

**C.V. of  
Dr. Grigorios Amoutzias**

**Associate Professor of  
Bioinformatics with emphasis in Microbiology  
Department of Biochemistry & Biotechnology,  
University of Thessaly, Greece**

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## **PERSONAL DETAILS**

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Scopus author profile:

<https://www.scopus.com/authid/detail.uri?authorId=20733668700>

Google Scholar author profile:

<https://scholar.google.gr/citations?user=3kEqBHwAAAAJ&hl=en&oi=ao>

## **ACADEMIC CAREER**

### **Faculty/Research Positions**

- August 2019 – present: Associate Professor of Bioinformatics with emphasis in Microbiology, Department of Biochemistry and Biotechnology, University of Thessaly, Greece. Elected in April 2019.
- January 2014 – August 2019: Assistant Professor of Bioinformatics in Genomics, Department of Biochemistry and Biotechnology, University of Thessaly, Greece.
- July 2010 – January 2014: Lecturer of Bioinformatics in Genomics, Department of Biochemistry and Biotechnology, University of Thessaly, Greece.
- February 2010 – June 2010: Postdoctoral researcher at the Systems Biology group of Prof. Stephen G. Oliver, Department of Biochemistry, University of Cambridge, UK.
- February 2008 – January 2010: EMBO long term fellow at Prof. Yves Van de Peer's group, at the Bioinformatics and Evolutionary Genomics Group, Department of Plant Systems Biology, UGent & VIB, Gent, Belgium.
- July 2007 – January 2008: Postdoctoral researcher at the Bioinformatics and Evolutionary Genomics Group of Prof. Yves Van de Peer, Department of Plant Systems Biology, UGent & VIB, Gent, Belgium.
- April 2007 – July 2007: Visiting scientist at the Bioinformatics group of Dr. Christos Ouzounis, Institute of Agrobiotechnology, INA, EKETA, Thessaloniki, Greece.
- October 2005 - March 2007: First assistant at the Bioinformatics group of Prof. Marc Robinson-Rechavi, Department of Ecology and Evolution, Faculty of Medicine and Biology, University of Lausanne, Switzerland.
- March 2004 – September 2004. CASE (AstraZeneca) funded PhD placement in text mining, at the Pathways group of Dr David De Graaf, in the pharmaceutical company AstraZeneca PLC, Macclesfield, UK and Waltham, MA, USA.

## Education

- 2001-2005: PhD in Bioinformatics, Manchester University, UK. Supervisor: Prof Stephen G. Oliver.
- 2000-2001: MRes in Bioinformatics (with Distinction), Leeds University, UK
- 1998-1999: Exchange student with Erasmus/Socrates programme, Queen's University of Belfast, UK.
- 1994-1999: BSc in Biology, Aristotle University of Thessaloniki, Greece.
- Mathematical modelling: 3 weeks training (July - August 2012) in principles of Metabolic Simulations with Flux Balance Analysis in the group of Prof. Stephen G. Oliver, Department of Biochemistry, University of Cambridge, UK.

## Awards-scholarships-distinctions

- 2008 – 2010: EMBO long-term postdoctoral fellowship (ALTF-930-2007).  
[http://www.embo.org/fellowships/autumn\\_07.html](http://www.embo.org/fellowships/autumn_07.html)
- 2005: Best published PhD research of the year 2004 in the Faculty of Life Sciences, University of Manchester, UK. £1200 prize (see page 6 of document in url below, section: Faculty Research Symposium).  
<http://documents.manchester.ac.uk/display.aspx?DocID=7475>
- 2001-2004: EPSRC studentship for PhD studies.
- 2001-2004: CASE (AstraZeneca) studentship for PhD studies.
- 2004: Travel funding to attend the Gordon Conference on Molecular Evolution. Ventura, CA, USA. Poster presentation of the article published in EMBO reports (Amoutzias et al., 2004).
- Article in EMBO reports (Amoutzias et al., 2004) commented in:  
<http://www.nature.com/embor/journal/v5/n4/full/7400129.html>

## **TEACHING/SUPERVISION**

### **Teaching experience**

Since 2010, teaching duties in the Department of Biochemistry and Biotechnology, University of Thessaly, include/d:

- 2010 – present: Bioinformatics -4<sup>th</sup>/8<sup>th</sup> semester, core undergraduate course. Responsible for the preparation and teaching of 11 X 2h lectures and 3X6h practical courses.
- 2013 – present: Informatics – 1<sup>st</sup> semester core undergraduate course. Teaching of 11 X 3h lectures and 4X6h practical courses.
- 2013 – present: Introduction to Programming – 8<sup>th</sup> semester elective undergraduate course. Responsible for the preparation and teaching of 6 X 3h lectures/practicals.
- 2011 – 2017: Evolution – 7<sup>th</sup> semester core undergraduate course. Teaching of 2 X 3h lectures.
- 2010 – present: Bioinformatics – 1<sup>st</sup> semester core MSc course in Molecular Biology and Genetics Applications. Responsible for the preparation and teaching of 4 X 3h lectures/practicals.
- 2015 – 2019: Toxicogenomics. 1<sup>st</sup> semester core MSc course in Toxicology. Teaching of 1 X 3h lectures and 3 X 4h practicals.
- 2016: Genomics. 1<sup>st</sup> semester core MSc course in Bio-Enterprising. Teaching of a 3h lecture in Genomics and Bioinformatics. Course took place in Athens.
- 2015: Biological Databases. PEGA course on Life-long Learning. Teaching of 3 X 3h lectures (2 lectures in Larisa, 1 lecture in Patra).

For the teaching of most of the above courses, new teaching material (powerpoint presentations + practicals-manuals) had to be prepared by me. The courses that have been taught for more than one year have been updated regularly.

I was a lecturer and trainer in a training school of three days on “Basic bioinformatics analysis for NGS data from small RNA libraries“, held in Thessaloniki, Greece during 13-15 April 2016, as part of the DIVAS (Deep Investigation on Viral Associated Sequences) COST

action FA 1407. In addition, I prepared the IT infrastructure of 30 virtual linux machines and their necessary bioinformatics software for NGS analysis in the Okeanos computer cloud.

As a result of the above training school, I was invited by Prof. Margit Laimer (who attended the above school), at the Institute of Biotechnology, University of Natural Resources and Life Sciences, BOKU, Vienna, Austria to give a series of Lectures/Practicals on Linux and Microbial Genomics, within the Erasmus Exchange Programme. I visited the Institute between 28 September – 8 October 2016 and gave 16 hours of Lectures/Practicals (teaching material was prepared in English) that were attended by students and Faculty members.

I have also been invited and given lectures (concerning Bioinformatics, Genomics and Proteomics) in MSc courses at i) the Department of Medicine, University of Ioannina, Greece, by Prof. Friligos (since 2016), ii) at the Department of Molecular Biology and Genetics, University of Thrace, for three different MSc courses (since 2017) by Assoc. Prof. Glykos, Assoc. Prof. Galanis, Prof. Sandaltzopoulos, Prof. Chlichlia, Prof. Papageorgiou, iii) at the Department of Medicine, University of Thessaly, by Prof. Simos and by Prof. Tsezou for two different MSc courses (in 2018), and iv) at the Department of Ichthyology and Marine Environment of University of Thessaly, by Prof. Exadactylos (2020 - 2022).

### **Supervision experience**

During their undergraduate, MSc and PhD thesis, several students of the group who have finished or are currently doing their theses in my Bioinformatics laboratory, have published papers in peer-reviewed journals, some of them of high impact in their field, like Nucleic Acids Research, Molecular Biology and Evolution, Gigascience, Viruses, Virology.

### **Supervised Undergraduate Theses that have been completed**

- Vergou A. 2022. Core genome analysis of *Salmonella* strains.
- Banti E. 2022. Core genome analysis of the *Staphylococcus* genus with Bioinformatics methods.
- Kapetanos D. 2022. Core genome analysis of *E.coli* strains with Bioinformatics

methods.

