

George Vasmatzis

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

105
papers

2,997
citations

29
h-index

53
g-index

107
ext. papers

3,552
ext. citations

4.5
avg, IF

4.71
L-index

#	Paper	IF	Citations
105	Identification of EWSR1 rearrangements in patients with immature hematopoietic neoplasms: A case series and review of literature.. <i>Annals of Diagnostic Pathology</i> , 2022 , 58, 151942	2.2	0
104	Utilizing next-generation sequencing to characterize a case of acute myeloid leukemia with t(4;12)(q12;p13) in the absence of ETV6/CHIC2 and ETV6/PDGFR A gene fusions. <i>Cancer Genetics</i> , 2021 , 260-261, 1-5	2.3	
103	Tumor Junction Burden and Antigen Presentation as Predictors of Survival in Mesothelioma Treated With Immune Checkpoint Inhibitors. <i>Journal of Thoracic Oncology</i> , 2021 ,	8.9	3
102	The Role of Hydrophobicity in Peptide-MHC Binding. <i>Lecture Notes in Computer Science</i> , 2021 , 24-37	0.9	0
101	In search for biomarkers and potential drug targets for uterine serous endometrial cancer. <i>Journal of Cancer Research and Clinical Oncology</i> , 2021 , 147, 1647-1658	4.9	2
100	Theragnostic chromosomal rearrangements in treatment-naive pancreatic ductal adenocarcinomas obtained via endoscopic ultrasound. <i>Journal of Cellular and Molecular Medicine</i> , 2021 , 25, 4110-4123	5.6	1
99	Chromosomal Junction Detection from Whole-Genome Sequencing on Formalin-Fixed, Paraffin-Embedded Tumors. <i>Journal of Molecular Diagnostics</i> , 2021 , 23, 375-388	5.1	
98	Personalized tumor-specific DNA junctions to detect circulating tumor in patients with endometrial cancer. <i>PLoS ONE</i> , 2021 , 16, e0252390	3.7	0
97	Assessment of isochromosome 12p and 12p abnormalities in germ cell tumors using fluorescence in situ hybridization, single-nucleotide polymorphism arrays, and next-generation sequencing/mate-pair sequencing. <i>Human Pathology</i> , 2021 , 112, 20-34	3.7	2
96	Biology and grading of pleomorphic xanthoastrocytoma-what have we learned about it?. <i>Brain Pathology</i> , 2021 , 31, 20-32	6	8
95	Detection of a Cryptic EP300/ZNF384 Gene Fusion by Chromosomal Microarray and Next-Generation Sequencing Studies in a Pediatric Patient with B-Lymphoblastic Leukemia. <i>Laboratory Medicine</i> , 2021 , 52, 297-302	1.6	
94	Identification of a novel KMT2A/GIMAP8 gene fusion in a pediatric patient with acute undifferentiated leukemia. <i>Genes Chromosomes and Cancer</i> , 2021 , 60, 108-111	5	1
93	Prenatal characterization of a novel inverted duplication by mate pair sequencing in a fetus with dextrocardia. <i>Clinical Case Reports (discontinued)</i> , 2021 , 9, 769-774	0.7	
92	Myeloid malignancies with 5q and 7q deletions are associated with extreme genomic complexity, biallelic TP53 variants, and very poor prognosis. <i>Blood Cancer Journal</i> , 2021 , 11, 18	7	3
91	Clinical utility of next generation sequencing to detect IGH/IL3 rearrangements [t(5;14)(q31.1;q32.1)] in B-lymphoblastic leukemia/lymphoma. <i>Annals of Diagnostic Pathology</i> , 2021 , 53, 151761	2.2	0
90	NKG7 is a T-cell intrinsic therapeutic target for improving antitumor cytotoxicity and cancer immunotherapy.. <i>Cancer Immunology Research</i> , 2021 ,	12.5	2
89	Optimizing clinical cytology touch preparations for next generation sequencing. <i>Genomics</i> , 2020 , 112, 5313-5323	4.3	1

