

CURRICULUM VITAE

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PANAGIOTIS ADAMOPOULOS

Assistant Professor

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Languages : Greek and English

Education

08/2024 – 10/2024 **Postdoctoral Research**
Lunenfeld - Tanenbaum Research Institute (LTRI), Sinai Health System, University of Toronto, Canada.

2018 – 2024 **Postdoctoral Research**
Department of Biochemistry and Molecular Biology, Faculty of Biology, National and Kapodistrian University of Athens, Athens, Greece.

2014 – 2018 **Doctoral Thesis (Ph.D.)**
Department of Biochemistry and Molecular Biology, Faculty of Biology, National and Kapodistrian University of Athens, Athens, Greece.
Ph.D. Thesis Title: *Identification and expression analysis of novel mRNA isoforms of kallikrein genes and RNase κ, as well as the miRNAs targeting them in cancer cells and solid tumors.*

2008 – 2013 **B.Sc. in Biology**
Faculty of Biology, National and Kapodistrian University of Athens, Athens, Greece.

Current Position

Assistant Professor (09/2025 -): Department of Biochemistry and Molecular Biology, Faculty of Biology, National and Kapodistrian University of Athens, Athens, Greece.

Principal Investigator in research grants

1. Deciphering the mRNA epitranscriptomic landscape of the human apoptosis-related genes in breast cancer.

Funded by: Hellenic Foundation for Research and Innovation (HFRI).

Duration: 2023 – 2025.

2. Identification, characterization, and clinical evaluation of tRNA-derived RNA fragments (tRFs) in colorectal cancer and other human malignancies using next-generation sequencing (NGS) and ultrasensitive molecular methodologies.

Funded by: Call for Postdoctoral Research fellowships from the Bodossaki Foundation.

Duration: 2019 – 2022.

Participation as team member in research grants

1. Investigation of the m6A epitranscriptome in bladder cancer.

Research Program: Hellenic Foundation for Research and Innovation (HFRI).

Duration: 2022 – 2023.

Principal Investigator: Prof. A. Scorilas

2. Non-invasive molecular methodology for diagnosis and personalized post-treatment monitoring of bladder cancer.

Research Program: Research – Create – Innovate (2nd Cycle).

Duration: 2022 – 2023.

Principal Investigator: Prof. A. Scorilas.

3. Design and development of innovative compounds based on bioactive metabolites of the olive tree (*Olea europaea*) with anti-inflammatory and anticancer activity.

Research Program: Research – Create – Innovate (2nd Cycle).

Duration: 2022 – 2023.

Principal Investigator: Prof. L. Skaltsounis.

4. Study of the molecular profile of small non-coding RNAs (sncRNAs) in breast cancer: Evaluation of their clinical significance in early diagnosis, personalized prognosis, and prediction of treatment response.

Research Program: Hellenic Society of Medical Oncology.

Duration: 2019 – 2022.

Principal Investigator: Dr. G. Ardavanis.

5. Expression analysis and functional investigation of non-coding RNAs targeting apoptotic genes using next-generation sequencing and ultrasensitive molecular methodologies in breast cancer cells sensitive or resistant to apoptosis induced by anticancer drugs.

Research Program: Hellenic Society of Medical Oncology.

Duration: 2017 – 2021.

Principal Investigator: Dr. M. Drizou.

6. Sequencing the transcriptome of *Helix aspersa* Müller, 1774.

Research Program: Onassis Foundation Scholarships.

Duration: 2014 – 2016.

Principal Investigator: Assoc. Prof. A. Parmakelis.

7. Utilization of bioinformatics and microchip emerging technologies towards a next generation architecture health system for diabetes mellitus type 2 management, prevention and personalized medical care.

Research Program: SYNERGASIA II, 2013–2015.

Duration: 2015.

Principal Investigator: Prof. Emm. G. Fragoulis.

8. Understanding the impact of production processes on the ecology of spoilage and contaminating microorganisms in dairy products (ESL, evaporated milk) and fresh fruit juices – Development of molecular methodologies and mathematical models for predicting shelf life.

Research Program: SYNERGASIA I, 2011–2015.

Duration: 2014.

Principal Investigator: Prof. A. Scorilas.

