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	Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.	27.8	8,060
2	Genomic Classification and Prognosis in Acute Myeloid Leukemia. New England Journal of Medicine, 2016, 374, 2209-2221.	27.0	3,067
3	Mutational Processes Molding the Genomes of 21 Breast Cancers. Cell, 2012, 149, 979-993.	28.9	1,673
4	Clinical and biological implications of driver mutations in myelodysplastic syndromes. Blood, 2013, 122, 3616-3627.	1.4	1,562
5	The landscape of cancer genes and mutational processes in breast cancer. Nature, 2012, 486, 400-404.	27.8	1,535
6	The Life History of 21 Breast Cancers. Cell, 2012, 149, 994-1007.	28.9	1,249
7	The evolutionary history of lethal metastatic prostate cancer. Nature, 2015, 520, 353-357.	27.8	1,185
8	SomaticSF3B1Mutation in Myelodysplasia with Ring Sideroblasts. New England Journal of Medicine, 2011, 365, 1384-1395.	27.0	1,094
9	Prediction of acute myeloid leukaemia risk in healthy individuals. Nature, 2018, 559, 400-404.	27.8	617
10	Effect of Mutation Order on Myeloproliferative Neoplasms. New England Journal of Medicine, 2015, 372, 601-612.	27.0	467
11	Clinical significance of SF3B1 mutations in myelodysplastic syndromes and myelodysplastic/myeloproliferative neoplasms. Blood, 2011, 118, 6239-6246.	1.4	457
12	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
13	Classification and Personalized Prognosis in Myeloproliferative Neoplasms. New England Journal of Medicine, 2018, 379, 1416-1430.	27.0	442
14	Clinical significance of somatic mutation in unexplained blood cytopenia. Blood, 2017, 129, 3371-3378.	1.4	379
15	Implications of TP53 allelic state for genome stability, clinical presentation and outcomes in myelodysplastic syndromes. Nature Medicine, 2020, 26, 1549-1556.	30.7	372
16	Cancer therapy shapes the fitness landscape of clonal hematopoiesis. Nature Genetics, 2020, 52, 1219-1226.	21.4	367
17	SF3B1 mutation identifies a distinct subset of myelodysplastic syndrome with ring sideroblasts. Blood, 2015, 126, 233-241.	1.4	361
18	Recurrent SETBP1 mutations in atypical chronic myeloid leukemia. Nature Genetics, 2013, 45, 18-24.	21.4	359

#	Article	IF	Citations
19	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. Science, 2014, 345, 1251343.	12.6	348
20	Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer. ELife, 2014, 3, .	6.0	318
21	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
22	Enasidenib induces acute myeloid leukemia cell differentiation to promote clinical response. Blood, 2017, 130, 732-741.	1.4	300
23	Molecular International Prognostic Scoring System for Myelodysplastic Syndromes. , 2022, 1, .		259
24	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
25	Variation in CDKN2A at 9p21.3 influences childhood acute lymphoblastic leukemia risk. Nature Genetics, 2010, 42, 492-494.	21.4	248
26	Whole exome sequencing of adenoid cystic carcinoma. Journal of Clinical Investigation, 2013, 123, 2965-2968.	8.2	233
27	Precision oncology for acute myeloid leukemia using a knowledge bank approach. Nature Genetics, 2017, 49, 332-340.	21.4	229
28	Driver somatic mutations identify distinct disease entities within myeloid neoplasms with myelodysplasia. Blood, 2014, 124, 1513-1521.	1.4	222
29	Combining gene mutation with gene expression data improves outcome prediction in myelodysplastic syndromes. Nature Communications, 2015, 6, 5901.	12.8	196
30	TP53 mutation status divides myelodysplastic syndromes with complex karyotypes into distinct prognostic subgroups. Leukemia, 2019, 33, 1747-1758.	7.2	195
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	Single cell dissection of plasma cell heterogeneity in symptomatic and asymptomatic myeloma. Nature Medicine, 2018, 24, 1867-1876.	30.7	179
33	Impact of spliceosome mutations on RNA splicing in myelodysplasia: dysregulated genes/pathways and clinical associations. Blood, 2018, 132, 1225-1240.	1.4	168
34	Mechanisms of clonal evolution in childhood acute lymphoblastic leukemia. Nature Immunology, 2015, 16, 766-774.	14.5	163
35	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
36	Analysis of the genomic landscape of multiple myeloma highlights novel prognostic markers and disease subgroups. Leukemia, 2018, 32, 2604-2616.	7.2	137