- Fragkou N. 2022. Bioinformatic and phylogenomic analysis of the core genome amongst members of the genus *Streptomyces*.
- Kalogianni G. 2022. Bioinformatics and Evolutionary Analysis of Glucose Carriers and Their Relationship with Species Adaptability.
- Kostopoulos K. 2022. Evolutionary and Bioinformatic analysis of *Bacillus cereus* group representatives.
- Sforou V. 2021. Evolutionary analysis of Adenoviruses using Bioinformatics methods.
- Bakoulas A. 2021. Evolutionary analysis of HPV16 using Bioinformatics methods.
- Bramis C. 2020. Evolutionary analysis of Coronaviruses using Bioinformatics Methods.
- Nikolaidis M. 2019. Development of a Bioinformatics tool for the identification and evolutionary classification of the eukaryotic MFS superfamily of sugar transporters.
- Pateraki G. 2019. Prediction of N-glycosylation sites with machine learning methods.
- Mpachoumis G. 2019. BAC-TRECs: A Computational tool that detects recombination events among bacterial genomes.
- Ntountoumi C. 2018. Bioinformatic analysis of Low Complexity Regions in prokaryotes.
- Flatoura V. 2018. Prediction of methylation sites in eukaryotic proteins with machine learning algorithms.
- Diakogeorgiou A. 2018. Bioinformatic and evolutionary analysis of the Major Facilitator Superfamily Sugar Transporters.
- Tsimpidis M. 2014. Genomic and evolutionary analysis of human Enteroviruses with Bioinformatics methods.
- Chaliotis A. 2012. Detection of microbial tRNA-synthetases with bioinformatics methods.

### **Supervised Postgraduate Theses that have been completed:**

- Makri S. 2022. Predicting post-translational modifications of proteins using machine learning methods.
- Nikolaidis M. 2021. Phylogenomic and comparative genomic analysis of the bacillus evolutionary group *B. altitudinis* - *B. pumilus* - *B. safensis* with bioinformatic methods
- Spetsarias S. 2018. Development of a Bioinformatics protocol for genome analysis of microbes with toxicological and forensic interest, using Illumina and Pacific

## Biosciences technologies

- Tsionos G. 2018. Prediction of phosphorylation sites in rat proteins with machine learning methods.
- Chaliotis A. 2017. The complex evolutionary history of aminoacyl-tRNA synthetases.
- Tsimpidis M. 2016. T-RECs: Rapid and large-scale detection of recombination events among different evolutionary lineages of viral genomes.
- Kyriakidou, P. 2016. Literature mining and bioinformatics analyses of publicly available phosphoproteomics datasets.
- Tsouhliou P. 2015. Bioinformatics and evolutionary analysis of RNA-Sequencing data from Bivalvia.
- Chalvopoulou P. 2014. Bioinformatic analysis of microbial metagenomes from Next-Generation Sequencing data.
- Sini C. 2013. Bioinformatics analysis of Human Exome data from Next-Generation Sequencing technologies.
- Doxara A. 2012. Bioinformatics analysis of Mitochondrial gene networks and related diseases from Genomic and Systems Biology data.

## PhD Theses

- Nikolaidis M. Ongoing, since Oct 2020. I am supervisor. PhD thesis title: Development of Bioinformatics tools and computational analyses for comparative genomics. During his thesis and his stay in the Bioinformatics Laboratory (since he has been a first year undergraduate student), Mr Nikolaidis has already published 20 peer-reviewed papers, with seven of them as first author (one of them in the prestigious journal *Molecular Biology and Evolution*) and has developed two published computational tools. Mr Nikolaidis has been the recipient of a Bodossakis MSc studentship and of a University of Thessaly PhD studentship (DEKA).
- Vlastaridis P. 2020. I was supervisor. PhD thesis title: Bioinformatics Analysis, Management and Organization of Biological Data related to Post-Translational Regulation. During his thesis, Dr Vlastaridis published 6 peer-reviewed papers (two of them in the prestigious journal *Nucleic Acids Research*), and participated in the development of 5 computational tools.



- I have participated in the three-member advisory board of the PhD theses of Dr. Gkoutzourelas, Dr. Daskou and I am also serving in the three-member advisory board of the PhD candidate Mr. Aggelos Yfantis, from the Department of Medicine, University of Thessaly, supervised by Prof. Simos.

### **Advisor/Examiner**

Member of the examining committee that evaluated the PhD defence of:

- Dr. Ying He, University of Ghent, Belgium (Supervised by Prof. Yves Van de Peer).
- Dr. Dimitrios Tsakogiannis, Dept of Biochemistry and Biotechnology, University of Thessaly, Greece. 2014.
- Dr. Eirini Rouether, Dept of Biochemistry and Biotechnology, University of Thessaly, Greece. 2014
- Dr. Nikolaos Goutzourelas, Dept of Biochemistry and Biotechnology, University of Thessaly, Greece. 2016
- Dr Tilemaxos Dimitriou, Dept of Biochemistry and Biotechnology, University of Thessaly, Greece. 2017.
- Dr. Athina Dimopoulou, Dept of Biochemistry and Biotechnology, University of Thessaly, Greece. 2017.
- Dr. Stella Tamana, Dept of Biological Sciences, University of Cyprus. 2018.
- Dr Serafim Chaidoutis, Dept of Veterinary Sciences, Aristotle University of Thessaloniki. 2019.
- Dr. Panagiota Lazou, School of Medicine, University of Ioannina. 2021.
- Dr. Maria Daskou, Dept of Biochemistry and Biotechnology, University of Thessaly. 2021.
- Dr. Aikaterini Tatsaki. School of Medicine, University of Ioannina. 2021.

[https://www.didaktorika.gr/eadd/simple-search?query=%CE%91%CE%BC%CE%BF%CF%85%CF%84%CE%B6%CE%B9%CE%B1%CF%82&submit\\_search.x=0&submit\\_search.y=0](https://www.didaktorika.gr/eadd/simple-search?query=%CE%91%CE%BC%CE%BF%CF%85%CF%84%CE%B6%CE%B9%CE%B1%CF%82&submit_search.x=0&submit_search.y=0)

## **ADMINISTRATION**

### **Establishment of the Bioinformatics Research Laboratory.**

I established unofficially the Bioinformatics research laboratory of the Dept of Biochemistry and Biotechnology in 2010. The laboratory obtained legal status in 2015 (ΦΕΚ: 511/3.4.2015) with me as its Director since then.

In the Bioinformatics laboratory, undergraduate and postgraduate students learn to work primarily with Linux and Perl. Other programming languages may also be used, depending on the project and informatics expertise of the student, such as Python, Java, Javascript, Visual Basic, SQL, PHP, Graph Databases, Matlab. Student projects vary from analyzing large and diverse biological data (phylogenetics, phylogenomics, genomic recombination, RNA-Seq, High-throughput phosphoproteomic data) to developing computational tools (viral genotyping and recombination tools, protein motif detection, databases, prediction of phosphorylation sites with machine learning) or a combination of data analysis and software development.

### **Other Departmental and extra-Departmental Administration duties**

- In charge of the three-member committee that supervised the electronic election procedure for the position of the Head of the Department of Biochemistry and Biotechnology, University of Thessaly in 2022.
- Responsible for the Informatics Teaching Laboratory of the Department.
- Member of the advisory board of the MSc course of Molecular Diagnostics/Molecular Biomarkers that is hosted by the Department.
- Member of the advisory board of the MSc course of Toxicology that is hosted by the Department.
- Member of the Departmental committee that follows the progress of the PhD theses of the Department of Biochemistry and Biotechnology.
- Member of the tri-partite committee who evaluated the application of Assoc. Prof. Kyriakopoulou to join the Department of Biochemistry and Biotechnology, in 2020.
- Member of the tri-partite committee who prepared the evaluation report for the

election of Ioannis Iliopoulos, Assoc. Prof. of Molecular Biology and Bioinformatics, at the School of Medicine, University of Crete, in 2020. I also served as one of the 11-member committee who evaluated this application.

- Member of the five-member committee for the evaluation and selection of a Research Scientist (Level C) at the Department of Basic Biomedical Research of the Alexander Fleming Research Center, Athens, in 2020.
- I served as one of the 11-member committee who evaluated the candidacies for the position of Assistant Professor of Molecular Microbial Ecology and Genomics, at the Dept. of Biochemistry and Biotechnology, University of Thessaly, in 2020.
- I served as one of the 11-member committee who evaluated the tenure application of Dr Kolovos, Assist. Prof of Systems Biology, at the Dept. of Molecular Biology and Genetics, University of Thrace, in 2022.
- I served as one of the 11-member committee who evaluated the candidacies for the position of Assistant Professor of Microbial Biotechnology, at the Dept. of Biochemistry and Biotechnology, University of Thessaly, in 2022.

## **REVIEWER EXPERIENCE**

- One hundred and fifty three (153) **verified** (in Publons.com, now WebofScience) reviews for 56 peer-reviewed international journals, including prestigious bioinformatics journals like *Nucleic Acids Research*, *eLife*, *Virus Research*, *Bioinformatics*, *Genome Biology and Evolution*, *PLOS Computational Biology*, *BMC Biology*. Reviews for journals that belong in the field of Microbiology include *Virus Evolution*, *Infection*, *Genetics and Evolution*, *Fungal Biology*, *Intervirology*, *Journal of General Virology*, *Journal of Medical Virology*, *Pathogens*, *Microorganisms*, *Vaccines*, *Viruses*, *Virology*.
- Grant application reviewer (panel reviewer) for Qatar National Research Fund.
- Grant application reviewer for the Research Foundation - Flanders (Fonds Wetenschappelijk Onderzoek -Vlaanderen, FWO).
- Grant application reviewer for National Science Center of Poland.
- Grant application reviewer for the General Secretariat of Research and Technology (ΓΓΕΤ) and for ΕΛΙΔΕΚ.
- Reviewer for the Kalippos framework of open access online scientific books for the Greek Academia.