Research activity

- Profiling of post-transcriptional modifications in mRNAs and investigation of their significance in mRNA stability and translational efficiency.
- Exploration of the biochemical roles of human mRNA methyltransferases and demethylases through gene silencing molecular methodologies.
- Identification, characterization, and structural analysis of novel alternative mRNA transcripts, and investigation of their role and function in cancer progression.
- Proteomic profiling of the kallikrein gene family and evaluation of its significance in human diseases.
- Study of point mutations and gene expansion events associated with epitranscriptomic mechanisms and elucidation of their role in urothelial cancer samples.
- Investigation of gene expression regulation by microRNAs (miRNAs) and tRNA-derived fragments (tRFs) in cancer cells.
- Study of the role, biosynthesis, regulation, and significance of non-coding RNAs, including miRNAs and long non-coding RNAs (lncRNAs), in colorectal cancer and other human malignancies.
- Development of high-throughput sequencing methodologies for the analysis of SARS-CoV-2 mutations and their impact on the structure and function of the Spike protein.
- Design and development of computational tools for omics data analysis, including de novo genome/transcriptome assembly, differential gene expression, DNA/RNA methylation, miRNA target discovery, transcription factor binding site prediction, and mutation detection and characterization in living organisms.

Research Performance Indicators

- **63 publications** in peer-reviewed international scientific journals.
 - **First** author in **26** publications.
 - **Second** author in **19** publications.
 - **Corresponding author** in **11** publications.
 - Publications in high-impact journals in the field, such as: *Genome Research*, *FEBS Journal*, *RNA Biology*, *Genomics*, *Apoptosis*, *Cancer Letters*, *British Journal of Cancer*, *International Journal of Biochemistry & Cell Biology*, *Scientific Reports*, *BMC Genomics*, *Epigenomics*.
- **Total Citations:** 1514 ([Google Scholar](#)).
- **h-Index:** 21 ([Google Scholar](#)).
- **3** patents.
- **3 chapters** in international scientific books.
- **>300 original entries** published in the international gene bank (GenBank® of NCBI).
- **>50 publications** (including 5 oral presentations) in proceedings of international and national conferences.