#	Article	IF	Citations
37	Genomic Classification in Acute Myeloid Leukemia. New England Journal of Medicine, 2016, 375, 900-901.	27.0	134
38	Pegylated interferon alfa-2a for polycythemia vera or essential thrombocythemia resistant or intolerant to hydroxyurea. Blood, 2019, 134, 1498-1509.	1.4	123
39	Subclonal variant calling with multiple samples and prior knowledge. Bioinformatics, 2014, 30, 1198-1204.	4.1	122
40	Recurrent ETNK1 mutations in atypical chronic myeloid leukemia. Blood, 2015, 125, 499-503.	1.4	115
41	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
42	Inactivating CUX1 mutations promote tumorigenesis. Nature Genetics, 2014, 46, 33-38.	21.4	111
43	Single-cell mutational profiling and clonal phylogeny in cancer. Genome Research, 2013, 23, 2115-2125.	5.5	105
44	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
45	Integrative Genomics Identifies the Molecular Basis of Resistance to Azacitidine Therapy in Myelodysplastic Syndromes. Cell Reports, 2017, 20, 572-585.	6.4	99
46	Timing the initiation of multiple myeloma. Nature Communications, 2020, 11, 1917.	12.8	99
47	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
48	Contrasting requirements during disease evolution identify EZH2 as a therapeutic target in AML. Journal of Experimental Medicine, 2019, 216, 966-981.	8.5	91
49	The transporter ABCB7 is a mediator of the phenotype of acquired refractory anemia with ring sideroblasts. Leukemia, 2013, 27, 889-896.	7.2	89
50	Genomic landscape and evolution of metastatic chromophobe renal cell carcinoma. JCI Insight, 2017, 2, .	5.0	89
51	Processed pseudogenes acquired somatically during cancer development. Nature Communications, 2014, 5, 3644.	12.8	86
52	Revealing the Impact of Structural Variants in Multiple Myeloma. Blood Cancer Discovery, 2020, 1, 258-273.	5.0	81
53	Clonal hematopoiesis is associated with risk of severe Covid-19. Nature Communications, 2021, 12, 5975.	12.8	81
54	Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. Genome Research, 2015, 25, 814-824.	5.5	69

#	Article	IF	Citations
55	SF3B1-initiating mutations in MDS-RSs target lymphomyeloid hematopoietic stem cells. Blood, 2017, 130, 881-890.	1.4	66
56	Single cell analysis of clonal architecture in acute myeloid leukaemia. Leukemia, 2019, 33, 1113-1123.	7.2	65
57	Interplay between chromosomal alterations and gene mutations shapes the evolutionary trajectory of clonal hematopoiesis. Nature Communications, 2021, 12, 338.	12.8	64
58	Managing Clonal Hematopoiesis in Patients With Solid Tumors. Journal of Clinical Oncology, 2019, 37, 7-11.	1.6	60
59	Ezh2 and Runx1 Mutations Collaborate to Initiate Lympho-Myeloid Leukemia in Early Thymic Progenitors. Cancer Cell, 2018, 33, 274-291.e8.	16.8	58
60	Inappropriately low hepcidin levels in patients with myelodysplastic syndrome carrying a somatic mutation of SF3B1. Haematologica, 2013, 98, 420-423.	3.5	51
61	Characterisation of the genomic landscape of CRLF2â€rearranged acute lymphoblastic leukemia. Genes Chromosomes and Cancer, 2017, 56, 363-372.	2.8	49
62	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
63	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
64	The Clinical Management of Clonal Hematopoiesis. Hematology/Oncology Clinics of North America, 2020, 34, 357-367.	2.2	42
65	Accelerated single cell seeding in relapsed multiple myeloma. Nature Communications, 2020, 11, 3617.	12.8	41
66	Comprehensive detection of recurring genomic abnormalities: a targeted sequencing approach for multiple myeloma. Blood Cancer Journal, 2019, 9, 101.	6.2	40
67	Cohesin-dependent regulation of gene expression during differentiation is lost in cohesin-mutated myeloid malignancies. Blood, 2019, 134, 2195-2208.	1.4	39
68	Role of AID in the temporal pattern of acquisition of driver mutations in multiple myeloma. Leukemia, 2020, 34, 1476-1480.	7.2	39
69	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
70	Baseline mutational patterns and sustained MRD negativity in patients with high-risk smoldering myeloma. Blood Advances, 2017, 1, 1911-1918.	5.2	37
71	Genome-wide homozygosity signatures and childhood acute lymphoblastic leukemia risk. Blood, 2010, 115, 4472-4477.	1.4	36
72	Direct Transcriptional Consequences of Somatic Mutation in Breast Cancer. Cell Reports, 2016, 16, 2032-2046.	6.4	36

