

Panagiotis Moulos

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I am a bioinformatician with strong computational, mathematical and statistical backgrounds and rich experience in research as well as scientific software development. I believe that the progress of any modern scientific domain includes multidisciplinary and biology with statistics and computer science, which are now permanently bound together, are perfect examples of multidisciplinary scientific progress and the future of healthcare. One of my strongest points is my focus and my passion for perfectionism regarding my work and the success of any project I am involved in.

Key achievements

Research and development

- Active bioinformatics support and development of clinical reporting process in the precision medicine unit at BSRC Alexander Fleming, in the framework of the Hellenic Precision Medicine Network in Oncology and support of the underlying regulatory procedures
- Supervision and contribution in the development and assessment of clinical pharmacogenomics and nutrigenetic SNP panels in collaboration with the private sector (PMID: 33858454 and Kapellou et al., under review)
- Contribution in Fibromine development, a curated multi-omics resource in pulmonary fibrosis (PMID: 34741074)
- Active involvement in the analysis of SARS-CoV-2 genomes during the COVID19 pandemic in Greece (PMID: 34190583, 34576169, 34675930)
- Complete bioinformatics analysis for elucidating the role of non-pioneer transcription factors CEBP α and HNF4 α in transcriptional and epigenomic regulation and network interplays during liver development in mice (PMID: 32023452)
- Development of integrated algorithms for RNA-Seq data analysis focusing on immunity to normalization methods and unbiased downstream functional analysis (PMID: 32778872)
- Development of integrated algorithms for the detection of differential splicing and isoform expression from RNA-Seq data using Machine Learning techniques (PMID: 34698224)
- Bioinformatics insights in refining a steroidogenic model from *Bombyx mori* prothoracic glands through the analysis of respective RNA-Seq data (PMID: 30005604)
- Bioinformatics insights in the elucidation of Kmt5a as a major controller in hepatic metabolic pathways through mediating H4K20 monomethylation (PMID: 28746875)
- Bioinformatics insights in the elucidation of Smyd3 as a key player among multiple cancer-promoting genes required for liver and colon cancer development (PMID: 26908355, 27245698)
- Integrative bioinformatics analysis, including handling of big datasets (TCGA consortium), assisting in the discovery of a positive regulatory loop between a Wnt-Regulated, with potential therapeutic properties, non-coding RNA and the ASCL2 gene which controls intestinal stem cell fate (PMID: 27292638)
- Gene expression analysis during the investigation of Set8 as a potential player in the development of hepatocellular carcinoma (PMID: 25515659)
- Bioinformatics transcriptome analysis of UUO mouse models in renal fibrosis (PMID: 27189340)
- PANDORA algorithm for systematic integration of RNA-Seq statistical algorithms for accurate detection of differential gene expression patterns (PMID: 25452340, 32778872)
- A novel method and web application for the identification of internal standards for the normalization of CE/MS data (PMID: 27694997)

Software

- *recoup*: an R/Bioconductor package for comprehensive analysis, summarization and visualization of Next Generation Sequencing signals (PMID: 33407065, <https://github.com/pmoulos/recoup>)

- *metaseqR2*: an R/Bioconductor package for the systematic integration of RNA-Seq statistical algorithms, robust data normalization, comprehensive downstream analysis and fully interactive result reporting (PMID: 32778872, <https://github.com/pmoulos/metaseqR2>)
- *SeqCVIBE*: an R Shiny application for the analysis, exploration, curation and visualization of big RNA-Seq datasets (manuscript in preparation, <https://github.com/hybridstat/seqcvibe>)
- *metaseqR*: an R/Bioconductor package for the systematic integration of RNA-Seq statistical algorithms and interactive result reporting (PMID: 25452340)
- The Kidney and Urinary Pathway Knowledge Base (*KUPKB*) and the *KUPNetViz* applications for knowledge mining and gene network visualization in kidney disease (www.kupkb.org, PMID: 23883183, 22345404)
- *cinnamoned*: a web application for the CE/MS data processing and normalization based on internal standards (PMID: 27694997, <https://github.com/pmoulos/cinnamoned>)
- *StRAnGER*: Hybrid parametric and non-parametric prioritization and enrichment analysis of Gene Ontology annotations (<http://grissom.gr/stranger/>, PMID: 21293737)
- *Gene ARMADA*: software for the analysis of gene expression microarray data (<https://github.com/pmoulos/gene-armada>, PMID: 19860866)