88	Detection of cryptic CCND1 rearrangements in mantle cell lymphoma by next generation sequencing. <i>Annals of Diagnostic Pathology</i> , 2020 , 46, 151533	2.2	3
87	Chromosomal rearrangements and their neoantigenic potential in mesothelioma. <i>Translational Lung Cancer Research</i> , 2020 , 9, S92-S99	4.4	9
86	Characterizing false-positive fluorescence in situ hybridization results by mate-pair sequencing in a patient with chronic myeloid leukemia and progression to myeloid blast crisis. <i>Cancer Genetics</i> , 2020 , 243, 48-51	2.3	2
85	Clinical Value of Next Generation Sequencing in the Detection of Recurring Structural Rearrangements and Copy Number Abnormalities in Acute Myeloid Leukemia. <i>Blood</i> , 2020 , 136, 21-22	2.2	
84	Integration of Comprehensive Genomic Analysis and Functional Screening of Affected Molecular Pathways to Inform Cancer Therapy. <i>Mayo Clinic Proceedings</i> , 2020 , 95, 306-318	6.4	3
83	Secondary acquisition of BCR-ABL1 fusion in de novo GATA2-MECOM positive acute myeloid leukemia with subsequent emergence of a rare KMT2A-ASXL2 fusion. <i>Cancer Genetics</i> , 2020 , 241, 67-71	2.3	1
82	Characterization of a cryptic fusion by mate-pair sequencing in a case of acute promyelocytic leukemia with a normal karyotype and negative FISH studies. <i>Leukemia and Lymphoma</i> , 2020 , 61, 975-978	1.9	4
81	Novel strategy for manufacturing autologous dendritic cell/allogeneic tumor lysate vaccines for glioblastoma. <i>Neuro-Oncology Advances</i> , 2020 , 2, vdaa105	0.9	2
80	Cryptic and atypical KMT2A-USP2 and KMT2A-USP8 rearrangements identified by mate pair sequencing in infant and childhood leukemia. <i>Genes Chromosomes and Cancer</i> , 2020 , 59, 422-427	5	4
79	Immune Cell Infiltration May Be a Key Determinant of Long-Term Survival in Small Cell Lung Cancer. <i>Journal of Thoracic Oncology</i> , 2019 , 14, 1286-1295	8.9	32
78	Characterization of a t(1;2)(p36;p21) involving the PRDM16 gene region by mate-pair sequencing (MPseq) in a patient with newly diagnosed acute myeloid leukemia with myelodysplasia-related changes. <i>Journal of Hematopathology</i> , 2019 , 12, 85-90	0.4	
77	Characterization of a cryptic KMT2A/AFF1 gene fusion by mate-pair sequencing (MPseq) in a young adult with newly diagnosed B-lymphoblastic leukemia. <i>Journal of Hematopathology</i> , 2019 , 12, 99-104	0.4	0
76	Elucidating a false-negative break-apart fluorescence in situ hybridization probe study by next-generation sequencing in a patient with high-grade B-cell lymphoma with and rearrangements. <i>Journal of Physical Education and Sports Management</i> , 2019 , 5,	2.8	8
75	Shared and unique genomic structural variants of different histological components within testicular germ cell tumours identified with mate pair sequencing. <i>Scientific Reports</i> , 2019 , 9, 3586	4.9	3
74	A comparison of adult rhabdomyosarcoma and high-grade neuroendocrine carcinoma of the urinary bladder reveals novel PPP1R12A fusions in rhabdomyosarcoma. <i>Human Pathology</i> , 2019 , 88, 48-59	3.7	1
73	Detection of a cryptic gene fusion by mate-pair sequencing (MPseq) in a newly diagnosed case of pediatric T-lymphoblastic leukemia. <i>Journal of Physical Education and Sports Management</i> , 2019 , 5,	2.8	7
72	Using Genomics to Differentiate Multiple Primaries From Metastatic Lung Cancer. <i>Journal of Thoracic Oncology</i> , 2019 , 14, 1567-1582	8.9	28
71	Whole Genome Mate-pair Sequencing of Plasma Cell Neoplasm as a Novel Diagnostic Strategy: A Case of Unrecognized t(2;11) Structural Variation. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2019 , 19, 598-602	2	2