Original research articles in international peer-reviewed scientific journals

1. **Adamopoulos PG**, Athanasopoulou K, Scorilas A. A versatile type VI CRISPR-based approach for targeted m6A demethylation in mRNAs. *Genome Res.* 2025 (Accepted).
2. Athanasopoulou K, **Adamopoulos PG**, Tsiakanikas P, Daneva GN, Prassas I, Yousef GM, Diamandis EP, Scorilas A. Deciphering the m6A Epitranscriptomic Landscape of mRNAs in Breast Cancer Cells. *Mol Cell Biol.* 2025 Oct 6:1-20. doi: [10.1080/10985549.2025.2560956](https://doi.org/10.1080/10985549.2025.2560956).
3. Athanasopoulou K, **Adamopoulos PG**, Tsiakanikas P, Scorilas A. Exploring the m⁵C epitranscriptome of mRNAs in breast cancer cells through genome engineering and long-read sequencing approaches. *Funct Integr Genomics.* 2025 Jun 25;25(1):136. doi: [10.1007/s10142-025-01648-4](https://doi.org/10.1007/s10142-025-01648-4).
4. **Adamopoulos PG**, Boti MA, Athanasopoulou K, Tsiakanikas P, Daneva GN, Scorilas A. Decoding the Transcriptional Complexity of the Human BRCA2 DNA Repair Gene Using Hybrid-seq. *Biochem Genet.* 2025 Jul 10. doi: [10.1007/s10528-025-11180-6](https://doi.org/10.1007/s10528-025-11180-6).
5. **Adamopoulos PG**, Bartzoka N, Tsiakanikas P, Scorilas A. Characterization of novel ACE2 mRNA transcripts: The potential role of alternative splicing in SARS-CoV-2 infection. *Gene.* 2025; 5:936:149092. doi: [10.1016/j.gene.2024.149092](https://doi.org/10.1016/j.gene.2024.149092).
6. Athanasopoulou K, **Adamopoulos PG**, Scorilas A. New insights into the dynamics of m6A epitranscriptome: hybrid-seq identifies novel mRNAs of the m6A writers METTL3/14. *Epigenomics.* 2024; 1-16. doi: [10.1080/17501911.2024.2390818](https://doi.org/10.1080/17501911.2024.2390818).
7. Diamantopoulos MA, **Adamopoulos PG**, Tsiakanikas P, Nisotakis T, Skourou PC, Scorilas A. Unraveling novel mRNA transcripts of the human DNA N-glycosylase (NTHL1) gene with the implementation of an innovative targeted DNA-seq assay. *Gene.* 2024; 930:148856. doi: [10.1016/j.gene.2024.148856](https://doi.org/10.1016/j.gene.2024.148856).
8. **Adamopoulos PG**, Diamantopoulos MA, Boti MA, Zafeiriadou A, Galani A, Kostakis M, Markou A, Sideris DC, Avgeris M, Thomaidis NS, Scorilas A. Spike-Seq: An amplicon-based high-throughput sequencing approach for the sensitive detection and characterization of SARS-CoV-2 genetic variations in environmental samples. *Sci Total Environ.* 2024; 914:169747. doi: [10.1016/j.scitotenv.2023.169747](https://doi.org/10.1016/j.scitotenv.2023.169747).
9. Soureas K, Papadimitriou MA, Malandrakis P, Papanota AM, **Adamopoulos PG**, Ntanasis-Stathopoulos I, Liacos CI, Gavriatopoulou M, Sideris DC, Kastritis E, Dimopoulos MA, Scorilas A, Terpos E, Avgeris M. Small RNA-seq and clinical evaluation of tRNA-derived fragments in multiple myeloma: Loss of mitochondrial i-tRF^{HisGTG} results in patients' poor treatment outcome. *Br J Haematol.* 2024; 204(5):1790-1800. doi: [10.1111/bjh.19332](https://doi.org/10.1111/bjh.19332).
10. **Adamopoulos PG**, Athanasopoulou K, Boti MA, Dimitroulis G, Daneva GN, Tsiakanikas P, Scorilas A. Hybrid-seq deciphers the complex transcriptional profile of the human *BRCA1* DNA repair associated gene. *RNA Biol.* 2023; 20(1):281-295. doi: [10.1080/15476286.2023.2220210](https://doi.org/10.1080/15476286.2023.2220210).
11. Boti MA, **Adamopoulos PG**, Vassilacopoulou D, Scorilas A. Unraveling the Concealed Transcriptomic Landscape of PTEN in Human Malignancies. *Curr Genomics.* 2023; 24(4):250-262. doi: [10.2174/0113892029265367231013113304](https://doi.org/10.2174/0113892029265367231013113304).
12. Papadimitriou MA, Soureas K, Papanota AM, Tsiakanikas P, **Adamopoulos PG**, Ntanasis-Stathopoulos I, Malandrakis P, Gavriatopoulou M, Sideris DC, Kastritis E, Avgeris M,