Education

3/2007 – 3/2011: PhD in Bioinformatics, School of Chemical Engineering, National Technical University of Athens, Thesis Title: Development of Bioinformatics Methodologies for the Study of Highly Complex Biological Systems

9/2004 – 7/2005: DEA (MSc) Bioinformatique, Université Libre de Bruxelles, Thesis Title: Feature Selection and Stability Analysis for Classification using Microarray Data

9/1999 – 7/2004: School of Applied Mathematics and Physics, National Technical University of Athens, Majors: Computer Science Mathematics, Statistics, Thesis Title: Models of Cellular Control and Emergent Phenomena in Multicellular Systems

Positions

10/2020 – Present: External collaborator in Bioinformatics, Center of New Biotechnologies & Precision Medicine, pMedGR, Athens Medical School, National Kapodistrian University of Athens.

8/2020 – Present: Associate Staff Scientist, Bioinformatics, Biomedical Sciences Research Center ‘Alexander Fleming’, Vari, Greece.

8/2017 – 7/2020: “Stavros Niarchos” Foundation Researcher in Bioinformatics, Biomedical Sciences Research Center ‘Alexander Fleming’, Vari, Greece with focus on the development of novel integrated analysis algorithms for genomics data.

4/2014 – Present: Co-founder at HybridStat Predictive Analytics (www.hybridstat.com): Bioinformatics consulting and services, software development for the analysis of big biological data.

6/2012 – 7/2017: Post-doctoral researcher at the Biomedical Sciences Research Center ‘Alexander Fleming’, Vari, Greece, working on the analysis of Next Generation Sequencing data and the development of new analytical approaches for deep sequencing data.

5/2011 – 5/2012: Post-doctoral researcher at Inserm (U1048, I2MC), Toulouse, France, working on the development of a pipeline for the analysis of CE/MS data with focus on the statistical identification of internal normalization standards and of a visualization interface for visualizing Semantic Web relationships stored in the Kidney and Urinary Pathway Knowledge Base (*KUPKB*).

9/2006 – 3/2011: Bioinformatics research assistant with focus on the analysis and meta-analysis of high-throughput functional genomics data, Metabolic Engineering and Bioinformatics Group, Institute of Biological Research and Biotechnology, National Hellenic Research Foundation.

4/2008 – 12/2008: Visiting researcher/bioinformatician in the laboratory of Prof. Henk G. Stunnenberg (NCMLS, Radboud University, Nijmegen, Netherlands), working on standardization, normalization, statistical analysis and analysis workflow organization for Next Generation Sequencing (ChIP-Seq) data.

1/2002 – 12/2009: Other activities: Statistical analysis of questionnaires and technical report writings, private courses in Statistics to students (university level), IT training of SME employees and IT support, teaching assistance during PhD.

Languages

English (excellent), French (excellent), Greek (mother tongue)

Skills

- Excellence with the use of various bioinformatics analysis tools and methodologies with focus on genome bioinformatics/genomics. Indicatively:
 - Next Generation Sequencing data analysis (computational pipelines setup for a variety of -Seq protocols, sequence alignment, data preprocessing, normalization, analysis and visualization)
 - DNA microarray data analysis (data preprocessing, normalization, statistical analysis, data mining, pathway and network analysis)
 - Biological sequence and DNA motif analysis
- Familiarity with a variety of biological databases with focus on genomic and small molecule data:

- Biological sequences and DNA motifs (RefSeq, GenBank, TRANSFAC, JASPAR etc.).
- High-throughput genomic data (GEO, SRA, ArrayExpress, SMD, ArrayTrack etc.).
- Biological small molecules (KEGG Compound, ChEBI, HMDB, METLIN)
- Databases of clinical focus (Clinvar, gNOMAD, DisGeNET, HPO, dbSNP, dbNSFP, PharmGKB etc).
- Metabolomic MS data analysis (preprocessing, peak detection, normalization, statistics, database search).
- Excellent operation of engineering and statistical packages R, MatLab, Minitab, SPSS.
- Experience in regulatory process development, application and maintenance for clinical labs and clinical software management (ISO 15189, ISO 13485).
- Application programming/development
 - Programming languages: Perl, Python, MatLab, R
 - Web development: PHP, HTML, JavaScript, jQuery, Meteor.js, R Shiny
 - Database systems: MongoDB, MySQL
- Excellent familiarity with data mining techniques (feature selection, classification and regression algorithms)

