh2 and Runx1 Mutations Collaborate to Initiate Lympho-Myeloid Leukemia in Early Thymic Progenitors. Cancer Cell, 2018, 33, 274-291.e8.	16.8	58
64	A recurrent novel MGAâ€“NUTM1 fusion identifies a new subtype of high-grade spindle cell sarcoma. Journal of Physical Education and Sports Management, 2018, 4, a003194.	1.2	32
65	Single cell dissection of plasma cell heterogeneity in symptomatic and asymptomatic myeloma. Nature Medicine, 2018, 24, 1867-1876.	30.7	179
66	Classification and Personalized Prognosis in Myeloproliferative Neoplasms. New England Journal of Medicine, 2018, 379, 1416-1430.	27.0	442
67	PHF6 and DNMT3A mutations are enriched in distinct subgroups of mixed phenotype acute leukemia with T-lineage differentiation. Blood Advances, 2018, 2, 3526-3539.	5.2	42
68	Analysis of the genomic landscape of multiple myeloma highlights novel prognostic markers and disease subgroups. Leukemia, 2018, 32, 2604-2616.	7.2	137
69	Prediction of acute myeloid leukaemia risk in healthy individuals. Nature, 2018, 559, 400-404.	27.8	617
70	Impact of spliceosome mutations on RNA splicing in myelodysplasia: dysregulated genes/pathways and clinical associations. Blood, 2018, 132, 1225-1240.	1.4	168
71	Outcomes of Relapsed/Refractory Patients with IDH1/2 Mutated AML Treated with Non-Targeted Therapy: Results from the NCRI AML Trials. Blood, 2018, 132, 664-664.	1.4	2
72	Capture Rate of the Adaptive Next Generation Sequencing VDJ Assay in Multiple Myeloma. Blood, 2018, 132, 3184-3184.	1.4	3

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73	Whole Genome Sequencing of Extramedullary Myeloma Autopsy Tumors Reveals a Genomic Portrait at Culmination of Clonal Convergence. Blood, 2018, 132, 3169-3169.	1.4	1
74	Molecular Predictors and Current Management of Minimal Residual Disease (MRD) Following Induction Chemotherapy for Acute Myeloid Leukemia (AML). Blood, 2018, 132, 292-292.	1.4	1
75	PHF6 Mutations Are Mutually Exclusive to TP53 Mutations, and Define a Distinct Subgroup of Secondary Acute Myeloid Leukemia Associated with a Primitive Stem/Progenitor Immunophenotype, Absent Complex Karyotype and Relatively Better Outcomes. Blood, 2018, 132, 2788-2788.	1.4	0
76	Development of a Data Portal for Aggregation and Analysis of Genomics Data in Familial Platelet Disorder with Predisposition to Myeloid Malignancy - the RUNX1.DB. Blood, 2018, 132, 5241-5241.	1.4	0
77	Modelling the Progression of a Preleukemic Stage to Overt Leukemia in Children with Down Syndrome. Blood, 2018, 132, 543-543.	1.4	1
78	V(D)J Sequence Capture for DNA-Based Minimal Residual Disease Detection in Multiple Myeloma. Blood, 2018, 132, 4444-4444.	1.4	0
79	Mytype: A Capture Based Sequencing Approach to Detect Somatic Mutations, Copy Number Changes and IGH Translocations in Multiple Myeloma. Blood, 2018, 132, 5588-5588.	1.4	0
80	Precision oncology for acute myeloid leukemia using a knowledge bank approach. Nature Genetics, 2017, 49, 332-340.	21.4	229
81	Stage-Specific Human Induced Pluripotent Stem Cells Map the Progression of Myeloid Transformation to Transplantable Leukemia. Cell Stem Cell, 2017, 20, 315-328.e7.	11.1	114
82	Clinical significance of somatic mutation in unexplained blood cytopenia. Blood, 2017, 129, 3371-3378.	1.4	379
83	SF3B1-initiating mutations in MDS-RSs target lymphomyeloid hematopoietic stem cells. Blood, 2017, 130, 881-890.	1.4	66
84	Enasidenib induces acute myeloid leukemia cell differentiation to promote clinical response. Blood, 2017, 130, 732-741.	1.4	300
85	Characterisation of the genomic landscape of CRLF2â€rearranged acute lymphoblastic leukemia. Genes Chromosomes and Cancer, 2017, 56, 363-372.	2.8	49
86	Integrative Genomics Identifies the Molecular Basis of Resistance to Azacitidine Therapy in Myelodysplastic Syndromes. Cell Reports, 2017, 20, 572-585.	6.4	99
87	Persistent Severe Hyperlactatemia and Metabolic Derangement in Lethal SDHB-Mutated Metastatic Kidney Cancer: Clinical Challenges and Examples of Extreme Warburg Effect. JCO Precision Oncology, 2017, 1, 1-14.	3.0	9
88	Baseline mutational patterns and sustained MRD negativity in patients with high-risk smoldering myeloma. Blood Advances, 2017, 1, 1911-1918.	5.2	37
89	Classification and risk assessment in AML: integrating cytogenetics and molecular profiling. Hematology American Society of Hematology Education Program, 2017, 2017, 37-44.	2.5	49
90	Successful Targeted Therapy of Refractory Pediatric ETV6-NTRK3 Fusion-Positive Secretory Breast Carcinoma. JCO Precision Oncology, 2017, 2017, 1-8.	3.0	31

