# George Vasmatzis

## List of Publications by Citations



| | | | |
|---|---|---|---|
| 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 | Determination of atomic desolvation energies from the structures of crystallized proteins. *Journal of Molecular Biology*, **1997**, 267, 707-26 | 6.5 | 433 |
| 104 | Discovery of recurrent t(6;7)(p25.3;q32.3) translocations in ALK-negative anaplastic large cell lymphomas by massively parallel genomic sequencing. *Blood*, **2011**, 117, 915-9 | 2.2 | 223 |
| 103 | Fibroblast growth factor receptor 2 translocations in intrahepatic cholangiocarcinoma. *Human Pathology*, **2014**, 45, 1630-8 | 3.7 | 179 |
| 102 | Genome-wide analysis reveals recurrent structural abnormalities of TP63 and other p53-related genes in peripheral T-cell lymphomas. *Blood*, **2012**, 120, 2280-9 | 2.2 | 164 |
| 101 | Anaplastic lymphoma kinase immunoreactivity correlates with ALK gene rearrangement and transcriptional up-regulation in non-small cell lung carcinomas. *Human Pathology*, **2009**, 40, 1152-8 | 3.7 | 157 |
| 100 | Novel markers for enterochromaffin cells and gastrointestinal neuroendocrine carcinomas. *Modern Pathology*, **2009**, 22, 261-72 | 9.8 | 110 |
| 99 | Heterogeneity of Programmed Cell Death Ligand 1 Expression in Multifocal Lung Cancer. *Clinical Cancer Research*, **2016**, 22, 2177-82 | 12.9 | 92 |
| 98 | Integrated mate-pair and RNA sequencing identifies novel, targetable gene fusions in peripheral T-cell lymphoma. *Blood*, **2016**, 128, 1234-45 | 2.2 | 77 |
| 97 | The role of desmoglein-3 in the diagnosis of squamous cell carcinoma of the lung. *American Journal of Pathology*, **2009**, 174, 1629-37 | 5.8 | 67 |
| 96 | BIMA V3: an aligner customized for mate pair library sequencing. *Bioinformatics*, **2014**, 30, 1627-9 | 7.2 | 66 |
| 95 | Neoantigenic Potential of Complex Chromosomal Rearrangements in Mesothelioma. *Journal of Thoracic Oncology*, **2019**, 14, 276-287 | 8.9 | 61 |
| 94 | 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. *Oncotarget*, **2016**, 7, 54526-54536 | 3.3 | 59 |
| 93 | SVAtools for junction detection of genome-wide chromosomal rearrangements by mate-pair sequencing (MPseq). *Cancer Genetics*, **2018**, 221, 1-18 | 2.3 | 57 |
| 92 | The ability of biomarkers to predict systemic progression in men with high-risk prostate cancer treated surgically is dependent on ERG status. *Cancer Research*, **2010**, 70, 8994-9002 | 10.1 | 52 |
| 91 | Mate pair sequencing of whole-genome-amplified DNA following laser capture microdissection of prostate cancer. *DNA Research*, **2012**, 19, 395-406 | 4.5 | 52 |
| 90 | Identification of differentially expressed genes in normal and malignant prostate by electronic profiling of expressed sequence tags. *Cancer Research*, **2002**, 62, 3308-14 | 10.1 | 49 |
| 89 | TFEB-VEGFA (6p21.1) co-amplified renal cell carcinoma: a distinct entity with potential implications for clinical management. *Modern Pathology*, **2017**, 30, 998-1012 | 9.8 | 48 |

| | | | |
|---|---|---|---|
| 88 | The cistrome and gene signature of androgen receptor splice variants in castration resistant prostate cancer cells. *Journal of Urology*, **2015**, 193, 690-8 | 2.5 | 48 |
| 87 | 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 |
| 86 | Novel TRAF1-ALK fusion identified by deep RNA sequencing of anaplastic large cell lymphoma. *Genes Chromosomes and Cancer*, **2013**, 52, 1097-102 | 5 | 45 |
| 85 | Lineage relationship of Gleason patterns in Gleason score 7 prostate cancer. *Cancer Research*, **2013**, 73, 3275-84 | 10.1 | 45 |
| 84 | Quantification of Somatic Chromosomal Rearrangements in Circulating Cell-Free DNA from Ovarian Cancers. *Scientific Reports*, **2016**, 6, 29831 | 4.9 | 42 |