70	Characterization of a rarely reported STAT5B/RARA gene fusion in a young adult with newly diagnosed acute promyelocytic leukemia with resistance to ATRA therapy. <i>Cancer Genetics</i> , 2019 , 237, 51-54	2.3	3
69	Characterization of TCF3 rearrangements in pediatric B-lymphoblastic leukemia/lymphoma by mate-pair sequencing (MPseq) identifies complex genomic rearrangements and a novel TCF3/TEF gene fusion. <i>Blood Cancer Journal</i> , 2019 , 9, 81	7	9
68	Differentiating between Hyperdiploidy and Pseudo-Hyperdiploidy in B-Lymphoblastic Leukemia Utilizing Low-Coverage Mate-Pair Sequencing. <i>Blood</i> , 2019 , 134, 5212-5212	2.2	
67	Acute leukemias harboring KMT2A/MLLT10 fusion: a 10-year experience from a single genomics laboratory. <i>Genes Chromosomes and Cancer</i> , 2019 , 58, 567-577	5	11
66	Proposal for Modification of CahanQ Criteria Utilizing Molecular Genetic Analyses for Cases without Baseline Histopathology: A Unique Method Applicable to Primary Radiosurgery. <i>Journal of Neurological Surgery, Part B: Skull Base</i> , 2019 , 80, 10-17	1.5	1
65	Investigation of somatic CNVs in brains of synucleinopathy cases using targeted SNCA analysis and single cell sequencing. <i>Acta Neuropathologica Communications</i> , 2019 , 7, 219	7.3	22
64	Mate pair sequencing outperforms fluorescence in situ hybridization in the genomic characterization of multiple myeloma. <i>Blood Cancer Journal</i> , 2019 , 9, 103	7	18
63	Large Chromosomal Rearrangements Yield Biomarkers to Distinguish Low-Risk From Intermediate- and High-Risk Prostate Cancer. <i>Mayo Clinic Proceedings</i> , 2019 , 94, 27-36	6.4	4
62	Neoantigenic Potential of Complex Chromosomal Rearrangements in Mesothelioma. <i>Journal of Thoracic Oncology</i> , 2019 , 14, 276-287	8.9	61
61	False-negative rates for fluorescence hybridization probes in B-cell neoplasms. <i>Haematologica</i> , 2019 , 104, e248-e251	6.6	16
60	Targeting HER2 in patient-derived xenograft ovarian cancer models sensitizes tumors to chemotherapy. <i>Molecular Oncology</i> , 2019 , 13, 132-152	7.9	14
59	Constitutional chromosome rearrangements that mimic the 2017 world health organization "acute myeloid leukemia with recurrent genetic abnormalities": A study of three cases and review of the literature. <i>Cancer Genetics</i> , 2019 , 230, 37-46	2.3	4
58	Use of mate-pair sequencing to characterize a complex cryptic BCR/ABL1 rearrangement observed in a newly diagnosed case of chronic myeloid leukemia. <i>Human Pathology</i> , 2019 , 89, 109-114	3.7	6
57	Mate pair sequencing improves detection of genomic abnormalities in acute myeloid leukemia. <i>European Journal of Haematology</i> , 2019 , 102, 87-96	3.8	23
56	Novel targeted therapy strategies for biliary tract cancers and hepatocellular carcinoma. <i>Future Oncology</i> , 2018 , 14, 553-566	3.6	20
55	SVAtools for junction detection of genome-wide chromosomal rearrangements by mate-pair sequencing (MPseq). <i>Cancer Genetics</i> , 2018 , 221, 1-18	2.3	57
54	Genome U-Plot: a whole genome visualization. <i>Bioinformatics</i> , 2018 , 34, 1629-1634	7.2	21
53	Chromoanasythesis is a common mechanism that leads to ERBB2 amplifications in a cohort of early stage HER2 breast cancer samples. <i>BMC Cancer</i> , 2018 , 18, 738	4.8	10