## **DISSEMINATION/OUTREACH/CONTRIBUTION TO SOCIETY**

During the COVID19 pandemic, I collaborated with the Laboratory of Epidemiology and Hygiene, (Prof. Hadjichristodoulou), where I worked gratis to develop a machine learning method based on Random Forests, in order to estimate the number of COVID19 cases from measurements of communal wastewater, for the cities of Larisa and Volos, in Thessaly. Due to the sensitive nature of this work, I gave it complete priority over all other ongoing research. This work was used for routine surveillance in Thessaly and was published in a peer-reviewed journal (Publication No. 65; Koureas, Amoutzias et al., 2021). My work in Coronavirus evolution (Publications No. 68–70) has also implications for the development of the next generation of COVID-19 vaccines. Especially the work in coronavirus recombination has been mentioned in an article of a world-renowned expert (Prof. Haseltine) in Forbes Magazine:

<https://www.forbes.com/sites/williamhaseltine/2022/04/01/coronaviruses-can-recombine-with-cellular-and-heterologous-viruses-to-create-unexpected-variants/>

I organized the IT infrastructure of the DIVAS COST action FA 1407 training School (mentioned in detail above in Teaching Section) and also provided lectures/practicals within that framework.

I also visited the Laboratory of Prof. Margit Laimer at the University of Natural Resources and Life Sciences (BOKU), Vienna, Austria within the Erasmus Exchange Programme and provided consultation in matters of NGS analysis as well as a series of Lectures/practicals on Linux and Genomics.

### **Conferences and invited talks**

I have given the following oral presentations in Conferences and Academic Institutes within the last 7 years:

- June 2022. Oral Presentation. The contribution of Genomics and Bioinformatics in confronting hybrid bio-threats. In: 2nd Forum on Hybrid Threats, Cyber-security, and Artificial Intelligence, Athens. The meeting was attended by high-ranking Greek Government Officials specializing in Cyber-Security and Cyber/Hybrid-threats.  
<https://fhtcsai2022.fainst.eu/>
- November 2018. Plenary Lecture: Post-translational modifications in the era of Proteomics and Bioinformatics. In Hellenic Society of Biochemistry and Molecular Biology annual conference.
- August 2017. Oral presentation. Estimating the total number of phosphoproteins and phosphorylation sites in eukaryotic proteomes. In the Gordon Research Conference, Hong Kong.
- May 2017. Oral presentation. T-RECs: rapid and large-scale detection of recombination events among different evolutionary lineages of viral genomes. In Hellenic Society of Virology conference.
- May 2017. Invited Talk. The properties of the eukaryotic phosphoproteome through the bioinformatics lens. In Hellenic society of Biological Sciences annual conference.
- January 2017. Title: The phosphoproteome through the Bioinformatics prism. Dept of Medicine, University of Ioannina, Greece. Invited talk by Prof. Friligos.
- November 2016. Title: The complex evolutionary history of aminoacyl tRNA synthetases. Oral Presentation In Hellenic Society of Biochemistry and Molecular Biology annual conference.
- February 2016. Title: The phosphoproteome through the Bioinformatics prism. Demokritos Research Center, Athens, Greece. Invited talk by Dr. Stratikos.
- October 2015. Title: Phosphoproteomics, a critical view through the Bioinformatics lens. Oral Presentation in CIBB 2015, Naples, Italy.
- May 2015. Title: The phosphoproteome through the bioinformatics prism: evaluation and properties. Dept. of Medicine, University of Patra. Invited talk by Prof. Stathopoulos.

## **RESEARCH**

### **Keywords**

Bioinformatics, Prokaryotes, Viruses, Evolution, Gene Regulation, Transcription Factors, Phosphorylation, Molecular Networks, Secondary Metabolism, Genomics, Proteomics, Phylogenetics, Data Integration, Text Mining.

### **Research interests**

During my PhD and other research posts, I focused on the integration of data from genomic, various functional 'omic' sources, and from literature. This data integration, combined with statistical, phylogenetic and domain architecture analyses gave insight about the properties, functions and evolution of molecular networks, especially at the level of post-translational regulation. Specifically, the work on dimerizing TFs provided for the first time a detailed and yet simple model for convergent evolution of protein interaction networks. Moreover, it generated new hypotheses about dimerization patterns in oncogenic TFs, that may be targeted and exploited therapeutically in the future. Peer-reviewed papers that were published from this line of research include publications No. 2-9, 11, 12, 14. Publication No. 14 has been cited by a Patent from Prof. Richard Young at the Whitehead Institute, concerning methods of altering gene expression by perturbing transcription factor multimers that structure regulatory loops.

During my postdoctoral positions at the University of Ghent, Belgium, at the University of Cambridge, UK and as a faculty member at the Department of Biochemistry and Biotechnology, University of Thessaly, I worked on the evolution and properties of post-translational modifications in model eukaryotes, like the yeast *S. cerevisiae*. My team have been integrating high-throughput MS/MS proteomic with genomic and functional genomic data. Published and ongoing work has demonstrated the global properties of the yeast phosphoproteome, the intricacies of its evolution and also that post-translational regulation

affects the evolution of the genome, specifically by affecting the survival rate of duplicated genes. Peer-reviewed papers that were published from this line of research include publications No. 18, 21, 30, 36, 38, 76.

Another current major research theme is virus evolution and recombination, particularly in Enteroviruses, Noroviruses, HPV16, and lately Coronaviruses, where data have been analysed and computational tools have been developed. Peer-reviewed papers that were published from this line of research include publications No. 23-29, 31, 34, 35, 39-41, 45-47, 50, 55, 59, 65-70, 75.

Also, evolution of certain bacteria (phylogenomics, core genome analysis) and evolution of bacterial protein families that are important for the primary and secondary metabolism are another major research theme. Peer-reviewed papers that were published from this line of research include publications No. 10, 16, 17, 32, 37, 43, 44, 48, 52, 54, 57, 58, 60-63, 71, 72, 74.

### **Accepted Research Proposals.**

- 2014 - 2015: Aristeia II national research framework for the **F**iltering, **A**nnotation and **B**ioinformatics analyses of high-throughput **P**hosphoproteomic data (FAB-Phos). Budget: €200,000. Principal Investigator: Dr. Amoutzias.
- 2011 – 2012: Processing and analysis of human genomic and phosphoproteomic data. Funded by the Research Committee of the University of Thessaly. Budget: €3,330. Principal Investigator: Dr. Amoutzias.
- 2008 – 2010: EMBO long-term postdoctoral fellowship (ALTF-930-2007).

As a member of my research group, Mr Nikolaidis has been the recipient of a Bodossakis studentship and of a University of Thessaly PhD studentship (DEKA).

### **Development of computational tools**

My group has developed and made publicly available the following computational tools:



A webserver for the detection and functional annotation of prokaryotic tRNA-synthetases

<http://bioinf.bio.uth.gr/aars/#/upload>

Published in Nucleic Acids Research in 2017 (Chaliotis et al., 2017)

A database of prokaryotic tRNA-synthetases

<http://bioinf.bio.uth.gr/aars/#/searchall>

Published in Nucleic Acids Research in 2017 (Chaliotis et al., 2017)

A software (T-RECs) that identifies recombination events in viral genomes

<http://bioinf.bio.uth.gr/t-recs.html>

Published in BMC Bioinformatics in 2017 (Tsimpidis et al., 2017)

A webserver (NAT/NCS2 hound) for the detection and functional/evolutionary classification of prokaryotic and eukaryotic NAT/NCS2 nucleobase transporters.

<http://bioinf.bio.uth.gr/nat-ncs2/#/>

Published in Gigascience in 2018 (Chaliotis et al., 2018)

A Neural Network webserver for the detection and functional prediction of prokaryotic low complexity regions

<http://bioinf.bio.uth.gr/lcr/#/>

Published in Nucleic Acids Research (Ntountoumi et al., 2019)

A Python program that performs analysis of core proteomes.

Published in Diversity in 2020 (Nikolaidis et al., 2020).

A python program that performs risk-assessment, lineage genotyping and recombination detection in HPV16 sequences.

