

# George S Vassiliou

## List of Publications by Year in descending order

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Version: 2024-02-01

93  
papers

11,388  
citations

81900

39  
h-index

46799

89  
g-index

108  
all docs

108  
docs citations

108  
times ranked

15586  
citing authors

#	ARTICLE	IF	CITATIONS
1	Acquired mutation of the tyrosine kinase JAK2 in human myeloproliferative disorders. <i>Lancet</i> , The, 2005, 365, 1054-1061.	13.7	3,100
2	Promoter-bound METTL3 maintains myeloid leukaemia by m6A-dependent translation control. <i>Nature</i> , 2017, 552, 126-131.	27.8	833
3	Prediction of acute myeloid leukaemia risk in healthy individuals. <i>Nature</i> , 2018, 559, 400-404.	27.8	617
4	A CRISPR Dropout Screen Identifies Genetic Vulnerabilities and Therapeutic Targets in Acute Myeloid Leukemia. <i>Cell Reports</i> , 2016, 17, 1193-1205.	6.4	556
5	Small-molecule inhibition of METTL3 as a strategy against myeloid leukaemia. <i>Nature</i> , 2021, 593, 597-601.	27.8	531
6	Effect of Mutation Order on Myeloproliferative Neoplasms. <i>New England Journal of Medicine</i> , 2015, 372, 601-612.	27.0	467
7	Leukemia-Associated Somatic Mutations Drive Distinct Patterns of Age-Related Clonal Hemopoiesis. <i>Cell Reports</i> , 2015, 10, 1239-1245.	6.4	443
8	Evolutionary routes and KRAS dosage define pancreatic cancer phenotypes. <i>Nature</i> , 2018, 554, 62-68.	27.8	328
9	PPM1D Mutations Drive Clonal Hematopoiesis in Response to Cytotoxic Chemotherapy. <i>Cell Stem Cell</i> , 2018, 23, 700-713.e6.	11.1	272
10	<i>PiggyBac</i> Transposon Mutagenesis: A Tool for Cancer Gene Discovery in Mice. <i>Science</i> , 2010, 330, 1104-1107.	12.6	217
11	Mutant nucleophosmin and cooperating pathways drive leukemia initiation and progression in mice. <i>Nature Genetics</i> , 2011, 43, 470-475.	21.4	194
12	A Genetic Progression Model of BrafV600E-Induced Intestinal Tumorigenesis Reveals Targets for Therapeutic Intervention. <i>Cancer Cell</i> , 2013, 24, 15-29.	16.8	183
13	CRISPR/Cas9 somatic multiplex-mutagenesis for high-throughput functional cancer genomics in mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13982-13987.	7.1	172
14	Targeting Chromatin Regulators Inhibits Leukemogenic Gene Expression in <i>NPM1</i> Mutant Leukemia. <i>Cancer Discovery</i> , 2016, 6, 1166-1181.	9.4	171
15	Clonal dynamics of haematopoiesis across the human lifespan. <i>Nature</i> , 2022, 606, 343-350.	27.8	160
16	Clonal heterogeneity of acute myeloid leukemia treated with the IDH2 inhibitor enasidenib. <i>Nature Medicine</i> , 2018, 24, 1167-1177.	30.7	157
17	METTL1-mediated m7G modification of Arg-TCT tRNA drives oncogenic transformation. <i>Molecular Cell</i> , 2021, 81, 3323-3338.e14.	9.7	153
18	Acute myeloid leukaemia: a paradigm for the clonal evolution of cancer?. <i>DMM Disease Models and Mechanisms</i> , 2014, 7, 941-951.	2.4	148