52	Copy number variant analysis using genome-wide mate-pair sequencing. <i>Genes Chromosomes and Cancer</i> , 2018 , 57, 459-470	5	38
51	YAP-associated chromosomal instability and cholangiocarcinoma in mice. <i>Oncotarget</i> , 2018 , 9, 5892-5905	3.3	30
50	Identification of a pyruvate-to-lactate signature in pancreatic intraductal papillary mucinous neoplasms. <i>Pancreatology</i> , 2018 , 18, 46-53	3.8	6
49	Frequently rearranged and overexpressed Eatenin is responsible for low sensitivity of prostate cancer cells to androgen receptor and Eatenin antagonists. <i>Oncotarget</i> , 2018 , 9, 24428-24442	3.3	2
48	Enhanced mRNA FISH with compact quantum dots. <i>Nature Communications</i> , 2018 , 9, 4461	17.4	27
47	Next Generation Sequencing of Sporadic Vestibular Schwannoma: Necessity of Biallelic NF2 Inactivation and Implications of Accessory Non-NF2 Variants. <i>Otology and Neurotology</i> , 2018 , 39, e860-e871	2.6	17
46	Mantle cell lymphoma with a novel t(11;12)(q13;p11.2): a proposed alternative mechanism of CCND1 up-regulation. <i>Human Pathology</i> , 2017 , 64, 207-212	3.7	5
45	Genomic rearrangements in sporadic lymphangiomyomatosis: an evolving genetic story. <i>Modern Pathology</i> , 2017 , 30, 1223-1233	9.8	3
44	A novel cytogenetic and molecular characterization of renal metanephric adenoma: Identification of partner genes involved in translocation t(9;15)(p24;q24). <i>Cancer Genetics</i> , 2017 , 214-215, 9-15	2.3	6
43	TFEB-VEGFA (6p21.1) co-amplified renal cell carcinoma: a distinct entity with potential implications for clinical management. <i>Modern Pathology</i> , 2017 , 30, 998-1012	9.8	48
42	Trinucleotide Repeat Expansion in the Transcription Factor 4 (TCF4) Gene Leads to Widespread mRNA Splicing Changes in Fuchs Endothelial Corneal Dystrophy 2017 , 58, 343-352		48
41	Retention of Interstitial Genes between and Is Associated with Low-Risk Prostate Cancer. <i>Cancer Research</i> , 2017 , 77, 6157-6167	10.1	7
40	Common fragile sites (CFS) and extremely large CFS genes are targets for human papillomavirus integrations and chromosome rearrangements in oropharyngeal squamous cell carcinoma. <i>Genes Chromosomes and Cancer</i> , 2017 , 56, 59-74	5	29
39	EGFR mediates activation of RET in lung adenocarcinoma with neuroendocrine differentiation characterized by ASCL1 expression. <i>Oncotarget</i> , 2017 , 8, 27155-27165	3.3	8
38	Management of Multifocal Lung Cancer: Results of a Survey. <i>Journal of Thoracic Oncology</i> , 2017 , 12, 1398-1402	8.4	13
37	Custom Gene Capture and Next-Generation Sequencing to Resolve Discordant ALK Status by FISH and IHC in Lung Adenocarcinoma. <i>Journal of Thoracic Oncology</i> , 2016 , 11, 1891-1900	8.9	30
36	Integrated mate-pair and RNA sequencing identifies novel, targetable gene fusions in peripheral T-cell lymphoma. <i>Blood</i> , 2016 , 128, 1234-45	2.2	77
35	Quantification of Somatic Chromosomal Rearrangements in Circulating Cell-Free DNA from Ovarian Cancers. <i>Scientific Reports</i> , 2016 , 6, 29831	4.9	42

34	Heterogeneity of Programmed Cell Death Ligand 1 Expression in Multifocal Lung Cancer. <i>Clinical Cancer Research</i> , 2016 , 22, 2177-82	12.9	92
33	Magnetophoretic-based microfluidic device for DNA Concentration. <i>Biomedical Microdevices</i> , 2016 , 18, 28	3.7	7
32	Integrated Genomic Analysis of Pancreatic Ductal Adenocarcinomas Reveals Genomic Rearrangement Events as Significant Drivers of Disease. <i>Cancer Research</i> , 2016 , 76, 749-61	10.1	23
31	Integrated analysis of the genomic instability of PTEN in clinically insignificant and significant prostate cancer. <i>Modern Pathology</i> , 2016 , 29, 143-56	9.8	28
30	Targeted next generation sequencing of endoscopic ultrasound acquired cytology from ampullary and pancreatic adenocarcinoma has the potential to aid patient stratification for optimal therapy selection. <i>Oncotarget</i> , 2016 , 7, 54526-54536	3.3	59
29	Molecular cytology genotyping of primary and metastatic GI stromal tumors by using a custom two-gene targeted next-generation sequencing panel with therapeutic intent. <i>Gastrointestinal Endoscopy</i> , 2016 , 84, 950-958.e3	5.2	5
28	The cistrome and gene signature of androgen receptor splice variants in castration resistant prostate cancer cells. <i>Journal of Urology</i> , 2015 , 193, 690-8	2.5	48
27	Chromosomal rearrangements and copy number abnormalities of TP63 correlate with p63 protein expression in lung adenocarcinoma. <i>Modern Pathology</i> , 2015 , 28, 359-66	9.8	10
26	Topoisomerase 2 Alpha Cooperates with Androgen Receptor to Contribute to Prostate Cancer Progression. <i>PLoS ONE</i> , 2015 , 10, e0142327	3.7	26
25	Transcriptomic and Immunohistochemical Profiling of SLC6A14 in Pancreatic Ductal Adenocarcinoma. <i>BioMed Research International</i> , 2015 , 2015, 593572	3	20
24	Chromosomal catastrophe is a frequent event in clinically insignificant prostate cancer. <i>Oncotarget</i> , 2015 , 6, 29087-96	3.3	19
23	A simple method for gene phasing using mate pair sequencing. <i>BMC Medical Genetics</i> , 2014 , 15, 19	2.1	7
22	Mate pair sequencing of oropharyngeal squamous cell carcinomas reveals that HPV integration occurs much less frequently than in cervical cancer. <i>Journal of Clinical Virology</i> , 2014 , 59, 195-200	14.5	33
21	Genomic rearrangements define lineage relationships between adjacent lepidic and invasive components in lung adenocarcinoma. <i>Cancer Research</i> , 2014 , 74, 3157-67	10.1	18
20	Fibroblast growth factor receptor 2 translocations in intrahepatic cholangiocarcinoma. <i>Human Pathology</i> , 2014 , 45, 1630-8	3.7	179
19	BIMA V3: an aligner customized for mate pair library sequencing. <i>Bioinformatics</i> , 2014 , 30, 1627-9	7.2	66
18	Novel TRAF1-ALK fusion identified by deep RNA sequencing of anaplastic large cell lymphoma. <i>Genes Chromosomes and Cancer</i> , 2013 , 52, 1097-102	5	45
17	Lineage relationship of Gleason patterns in Gleason score 7 prostate cancer. <i>Cancer Research</i> , 2013 , 73, 3275-84	10.1	45