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91	Genomic landscape and evolution of metastatic chromophobe renal cell carcinoma. JCI Insight, 2017, 2, .	5.0	89
92	Genomic Classification in Acute Myeloid Leukemia. New England Journal of Medicine, 2016, 375, 900-901.	27.0	134
93	Direct Transcriptional Consequences of Somatic Mutation in Breast Cancer. Cell Reports, 2016, 16, 2032-2046.	6.4	36
94	Genomic Classification and Prognosis in Acute Myeloid Leukemia. New England Journal of Medicine, 2016, 374, 2209-2221.	27.0	3,067
95	Aberrant splicing of genes involved in haemoglobin synthesis and impaired terminal erythroid maturation in <scp>SF</scp>3B1 mutated refractory anaemia with ring sideroblasts. British Journal of Haematology, 2015, 171, 478-490.	2.5	37
96	Recurrent ETNK1 mutations in atypical chronic myeloid leukemia. Blood, 2015, 125, 499-503.	1.4	115
97	Mechanisms of clonal evolution in childhood acute lymphoblastic leukemia. Nature Immunology, 2015, 16, 766-774.	14.5	163
98	Effect of Mutation Order on Myeloproliferative Neoplasms. New England Journal of Medicine, 2015, 372, 601-612.	27.0	467
99	Combining gene mutation with gene expression data improves outcome prediction in myelodysplastic syndromes. Nature Communications, 2015, 6, 5901.	12.8	196
100	SF3B1 mutation identifies a distinct subset of myelodysplastic syndrome with ring sideroblasts. Blood, 2015, 126, 233-241.	1.4	361
101	Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. Genome Research, 2015, 25, 814-824.	5.5	69
102	The evolutionary history of lethal metastatic prostate cancer. Nature, 2015, 520, 353-357.	27.8	1,185
103	Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer. ELife, 2014, 3, .	6.0	318
104	Processed pseudogenes acquired somatically during cancer development. Nature Communications, 2014, 5, 3644.	12.8	86
105	Subclonal variant calling with multiple samples and prior knowledge. Bioinformatics, 2014, 30, 1198-1204.	4.1	122
106	RAG-mediated recombination is the predominant driver of oncogenic rearrangement in ETV6-RUNX1 acute lymphoblastic leukemia. Nature Genetics, 2014, 46, 116-125.	21.4	313
107	Inactivating CUX1 mutations promote tumorigenesis. Nature Genetics, 2014, 46, 33-38.	21.4	111
108	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. Science, 2014, 345, 1251343.	12.6	348

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109	Association of a germline copy number polymorphism of APOBEC3A and APOBEC3B with burden of putative APOBEC-dependent mutations in breast cancer. Nature Genetics, 2014, 46, 487-491.	21.4	254
110	Driver somatic mutations identify distinct disease entities within myeloid neoplasms with myelodysplasia. Blood, 2014, 124, 1513-1521.	1.4	222
111	Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.	27.8	8,060
112	Clinical and biological implications of driver mutations in myelodysplastic syndromes. Blood, 2013, 122, 3616-3627.	1.4	1,562
113	Recurrent SETBP1 mutations in atypical chronic myeloid leukemia. Nature Genetics, 2013, 45, 18-24.	21.4	359
114	Single-cell mutational profiling and clonal phylogeny in cancer. Genome Research, 2013, 23, 2115-2125.	5.5	105
115	The transporter ABCB7 is a mediator of the phenotype of acquired refractory anemia with ring sideroblasts. Leukemia, 2013, 27, 889-896.	7.2	89
116	Inappropriately low hepcidin levels in patients with myelodysplastic syndrome carrying a somatic mutation of SF3B1. Haematologica, 2013, 98, 420-423.	3.5	51
117	Whole exome sequencing of adenoid cystic carcinoma. Journal of Clinical Investigation, 2013, 123, 2965-2968.	8.2	233
118	The landscape of cancer genes and mutational processes in breast cancer. Nature, 2012, 486, 400-404.	27.8	1,535
119	Mutational Processes Molding the Genomes of 21 Breast Cancers. Cell, 2012, 149, 979-993.	28.9	1,673
120	The Life History of 21 Breast Cancers. Cell, 2012, 149, 994-1007.	28.9	1,249
121	Clinical significance of SF3B1 mutations in myelodysplastic syndromes and myelodysplastic/myeloproliferative neoplasms. Blood, 2011, 118, 6239-6246.	1.4	457
122	Identification of Novel Somatic Mutations in SF3B1, a Gene Encoding a Core Component of RNA Splicing Machinery, in Myelodysplasia with Ring Sideroblasts and Other Common Cancers. European Journal of Cancer, 2011, 47, 7.	2.8	3
123	SomaticSF3B1Mutation in Myelodysplasia with Ring Sideroblasts. New England Journal of Medicine, 2011, 365, 1384-1395.	27.0	1,094
124	MHC variation and risk of childhood B-cell precursor acute lymphoblastic leukemia. Blood, 2011, 117, 1633-1640.	1.4	24
125	Verification of the susceptibility loci on 7p12.2, 10q21.2, and 14q11.2 in precursor B-cell acute lymphoblastic leukemia of childhood. Blood, 2010, 115, 1765-1767.	1.4	142
126	Genome-wide homozygosity signatures and childhood acute lymphoblastic leukemia risk. Blood, 2010, 115, 4472-4477.	1.4	36

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127	Variation in CDKN2A at 9p21.3 influences childhood acute lymphoblastic leukemia risk. Nature Genetics, 2010, 42, 492-494.	21.4	248
128	Loci on 7p12.2, 10q21.2 and 14q11.2 are associated with risk of childhood acute lymphoblastic leukemia. Nature Genetics, 2009, 41, 1006-1010.	21.4	445