<http://bioinf.bio.uth.gr/hpv16-genotyper.html>

Published in Diversity in 2021 (Nikolaidis et al., 2021).

A Neural Network webserver for the prediction of phosphorylation and methylation sites in eukaryotic proteins

<http://bioinf.bio.uth.gr/meth-phos-prometheus/#/>

Manuscript in preparation (Ntountoumi, Vlastaridis et al.,)

A database of human and yeast phosphorylation sites

<http://bioinf.bio.uth.gr/phospho-prometheus-db/#/>

Manuscript in preparation (Vlastaridis et al.,)

## Publications of Dr. Grigorios D. Amoutzias

I have co-authored 79 peer-reviewed papers (15 as first author, 16 as corresponding author), 3 book chapters in the field of Bioinformatics and also translated (in Greek) four book chapters of University student text-books, on Bioinformatics, Genomics, Proteomics and Systems Biology. All my work is purely computational. According to Google Scholar (search on 26-04-2023), my work has been cited 3334 times and has an H-index of 28 and i10 index of 51. According to Scopus (search on 26-04-2023), my work has been cited 2268 times (2175 times, excluding self-citations of selected author; 1846 times, excluding self-citations of all authors) and has an H-index of 23. The cumulative five-year impact factor (based on Web of Science, for the year 2021) is 519.

### Summary Statistics (search on 26-04-2023)

| Paper No. | Auth. Pos.   | Type              | Journal                                     | Year | Scopus Cit. excl.all authors | ISI I.F. 2021 |
|-----------|--------------|-------------------|---|------|------------------------------|---------------|
| 79        | 7/7<br>Corr. | Research          | Microbial Genomics                          | 2023 | 0                            | 7.1           |
| 78        | 13/14        | Research          | Foods                                       | 2023 | 0                            | 5.9           |
| 77        | 5/7          | Review + Analysis | Cells                                       | 2023 | 0                            | 7.7           |
| 76        | 3/7          | Research          | International Journal of Molecular Sciences | 2023 | 0                            | 6.6           |
| 75        | 9/10         | Review + Analysis | Viruses                                     | 2022 | 0                            | 5.8           |
| 74        | 7/8          | Research          | Applied Sciences                            | 2022 | 0                            | 2.9           |
| 73        | 5/9          | Research          | International Journal of Molecular Sciences | 2022 | 0                            | 6.6           |
| 72        | 6/6<br>Corr  | Research          | Microorganisms                              | 2022 | 2                            | 5.1           |
| 71        | 1/3<br>Corr  | Review + Analysis | Microorganisms                              | 2022 | 5                            | 5.1           |
| 70        | 6/6<br>Corr  | Research          | Viruses                                     | 2022 | 20                           | 5.8           |
| 69        | 5/5<br>Corr  | Research          | Mol. Bio. Evol.                             | 2022 | 16                           | 20.1          |
| 68        | 1/6<br>Corr  | Review            | Viruses                                     | 2022 | 35                           | 5.8           |

|    |                |          |                                 |      |    |      |
|----|----------------|----------|---------------------------------|------|----|------|
| 67 | 3/7            | Review   | Exp. Rev. Mol. Med.             | 2021 | 4  | 7.3  |
| 66 | 8/8<br>Corr.   | Research | Diversity                       | 2021 | 1  | 2.9  |
| 65 | 2/13           | Research | Environmental Research          | 2021 | 11 | 8.4  |
| 64 | 6/10           | Research | Nucleic Acids Res               | 2021 | 6  | 17.2 |
| 63 | 5/7            | Research | Applied Sciences                | 2021 | 4  | 2.9  |
| 62 | 8/10           | Research | Antibiotics                     | 2021 | 6  | 5.4  |
| 61 | 7/8            | Research | Foods                           | 2021 | 13 | 5.9  |
| 60 | 6/8            | Research | Microb Drug Resist              | 2021 | 4  | 2.9  |
| 59 | 6/8            | Research | J Virol Methods                 | 2021 | 1  | 2.2  |
| 58 | 2/3            | Review   | Eur Food Res Technol            | 2021 | 22 | 3.5  |
| 57 | 7/8            | Research | Front Microbiol.                | 2021 | 21 | 6.8  |
| 56 | 3/6            | Research | Molecules                       | 2021 | 8  | 5.1  |
| 55 | 5/8            | Research | J Appl Microbiol                | 2021 | 7  | 4.4  |
| 54 | 4/5            | Review   | Antibiotics                     | 2020 | 32 | 5.4  |
| 53 | 3/6            | Research | Metabolites                     | 2020 | 31 | 5.5  |
| 52 | 4/4<br>Corr.   | Research | Diversity                       | 2020 | 16 | 2.9  |
| 51 | 9/11           | Research | J Exp Bot.                      | 2020 | 4  | 8.3  |
| 50 | 6/7            | Research | Virus Genes                     | 2020 | 2  | 1.9  |
| 49 | 9/15           | Research | NAR Genomics and Bioinformatics | 2020 | 0  | 0    |
| 48 | 8/8<br>Corr.   | Research | <i>Nucleic Acids Res</i>        | 2019 | 26 | 17.2 |
| 47 | 4/8            | Research | <i>J Virol Methods</i>          | 2019 | 16 | 2.2  |
| 46 | 6/9            | Research | <i>Mol Cell Probes</i>          | 2019 | 1  | 2.8  |
| 45 | 7/7<br>Corr.   | Research | Virology                        | 2019 | 28 | 3.5  |
| 44 | 10/10<br>Corr. | Research | Gigascience                     | 2018 | 4  | 8.4  |
| 43 | 3/7            | Research | Microbiologyopen                | 2018 | 22 | 4.1  |
| 42 | 6/8            | Research | Mech Ageing Dev.                | 2018 | 6  | 5.2  |
| 41 | 5/8            | Research | J Med Virol                     | 2018 | 5  | 12.2 |
| 40 | 2/6            | Research | Arch Virol                      | 2018 | 3  | 2.5  |
| 39 | 5/9            | Research | Lett Appl Microbiol             | 2017 | 0  | 3.1  |
| 38 | 6/6<br>Corr.   | Research | Genes, Genomes, Genetics        | 2017 | 15 | 3.5  |

|    |              |                         |                                  |      |     |                |
|----|--------------|-------------------------|----------------------------------|------|-----|----------------|
| 37 | 7/7<br>Corr. | Research                | Nucleic Acids Research.          | 2017 | 41  | 17.2           |
| 36 | 6/6<br>Corr. | Research                | Gigascience                      | 2017 | 67  | 8.4            |
| 35 | 7/7<br>Corr. | Research                | BMC Bioinformatics               | 2017 | 5   | 4.3            |
| 34 | 7/8          | Research                | Viral Immunol.                   | 2016 | 1   | 2.2            |
| 33 | 1/7          | Research                | PLoS One.                        | 2016 | 4   | 4.1            |
| 32 | 1/3          | Review<br>+<br>Analysis | Mar Drugs.                       | 2016 | 51  | 6              |
| 31 | 3/4          | Research                | Arch Virol.                      | 2016 | 8   | 2.5            |
| 30 | 4/4<br>Corr. | Review                  | Lecture Notes in Bioinformatics. | 2016 | 1   | 0              |
| 29 | 3/5          | Research                | Plant Pathology                  | 2015 | 12  | 3.1            |
| 28 | 5/8          | Research                | Infect Genet Evol                | 2015 | 7   | 3.7            |
| 27 | 3/4          | Review<br>+<br>Analysis | Virus Genes                      | 2015 | 40  | 1.9            |
| 26 | 4/8          | Research                | J Med Microbiol                  | 2014 | 7   | 3              |
| 25 | 5/8          | Research                | Mol Cell Probes                  | 2014 | 6   | 2.8            |
| 24 | 7/8          | Research                | Arch Virol                       | 2014 | 5   | 2.5            |
| 23 | 3/7          | Research                | Arch Virol                       | 2013 | 4   | 2.5            |
| 22 | 1/5          | Research                | Mol Cell Proteomics              | 2012 | 40  | 6.6            |
| 21 | 2/6          | Review                  | Food Chem Toxicol                | 2012 | 130 | 5.7            |
| 20 | 5/84         | Review                  | Advances in Botanical Research   | 2012 | 7   | 3.4            |
| 19 | 6/77         | Research                | Nature                           | 2010 | 415 | 63.6           |
| 18 | 1/6          | Research                | Proc Natl Acad Sci U S A         | 2010 | 41  | 13.5           |
| 17 | 2/2          | Review                  | Int J Med Microbiol              | 2009 | 18  | 3.9            |
| 16 | 1/3          | Review                  | Future Microbiol                 | 2008 | 25  | 3.8            |
| 15 | 1/2          | Preview                 | Dev Cell                         | 2008 | 11  | 13.3           |
| 14 | 1/4          | Review                  | Trends Biochem Sci.              | 2008 | 173 | 20.8           |
| 13 | 3/5          | Research                | Comput Biol Chem                 | 2008 | 5   | 2.9            |
| 12 | 2/4          | Research                | Proc Natl Acad Sci U S A.        | 2007 | 31  | 13.5           |
| 11 | 4/5          | Research                | BMC Bioinformatics               | 2007 | 3   | 4.3            |
| 10 | 2/2          | Review                  | Future Microbiol                 | 2007 | 16  | 3.8            |
| 9  | 1/9          | Research                | BMC Syst Biol                    | 2007 | 28  | 2.4*<br>(2018) |
| 8  | 1/7          | Research                | Mol Biol Evol                    | 2007 | 113 | 20             |
| 7  | 1/4          | Research                | BMC Genomics                     | 2006 | 21  | 4.9            |