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19	Therapeutic targeting of preleukemia cells in a mouse model of <i>NPM1</i> mutant acute myeloid leukemia. <i>Science</i> , 2020, 367, 586-590.	12.6	145
20	The longitudinal dynamics and natural history of clonal haematopoiesis. <i>Nature</i> , 2022, 606, 335-342.	27.8	136
21	Network properties derived from deep sequencing of human B-cell receptor repertoires delineate B-cell populations. <i>Genome Research</i> , 2013, 23, 1874-1884.	5.5	128
22	UTX-mediated enhancer and chromatin remodeling suppresses myeloid leukemogenesis through noncatalytic inverse regulation of ETS and GATA programs. <i>Nature Genetics</i> , 2018, 50, 883-894.	21.4	117
23	Glutaminolysis is a metabolic dependency in FLT3ITD acute myeloid leukemia unmasked by FLT3 tyrosine kinase inhibition. <i>Blood</i> , 2018, 131, 1639-1653.	1.4	114
24	Genome-wide analyses of 200,453 individuals yield new insights into the causes and consequences of clonal hematopoiesis. <i>Nature Genetics</i> , 2022, 54, 1155-1166.	21.4	109
25	HBO1 is required for the maintenance of leukaemia stem cells. <i>Nature</i> , 2020, 577, 266-270.	27.8	105
26	Contrasting requirements during disease evolution identify EZH2 as a therapeutic target in AML. <i>Journal of Experimental Medicine</i> , 2019, 216, 966-981.	8.5	91
27	Promiscuous targeting of bromodomains by bromosporine identifies BET proteins as master regulators of primary transcription response in leukemia. <i>Science Advances</i> , 2016, 2, e1600760.	10.3	90
28	A conditional piggyBac transposition system for genetic screening in mice identifies oncogenic networks in pancreatic cancer. <i>Nature Genetics</i> , 2015, 47, 47-56.	21.4	77
29	Activity of a heptad of transcription factors is associated with stem cell programs and clinical outcome in acute myeloid leukemia. <i>Blood</i> , 2013, 121, 2289-2300.	1.4	72
30	The long non-coding RNA HOXB-AS3 regulates ribosomal RNA transcription in NPM1-mutated acute myeloid leukemia. <i>Nature Communications</i> , 2019, 10, 5351.	12.8	71
31	Mutant calreticulin knockin mice develop thrombocytosis and myelofibrosis without a stem cell self-renewal advantage. <i>Blood</i> , 2018, 131, 649-661.	1.4	70
32	TET2 binding to enhancers facilitates transcription factor recruitment in hematopoietic cells. <i>Genome Research</i> , 2019, 29, 564-575.	5.5	66
33	Molecular synergy underlies the co-occurrence patterns and phenotype of NPM1-mutant acute myeloid leukemia. <i>Blood</i> , 2017, 130, 1911-1922.	1.4	63
34	Capturing needles in haystacks: a comparison of B-cell receptor sequencing methods. <i>BMC Immunology</i> , 2014, 15, 29.	2.2	62
35	SRPK1 maintains acute myeloid leukemia through effects on isoform usage of epigenetic regulators including BRD4. <i>Nature Communications</i> , 2018, 9, 5378.	12.8	60
36	Synergistic targeting of <i>FLT3</i> mutations in AML via combined menin-MLL and FLT3 inhibition. <i>Blood</i> , 2020, 136, 2442-2456.	1.4	59

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37	A single-copy Sleeping Beauty transposon mutagenesis screen identifies new PTEN-cooperating tumor suppressor genes. <i>Nature Genetics</i> , 2017, 49, 730-741.	21.4	53
38	Development and validation of a comprehensive genomic diagnostic tool for myeloid malignancies. <i>Blood</i> , 2016, 128, e1-e9.	1.4	49
39	Characterization of gene mutations and copy number changes in acute myeloid leukemia using a rapid target enrichment protocol. <i>Haematologica</i> , 2015, 100, 214-222.	3.5	43
40	Aging as a driver of leukemogenesis. <i>Science Translational Medicine</i> , 2015, 7, 306fs38.	12.4	42
41	JAK2 V617F hematopoietic clones are present several years prior to MPN diagnosis and follow different expansion kinetics. <i>Blood Advances</i> , 2017, 1, 968-971.	5.2	42
42	The Cancer Therapy-Related Clonal Hematopoiesis Driver Gene <i>Ppm1d</i> Promotes Inflammation and Non-Ischemic Heart Failure in Mice. <i>Circulation Research</i> , 2021, 129, 684-698.	4.5	42
43	Genome-wide transposon screening and quantitative insertion site sequencing for cancer gene discovery in mice. <i>Nature Protocols</i> , 2017, 12, 289-309.	12.0	41
44	Concordance for clonal hematopoiesis is limited in elderly twins. <i>Blood</i> , 2020, 135, 269-273.	1.4	38
45	PiggyBac transposon tools for recessive screening identify B-cell lymphoma drivers in mice. <i>Nature Communications</i> , 2019, 10, 1415.	12.8	37
46	Clinical relevance of clonal hematopoiesis in persons aged ≥80 years. <i>Blood</i> , 2021, 138, 2093-2105.	1.4	37
47	Genetic modification of primary human B cells to model high-grade lymphoma. <i>Nature Communications</i> , 2019, 10, 4543.	12.8	36
48	A novel mouse model identifies cooperating mutations and therapeutic targets critical for chronic myeloid leukemia progression. <i>Journal of Experimental Medicine</i> , 2015, 212, 1551-1569.	8.5	35
49	Enhancing the genome editing toolbox: genome wide CRISPR arrayed libraries. <i>Scientific Reports</i> , 2017, 7, 2244.	3.3	35
50	SOCS2 is part of a highly prognostic 4-gene signature in AML and promotes disease aggressiveness. <i>Scientific Reports</i> , 2019, 9, 9139.	3.3	34
51	Preventing chemotherapy-induced myelosuppression by repurposing the FLT3 inhibitor quizartinib. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	33
52	Vitamin D Receptor Controls Cell Stemness in Acute Myeloid Leukemia and in Normal Bone Marrow. <i>Cell Reports</i> , 2020, 30, 739-754.e4.	6.4	32
53	meCLICK-Seq, a Substrate-Hijacking and RNA Degradation Strategy for the Study of RNA Methylation. <i>ACS Central Science</i> , 2020, 6, 2196-2208.	11.3	31
54	Targeting MEK in vemurafenib-resistant hairy cell leukemia. <i>Leukemia</i> , 2019, 33, 541-545.	7.2	26