Journal publications

- Kapellou, A., Ntoumou, E., Panagiotou, N., Bothos, E., **Moulos, P.**, Papassava, M., Kalliandasi, K., Katsarou, M., Drakoulis, N.: *Nutrigenetic Contributors of Obesity in a Southeastern European Caucasian Population*, under review in Front. Medicine.
- Röling, M., Mollapour, S.M., Ne, E., **Moulos, P.**, Crespo, R., Stoszko, M., De Crignis, E., Bodmer, H., Kan, T.W., Akbarzadeh, M., Harokopos, V., Hatzis, P., Palstra, R.J., Mahmoudi, T.: *A Two-Color Haploid Genetic Screen Identifies Novel Host Factors Involved in HIV-1 Latency*, mBio. 2021, 12(6):e0298021.
- Fanidis, D., **Moulos, P.**, Aidinis, V.: *Fibromine is a multi-omics database and mining tool for target discovery in pulmonary fibrosis*, Sci Rep. 2021, 11(1):21712.
- Dimopoulos, A., Koukoutegos, K., Psomopoulos, E.F., **Moulos, P.**: *Combining multiple RNA-Seq data analysis algorithms using Machine Learning improves differential isoform expression analysis*, Methods Protoc. 2021, 4(4):68.
- Sfikakis, P., Verrou, K.M., Ampatziadis-Michailidis, G., Tsitsilonis, O., Paraskevis, D., Kastiris, E., Lianidou, E., Moutsatsou, P., Terpos, E., Trougakos, E., Chini, V., Manoloukos, M., **Moulos, P.**, Pavlopoulos, G.A., Kollias, G., Hatzis, P., Dimopoulos, M.A.: *Blood Transcriptomes of Anti-SARS-CoV-2 Antibody-Positive Healthy Individuals Who Experienced Asymptomatic Versus Clinical Infection*, Front Immunol. 2021, 12:746203.
- Nikitopoulou, I., Fanidis, D., Ntatsoulis, K., **Moulos, P.**, Mpekoulis, G., Evangelidou, M., Vassiliou, A.G., Dimakopoulou, V., Jahaj, E., Tsipilis, S., Orfanos, S.E., Dimopoulou, I., Angelakis, E., Akinosoglou, K., Vassilaki, N., Tzouveleakis, A., Kotanidou, A., Aidinis, V.: *Increased Autotaxin Levels in Severe COVID-19, Correlating with IL-6 Levels, Endothelial Dysfunction Biomarkers, and Impaired Functions of Dendritic Cells*, International Journal of Molecular Sciences 2021, 22(18):10006.
- De Crignis, E., Hossain, T., Romal, S., Carofiglio, F., **Moulos, P.**, Khalid, M.M., Rao, S., Bazrafshan, A., Versteegen, M.M., Pourfarzad, F., Koutsothanassis, C., Gehart, H., Kan, T.W., Palstra, R.J., Boucher, C., IJermans, J.N., Huch, M., Boj, S.F., Vries, R., Clevers, H., van der Laan, L.J., Hatzis, P., Mahmoudi, T.: *Application of human liver organoids as a patient-derived primary model for HBV infection and related hepatocellular carcinoma*, eLife 2021, 10:e60747.
- Kostaki, G.E., Pavlopoulos, G.A., Verrou, K.M., Ampatziadis-Michailidis, G., Harokopos, V., Hatzis, P., **Moulos, P.**, Sifakas, N., Pournaras, S., Hadjichristodoulou, C., Chatzopoulou, F., Chatzidimitriou, C., Panagopoulos, P., Lourida, P., Argyraki, A., Lytras, T., Sapounas, S., Gerolymatos, G., Panagiotakopoulos, G., Prezerakos, P., Tsiodras, S., Sypsa, V., Hatzakis, A., Anastassopoulou, C., Spanakis, N., Tsakris, A., Dimopoulos, M.A., Kotanidou, A., Sfikakis, P., Kollias, G., Magiorkinis, G., Paraskevis, D.: *Molecular epidemiology of SARS-CoV-2 in Greece reveals low rates of onward virus transmission after lifting of travel restrictions based on risk assessment during summer 2020*, mSphere 2021, 6(3):e0018021.
- Bothos, E., Ntoumou, E., Kelaidoni, K., Roukas, D., Drakoulis, N., Papasavva, M., Karakostis, F.A., **Moulos, P.**, Karakostis, K.: *Clinical pharmacogenomics in action: design, assessment and implementation of a novel pharmacogenetic panel supporting drug selection for diseases of the central nervous system (CNS)*, J Transl Med. 2021, 19(1):151.
- Verrou, K.M., Vlachogiannis, N.I., Ampatziadis-Michailidis, G., **Moulos, P.**, Pavlopoulos, G.A., Hatzis, P., Kollias, G., Sfikakis, P.P.: *Distinct transcriptional profile of blood mononuclear cells in Behcet's disease: insights into the central role of neutrophil chemotaxis*, Rheumatology 2021, keab052.
- **Moulos, P.**: *recoup: versatile signal visualization from genomic sequencing*, BMC Bioinformatics 2021, 22(1):2.
- Fanidis, D., **Moulos, P.**: *Integrative, normalization-insusceptible statistical analysis of RNA-Seq data, with improved differential expression and unbiased downstream functional analysis*, Briefings in Bioinformatics 2020, bbaa156.
- Gioulbasani, M., Galaras, A., Grammenoudi, S., **Moulos, P.**, Dent, A., Sigvardsson, M., Hatzis, P., Kee, B.L., Verykokakis, M.: *The transcription factor BCL6 controls early development of innate-like T cells*, Nature Immunology 2020, 21(9), 1058-1069.
- Buffin-Meyer, B., Klein, J., van der Zanden, L.F.M., Levchenko, E., **Moulos, P.**, Lounis, N., Conte-Auriol, F., Hindryckx, A., Wühl, E., Persico, N., Oepkes, D., Schreuder, M.F., Tkaczyk, M., Ariceta, G., Fossum, M., Parvex, P., Feitz, W., Olsen, H., Montini, G., Decramer, S., Schanstra, J.P.; ANTENATAL Consortium: *The ANTENATAL multicentre study to predict postnatal renal outcome in fetuses with posterior urethral valves: objectives and design*, Clin Kidney J. 2019, 13(3):371-379.