|   |     |          |                                      |      |    |      |
|---|-----|----------|--------------------------------------|------|----|------|
|   |     | h        |                                      |      |    |      |
| 6 | 4/5 | Research | J Bioinform Comput Biol.             | 2005 | 7  | 1.1  |
| 5 | 1/3 | Research | Gene                                 | 2005 | 4  | 3.5  |
| 4 | 1/4 | Research | EMBO Rep                             | 2004 | 48 | 10.7 |
| 3 | 1/3 | Review   | Comp Func Genomics                   | 2004 | 14 | 1.8  |
| 2 | 4/5 | Research | Proc IEEE Comput Syst Bioinform Conf | 2004 | 22 | 0    |
| 1 | 4/5 | Research | J Hered                              | 2003 | 4  | 3.2  |
|   |     |          |                                      |      |    | 519  |

## Selected Publications

Nikolaidis M, Markoulatos P, Van de Peer Y, Oliver SG, **Amoutzias GD**. The Neighborhood of the Spike Gene Is a Hotspot for Modular Intertypic Homologous and Nonhomologous Recombination in Coronavirus Genomes. *Mol Biol Evol*. 2022 Jan 7;39(1):msab292. doi: 10.1093/molbev/msab292.

Ntountoumi C, Vlastaridis P, Mossialos D, Stathopoulos C, Iliopoulos I, Promponas V, Oliver SG, **Amoutzias GD**. Low complexity regions in the proteins of prokaryotes perform important functional roles and are highly conserved. *Nucleic Acids Res*. 2019 Sep 4. pii: gkz730. doi: 10.1093/nar/gkz730.

Chalioitis A, Vlastaridis P, Mossialos D, Ibba M, Becker HD, Stathopoulos C, **Amoutzias GD**. The complex evolutionary history of aminoacyl-tRNA synthetases. *Nucleic Acids Res*. 2017 Feb 17;45(3):1059-1068.

Vlastaridis P, Kyriakidou P, Chalioitis A, Van de Peer Y, Oliver SG, **Amoutzias GD**. Estimating the total number of phosphoproteins and phosphorylation sites in eukaryotic proteomes. *Gigascience*. 2017 Feb 1;6(2):1-11. doi: 10.1093/gigascience/giw015. PMID:28327990

**Amoutzias GD**, He Y, Lilley KS, Van de Peer Y, Oliver SG. Evaluation and properties of the budding yeast phosphoproteome. *Mol Cell Proteomics*. 2012 Jun;11(6):M111.009555.

Cock MJ, Sterck L, Rouzé P, Scornet D, Allen AE, **Amoutzias G**, et al. The Ectocarpus genome and the independent evolution of multicellularity in brown algae. *Nature*. 2010 Jun 3;465(7298):617-21.

**Amoutzias GD**, He Y, Gordon J, Mossialos D, Oliver SG, Van de Peer Y. Posttranslational regulation impacts the fate of duplicated genes. *Proc Natl Acad Sci U S A*. 2010 Feb 16;107(7):2967-71.

**Amoutzias GD**, Robertson DL, Van de Peer Y, Oliver SG. Choose your partners: Dimerization in eukaryotic transcription factors. *Trends Biochem Sci*. 2008 May;33(5):220-9.

Pinney JW, **Amoutzias GD**, Rattray M, Robertson DL. Reconstruction of ancestral protein interaction networks for the bZIP transcription factors. *Proc Natl Acad Sci U S A*. 2007 Dec 18;104(51):20449-53

**Amoutzias G**, Veron A, Weiner A, Robinson-Rechavi M, Bornberg-Bauer E, Oliver S, Robertson D. One Billion Years of bZIP Transcription Factor Evolution: Conservation and Change in Dimerization, and DNA-Binding Site Specificity. *Mol Biol Evol*. 2007.

**Amoutzias GD**, Robertson DL, Oliver SG, Bornberg-Bauer E. Convergent evolution of gene networks by single-gene duplications in higher eukaryotes. *EMBO Rep*. 2004 Mar;5(3):274-9.

### Published Book Chapters

3) **Αμούτζιας Γρ.**, Ηλιόπουλος Ι. Μοριακή Γενετική του Ανθρώπου. Κεφάλαιο 11. Γονιδιωματική, Βιοπληροφορική και Πρωτεωμική.

2) **Amoutzias G.D.** and Van de Peer Y. Single-Gene and Whole-Genome duplications and the evolution of protein-protein interaction networks. In: *Evolutionary Genomics and Systems Biology*. 2010. pp. 413-429

1) **Αμούτζιας Γρ.**, Van de Peer Y. Η εξέλιξη των πρωτεϊνικών αλληλεπιδράσεων μέσα από το πρίσμα της Βιοπληροφορικής και της Βιολογίας Συστημάτων. In: *Βιοπληροφορική*. 2008. Επιμέλεια: Κοσσίδα Σ. Σελ. 187-204.

### Translations of Student text books

4) **Αμούτζιας Γρ.**, Ηλιόπουλος Ι., Φαδούλογλου Β. Κεφάλαιο 12. Πρωτεϊνική Ανάλυση και Πρωτεωμική. Βιοπληροφορική και Λειτουργική Γονιδιωματική, 3<sup>η</sup> έκδοση, Pevsner J. Επιστημονική επιμέλεια της μετάφρασης του κεφαλαίου.

3) **Αμούτζιας Γρ.**, Ηλιόπουλος Ι. Κεφάλαιο 5 Προηγμένα προγράμματα αναζήτησης σε βάσεις δεδομένων. Βιοπληροφορική και Λειτουργική Γονιδιωματική, 3<sup>η</sup> έκδοση, Pevsner J. Επιστημονική επιμέλεια της μετάφρασης του κεφαλαίου.

1 +2) Παπασιδέρη Ι, **Αμούτζιας Γρ.** Γονιδιωματική, Πρωτεομική, Βιολογία Συστημάτων.  
Κεφάλαιο 5 Φοιτητικού συγγράμματος «Το Κύτταρο-Μια Μοριακή προσέγγιση”.  
Επιστημονική επιμέλεια της μετάφρασης του κεφαλαίου για την 2<sup>η</sup> και 3<sup>η</sup> ελληνική έκδοση.

## Published Peer-reviewed Papers

\* denotes corresponding author

### 2023

79) Nikolaidis M, Hesketh A, Frangou N, Mossialos D, Van de Peer Y, Oliver SG, **Amoutzias GD\***. A panoramic view of the genomic landscape of the genus *Streptomyces*. *In press: Microbial Genomics*.

78) Goutzourelas N, Kevrekidis DP, Barda S, Malea P, Trachana V, Savvidi S, Kevrekidou A, Assimopoulou AN, Goutas A, Liu M, Lin X, Kollatos N, **Amoutzias GD**, Stagos D. Antioxidant Activity and Inhibition of Liver Cancer Cells' Growth of Extracts from 14 Marine Macroalgae Species of the Mediterranean Sea. *Foods*. 2023 Mar 19;12(6):1310. doi: 10.3390/foods12061310. PMID: 36981236; PMCID:PMC10048654.

77) Yfantis A, Mylonis I, Chachami G, Nikolaidis M, **Amoutzias GD**, Paraskeva E, Simos G. Transcriptional Response to Hypoxia: The Role of HIF-1-Associated Co-Regulators. *Cells*. 2023 Mar 3;12(5):798. doi: 10.3390/cells12050798. PMID:36899934; PMCID: PMC10001186.

76) Papanikolaou NA, Nikolaidis M, **Amoutzias GD**, Fouza A, Papaioannou M, Pandey A, Papavassiliou AG. The Dynamic and Crucial Role of the Arginine Methylproteome in Myoblast Cell Differentiation. *Int. J. Mol. Sci.* 2023, 24(3), 2124; <https://doi.org/10.3390/ijms24032124>.