- Dimopoulos MA, Terpos E, Scorilas A. miRNA-seq identification and clinical validation of CD138+ and circulating miR-25 in treatment response of multiple myeloma. *J Transl Med.* 2023; 21(1):245. doi: [10.1186/s12967-023-04034-5](https://doi.org/10.1186/s12967-023-04034-5).
13. Galani A, Markou A, Dimitrakopoulos L, Kontou A, Kostakis M, Kapes V, Diamantopoulos MA, **Adamopoulos PG**, Avgeris M, Lianidou E, Scorilas A, Paraskevis D, Tsiodras S, Dimopoulos MA, Thomaidis N. Delta SARS-CoV-2 variant is entirely substituted by the omicron variant during the fifth COVID-19 wave in Attica region. *Sci Total Environ.* 2023; 856(Pt 1):159062. doi: [10.1016/j.scitotenv.2022.159062](https://doi.org/10.1016/j.scitotenv.2022.159062).
14. **Adamopoulos PG**, Athanasopoulou K, Tsiakanikas P, Scorilas A. A comprehensive nanopore sequencing methodology deciphers the complete transcriptional landscape of cyclin-dependent kinase 4 (CDK4) in human malignancies. *FEBS J.* 2022; 289(3):712-729. doi: [10.1111/febs.16201](https://doi.org/10.1111/febs.16201).
15. **Adamopoulos PG**, Tsiakanikas P, Stolidi I, Scorilas A. A versatile 5' RACE- Seq methodology for the accurate identification of the 5' termini of mRNAs. *BMC Genomics.* 2022; 23(1):163. doi: [10.1186/s12864-022-08386-y](https://doi.org/10.1186/s12864-022-08386-y).
16. Athanasopoulou K, **Adamopoulos PG**, Scorilas A. Structural characterization and expression analysis of novel MAPK1 transcript variants with the development of a multiplexed targeted nanopore sequencing approach. *Int J Biochem Cell Biol.* 2022; 150:106272. doi: [10.1016/j.biocel.2022.106272](https://doi.org/10.1016/j.biocel.2022.106272).
17. Athanasopoulou K, **Adamopoulos PG**, Daneva GN, Scorilas A. Decoding the concealed transcriptional signature of the apoptosis-related BCL2 antagonist/killer 1 (BAK1) gene in human malignancies. *Apoptosis.* 2022; 27(11-12):869-882. doi: [10.1007/s10495-022-01753-w](https://doi.org/10.1007/s10495-022-01753-w).
18. Tsiakanikas P, **Adamopoulos PG**, Tsirba D, Artemaki PI, Papadopoulos IN, Kontos CK, Scorilas A. High Expression of a tRNA^{Pro} Derivative Associates with Poor Survival and Independently Predicts Colorectal Cancer Recurrence. *Biomedicines.* 2022; 10(5):1120. doi: [10.3390/biomedicines10051120](https://doi.org/10.3390/biomedicines10051120).
19. Papadimitriou MA, Papanota AM, **Adamopoulos PG**, Pilala KM, Liacos CI, Malandrakis P, Mavrianou-Koutsoukou N, Patseas D, Eleutherakis-Papaiakovou E, Gavriatopoulou M, Kastritis E, Avgeris M, Dimopoulos MA, Terpos E, Scorilas A. miRNA-seq and clinical evaluation in multiple myeloma: miR-181a overexpression predicts short-term disease progression and poor post-treatment outcome. *Br J Cancer.* 2022; 126(1):79-90. doi: [10.1038/s41416-021-01602-8](https://doi.org/10.1038/s41416-021-01602-8).
20. Galani A, Aalizadeh R, Kostakis M, Markou A, Alygizakis N, Lytras T, **Adamopoulos PG**, Peccia J, Thompson DC, Kontou A, Karagiannidis A, Lianidou ES, Avgeris M, Paraskevis D, Tsiodras S, Scorilas A, Vasiliou V, Dimopoulos MA, Thomaidis NS. SARS-CoV-2 wastewater surveillance data can predict hospitalizations and ICU admissions. *Sci Total Environ.* 2022; 804:150151. doi: [10.1016/j.scitotenv.2021.150151](https://doi.org/10.1016/j.scitotenv.2021.150151).
21. **Adamopoulos PG**, Tsiakanikas P, Boti MA, Scorilas A. Targeted Long-Read Sequencing Decodes the Transcriptional Atlas of the Founding RAS Gene Family Members. *Int J Mol Sci.* 2021; 22(24):13298. doi: [10.3390/ijms222413298](https://doi.org/10.3390/ijms222413298).
22. **Adamopoulos PG**, Tsiakanikas P, Adam EE, Scorilas A. Unraveling novel survivin mRNA transcripts in cancer cells using an in-house developed targeted high-throughput sequencing approach. *Genomics.* 2021; 113(1 Pt 2):573-581. doi: [10.1016/j.ygeno.2020.09.053](https://doi.org/10.1016/j.ygeno.2020.09.053).

