


PERSONAL INFORMATION

Oguzhan Kalyon

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[Linkedin](#)

EDUCATION

- 2021 - 2025 **PhD in Bioinformatics, Faculty of Medical Sciences
Newcastle University, UK**
Thesis: Investigating the role of structural variation in male infertility
- 2017 - 2020 **MSc in Bioinformatics, Department of Molecular Biology and Genetics
Yildiz Technical University, Turkiye**
Thesis: Automation of Genetic Diagnosis Based Next Generation Sequencing Data Processing and Reporting
- 2013 - 2017 **BSc Department of Molecular Biology and Genetics
Yildiz Technical University, Turkiye**

WORK EXPERIENCE

- 2026 - **Assistant Professor
Bogazici University / Department of Molecular Biology and Genetics**
- 2024 - 2026 **Postdoctoral Research Fellow
University of Exeter / University of Exeter Medical School**
- Investigated the role of structural variations in disorders of insulin secretion.
 - Exploring AI-driven variant interpretation.
 - Contributed to projects on the optimisation of mosaic variant calling and optimisation of detection of contamination in NGS data.
 - Managed research data with NHS through DNAnexus platform.
 - Contributed the departmental genome pipeline.
 - Co-supervised and provide data for 5 student projects.
 - Involved in teaching by recording a lecture for MSc Genomic Medicine and running 3 research Special Study Unit sessions for medical students.
- 2021 - 2024 **Teaching Assistant
Newcastle University / Faculty of Medical Sciences**
- Conducted demonstrations in the lab for various Biomedical Sciences modules.
 - Led the Cell Biology Module seminar.
 - Co-supervised two undergraduate projects.
 - Assisted with marking undergraduate assessments.
- 2020 -2021 **Project Manager
E Bilgisayar Software and Healthcare ind.trade.co.ltd.**
- Planned, organized and monitored project process, resources, staff and timing for developing web-based genomic data analysis platform.
- 2017 – 2020 **Bioinformatician
Next Genetic Centre**
- Developed, applied and benchmarked analytic tools and pipelines for exome sequencing.
 - Kept up to date on new computational methodologies and incorporate into internal pipelines as appropriate.
 - Interpretation of WES data results in clinical context.

PERSONAL SKILLS

Field Related Skills

- Experienced with genomic data analysis tools (bedtools, samtools, bcftools, gatk, etc)
- Experienced with Docker, GitHub and workflow management tools (snakemake, nextflow)
- Experienced with targeted-seq, WES and WGS data analysis in clinical context
- Project management

Computer Language Skills

- R and bash - Expert user
- Python – Intermediate User

PAPERS & BOOK & PRESENTATIONS & COURSES

Book

- Demirbaga, Ü., Aujla, G. S., Jindal, A., & **Kalyon, O.** (2024). **Big Data Analytics**. Springer Nature Switzerland. <https://doi.org/10.1007/978-3-031-55639-5>

Papers

- Flanagan, S. E., Lazaridi, I.-A., Männistö, J. M. E., Bennett, J. J., **Kalyon, O.**, Johnson, M. B., Wakeling, M. N., Houghton, J. A. L., & Laver, T. W. (2025). Large copy number variants are an important cause of congenital hyperinsulinism that should be screened for during routine testing. **Frontiers in Endocrinology**, 16. <https://doi.org/10.3389/fendo.2025.1514916>
- Dicke, A.-K., Ahmedani, A., Ma, L., Herrmann, L., van der Heijden, G. W., Koser, S. A., Krallmann, C., **Kalyon, O.**, Xavier, M. J., Veltman, J. A., Kliesch, S., Neuhaus, N., Kotaja, N., Tüttelmann, F., & Stallmeyer, B. (2025). NXT2 is a key component of the RNA nuclear export factor complex in the human testis and essential for spermatogenesis. **Nature Communications**, 16(1). <https://doi.org/10.1038/s41467-025-61463-0>
- Laver, T. W., Sriram, A., Wakeling, M. N., Şiklar, Z., Kobaisi, F., **Kalyon, O.**, Hattersley, A. T., Weedon, M. N., Flanagan, S. E., De Franco, E., Colclough, K., & Patel, K. A. (2026). Systematic analysis of loss-of-function variants across MODY genes demonstrates gene-specific effects and expands the spectrum of INS variants causing MODY. **Diabetologia**. <https://doi.org/10.1007/s00125-026-06685-7>
- Bennett, J. J., Laver, T. W., Männistö, J. M. E., Houghton, J. A. L., De Franco, E., **Kalyon, O.**, Wright, S., Johnson, A.-M., De Leon, D. D., Globa, E., Kummer, S., Banerjee, I., Dastamani, A., Akçay, T., Alhomidah, D. S., Bhavani, N., Miranda Cabrera, B. F., Demir, K., Fadiana, G., ... Flanagan, S. E. (2026). Low-level mosaic variants causing the pancreatic disease congenital hyperinsulinism can be detected from blood DNA. **eBioMedicine**, 128, 106308. <https://doi.org/10.1016/j.ebiom.2026.106308>