### 2022

75) Tsakogiannis D, Nikolaidis M, Zagouri F, Zografos E, Kottaridi C, Kyriakopoulou Z, Tzioga L, Markoulatos P, **Amoutzias GD**, Bletsas G. Mutation Profile of HPV16 L1 and L2 Genes in Different Geographic Areas. *Viruses* 2022 Dec 31;15(1):141. doi: 10.3390/v15010141.

74) Georgi I, Asoutis Didaras N, Nikolaidis M, Dimitriou TG, Charistos L, Hatjina F, **Amoutzias GD**, Mossialos D. The Impact of *Vairimorpha* (*Nosema*) *ceranae* Natural Infection on Honey Bee (*Apis mellifera*) and Bee Bread Microbiota. *Applied Sciences* (Switzerland), 2022, 12(22), 11476.

73) Baltasvia I, Theodosiou T, Papanikolaou N, Pavlopoulos GA, **Amoutzias GD**, Panagopoulou M, Chatzaki E, Andreakos E, Iliopoulos I. Prediction and Ranking of Biomarkers Using *multiple* UniReD. *Int J Mol Sci.* 2022 Sep 21;23(19):11112. doi: 10.3390/ijms231911112

72) Nikolaidis M, Hesketh A., Mossialos D. Iliopoulos I. Oliver S.G., **Amoutzias G.D\***. A Comparative Analysis of the Core Proteomes within and among the *Bacillus subtilis* and *Bacillus cereus* Evolutionary Groups Reveals the Patterns of Lineage- and Species-Specific Adaptations. *Microorganisms* 2022, 10(9), 1720; doi: 10.3390/microorganisms10091720.

71) **Amoutzias GD\***, Nikolaidis M, Hesketh A. The Notable Achievements and the Prospects of Bacterial Pathogen Genomics. *Microorganisms*. 2022 May 17;10(5):1040. doi: 10.3390/microorganisms10051040.

70) Nikolaidis M, Papakyriakou A, Chlichlia K, Markoulatos P, Oliver SG, **Amoutzias GD\***. Comparative Analysis of SARS-CoV-2 Variants of Concern, Including Omicron, Highlights Their Common and Distinctive Amino Acid Substitution Patterns, Especially at the Spike ORF. *Viruses*. 2022 Mar 29;14(4):707. doi: 10.3390/v14040707.

69) Nikolaidis M, Markoulatos P, Van de Peer Y, Oliver SG, **Amoutzias GD\***. The Neighborhood of the Spike Gene Is a Hotspot for Modular Intertypic Homologous and Nonhomologous Recombination in Coronavirus Genomes. *Mol Biol Evol.* 2022 Jan 7;39(1):msab292. doi: 10.1093/molbev/msab292.



Mention in Forbes Magazine:

<https://www.forbes.com/sites/williamhaseltine/2022/04/01/coronaviruses-can-recombine-with-cellular-and-heterologous-viruses-to-create-unexpected-variants/>

68) **Amoutzias GD\***, Nikolaidis M, Tryfonopoulou E, Chlichlia K, Markoulatos P, Oliver SG. The Remarkable Evolutionary Plasticity of Coronaviruses by Mutation and Recombination: Insights for the COVID-19 Pandemic and the Future Evolutionary Paths of SARS-CoV-2. *Viruses*. 2022 Jan 2;14(1):78. doi: 10.3390/v14010078.

## 2021

67) Bletsa G, Zagouri F, **Amoutzias GD**, Nikolaidis M, Zografos E, Markoulatos P, Tsakogiannis D. Genetic variability of the HPV16 early genes and LCR. Present and future perspectives. *Expert Rev Mol Med*. 2021 Dec 1;23:e19. doi: 10.1017/erm.2021.18.

66) Nikolaidis M, Tsakogiannis D, Bletsa G, Mossialos D, Kottaridi C, Iliopoulos I, Markoulatos P, **Amoutzias GD\***. HPV16-genotyper: A computational tool for risk-assessment, lineage genotyping and recombination detection in hpv16 sequences, based on a large-scale evolutionary analysis. *Diversity* Volume 13, Issue 10 October 2021 Article number 497

65) Koureas M, **Amoutzias GD**, Vontas A, Kyritsi M, Pinaka O, Papakonstantinou A, Dadouli K, Hatzinikou M, Koutsolioutsou A, Mouchtouri VA, Speletas M, Tsiodras S, Hadjichristodoulou C. Wastewater monitoring as a supplementary surveillance tool for capturing SARS-COV-2 community spread. A case study in two Greek municipalities. *Environ Res*. 2021 Sep;200:111749. doi: 10.1016/j.envres.2021.111749.

64) Theodorakis E, Antonakis AN, Baltsavia I, Pavlopoulos GA, Samiotaki M, **Amoutzias GD**, Theodosiou T, Acuto O, Efstathiou G, Iliopoulos I. ProteoSign v2: a faster and evolved user-friendly online tool for statistical analyses of differential proteomics. *Nucleic Acids Res*. 2021 Jul 2;49(W1):W573-W577. doi: 10.1093/nar/gkab329.

63) Tsadila C, Nikolaidis M, Dimitriou TG, Kafantaris I, **Amoutzias GD**, Pournaras S, Mossialos D. Antibacterial Activity and Characterization of Bacteria Isolated from Diverse Types of Greek Honey against Nosocomial and Foodborne Pathogens. *Applied Sciences* (Switzerland), Volume 11, Issue 131 July 2021 Article number 5801.

62) Didaras NA, Kafantaris I, Dimitriou TG, Mitsagga C, Karatasou K, Giavasis I, Stagos D, **Amoutzias GD**, Hatjina F, Mossialos D. Biological Properties of Bee Bread Collected from Apiaries Located across Greece. *Antibiotics* (Basel). 2021 May 10;10(5):555. doi: 10.3390/antibiotics10050555.

61) Kafantaris I, Tsadila C, Nikolaidis M, Tsavea E, Dimitriou TG, Iliopoulos I, **Amoutzias GD**, Mossialos D. Transcriptomic Analysis of *Pseudomonas aeruginosa* Response to Pine Honey via RNA Sequencing Indicates Multiple Mechanisms of Antibacterial Activity. *Foods*. 2021 Apr 24;10(5):936. doi: 10.3390/foods10050936.

60) Koutsianos D, Athanasiou LV, Dimitriou T, Nikolaidis M, Tsadila C, **Amoutzias G**, Mossialos D, Koutoulis KC. Antibiotic Resistance Patterns and *mcr-1* Detection in Avian Pathogenic *Escherichia coli* Isolates from Commercial Layer and Layer Breeder Flocks Demonstrating Colibacillosis in Greece. *Microb Drug Resist*. 2020 Sep 21. doi: 10.1089/mdr.2020.0057.

59) Daskou M, Tsakogiannis D, Alexopoulou DS, Dimitriou TG, Mossialos D, **Amoutzias GD**, Kottaridi C, Markoulatos P. A colorimetric IsoPCR for the rapid and sensitive visual detection of high-risk HPV16 in clinical samples with hydroxynaphthol blue. *J Virol Methods*. 2021 Apr;290:114072. doi: 10.1016/j.jviromet.2021.114072

58) Kafantaris, I., **Amoutzias, G.D.** & Mossialos, D. Foodomics in bee product research: a systematic literature review. *Eur Food Res Technol* (2020). <https://doi.org/10.1007/s00217-020-03634-5>

57) Samaras A, Nikolaidis M, Antequera-Gómez ML, Cámara-Almirón J, Romero D, Moschakis T, **Amoutzias GD**, Karaoglanidis GS. Whole Genome Sequencing and Root

Colonization Studies Reveal Novel Insights in the Biocontrol Potential and Growth Promotion by *Bacillus subtilis* MBI 600 on Cucumber. *Front Microbiol.* 2021 Jan 12;11:600393. doi: 10.3389/fmicb.2020.600393.

56) Koureas M, Kalompatsios D, **Amoutzias GD**, Hadjichristodoulou C, Gourgoulisanis K, Tsakalof A. Comparison of Targeted and Untargeted Approaches in Breath Analysis for the Discrimination of Lung Cancer from Benign Pulmonary Diseases and Healthy Persons. *Molecules.* 2021 Apr 29;26(9):2609. doi: 10.3390/molecules26092609.

55) Daskou M, Dimitriou TG, Alexopoulou DS, Tsakogiannis D, **Amoutzias GD**, Mossialos D, Kyriakopoulou Z, Markoulatos P. WarmStart colorimetric RT-LAMP for the rapid, sensitive and specific detection of Enteroviruses A-D targeting the 5'UTR region. *J Appl Microbiol.* 2021 Jan;130(1):292-301. doi: 10.1111/jam.14770.