- Karagianni, P., **Moulos, P.**, Odom, D., Talianidis, I.: *Bookmarking by non-pioneer transcription factors during liver development establishes competence for future gene activation*. Cell Rep. 2020, 30(5):1319-1328.e6¹.
- **Moulos, P.**, Alexandratos, A., Nellas, I., Dedos, S.G.: Refining a steroidogenic model: an analysis of RNA-seq datasets from insect prothoracic glands. BMC Genomics 2018, 19(1):537.
- Buffin-Meyer, B., Klein, J., Breuil, B., Muller, F., **Moulos, P.**, Groussolles, M., Bouali, O., Bascands, J.-L., Decramer, S., Schanstra, J.-P.: Combination of the fetal urinary metabolome and peptidome for the prediction of postnatal renal outcome in fetuses with PUV. J Proteomics 2018, 184:1-9.
- Nikolaou, K.C., **Moulos, P.**, Harokopos, V., Chalepakis, G., Talianidis, I.: *Kmt5a Controls Hepatic Metabolic Pathways by Facilitating RNA Pol II Release from Promoter-Proximal Regions*. Cell Rep. 2017, 20(4):909-922.
- Apostolou, G., Apostolou, N., **Moulos, P.**, Chatzipantelis, P.: Endometrial cytopathology. *An image analysis approach using the Ki-67 biomarker*. Cytopathology 2017, 28(5):385-390.
- Papadopoulos, T., Casemayou, A., Neau, E., Breuil, B., Caubet, C., Calise, D., Thornhill, B.A., Bachvarova, M., Belliere, J., Chevalier, R.L., **Moulos, P.**, Bachvarov, D., Buffin-Meyer, B., Decramer, S., Auriol, F.C., Bascands, J.L., Schanstra, J.P., Klein, J.: *Systems biology combining human- and animal-data miRNA and mRNA data identifies new targets in ureteropelvic junction obstruction*. BMC Syst Biol. 2017, 11(1):31.
- Boizard, F., Brunchault, V., **Moulos, P.**, Breuil, B., Klein, J., Lounis, N., Caubet, C., Tellier, S., Bascands, J.L., Decramer, S., Schanstra, J.P., Buffin-Meyer, B.: *A capillary electrophoresis coupled to mass spectrometry pipeline for long term comparable assessment of the urinary metabolome*. Sci Rep. 2016, 6:34453.
- **Moulos, P.**, Samiotaki, M., Panayotou, G., Dedos, S.G.: *Combinatory annotation of cell membrane receptors and signalling pathways of Bombyx mori prothoracic glands*. Sci Data. 2016, 3:160073.
- Giakountis, A., **Moulos, P.**, Sarris, M.E., Hatzis, P., Talianidis, I.: *Smyd3-associated regulatory pathways in cancer*. Semin Cancer Biol. 2016, S1044-579X(16)30041-4.
- Papadodima, O., **Moulos, P.**, Koryllou, A., Piroti, G., Kolisis, F., Chatziioannou, A., Pletsa, V.: *Modulation of Pathways Underlying Distinct Cell Death Mechanisms in Two Human Lung Cancer Cell Lines in Response to SN1 Methylating Agents Treatment*. PLoS One. 2016, 11(7):e0160248.
- Giakountis, A., **Moulos, P.**, Zarkou, V., Oikonomou, C., Harokopos, V., Hatzigeorgiou, A.G., Reczko, M., Hatzis, P.: *A Positive Regulatory Loop between a Wnt-Regulated Non-coding RNA and ASCL2 Controls Intestinal Stem Cell Fate*. Cell Reports. 2016, S2211-1247(16)30621-0.