23. Avgeris M, **Adamopoulos PG**, Galani A, Xagorari M, Gourgiotis D, Trougakovs IP, Voulgaris N, Dimopoulos MA, Thomaidis NS, Scorilas A. Novel Nested-Seq Approach for SARS-CoV-2 Real-Time Epidemiology and In-Depth Mutational Profiling in Wastewater. *Int J Mol Sci.* 2021; 22(16):8498. doi: [10.3390/ijms22168498](https://doi.org/10.3390/ijms22168498).
24. Boti MA, **Adamopoulos PG**, Tsiakanikas P, Scorilas A. Nanopore Sequencing Unveils Diverse Transcript Variants of the Epithelial Cell-Specific Transcription Factor Elf-3 in Human Malignancies. *Genes (Basel).* 2021; 12(6):839. doi: [10.3390/genes12060839](https://doi.org/10.3390/genes12060839).
25. Katsaraki K, **Adamopoulos PG**, Papageorgiou SG, Pappa V, Scorilas A, Kontos CK. A 3' tRNA-derived fragment produced by tRNA^{LeuAAG} and tRNA^{LeuTAG} is associated with poor prognosis in B-cell chronic lymphocytic leukemia, independently of classical prognostic factors. *Eur J Haematol.* 2021; 106(6):821-830. doi: [10.1111/ejh.13613](https://doi.org/10.1111/ejh.13613).
26. Papatsirou M, **Adamopoulos PG**, Artemaki PI, Georganti VP, Scorilas A, Vassilacopoulou D, Kontos CK. Next-generation sequencing reveals alternative L-DOPA decarboxylase (DDC) splice variants bearing novel exons, in human hepatocellular and lung cancer cells. *Gene.* 2021; 768:145262. doi: [10.1016/j.gene.2020.145262](https://doi.org/10.1016/j.gene.2020.145262).
27. Artemaki PI, Papatsirou M, Boti MA, **Adamopoulos PG**, Christodoulou S, Vassilacopoulou D, Scorilas A, Kontos CK. Revised Exon Structure of L-DOPA Decarboxylase (DDC) Reveals Novel Splice Variants Associated with Colorectal Cancer Progression. *Int J Mol Sci.* 2020; 21(22):8568. doi: [10.3390/ijms21228568](https://doi.org/10.3390/ijms21228568).
28. Karousi P, **Adamopoulos PG**, Papageorgiou SG, Pappa V, Scorilas A, Kontos CK. A novel, mitochondrial, internal tRNA-derived RNA fragment possesses clinical utility as a molecular prognostic biomarker in chronic lymphocytic leukemia. *Clin Biochem.* 2020; 85:20-26. doi: [10.1016/j.clinbiochem.2020.07.005](https://doi.org/10.1016/j.clinbiochem.2020.07.005).
29. Zisi Z, **Adamopoulos PG**, Kontos CK, Scorilas A. Identification and expression analysis of novel splice variants of the human carcinoembryonic antigen-related cell adhesion molecule 19 (CEACAM19) gene using a high-throughput sequencing approach. *Genomics.* 2020; 112(6):4268-4276. doi: [10.1016/j.ygeno.2020.06.043](https://doi.org/10.1016/j.ygeno.2020.06.043).
30. **Adamopoulos PG**, Kontos CK, Scorilas A, Sideris DC. Identification of novel alternative transcripts of the human Ribonuclease κ (RNASEK) gene using 3' RACE and high-throughput sequencing approaches. *Genomics.* 2020; 112(1):943-951. doi: [10.1016/j.ygeno.2019.06.010](https://doi.org/10.1016/j.ygeno.2019.06.010).
31. **Adamopoulos PG**, Koukouzeli FE, Kontos CK, Scorilas A. Identification of six novel alternative transcripts of the human kallikrein-related peptidase 15 (KLK15), using 3'RACE and high-throughput sequencing. *Gene.* 2020; 749:144708. doi: [10.1016/j.gene.2020.144708](https://doi.org/10.1016/j.gene.2020.144708).
32. Kalioraki MA, Artemaki PI, Sklirou AD, Kontos CK, **Adamopoulos PG**, Papadopoulos IN, Trougakovs IP, Scorilas A. Heat shock protein beta 3 (HSPB3) is an unfavorable molecular biomarker in colorectal adenocarcinoma. *Mol Carcinog.* 2020; 59(1):116-125. doi: [10.1002/mc.23133](https://doi.org/10.1002/mc.23133).
33. **Adamopoulos PG**, Tsiakanikas P, Kontos CK, Panagiotou A, Vassilacopoulou D, Scorilas A. Identification of novel alternative splice variants of the human L-DOPA decarboxylase (DDC) gene in human cancer cells, using high-throughput sequencing approaches. *Gene.* 2019; 719:144075. doi: [10.1016/j.gene.2019.144075](https://doi.org/10.1016/j.gene.2019.144075).