| 83 | Copy number variant analysis using genome-wide mate-pair sequencing. *Genes Chromosomes and Cancer*, **2018**, 57, 459-470 | 5 | 38 |
| 82 | Mate pair sequencing of oropharyngeal squamous cell carcinomas reveals that HPV integration occurs much less frequently than in cervical cancer. *Journal of Clinical Virology*, **2014**, 59, 195-200 | 14.5 | 33 |
| 81 | Immune Cell Infiltration May Be a Key Determinant of Long-Term Survival in Small Cell Lung Cancer. *Journal of Thoracic Oncology*, **2019**, 14, 1286-1295 | 8.9 | 32 |
| 80 | Computational determination of side chain specificity for pockets in class I MHC molecules. *Molecular Immunology*, **1996**, 33, 1231-9 | 4.3 | 32 |
| 79 | Custom Gene Capture and Next-Generation Sequencing to Resolve Discordant ALK Status by FISH and IHC in Lung Adenocarcinoma. *Journal of Thoracic Oncology*, **2016**, 11, 1891-1900 | 8.9 | 30 |
| 78 | YAP-associated chromosomal instability and cholangiocarcinoma in mice. *Oncotarget*, **2018**, 9, 5892-5905 | 5.3 | 30 |
| 77 | Common fragile sites (CFS) and extremely large CFS genes are targets for human papillomavirus integrations and chromosome rearrangements in oropharyngeal squamous cell carcinoma. *Genes Chromosomes and Cancer*, **2017**, 56, 59-74 | 5 | 29 |
| 76 | Integrated analysis of the genomic instability of PTEN in clinically insignificant and significant prostate cancer. *Modern Pathology*, **2016**, 29, 143-56 | 9.8 | 28 |
| 75 | Using Genomics to Differentiate Multiple Primaries From Metastatic Lung Cancer. *Journal of Thoracic Oncology*, **2019**, 14, 1567-1582 | 8.9 | 28 |
| 74 | Enhanced mRNA FISH with compact quantum dots. *Nature Communications*, **2018**, 9, 4461 | 17.4 | 27 |
| 73 | Topoisomerase 2 Alpha Cooperates with Androgen Receptor to Contribute to Prostate Cancer Progression. *PLoS ONE*, **2015**, 10, e0142327 | 3.7 | 26 |
| 72 | Integrated Genomic Analysis of Pancreatic Ductal Adenocarcinomas Reveals Genomic Rearrangement Events as Significant Drivers of Disease. *Cancer Research*, **2016**, 76, 749-61 | 10.1 | 23 |
| 71 | Mate pair sequencing improves detection of genomic abnormalities in acute myeloid leukemia. *European Journal of Haematology*, **2019**, 102, 87-96 | 3.8 | 23 |

| | | | |
|---|---|---|---|
| 70 | Investigation of somatic CNVs in brains of synucleinopathy cases using targeted SNCA analysis and single cell sequencing. *Acta Neuropathologica Communications*, **2019**, 7, 219 | 7.3 | 22 |
| 69 | Genome U-Plot: a whole genome visualization. *Bioinformatics*, **2018**, 34, 1629-1634 | 7.2 | 21 |
| 68 | Novel targeted therapy strategies for biliary tract cancers and hepatocellular carcinoma. *Future Oncology*, **2018**, 14, 553-566 | 3.6 | 20 |
| 67 | Transcriptomic and Immunohistochemical Profiling of SLC6A14 in Pancreatic Ductal Adenocarcinoma. *BioMed Research International*, **2015**, 2015, 593572 | 3 | 20 |
| 66 | Chromosomal catastrophe is a frequent event in clinically insignificant prostate cancer. *Oncotarget*, **2015**, 6, 29087-96 | 3.3 | 19 |
| 65 | Genomic rearrangements define lineage relationships between adjacent lepidic and invasive components in lung adenocarcinoma. *Cancer Research*, **2014**, 74, 3157-67 | 10.1 | 18 |
| 64 | Bioinformatics methods for prioritizing serum biomarker candidates. *Clinical Chemistry*, **2006**, 52, 2162-4 | 5.5 | 18 |
| 63 | Mate pair sequencing outperforms fluorescence in situ hybridization in the genomic characterization of multiple myeloma. *Blood Cancer Journal*, **2019**, 9, 103 | 7 | 18 |