- **Moulos, P.**, Sarris, M.E., Talianidis, I.: *Mechanism of gene-specificity of oncogenic regulators*. Cell Cycle. 2016 May 31:0. [Epub ahead of print]
- Arvaniti, E., **Moulos, P.**, Vakrakou, A., Chatziantoniou, C., Chadjichristos, C., Kavvadas, P., Charonis, A., Politis, P.K.: *Whole-transcriptome analysis of UUO mouse model of renal fibrosis reveals new molecular players in kidney diseases*. Sci Rep. 2016, 6:26235.
- Sarris, M.E., **Moulos, P.**, Haroniti, A., Giakountis, A., Talianidis, I.: *Smyd3 Is a Transcriptional Potentiator of Multiple Cancer-Promoting Genes and Required for Liver and Colon Cancer Development*. Cancer Cell. 2016, 29(3):354-66.
- Alexandratos, A., **Moulos, P.**, Nellas, I., Mavridis, K., Dedos, S.G.: *Reassessing ecdysteroidogenic cells from the cell membrane receptors' perspective*. Sci Rep. 2016, 6:2022.
- Milongo, D., Bascands, J.-L., Huart, A., Esposito, L., Breuil, B., **Moulos, P.**, Siwy, J., Ramirez-Torres, A., Ribes, D., Lavayssière, L., Del Bello, A., Muscari, F., Alric, L., Bureau, C., Rostaing, L., Schanstra, J.-P., Kamar, N.: *Pretransplant urinary proteome analysis does not predict development of chronic kidney disease after liver transplantation*. Liver Int. 2015, 35(7), 1893-901.
- Nikolaou, K.C., **Moulos, P.**, Chalepakis, G., Hatzis, P., Oda, H., Reinberg, D., Talianidis, I.: *Spontaneous development of hepatocellular carcinoma with cancer stem cell properties in PR-SET7-deficient livers*. EMBO J. 2015, 34(4), 430-47.
- **Moulos, P.**, Hatzis, P.: *Systematic integration of RNA-Seq statistical algorithms for accurate detection of differential gene expression patterns*. Nucleic Acids Res. 2015, 43(4), e25.
- **Moulos, P.**, Klein, J., Jupp, S., Stevens, R., Bascands, J.-L., Schanstra, J.P.: *The KUPNetViz: A biological network viewer for multiple -omics datasets in kidney diseases*. BMC Bioinformatics 2013, 14:235.
- Klein, J., Jupp, S., **Moulos, P.**, Fernandez, M., Buffin-Meyer, B., Chayaa, R., Charonis, A., Bascands, J.-L., Stevens, R., Schanstra, J.-P.: *The KUPKB: a novel Web application to access multiomics data on kidney disease*. FASEB J. 2012, 26(5), 2145-2153.
- Rao, N.A.S., McCalman, M.T., **Moulos, P.**, Francoijs, K.J., Chatziioannou, A., Kolisis, F.N., Alexis, M.N., Stunnenberg, H.G., Mitsiou, D.J.: *Coactivation of GR and NFKB alters the repertoire of their binding sites and target genes*. Genome Res. 2011, 21(9), 1404-1416¹.
- Chatziioannou, A., Kanaris, I., Doukas, C., **Moulos, P.**, Maglogiannis, I., Kolisis, F.N.: *The GRISSOM Platform: Enabling distributed Processing and Management of Biological Data through fusion of Grid and Web Technologies*. IEEE Transactions on Information Technology in Biomedicine 2011, 15(1), 83-92.