34. **Adamopoulos PG**, Mavrogiannis AV, Kontos CK, Scorilas A. Novel alternative splice variants of the human protein arginine methyltransferase 1 (PRMT1) gene, discovered using next-generation sequencing. *Gene*. 2019; 699:135-144. doi: [10.1016/j.gene.2019.02.072](https://doi.org/10.1016/j.gene.2019.02.072).
35. **Adamopoulos PG**, Kontos CK, Scorilas A. Discovery of novel transcripts of the human tissue kallikrein (KLK1) and kallikrein-related peptidase 2 (KLK2) in human cancer cells, exploiting Next-Generation Sequencing technology. *Genomics*. 2019; 111(4):642-652. doi: [10.1016/j.ygeno.2018.03.022](https://doi.org/10.1016/j.ygeno.2018.03.022).
36. **Adamopoulos PG**, Kontos CK, Diamantopoulos MA, Scorilas A. Molecular cloning of novel transcripts of the adaptor-related protein complex 2 alpha 1 subunit (AP2A1) gene, using Next-Generation Sequencing. *Gene*. 2018; 678:55-64. doi: [10.1016/j.gene.2018.08.008](https://doi.org/10.1016/j.gene.2018.08.008).
37. **Adamopoulos PG**, Theodoropoulou MC, Scorilas A. Alternative Splicing Detection Tool-a novel PERL algorithm for sensitive detection of splicing events, based on next-generation sequencing data analysis. *Ann Transl Med*. 2018; 6(12):244. doi: [10.21037/atm.2018.06.32](https://doi.org/10.21037/atm.2018.06.32).
38. Kourtis A, **Adamopoulos PG**, Papalois A, Iliopoulos DC, Babis GC, Scorilas A. Quantitative analysis and study of the mRNA expression levels of apoptotic genes *BCL2*, *BAX* and *BCL2L12* in the articular cartilage of an animal model of osteoarthritis. *Ann Transl Med*. 2018; 6(12):243. doi: [10.21037/atm.2018.05.47](https://doi.org/10.21037/atm.2018.05.47).
39. **Adamopoulos PG**, Kontos CK, Scorilas A. Novel splice variants of the human kallikrein-related peptidases 11 (KLK11) and 12 (KLK12), unraveled by next-generation sequencing technology. *Biol Chem*. 2018; 399(9):1065-1071. doi: [10.1515/hsz-2017-0294](https://doi.org/10.1515/hsz-2017-0294).
40. **Adamopoulos PG**, Raptis GD, Kontos CK, Scorilas A. Discovery and expression analysis of novel transcripts of the human SR-related CTD-associated factor 1 (SCAF1) gene in human cancer cells using Next-Generation Sequencing. *Gene*. 2018; 670:155-165. doi: [10.1016/j.gene.2018.05.044](https://doi.org/10.1016/j.gene.2018.05.044).
41. **Adamopoulos PG**, Kontos CK, Scorilas A. Molecular cloning of novel transcripts of human kallikrein-related peptidases 5, 6, 7, 8 and 9 (KLK5 - KLK9), using Next-generation sequencing. *Sci Rep*. 2017; 7(1):17299. doi: [10.1038/s41598-017-16269-6](https://doi.org/10.1038/s41598-017-16269-6).
42. Parmakelis A, Kotsakiozi P, Kontos CK, **Adamopoulos PG**, Scorilas A. The transcriptome of a "sleeping" invader: de novo assembly and annotation of the transcriptome of aestivating *Cornu aspersum*. *BMC Genomics*. 2017; 18(1):491. doi: [10.1186/s12864-017-3885-1](https://doi.org/10.1186/s12864-017-3885-1).
43. **Adamopoulos PG**, Kontos CK, Scorilas A. Identification and molecular cloning of novel transcripts of the human kallikrein-related peptidase 10 (KLK10) gene using next-generation sequencing. *Biochem Biophys Res Commun*. 2017; 487(4):776-781. doi: [10.1016/j.bbrc.2017.04.078](https://doi.org/10.1016/j.bbrc.2017.04.078).
44. Tsangaris GT, Papathanasiou C, **Adamopoulos PG**, Scorilas A, Vorgias CE, Prodromou N, Stathopoulou FT, Stravopodis DJ, Anagnostopoulos AK. Pediatric Ependymoma: A Proteomics Perspective. *Cancer Genomics Proteomics*. 2017; 14(2):127-136. doi: [10.21873/cgp.20025](https://doi.org/10.21873/cgp.20025).
45. **Adamopoulos PG**, Kontos CK, Tsiakanikas P, Scorilas A. Identification of novel alternative splice variants of the *BCL2L12* gene in human cancer cells using next-generation sequencing methodology. *Cancer Lett*. 2016; 373(1):119-129. doi: [10.1016/j.canlet.2016.01.019](https://doi.org/10.1016/j.canlet.2016.01.019).
46. Miltiades P, Lamprianidou E, Vassilakopoulos TP, Papageorgiou SG, Galanopoulos AG, Kontos CK, **Adamopoulos PG**, Nakou E, Vakalopoulou S, Garypidou V, Papaioannou M, Hatjiharissi E, Papadaki HA, Spanoudakis E, Pappa V, Scorilas A, Tsatalas C, Kotsianidis I; Hellenic MDS Study