| 62 | Prognostic value of discs large homolog 7 transcript levels in prostate cancer. *PLoS ONE*, **2013**, 8, e82833 | 3.7 | 17 |
| 61 | Next Generation Sequencing of Sporadic Vestibular Schwannoma: Necessity of Biallelic NF2 Inactivation and Implications of Accessory Non-NF2 Variants. *Otology and Neurotology*, **2018**, 39, e860-e871 | 2.6 | 17 |
| 60 | False-negative rates for fluorescence hybridization probes in B-cell neoplasms. *Haematologica*, **2019**, 104, e248-e251 | 6.6 | 16 |
| 59 | Targeting HER2 in patient-derived xenograft ovarian cancer models sensitizes tumors to chemotherapy. *Molecular Oncology*, **2019**, 13, 132-152 | 7.9 | 14 |
| 58 | Quantitating tissue specificity of human genes to facilitate biomarker discovery. *Bioinformatics*, **2007**, 23, 1348-55 | 7.2 | 13 |
| 57 | Management of Multifocal Lung Cancer: Results of a Survey. *Journal of Thoracic Oncology*, **2017**, 12, 1398-1402 | 8.9 | 13 |
| 56 | Acute leukemias harboring KMT2A/MLLT10 fusion: a 10-year experience from a single genomics laboratory. *Genes Chromosomes and Cancer*, **2019**, 58, 567-577 | 5 | 11 |
| 55 | Chromosomal rearrangements and copy number abnormalities of TP63 correlate with p63 protein expression in lung adenocarcinoma. *Modern Pathology*, **2015**, 28, 359-66 | 9.8 | 10 |
| 54 | Chromoanasynthesis is a common mechanism that leads to ERBB2 amplifications in a cohort of early stage HER2 breast cancer samples. *BMC Cancer*, **2018**, 18, 738 | 4.8 | 10 |
| 53 | Identification of submicroscopic genetic changes and precise breakpoint mapping in myelofibrosis using high resolution mate-pair sequencing. *American Journal of Hematology*, **2013**, 88, 741-6 | 7.1 | 10 |

| | | | |
|---|---|---|---|
| 52 | Chromosomal rearrangements and their neoantigenic potential in mesothelioma. *Translational Lung Cancer Research*, **2020**, 9, S92-S99 | 4.4 | 9 |
| 51 | 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. *Blood Cancer Journal*, **2019**, 9, 81 | 7 | 9 |
| 50 | 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. *Journal of Physical Education and Sports Management*, **2019**, 5, | 2.8 | 8 |
| 49 | EGFR mediates activation of RET in lung adenocarcinoma with neuroendocrine differentiation characterized by ASCL1 expression. *Oncotarget*, **2017**, 8, 27155-27165 | 3.3 | 8 |
| 48 | Biology and grading of pleomorphic xanthoastrocytoma-what have we learned about it?. *Brain Pathology*, **2021**, 31, 20-32 | 6 | 8 |
| 47 | Detection of a cryptic gene fusion by mate-pair sequencing (MPseq) in a newly diagnosed case of pediatric T-lymphoblastic leukemia. *Journal of Physical Education and Sports Management*, **2019**, 5, | 2.8 | 7 |
| 46 | Magnetophoretic-based microfluidic device for DNA Concentration. *Biomedical Microdevices*, **2016**, 18, 28 | 3.7 | 7 |
| 45 | A simple method for gene phasing using mate pair sequencing. *BMC Medical Genetics*, **2014**, 15, 19 | 2.1 | 7 |
| 44 | Retention of Interstitial Genes between and Is Associated with Low-Risk Prostate Cancer. *Cancer Research*, **2017**, 77, 6157-6167 | 10.1 | 7 |
| 43 | A novel cytogenetic and molecular characterization of renal metanephric adenoma: Identification of partner genes involved in translocation t(9;15)(p24;q24). *Cancer Genetics*, **2017**, 214-215, 9-15 | 2.3 | 6 |
| 42 | Identification of a pyruvate-to-lactate signature in pancreatic intraductal papillary mucinous neoplasms. *Pancreatology*, **2018**, 18, 46-53 | 3.8 | 6 |
| 41 | Use of mate-pair sequencing to characterize a complex cryptic BCR/ABL1 rearrangement observed in a newly diagnosed case of chronic myeloid leukemia. *Human Pathology*, **2019**, 89, 109-114 | 3.7 | 6 |