Presentations

- **ESHG 2026**, 13-16 June 2026, Gothenburgh, Sweden ([poster presentation](#))
O. Kalyon, R. Arumugam, D. Patel, S. Wright, J. Russ-Silsby, R. Donis, S. E. Flanagan, E. De Franco, T. W. Laver, K. Patel. (2026). "*Detection of mitochondrial DNA deletions by whole-genome sequencing improves diagnosis in syndromic paediatric diabetes: implications for routine clinical practice*"
- **ASHG 2025**, 14-18 October 2025, Boston, US ([poster presentation](#))
O. Kalyon, M. N. Wakeling, I.A. Lazaridi, E.D. Franco, S.E. Flanagan, T.W. Laver (2025). "*Investigating the Contribution of Copy Number Variants to Disorders of Insulin Secretion*"
- **ASHG 2025**, 14-18 October 2025, Boston, US ([oral presentation, presented by T.W. Laver](#))
T.W. Laver, P. Sangha, O. Kalyon, J. Fasham, A. Gunning (2025). "*Artificial intelligence cannot replace human intelligence: generative AI is not suitable for variant classification*"
- **ESHG 2023**, 10-13 June 2023, Glasgow, UK ([oral presentation](#))
O. Kalyon, B.K.S. Alobaidi, L.E. Batty, J. Coxhead, K. McEleny, G. W. van der Heijden, L. Ramos, M. S. Oud, M.J. Xavier, A. Mikulasova, G.S. Holt, J.A. Veltman (2023). "*Genome sequencing reveals copy number variants in known and novel candidate genes for idiopathic non-obstructive azoospermia*"
- **NUCoRE Rare Disease Seminar Series**, November 2023, Newcastle, UK ([invited speaker](#))
- **TÜSEB FUTURE HEALTH-GENOMICS 2023 Congress**, 8–9 December 2023, Istanbul, Turkiye ([oral presentation](#))
O. Kalyon, B.K.S. Alobaidi, L.E. Batty, J. Coxhead, K. McEleny, G. W. van der Heijden, L. Ramos, M. S. Oud, M.J. Xavier, A. Mikulasova, G.S. Holt, J.A. Veltman (2023). "*Genome sequencing reveals copy number variants in known and novel candidate genes for idiopathic non-obstructive azoospermia*"
- **What's Happening at the CFL Seminar Series**, February 2023, Newcastle, UK ([invited speaker](#))
- **Genetic Matters Public Event**, February 2023, Newcastle, UK ([oral presentation](#))
- **ESHG 2022**, 11-14 June 2022, Vienna ([poster presentation](#))
O. Kalyon, B.K.S. Alobaidi, L.E. Batty, M.J. Xavier, G.S. Holt, A. Mikulasova, J.A. Veltman (2022). "*Method optimisation for structural variant detection in the human genome*"
- **Functional Regulatory Genomics and Disease Conference**, 11-13 April 2022, Edinburgh, UK ([poster presentation](#))
O. Kalyon, B.K.S. Alobaidi, L.E. Batty, M.J. Xavier, G.S. Holt, A. Mikulasova, J.A. Veltman (2022). "*Method optimisation for structural variant detection in the human genome*"
- **HIBIT'19**, 17-19 October 2019, Izmir, Turkiye ([poster presentation](#))
O. Kalyon, A. Yilmaz, M.H. Muslumanoglu, (2019). "*Automation of Genetic Testing and Reporting with Snakemake*"
- **HIBIT'17**, 24-28 June 2017, Northern Cyprus ([poster presentation](#))
O. Kalyon, A. Yilmaz, (2017). "*Survey of Chimeric mRNA's in HIV Infected Patient RNA-Seq Data*"
- **International Molecular Biology And Biotechnology Congress**, 25-27 April 2018, Konya, Turkiye ([poster presentation](#))
O. Kalyon, N.S. Uluskan, L. Elmas, M. Secme, E. Tepeli, M.H. Muslumanoglu, (2018). "*Determination of The Cytotoxic Effect of Zerumbone on A172 And U87MG Human Glioblastoma Multiforme Cell Lines and The Effect of Apoptotic Genes*"

Courses

- The MUMC+ ESHG course Next-Generation Reproductive Medicine, 13-15 October 2022, Netherlands (Online)
- 33rd Course on Clinical Genomics and NGS jointly organized by ESHG and CEUB, May 6 – 11, 2021
- Genomics Education Programme (GEN) (e-course given by NHS)

MEMBERSHIPS & AWARDS

Memberships & Fellows

- Associate Fellowship with the Higher Education Academy (AFHEA)
- A member of European Society of Human Genetics, 2022-2023, 2025-...
- A member of American Society of Human Genetics, 2025-...
- A member of the Expert Panel of the ClinGen Neurodevelopmental Dosage Subgroup, 2022-...
- A member of Genetic Society UK, 2022-2023
- A member of The Network for Young Researchers in Andrology (NYRA), 2022-2023
- Welfare Officer of the Turkish Society at Newcastle University Student Union, 2022-2023
- A member of NEPG 2022 organisation committee, 2022

Awards

- Taking 1st place at AI in Healthcare / Bioinformatics competition in Türkiye, "*Phen2Treat: Category of AI-based Bioinformatic Analysis Methods Development*", Aerospace and Technology Festival, Türkiye, 2022.
- Ministry of National Education of Türkiye abroad postgraduate fellowship, Türkiye, 2018
- Genetics Society Conference Grant – Edinburgh 2022
- Newcastle University Doctoral Collage Travel Grant, 2022
- Nci+ Award, 2023
- HDR UK Biomedical Vacation Scholarship (NIHR Exeter BRC)
Secured funding for and supervised a summer research internship.