¹ equal first authorship

- Chatziioannou, A., **Moulos, P.**: *Exploiting statistical methodologies and controlled vocabularies for prioritized functional analysis of genomic experiments: The StRAnGER web application*. Front Neurosci. 2011, Jan 26, 5:8.
- **Moulos, P.**, Papadodima, O., Chatziioannou, A., Loutrari, H., Roussos, C., Kolisis, F.N.: *A transcriptomic computational analysis of mastic oil-treated Lewis lung carcinomas reveals molecular mechanisms targeting tumor cell growth and survival*. BMC Medical Genomics 2009, 2:68.
- Chatziioannou, A., **Moulos, P.**, Kolisis, F.N.: *Gene ARMADA: an integrated multi-analysis platform for microarray data implemented in MATLAB*. BMC Bioinformatics 2009 10:354.
- Nielsen, R., Pedersen, T.A., Hagenbeek, D., **Moulos, P.**, Siersbaek, R., Megens, E., Denissov, S., Borgesen, M., Francoijs, K.J., Mandrup, S., Stunnenberg, H.G.: *Genome-wide profiling of PPARgamma:RXR and RNA polymerase II occupancy reveals temporal activation of distinct metabolic pathways and changes in RXR dimer composition during adipogenesis*. Genes Dev 2008, 22(21):2953-2967.

Selected conference proceedings with peer-review

- Fanidis, D., **Moulos, P.**: *Combined statistics for differential expression analysis of RNA-sequencing data*, Conf Proc 19th IEEE Bioinformatics and Bioengineering (BIBE), 2019.
- **Moulos, P.**, Kanaris, I, Bontempi, G.: *Stability of feature selection algorithms for classification in high-throughput genomics datasets*. Conf Proc 13th IEEE Bioinformatics and Bioengineering (BIBE), 2013.
- Valavanis, I., **Moulos, P.**, Maglogiannis, I., Klein, J., Schanstra, J.-P., Chatziioannou, A.: *Intelligent Selection of human miRNAs and mouse mRNAs related to Obstructive Nephropathy*. IEEE AIAB 2011.
- **Moulos, P.**, Valavanis, I., Klein, J., Maglogiannis, I., Schanstra, J.-P., Chatziioannou, A.: *Unifying the Integration, Analysis and Interpretation of multi-omic datasets: Exploration of the disease networks of Obstructive Nephropathy in children*. IEEE EMBC 2011.
- Jupp, S., Klein, J., **Moulos, P.**, Schanstra, J.P.: *Ontologies come of age with the iKUP browser*, ISWC Workshop Ontologies Come of Age Semantic Web, OCAS, 2011.
- Chatziioannou, A., **Moulos, P.**, Pilalis, E., Kolisis, F.N., Maglogiannis, I., Doukas, C.: *GRISSOM web based grid portal: Exploiting the power of grid infrastructure for the interpretation and storage of DNA microarray experiments*, ITAB 2009:1-5.
- Chatziioannou, A., **Moulos, P.**: *Extending the Interpretation of Gene Profiling Microarray Experiments to Pathway Analysis Through the Use of Gene Ontology Terms*. ICCS 2007: 55-61, 22-27/7/2007, Sheffield, England.
- Chatziioannou, A., **Moulos, P.**: *ANDROMEDA: A MATLAB Automated cDNA Microarray Data Analysis Platform*. AIAI 2007: 127-136, 19-21/9/2007, Athens, Greece.