| 40 | Mantle cell lymphoma with a novel t(11;12)(q13;p11.2): a proposed alternative mechanism of CCND1 up-regulation. *Human Pathology*, **2017**, 64, 207-212 | 3.7 | 5 |
| 39 | Molecular cytology genotyping of primary and metastatic GI stromal tumors by using a custom two-gene targeted next-generation sequencing panel with therapeutic intent. *Gastrointestinal Endoscopy*, **2016**, 84, 950-958.e3 | 5.2 | 5 |
| 38 | Characterization of a cryptic fusion by mate-pair sequencing in a case of acute promyelocytic leukemia with a normal karyotype and negative FISH studies. *Leukemia and Lymphoma*, **2020**, 61, 975-978 | 1.9 | 4 |
| 37 | Large Chromosomal Rearrangements Yield Biomarkers to Distinguish Low-Risk From Intermediate- and High-Risk Prostate Cancer. *Mayo Clinic Proceedings*, **2019**, 94, 27-36 | 6.4 | 4 |
| 36 | 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. *Cancer Genetics*, **2019**, 230, 37-46 | 2.3 | 4 |
| 35 | Cryptic and atypical KMT2A-USP2 and KMT2A-USP8 rearrangements identified by mate pair sequencing in infant and childhood leukemia. *Genes Chromosomes and Cancer*, **2020**, 59, 422-427 | 5 | 4 |

| | | | |
|---|---|---|---|
| 34 | Genomic rearrangements in sporadic lymphangioleiomyomatosis: an evolving genetic story. *Modern Pathology*, **2017**, 30, 1223-1233 | 9.8 | 3 |
| 33 | Shared and unique genomic structural variants of different histological components within testicular germ cell tumours identified with mate pair sequencing. *Scientific Reports*, **2019**, 9, 3586 | 4.9 | 3 |
| 32 | Detection of cryptic CCND1 rearrangements in mantle cell lymphoma by next generation sequencing. *Annals of Diagnostic Pathology*, **2020**, 46, 151533 | 2.2 | 3 |
| 31 | Characterization of a rarely reported STAT5B/RARA gene fusion in a young adult with newly diagnosed acute promyelocytic leukemia with resistance to ATRA therapy. *Cancer Genetics*, **2019**, 237, 51-54 | 2.3 | 3 |
| 30 | Tumor Junction Burden and Antigen Presentation as Predictors of Survival in Mesothelioma Treated With Immune Checkpoint Inhibitors. *Journal of Thoracic Oncology*, **2021**, | 8.9 | 3 |
| 29 | Integration of Comprehensive Genomic Analysis and Functional Screening of Affected Molecular Pathways to Inform Cancer Therapy. *Mayo Clinic Proceedings*, **2020**, 95, 306-318 | 6.4 | 3 |
| 28 | Myeloid malignancies with 5q and 7q deletions are associated with extreme genomic complexity, biallelic TP53 variants, and very poor prognosis. *Blood Cancer Journal*, **2021**, 11, 18 | 7 | 3 |
| 27 | 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. *Cancer Genetics*, **2020**, 243, 48-51 | 2.3 | 2 |
| 26 | Whole Genome Mate-pair Sequencing of Plasma Cell Neoplasm as a Novel Diagnostic Strategy: A Case of Unrecognized t(2;11) Structural Variation. *Clinical Lymphoma, Myeloma and Leukemia*, **2019**, 19, 598-602 | 2 | 2 |
| 25 | Novel strategy for manufacturing autologous dendritic cell/allogeneic tumor lysate vaccines for glioblastoma. *Neuro-Oncology Advances*, **2020**, 2, vdaa105 | 0.9 | 2 |
| 24 | In search for biomarkers and potential drug targets for uterine serous endometrial cancer. *Journal of Cancer Research and Clinical Oncology*, **2021**, 147, 1647-1658 | 4.9 | 2 |
| 23 | 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. *Human Pathology*, **2021**, 112, 20-34 | 3.7 | 2 |
| 22 | Frequently rearranged and overexpressed catenin is responsible for low sensitivity of prostate cancer cells to androgen receptor and catenin antagonists. *Oncotarget*, **2018**, 9, 24428-24442 | 3.3 | 2 |
| 21 | NKG7 is a T-cell intrinsic therapeutic target for improving antitumor cytotoxicity and cancer immunotherapy.. *Cancer Immunology Research*, **2021**, | 12.5 | 2 |