#	Article	IF	Citations
73	PATZ1 fusions define a novel molecularly distinct neuroepithelial tumor entity with a broad histological spectrum. Acta Neuropathologica, 2021, 142, 841-857.	7.7	36
74	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
75	Successful Targeted Therapy of Refractory Pediatric ETV6-NTRK3 Fusion-Positive Secretory Breast Carcinoma. JCO Precision Oncology, 2017, 2017, 1-8.	3.0	31
76	Abnormal oxidative metabolism in a quiet genomic background underlies clear cell papillary renal cell carcinoma. ELife, 2019, 8, .	6.0	31
77	Feasibility of whole genome and transcriptome profiling in pediatric and young adult cancers. Nature Communications, 2022, 13, 2485.	12.8	31
78	Molecular underpinnings of clinical disparity patterns in African American vs. Caucasian American multiple myeloma patients. Blood Cancer Journal, 2019, 9, 15.	6.2	30
79	Isabl Platform, a digital biobank for processing multimodal patient data. BMC Bioinformatics, 2020, 21, 549.	2.6	26
80	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
81	MHC variation and risk of childhood B-cell precursor acute lymphoblastic leukemia. Blood, 2011, 117, 1633-1640.	1.4	24
82	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
83	11p15.5 epimutations in children with Wilms tumor and hepatoblastoma detected in peripheral blood. Cancer, 2020, 126, 3114-3121.	4.1	23
84	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
85	Epigenetic therapy of myelodysplastic syndromes connects to cellular differentiation independently of endogenous retroelement derepression. Genome Medicine, 2019, 11, 86.	8.2	20
86	ZBTB33 Is Mutated in Clonal Hematopoiesis and Myelodysplastic Syndromes and Impacts RNA Splicing. Blood Cancer Discovery, 2021, 2, 500-517.	5.0	17
87	The clinical implications of clonal hematopoiesis in hematopoietic cell transplantation. Blood Reviews, 2021, 46, 100744.	5.7	16
88	Comprehensive Molecular Profiling of Desmoplastic Small Round Cell Tumor. Molecular Cancer Research, 2021, 19, 1146-1155.	3.4	14
89	DNA Methylation Profiles of Ovarian Clear Cell Carcinoma. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 132-141.	2.5	12
90	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

#	Article	IF	Citations
91	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
92	Baseline VDJ clonotype detection using a targeted sequencing NGS assay: allowing for subsequent MRD assessment. Blood Cancer Journal, 2020, 10, 76.	6.2	9
93	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
94	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
95	Association of BRAF V600E mutations with vasoactive intestinal peptide syndrome in MYCNâ€amplified neuroblastoma. Pediatric Blood and Cancer, 2021, 68, e29265.	1.5	7
96	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
97	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
98	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
99	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
100	Use of Machine Learning in 2074 Cases of Acute Myeloid Leukemia for Genetic Risk Profiling. Blood, 2019, 134, 1392-1392.	1.4	6
101	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
102	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
103	Revealing the Impact of Recurrent and Rare Structural Variations in Multiple Myeloma. Blood, 2019, 134, 576-576.	1.4	5
104	Bone Marrow Surveillance of Pediatric Cancer Survivors Identifies Clones that Predict Therapy-Related Leukemia. Clinical Cancer Research, 2022, 28, 1614-1627.	7.0	4
105	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
106	Capture Rate of the Adaptive Next Generation Sequencing VDJ Assay in Multiple Myeloma. Blood, 2018, 132, 3184-3184.	1.4	3
107	Multifaceted modes of action of azacytidine: a riddle wrapped up in an enigma. Leukemia and Lymphoma, 2019, 60, 3277-3281.	1.3	2
108	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

#	Article	IF	Citations
109	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
110	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
111	Single Cell DNA Sequencing Identifies Combinatorial Mutation Patterns and Clonal Architecture in Myeloid Malignancies. Blood, 2019, 134, 913-913.	1.4	1
112	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
113	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
114	Modelling the Progression of a Preleukemic Stage to Overt Leukemia in Children with Down Syndrome. Blood, 2018, 132, 543-543.	1.4	1
115	Targeted Sequencing Predicts the Development of Myeloid Malignancies and Clinical Outcome in Patients with Unexplained Cytopenia. Blood, 2019, 134, 1712-1712.	1.4	1
116	Clonal Hematopoiesis and COVID-19 Severity in Cancer Patients. Blood, 2020, 136, 37-38.	1.4	1
117	Germline Contributions to Clonal Hematopoiesis in Solid Cancer Patients. Blood, 2020, 136, 30-31.	1.4	1
118	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
119	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
120	V(D)J Sequence Capture for DNA-Based Minimal Residual Disease Detection in Multiple Myeloma. Blood, 2018, 132, 4444-4444.	1.4	0
121	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
122	Timing the Initiation of Multiple Myeloma. Blood, 2019, 134, 573-573.	1.4	0
123	Molecular Characteristics That Predict Response to Azacitidine Therapy. Blood, 2019, 134, 4246-4246.	1.4	0
124	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
125	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
126	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

#	Article	IF	Citations
127	Interplay between Chromosomal Alterations and Gene Mutations Shapes the Evolutionary Trajectory of Clonal Hematopoiesis. Blood, 2020, 136, 29-30.	1.4	0
128	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