- Group. The Stat3/5 Signaling Biosignature in Hematopoietic Stem/Progenitor Cells Predicts Response and Outcome in Myelodysplastic Syndrome Patients Treated with Azacitidine. *Clin Cancer Res.* 2016; 22(8):1958-68. doi: [10.1158/1078-0432.CCR-15-1288](https://doi.org/10.1158/1078-0432.CCR-15-1288).
47. Kontos CK, **Adamopoulos PG**, Papageorgiou SG, Pappa V, Scorilas A. mRNA overexpression of kallikrein-related peptidase 14 (KLK14) is an independent predictor of poor overall survival in chronic lymphocytic leukemia patients. *Clin Chem Lab Med.* 2016; 54(2):315-24. doi: [10.1515/cclm-2015-0456](https://doi.org/10.1515/cclm-2015-0456).
48. **Adamopoulos PG**, Kontos CK, Papageorgiou SG, Pappa V, Scorilas A. KLKB1 mRNA overexpression: A novel molecular biomarker for the diagnosis of chronic lymphocytic leukemia. *Clin Biochem.* 2015; 48(13-14):849-54. doi: [10.1016/j.clinbiochem.2015.04.007](https://doi.org/10.1016/j.clinbiochem.2015.04.007).
49. **Adamopoulos PG**, Kontos CK, Rapti SM, Papadopoulos IN, Scorilas A. miR-224 overexpression is a strong and independent prognosticator of short-term relapse and poor overall survival in colorectal adenocarcinoma. *Int J Oncol.* 2015; 46(2):849-59. doi: [10.3892/ijo.2014.2775](https://doi.org/10.3892/ijo.2014.2775).

Review articles in international peer-reviewed scientific journals

50. Athanasopoulou K, Michalopoulou VI, Scorilas A, **Adamopoulos PG**. Integrating Artificial Intelligence in Next-Generation Sequencing: Advances, Challenges, and Future Directions. *Curr Issues Mol Biol.* 2025 Jun 19;47(6):470. doi: [10.3390/cimb47060470](https://doi.org/10.3390/cimb47060470).
51. Tsiakanikas P, Athanasopoulou K, Darioti IA, Agiassoti VT, Theocharis S, Scorilas A, **Adamopoulos PG**. Beyond the Chromosome: Recent Developments in Decoding the Significance of Extrachromosomal Circular DNA (eccDNA) in Human Malignancies. *Life (Basel).* 2024; 14(8):922. doi: [10.3390/life14080922](https://doi.org/10.3390/life14080922).
52. Athanasopoulou K, **Adamopoulos PG**, Scorilas A. Unveiling the Human Gastrointestinal Tract Microbiome: The Past, Present, and Future of Metagenomics. *Biomedicines.* 2023; 11(3):827. doi: [10.3390/biomedicines11030827](https://doi.org/10.3390/biomedicines11030827).
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Cancer letters	Scientific Reports
RNA Biology	International Journal of Molecular Sciences
BMC Cancer	Cancers
Gene	Biochemical and Biophysical Research Communications
Biomedicines	Diagnostics
Bioinformatics	Genes