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55	KAT7 is a genetic vulnerability of acute myeloid leukemias driven by MLL rearrangements. <i>Leukemia</i> , 2021, 35, 1012-1022.	7.2	26
56	Analysis pipelines for cancer genome sequencing in mice. <i>Nature Protocols</i> , 2020, 15, 266-315.	12.0	25
57	Combined Influence of B-Cell Receptor Rearrangement and Somatic Hypermutation on B-Cell Class-Switch Fate in Health and in Chronic Lymphocytic Leukemia. <i>Frontiers in Immunology</i> , 2018, 9, 1784.	4.8	22
58	Mutational synergy during leukemia induction remodels chromatin accessibility, histone modifications and three-dimensional DNA topology to alter gene expression. <i>Nature Genetics</i> , 2021, 53, 1443-1455.	21.4	19
59	PiggyBac mutagenesis and exome sequencing identify genetic driver landscapes and potential therapeutic targets of EGFR-mutant gliomas. <i>Genome Biology</i> , 2020, 21, 181.	8.8	18
60	Pharmacological Inhibition of the RNA m6a Writer METTL3 As a Novel Therapeutic Strategy for Acute Myeloid Leukemia. <i>Blood</i> , 2019, 134, 403-403.	1.4	18
61	Controlled masking and targeted release of redox-cycling ortho-quinones via a C-C bond-cleaving 1,6-elimination. <i>Nature Chemistry</i> , 2022, 14, 754-765.	13.6	18
62	Detection of cytoplasmic nucleophosmin expression by imaging flow cytometry. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2012, 81A, 896-900.	1.5	15
63	STAT1 is essential for HSC function and maintains MHCIIhi stem cells that resist myeloablation and neoplastic expansion. <i>Blood</i> , 2022, 140, 1592-1606.	1.4	15
64	NPM1c alters FLT3-D835Y localization and signaling in acute myeloid leukemia. <i>Blood</i> , 2019, 134, 383-388.	1.4	14
65	Dissecting the early steps of MLL induced leukaemogenic transformation using a mouse model of AML. <i>Nature Communications</i> , 2020, 11, 1407.	12.8	13
66	RNAmut: robust identification of somatic mutations in acute myeloid leukemia using RNA-sequencing. <i>Haematologica</i> , 2020, 105, e290-e293.	3.5	13
67	A macaque clonal hematopoiesis model demonstrates expansion of TET2-disrupted clones and utility for testing interventions. <i>Blood</i> , 2022, 140, 1774-1789.	1.4	13
68	Clonal haematopoiesis is not prevalent in survivors of childhood cancer. <i>British Journal of Haematology</i> , 2018, 181, 537-539.	2.5	12
69	<i>IL2RA</i> Promotes Aggressiveness and Stem Cell-Related Properties of Acute Myeloid Leukemia. <i>Cancer Research</i> , 2020, 80, 4527-4539.	0.9	12
70	SETBP1 overexpression acts in the place of class-defining mutations to drive FLT3-ITD mutant AML. <i>Blood Advances</i> , 2021, 5, 2412-2425.	5.2	10
71	Clonal hematopoiesis is not significantly associated with COVID-19 disease severity. <i>Blood</i> , 2022, 140, 1650-1655.	1.4	10
72	JAK2 V617F clonal disorders: fate or chance?. <i>Blood</i> , 2016, 128, 1032-1033.	1.4	9