Posters/oral presentations in conference with reviewers

- Fanidis, D., **Moulos, P.**: *Integrative Robust RNA-Seq Differential Expression Analysis with PANDORA*, 15th HSCBB conference, Athens, Greece, December, 2021 (Oral).
- Roukas, D., Bothos, E., Ntounou, E., Kelaidoni, K., Drakoulis, N., Papisavva, M., Karakostis, F.A., **Moulos, P.**, Karakostis, K.: *A rapid, concise and robust companion diagnostic PGx test supporting drug selection for diseases of the Central Nervous System*, 34th ECNP Congress, October 2-5, 2021, <https://www.ecnp.eu/Congress2021/ECNPcongress> (Poster)
- Rouskas, K., Katsareli, E., Amerikanou, C., Glentis, S., Dimopoulos, A.C., Bielser, D., Planchon, A., Romano, L., Panousis, N., Delaneau, O., Ongen, H., Griniatsos, I., Diamantis, T., **Moulos, P.**, Dermitzakis, E., Ragoussis, J., Dedoussis, G., Dimas, A. S.: *Dissecting the gene regulatory landscape of human adipose tissue*, 52nd European Society of Human Genetics (ESHG) 2019, London, UK (Poster).
- Georgaki, M., Giakountis, A., **Moulos, P.**: *Systematic comparison and integration of somatic mutation calling algorithms for reliable identification of cancer mutations*, ISCB Advances in Computational Biology Conference (AdvCompBio), 2019, <https://www.iscb.org/advcompbio2019> (Poster)
- **Moulos, P.**, recoup: *Advanced Next Generation Sequencing Signal Visualization*, ECCB, Athens, Greece, September 9-12, 2019, <http://eccb18.org> (Poster)
- **Moulos, P.**, Giakountis, A., Hatzis, P., *SeqCVIBE: Interactive Data Exploration, Analysis, Visualization and Genome Browsing of RNA-Seq Data*, ECCB, Athens, Greece, September 9-12, 2019, <http://eccb18.org> (Poster)
- Georgaki, M., Koutsothanassis, C., Bothos, E., **Moulos, P.**, *Evaluation of Multiple Variant Calling Algorithms Using Simulated and Real Whole Genome Sequencing Data*, ECCB, Athens, Greece, September 9-12, 2018, <http://eccb18.org> (Poster)
- Markopoulou, K., Hatzis, P., **Moulos, P.**, *Investigating the Discriminative Potential of Long non-coding RNAs in Cancer Using Dimensionality Reduction on RNA-Seq Data*, ECCB, Athens, Greece, September 9-12, 2019, <http://eccb18.org> (Poster)
- Giakountis, A., **Moulos, P.**, Zarkou, V., Oikonomou, C., Harokopos, V., Hatzigeorgiou, A., Reczko, M., Hatzis P., *A positive regulatory loop between a Wnt-regulated non-coding RNA and ASCL2 controls intestinal stem cell fate*, EMBO Wnt signalling conference, Brno, Czech Republic, 2016, <http://wnt2016.muni.cz/> (Poster)
- Karagianni, P., **Moulos, P.**, Schmidt, D., Schmitt, B., Martinez-Jimenez, C.P., Odom, D.T., Talianidis, I., *Developmental dynamics of transcription factor binding in the liver*. 66th HSBMB Conference, December 11-13, Athens, Greece, 2015, <http://www.eebmb2015.gr/> (Poster)

- Karagianni, P., **Moulos, P.**, Schmitt, B., Schmidt, D., Odom, D.T., Talianidis, I., Dynamics of transcription factor binding across liver development, Danube Conference on Epigenetics, November, Budapest, Hungary, 2014, <http://danube-epigenetics.weebly.com/archive.html> (Poster)
- Karagianni, P., **Moulos, P.**, Schmidt, D., Schmitt, B., Martinez-Jimenez, C.P., Odom, D.T., Talianidis, I., Developmental dynamics of transcription factor binding in the liver, Transcription and Chromatin, 11th EMBL Conference, August 23-26, Heidelberg, Germany, 2014, <https://www.embl.de/training/events/2014/TRM14-01/> (Poster)
- Karagianni, P., **Moulos, P.**, Schmidt, D., Schmitt, B., Martinez-Jimenez, C.P., Odom, D.T., Talianidis, I., Analysis of C/EBP α hepatic transcription function, 64th HSBMB Conference, December, Athens, Greece, 2013, <http://www.eebmb2013.gr/> (Poster)
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