## 2020

54) Didaras NA, Karatasou K, Dimitriou TG, **Amoutzias GD**, Mossialos D. Antimicrobial Activity of Bee-Collected Pollen and Beebread: State of the Art and Future Perspectives. *Antibiotics (Basel).* 2020 Nov 14;9(11):811. doi: 10.3390/antibiotics9110811.

53) Koureas M, Kirgou P, **Amoutzias G**, Hadjichristodoulou C, Gourgoulisanis K, Tsakalof A. Target Analysis of Volatile Organic Compounds in Exhaled Breath for Lung Cancer Discrimination from Other Pulmonary Diseases and Healthy Persons. *Metabolites.* 2020 Aug 3;10(8):317. doi: 10.3390/metabo10080317.

52) Nikolaidis M, Mossialos D, Oliver SG, **Amoutzias GD\***. Comparative Analysis of the Core Proteomes among the *Pseudomonas* Major Evolutionary Groups Reveals Species-Specific Adaptations for *Pseudomonas aeruginosa* and *Pseudomonas chlororaphis*. *Diversity* 2020, 12(8), 289; <https://doi.org/10.3390/d12080289>

51) Komaitis F, Kalliampakou K, Botou M, Nikolaidis M, Kalloniati C, Skliros D, Du B, Rennenberg H, **Amoutzias GD**, Frillingos S, Fletmetakis E. Molecular and physiological

characterization of the monosaccharide transporters gene family in *Medicago truncatula*. *J Exp Bot.* 2020 May 30;71(10):3110-3125. doi: 10.1093/jxb/eraa055.

50) Daskou M, Dimitriou TG, Kouklamani-Giannouli G, Nikolaidis M, Mossialos D, **Amoutzias GD**, Markoulatos P. Development of a reverse transcription loop-mediated isothermal amplification assay (RT-LAMP) that detects enteroviruses by targeting the highly conserved 5'-UTR region. *Virus Genes.* 2020 Apr;56(2):194-201. doi: 10.1007/s11262-020-01732-w. Epub 2020 Jan 18. PMID: 31955385

49) Theodosiou T, Papanikolaou N, Savvaki M, Bonetto G, Maxouri S, Fakourelis E, Eliopoulos AG, Tavernarakis N, **Amoutzias GD**, Pavlopoulos GA, Aivaliotis M, Nikolettou V, Tzamaras D, Karagogeos D, Iliopoulos I. UniProt-Related Documents (UniReD): assisting wet lab biologists in their quest on finding novel counterparts in a protein network. *NAR Genomics and Bioinformatics*, 2020 1–13. doi: 10.1093/nargab/lqaa005.

## 2019

48) Ntountoumi C, Vlastaridis P, Mossialos D, Stathopoulos C, Iliopoulos I, Promponas V, Oliver SG, **Amoutzias GD\***. Low complexity regions in the proteins of prokaryotes perform important functional roles and are highly conserved. *Nucleic Acids Res.* 2019 Sep 4. pii: gkz730. doi: 10.1093/nar/gkz730.

47) Daskou M, Tsakogiannis D, Dimitriou TG, **Amoutzias GD**, Mossialos D, Kottaridi C, Gartzonika C, Markoulatos P. WarmStart colorimetric LAMP for the specific and rapid detection of HPV16 and HPV18 DNA. *J Virol Methods.* 2019 Apr 28;270:87-94.

46) Daskou M, Tsakogiannis D, Dimitriou TG, Manali M, Aptsis C, **Amoutzias GD**, Mossialos D, Kottaridi C, Markoulatos P. A 2-stage, nested-like nucleic acid amplification method (IsoPCR) for the highly sensitive detection of HPV16 and HPV18 DNA. *Mol Cell Probes.* 2019 Mar 19. pii: S0890-8508(18)30307-4.

45) Nikolaidis M, Mimouli K, Kyriakopoulou Z, Tsimpidis M, Tsakogiannis D, Markoulatos P, **Amoutzias GD\***. Large-scale genomic analysis reveals recurrent patterns of intertypic recombination in human enteroviruses. *Virology*. 2019 Jan 2;526:72-80.

## 2018

44) Chaliotis A, Vlastaridis P, Ntountoumi, C, Botou M, Yalellis V, Lazou P, Tatsaki E, Mossialos D, Frillingos S\* and **Amoutzias GD\***. NAT/NCS2-hound: A webserver for the detection and evolutionary classification of prokaryotic and eukaryotic nucleobase-cation symporters of the NAT/NCS2 family. *Gigascience*. 2018 Dec 1;7(12). doi: 10.1093/gigascience/giy133.

43) Karakasidou K, Nikolouli K, **Amoutzias GD**, Pournou A, Manassis C, Tsiamis G, Mossialos D. Microbial diversity in biodeteriorated Greek historical documents dating back to the 19th and 20th century: A case study. *Microbiologyopen*. 2018 Oct;7(5):e00596. doi: 10.1002/mbo3.596.

42) Priftis A, Goutzourelas N, Chalabalaki M, Ntasi G, Stagos D, **Amoutzias GD**, Skaltsounis LA, Kouretas D. Effect of polyphenols from coffee and grape on gene expression in myoblasts. *Mech Ageing Dev*. 2017 Nov 23. pii: S0047-6374(17)30155-0. doi: 10.1016/j.mad.2017.11.015.

41) Tsakogiannis D, Moschonas GD, Bella E, Kyriakopoulou Z, **Amoutzias GD**, Dimitriou TG, Kottaridi C, Markoulatos P. Association of p16 (CDKN2A) polymorphisms with the development of HPV16-related precancerous lesions and cervical cancer in the Greek population. *J Med Virol*. 2017 Nov 23. doi: 10.1002/jmv.24996.

40) Kyriakopoulou Z, **Amoutzias GD**, Dimitriou TG, Tsakogiannis D, Mossialos D, Markoulatos P. Intra- and inter-serotypic recombinations in the 5' UTR-VP4 region of Echovirus 30 strains. *Arch Virol*. 2017 Oct 30. doi: 10.1007/s00705-017-3600-1.

## 2017

39) Fikatas A, Dimitriou TG, Kyriakopoulou Z, Moschonas GD, **Amoutzias GD**, Mossialos D, Gartzonika C, Levidiotou-Stefanou S, Markoulatos P. Detection of negative and positive RNA strand of poliovirus Sabin 1 and echovirus E19 by a stem-loop reverse transcription PCR. *Lett Appl Microbiol*. 2017 Jun 20. doi: 10.1111/lam.12766. PMID: 28631392.

38) Vlastaridis P., Papakyriakou A., Chaliotis A., Stratikos E., Oliver SG. and **Amoutzias GD\***. The pivotal role of protein phosphorylation in the control of yeast central metabolism. *G3: Genes, Genomes, Genetics* 2017 Mar 1. pii: g3.116.037218.

37) Chaliotis A, Vlastaridis P, Mossialos D, Ibba M, Becker HD, Stathopoulos C and **Amoutzias GD\***. The complex evolutionary history of aminoacyl-tRNA synthetases. *Nucleic Acids Res*. 2017 Feb 17;45(3):1059-1068.

36) Vlastaridis P, Kyriakidou P, Chaliotis A, Van de Peer Y, Oliver SG, **Amoutzias GD\***. Estimating the total number of phosphoproteins and phosphorylation sites in eukaryotic proteomes. *Gigascience*. 2017 Feb 1;6(2):1-11. doi: 10.1093/gigascience/giw015. PMID:28327990

35) Tsimpidis M, Bachoumis G, Mimouli K, Kuriakopoulou Z, Robertson DL, Markoulatos P, **Amoutzias GD\***. T-RECs: Rapid and large-scale detection of recombination events among different evolutionary lineages of viral genomes. *BMC Bioinformatics*. 2017 Jan 5;18(1):13.

## 2016

34) Fikatas A, Dimitriou TG, Kyriakopoulou Z, Tsachouridou O, Gartzonika C, Levidiotou-Stefanou S, **Amoutzias GD**, Markoulatos P. Serum neutralization assay for the determination of antibody levels against non-polio enterovirus strains in Central and Western Greece. *Viral Immunol*. 2016 Sep;29(7):444-50.

33) **Amoutzias GD**, Giannoulis T, Moutou KA, Psarra AG, Stamatis C, Tsipourlianos A, Mamuris Z. SNP identification through transcriptome analysis of the European brown hare (*Lepus europaeus*): cellular energetics and mother's curse. *PLoS One*. 2016 Jul 26;11(7).