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73	Genetic Vulnerabilities of DNMT3AR882H in Myeloid Malignancies. <i>Blood</i> , 2019, 134, 111-111.	1.4	8
74	Recurrent histone mutations in Tâ€œcell acute lymphoblastic leukaemia. <i>British Journal of Haematology</i> , 2019, 184, 676-679.	2.5	7
75	Identification of a germline F692L drug resistance variant in cis with Flt3-internal tandem duplication in knock-in mice. <i>Haematologica</i> , 2016, 101, e328-e331.	3.5	5
76	The curious incident of TdT-mediated mutations in AML. <i>Blood</i> , 2019, 134, 2229-2231.	1.4	5
77	Evi1 Counteracts Anti-Leukemic and Stem Cell Inhibitory Effects of All-Trans Retinoic Acid on Flt3-ITD/Npm1c-Driven Acute Myeloid Leukemia Cells. <i>Biomedicines</i> , 2020, 8, 385.	3.2	4
78	Rapid parallel acquisition of somatic mutations after <i><scp>NPM</scp>1</i> in acute myeloid leukaemia evolution. <i>British Journal of Haematology</i> , 2017, 176, 825-829.	2.5	3
79	Genome-scale drop-out screens to identify cancer cell vulnerabilities in AML. <i>Current Opinion in Genetics and Development</i> , 2019, 54, 83-87.	3.3	3
80	Home and away: clonal hematopoiesis in sibling transplants. <i>Blood</i> , 2020, 135, 1511-1512.	1.4	3
81	Mouse Models of Myeloid Malignancies. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2021, 11, a035535.	6.2	3
82	The<i>CADM1</i> tumor suppressor gene is a major candidate gene in MDS with deletion of the long arm of chromosome 11. <i>Blood Advances</i> , 2022, 6, 386-398.	5.2	3
83	An acquired translocation in JAK2 Val617Phe-negative essential thrombocythemia associated with autosomal spread of X-inactivation. <i>Haematologica</i> , 2006, 91, 1100-4.	3.5	3
84	NPM1 gene mutations can be confidently identified in blood DNA months before de novo AML onset. <i>Blood Advances</i> , 2022, 6, 2409-2413.	5.2	3
85	Mutational Synergy Coordinately Remodels Chromatin Accessibility, Enhancer Landscape and 3-Dimensional DNA Topology to Alter Gene Expression during Leukemia Induction. <i>Blood</i> , 2019, 134, 278-278.	1.4	2
86	Combinatorial genetics reveals the Dock1-Rac2 axis as a potential target for the treatment of NPM1;Cohesin mutated AML. <i>Leukemia</i> , 2022, 36, 2032-2041.	7.2	2
87	Design and Application of Multiplex PCR Seq for the Detection of Somatic Mutations Associated with Myeloid Malignancies. <i>Methods in Molecular Biology</i> , 2017, 1633, 87-99.	0.9	1
88	Triple-mutant AML: too clever by HLF?. <i>Blood</i> , 2019, 134, 222-224.	1.4	1
89	Npm1 Haploinsufficiency in collaboration with MEIS1 is sufficient to induce AML in mice. <i>Blood Advances</i> , 2022, , .	5.2	1
90	The PML-RARA fusion is not detectable in historical blood samples of acute promyelocytic leukaemia patients. <i>Annals of Hematology</i> , 2021, , 1.	1.8	0

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91	Abstract 391: Evolutionary trajectories andKRASgene dosage define pancreatic cancer phenotypes. , 2018, , .		0
92	High Prevalence of PPM1D Mutations in Therapy-Related AML/MDS Is Due to Context-Specific Clonal Hematopoiesis. Blood, 2018, 132, 746-746.	1.4	0
93	Abstract 3841: Therapeutic targeting of<i>FLT3</i> mutations in AML via menin-MLL1 and FLT3 inhibition. , 2019, , .		0