| 20 | A comparison of adult rhabdomyosarcoma and high-grade neuroendocrine carcinoma of the urinary bladder reveals novel PPP1R12A fusions in rhabdomyosarcoma. *Human Pathology*, **2019**, 88, 48-59 | 3.7 | 1 |
| 19 | Optimizing clinical cytology touch preparations for next generation sequencing. *Genomics*, **2020**, 112, 5313-5323 | 4.3 | 1 |
| 18 | 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. *Blood*, **2010**, 116, 633-633 | 2.2 | 1 |
| 17 | Activation Of TAK1 By MYD88 L265P Drives Malignant B Cell Growth In Non-Hodgkin Lymphomas. *Blood*, **2013**, 122, 245-245 | 2.2 | 1 |

| | | | |
|---|---|---|---|
| 16 | Secondary acquisition of BCR-ABL1 fusion in de novo GATA2-MECOM positive acute myeloid leukemia with subsequent emergence of a rare KMT2A-ASXL2 fusion. *Cancer Genetics*, **2020**, 241, 67-71 | 2.3 | 1 |
| 15 | Theragnostic chromosomal rearrangements in treatment-naive pancreatic ductal adenocarcinomas obtained via endoscopic ultrasound. *Journal of Cellular and Molecular Medicine*, **2021**, 25, 4110-4123 | 5.6 | 1 |
| 14 | Proposal for Modification of Cahan's Criteria Utilizing Molecular Genetic Analyses for Cases without Baseline Histopathology: A Unique Method Applicable to Primary Radiosurgery. *Journal of Neurological Surgery, Part B: Skull Base*, **2019**, 80, 10-17 | 1.5 | 1 |
| 13 | Identification of a novel KMT2A/GIMAP8 gene fusion in a pediatric patient with acute undifferentiated leukemia. *Genes Chromosomes and Cancer*, **2021**, 60, 108-111 | 5 | 1 |
| 12 | Characterization of a cryptic KMT2A/AFF1 gene fusion by mate-pair sequencing (MPseq) in a young adult with newly diagnosed B-lymphoblastic leukemia. *Journal of Hematopathology*, **2019**, 12, 99-104 | 0.4 | 0 |
| 11 | The Role of Hydrophobicity in Peptide-MHC Binding. *Lecture Notes in Computer Science*, **2021**, 24-37 | 0.9 | 0 |
| 10 | Personalized tumor-specific DNA junctions to detect circulating tumor in patients with endometrial cancer. *PLoS ONE*, **2021**, 16, e0252390 | 3.7 | 0 |
| 9 | Clinical utility of next generation sequencing to detect IGH/IL3 rearrangements [t(5;14)(q31.1;q32.1)] in B-lymphoblastic leukemia/lymphoma. *Annals of Diagnostic Pathology*, **2021**, 53, 151761 | 2.2 | 0 |
| 8 | Identification of EWSR1 rearrangements in patients with immature hematopoietic neoplasms: A case series and review of literature.. *Annals of Diagnostic Pathology*, **2022**, 58, 151942 | 2.2 | 0 |
| 7 | 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. *Journal of Hematopathology*, **2019**, 12, 85-90 | 0.4 | |
| 6 | Clinical Value of Next Generation Sequencing in the Detection of Recurring Structural Rearrangements and Copy Number Abnormalities in Acute Myeloid Leukemia. *Blood*, **2020**, 136, 21-22 | 2.2 | |
| 5 | 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/PDGFRA gene fusions. *Cancer Genetics*, **2021**, 260-261, 1-5 | 2.3 | |
| 4 | Differentiating between Hyperdiploidy and Pseudo-Hyperdiploidy in B-Lymphoblastic Leukemia Utilizing Low-Coverage Mate-Pair Sequencing. *Blood*, **2019**, 134, 5212-5212 | 2.2 | |
| 3 | Chromosomal Junction Detection from Whole-Genome Sequencing on Formalin-Fixed, Paraffin-Embedded Tumors. *Journal of Molecular Diagnostics*, **2021**, 23, 375-388 | 5.1 | |
| 2 | Detection of a Cryptic EP300/ZNF384 Gene Fusion by Chromosomal Microarray and Next-Generation Sequencing Studies in a Pediatric Patient with B-Lymphoblastic Leukemia. *Laboratory Medicine*, **2021**, 52, 297-302 | 1.6 | |
| 1 | Prenatal characterization of a novel inverted duplication by mate pair sequencing in a fetus with dextrocardia. *Clinical Case Reports (discontinued)*, **2021**, 9, 769-774 | 0.7 | |