32) **Amoutzias GD**, Chaliotis A, Mossialos D. Discovery Strategies of Bioactive Compounds Synthesized by Nonribosomal Peptide Synthetases and Type-I Polyketide Synthases Derived from Marine Microbiomes. *Mar Drugs*. 2016 Apr 16;14(4). pii: E80.

31) Pappi PG, Maliogka VI, **Amoutzias GD**, Katis NI. Genetic variation of eggplant mottled dwarf virus from annual and perennial plant hosts. *Arch Virol*. 2016 Mar;161(3):631-9.

30) Vlastaridis P, Oliver SG, Van de Peer Y, **Amoutzias GD\***. The Challenges of Interpreting Phosphoproteomics Data: A Critical View Through the Bioinformatics Lens. *Lecture Notes in Bioinformatics*. 2016. 9874, pp. 196-204.

## 2015

29) Katsiani, A.T., Maliogka, V.I., **Amoutzias, G.D.**, Efthimiou, K.E., Katis, N.I. Insights into the genetic diversity and evolution of Little cherry virus 1. *Plant Pathology* 2015, 64 (4), pp. 817-824

28) Kyriakopoulou Z, Bletsa M, Tsakogiannis D, Dimitriou TG, **Amoutzias GD**, Gartzonika C, Levidiotou-Stefanou S, Markoulatos P. Molecular epidemiology and evolutionary dynamics of Echovirus 3 serotype. *Infect Genet Evol*. 2015 Jun;32:305-12.

27) Kyriakopoulou Z, Pliaka V, **Amoutzias GD**, Markoulatos P. Recombination among human non-polio enteroviruses: implications for epidemiology and evolution. *Virus Genes*. 2015 Apr;50(2):177-88

## 2014

26) Tsakogiannis D, Kyriakopoulou Z, Ruether IG, **Amoutzias GD**, Dimitriou TG, Diamantidou V, Kotsovassilis C, Markoulatos P. Determination of HPV16 physical status through E1/E6 and E2/E6 ratio analysis. *J Med Microbiol*. 2014 Sep 11. pii: jmm.0.076810-0.

25) Ruether IG, Dimitriou TG, Tsakogiannis D, Kyriakopoulou Z, **Amoutzias GD**, Gartzonika C, Levidiotou-Stefanou S, Markoulatos P. Characterization of novel intergenogroup and intergenotype recombinant noroviruses from central Greece. *Mol Cell Probes*. 2014 Aug;28(4):204-10.

24) Tsakogiannis D, Darmis F, Gortsilas P, Ruether IG, Kyriakopoulou Z, Dimitriou TG, **Amoutzias G**, Markoulatos P. Nucleotide polymorphisms of the human papillomavirus 16 E1 gene. *Arch Virol*. 2014 Jan;159(1):51-63.

### 2013

23) Tsakogiannis D, Kyriakopoulou Z, **Amoutzias G**, Ruether IG, Dimitriou TG, Panotopoulou E, Markoulatos P. Identification of novel E6-E7 sequence variants of human papillomavirus 16. *Arch Virol*. 2013 Apr;158(4):821-8.

### 2012

22) **Amoutzias GD**, He Y, Lilley KS, Van de Peer Y, Oliver SG. Evaluation and properties of the budding yeast phosphoproteome. *Mol Cell Proteomics*. 2012 Jun;11(6):M111.009555.

21) Stagos D, **Amoutzias GD**, Matakos A, Spyrou A, Tsatsakis AM, Kouretas D. Chemoprevention of liver cancer by plant polyphenols. *Food Chem Toxicol*. 2012 Jun;50(6):2155-70.

20) Cock MJ, Sterck L, Rouzé P, Scornet D, Allen AE, **Amoutzias G**, et al. The Ectocarpus Genome and Brown Algal Genomics. The Ectocarpus Genome Consortium. *Advances in Botanical Research*. 2012. Volume 64, 2012, Pages 141-184

### 2010

19) Cock MJ, Sterck L, Rouzé P, Scornet D, Allen AE, **Amoutzias G**, et al. The Ectocarpus genome and the independent evolution of multicellularity in brown algae. *Nature*. 2010 Jun 3;465(7298):617-21.



18) **Amoutzias GD**, He Y, Gordon J, Mossialos D, Oliver SG, Van de Peer Y. Posttranslational regulation impacts the fate of duplicated genes. *Proc Natl Acad Sci U S A*. 2010 Feb 16;107(7):2967-71.

## 2009

17) Mossialos D, **Amoutzias GD**. Role of siderophores in cystic fibrosis (CF) pathogenesis: foes or friends? *Int J Med Microbiol*. 2009 Feb;299(2):87-98.

## 2008

16) **Amoutzias GD**, Van de Peer Y, Mossialos D. Evolution and taxonomic distribution of non-ribosomal peptide and polyketide synthases. *Future Microbiol*. 2008 Jun;3:361-70.

15) **Amoutzias G**, Van de Peer Y. Together we stand: genes cluster to coordinate regulation. *Dev Cell*. 2008 May;14(5):640-2.

14) **Amoutzias GD**, Robertson DL, Van de Peer Y, Oliver SG. Choose your partners: Dimerization in eukaryotic transcription factors. *Trends Biochem Sci*. 2008 May;33(5):220-9.

## 2007

13) Pampalakis G, Arampatzidou M, **Amoutzias G**, Kossida S, Sotiropoulou G. Identification and analysis of mammalian KLK6 orthologue genes for prediction of physiological substrates. *Comput Biol Chem*. 2007 Nov 29

12) Pinney JW, **Amoutzias GD**, Rattray M, Robertson DL. Reconstruction of ancestral protein interaction networks for the bZIP transcription factors. *Proc Natl Acad Sci U S A*. 2007 Dec 18;104(51):20449-53

11) Holden BJ, Pinney JW, Lovell SC, **Amoutzias GD** & Robertson DL. An exploration of alternative visualizations of the basic helix-loop-helix protein interaction network. *BMC Bioinformatics*. 2007 Aug 6;8(1):289.

10) Mossialos D, **Amoutzias G**. Siderophores in fluorescent pseudomonads: new tricks from an old dog. *Future Microbiol*. 2007 Aug;2:387-95.

9) **Amoutzias GD**, Pichler EE, Mian N, De Graaf D, Imsiridou A, Robinson-Rechavi M, Bornberg-Bauer E, Robertson DL, Oliver SG. A protein interaction atlas for the nuclear receptors: Properties and quality of a hub-based dimerisation network. *BMC Syst Biol*. 2007 Jul 31;1(1):34.

8) **Amoutzias G**, Veron A, Weiner A, Robinson-Rechavi M, Bornberg-Bauer E, Oliver S, Robertson D. One Billion Years of bZIP Transcription Factor Evolution: Conservation and Change in Dimerization, and DNA-Binding Site Specificity. *Mol Biol Evol*. 2006 Dec 28.

## 2006

7) **Amoutzias GD**, Bornberg-Bauer E, Oliver SG, Robertson DL. The Reduction/oxidation-phosphorylation control of the DNA binding of the bZIP family is linked with its dimerization network. *BMC Genomics* 2006 May 4;7:107

## 2005

6) Podowski RM, Cleary JG, Goncharoff NT, **Amoutzias G**, Hayes WS. Suregene, a scalable system for automated term disambiguation of gene and protein names. *J Bioinform Comput Biol*. 2005 Jun;3(3):743-70.

5) **Amoutzias GD**, Weiner J, Bornberg-Bauer E. Phylogenetic profiling of protein interaction networks in eukaryotic transcription factors reveals focal proteins being ancestral to hubs. *Gene*. 2005 Feb 23

**2004**

4) **Amoutzias GD**, Robertson DL, Oliver SG, Bornberg-Bauer E. Convergent evolution of gene networks by single-gene duplications in higher eukaryotes.. *EMBO Rep.* 2004 Mar;5(3):274-9.

Commented in:

<http://www.nature.com/embor/journal/v5/n4/full/7400129.html>

Awarded:

<http://documents.manchester.ac.uk/display.aspx?DocID=7475>

3) **Amoutzias GD**, Robertson DL, Bornberg-Bauer E. The evolution of protein interaction networks in regulatory proteins. *Comp Func Genomics* 2004; 5: 79-84

2) Podowski RM, Cleary JG, Goncharoff NT, **Amoutzias G**, Hayes WS. AZuRE, a scalable system for automated term disambiguation of gene and protein names. *Proc IEEE Comput Syst Bioinform Conf.* 2004;:415-24.

**2003**

1) Imsiridou A, Hardy H, Maudling N, **Amoutzias G**, Zaldivar Comenges JM. Web database of molecular genetic data from fish stocks. *J Hered.* 2003 May-Jun;94(3):265-7.