16	Identification of submicroscopic genetic changes and precise breakpoint mapping in myelofibrosis using high resolution mate-pair sequencing. <i>American Journal of Hematology</i> , 2013 , 88, 741-6	7.1	10
15	Prognostic value of discs large homolog 7 transcript levels in prostate cancer. <i>PLoS ONE</i> , 2013 , 8, e82833	3.7	17
14	Activation Of TAK1 By MYD88 L265P Drives Malignant B Cell Growth In Non-Hodgkin Lymphomas. <i>Blood</i> , 2013 , 122, 245-245	2.2	1
13	Genome-wide analysis reveals recurrent structural abnormalities of TP63 and other p53-related genes in peripheral T-cell lymphomas. <i>Blood</i> , 2012 , 120, 2280-9	2.2	164
12	Mate pair sequencing of whole-genome-amplified DNA following laser capture microdissection of prostate cancer. <i>DNA Research</i> , 2012 , 19, 395-406	4.5	52
11	Discovery of recurrent t(6;7)(p25.3;q32.3) translocations in ALK-negative anaplastic large cell lymphomas by massively parallel genomic sequencing. <i>Blood</i> , 2011 , 117, 915-9	2.2	223
10	The ability of biomarkers to predict systemic progression in men with high-risk prostate cancer treated surgically is dependent on ERG status. <i>Cancer Research</i> , 2010 , 70, 8994-9002	10.1	52
9	Massively Parallel Mate Pair DNA Library Sequencing for Translocation Discovery: Recurrent t(6;7)(p25.3;q32.3) Translocations In ALK-Negative Anaplastic Large Cell Lymphomas. <i>Blood</i> , 2010 , 116, 633-633	2.2	1
8	Novel markers for enterochromaffin cells and gastrointestinal neuroendocrine carcinomas. <i>Modern Pathology</i> , 2009 , 22, 261-72	9.8	110
7	Anaplastic lymphoma kinase immunoreactivity correlates with ALK gene rearrangement and transcriptional up-regulation in non-small cell lung carcinomas. <i>Human Pathology</i> , 2009 , 40, 1152-8	3.7	157
6	The role of desmoglein-3 in the diagnosis of squamous cell carcinoma of the lung. <i>American Journal of Pathology</i> , 2009 , 174, 1629-37	5.8	67
5	Quantitating tissue specificity of human genes to facilitate biomarker discovery. <i>Bioinformatics</i> , 2007 , 23, 1348-55	7.2	13
4	Bioinformatics methods for prioritizing serum biomarker candidates. <i>Clinical Chemistry</i> , 2006 , 52, 2162-4	5.5	18
3	Identification of differentially expressed genes in normal and malignant prostate by electronic profiling of expressed sequence tags. <i>Cancer Research</i> , 2002 , 62, 3308-14	10.1	49
2	Determination of atomic desolvation energies from the structures of crystallized proteins. <i>Journal of Molecular Biology</i> , 1997 , 267, 707-26	6.5	433
1	Computational determination of side chain specificity for pockets in class I MHC molecules. <i>Molecular Immunology</i> , 1996 , 33, 1231-9	4.3	32