

Curriculum vitae: Krzysztof Kuś

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ORCID: 0000-0003-4791-9658

Passports: Polish, British

Research Experience

- 2017 – Now **Postdoctoral Research Associate**, Department of Biochemistry, University of Oxford.
Research on transcriptional regulation in Lidia Vasilieva laboratory.
- 2011 – 2016 **Ph.D. Student**, Protein-Nucleic Acids Interactions Group, Instituto Gulbenkian de Ciência.
Studies on nucleic acids recognition by Z-DNA/Z-RNA binding domains.
- 2009 – 2010 **Master Student**, Faculty of Biochemistry, Biophysics and Biotechnology, Jagiellonian University.
Mathematical modeling of the tricarboxylic acid cycle.
- 2009 **Summer Undergraduate Fellow**, Science Foundation Ireland Biomedical Research Network.
Project: Predicting the methylation status of CG clusters in mouse germ cells.

Education

- 2010 – 2016 **Ph.D., Instituto Gulbenkian de Ciência**, Structural Biology, Integrative Biomedical Sciences, Portugal
- 2005 – 2010 **M.Sc. Biotechnology, Jagiellonian University** Faculty of Biochemistry, Biophysics and Biotechnology, Poland

Research Publications

† Co-corresponding author * Co-first author

- 1 **K. Kuś**[†], S. Nielsen, N. Zenkin, and L. Vasiljeva, “Conserved protein Seb1 that interacts with RNA polymerase II and RNA is an antipausing transcription elongation factor,” *RNA*, vol. 32, no. 1, pp. 71–81, 2026.
- 2 M. Ahrar, L. Glenn, M. Held, A. Jackson, **K. Kuś**, G. D. Hurst, and E. Chrostek, “Development of antisense tools to study *Bodo saltans* and its intracellular symbiont,” *MicrobiologyOpen*, vol. 14, no. 2, e70018, 2025.
- 3 A. Au, A. Southers, **K. Kuś**^{*}, N. Schoemaker, E. Balikci-Akil, C. Hewes, M. Fournier, E. Aydin, S. S. Hassanein, C. Kilchert, J. M. Grimes, and L. Vasiljeva, “The PP1 phosphatase complex coordinates pre-mRNA 3’ end processing and termination of RNA polymerase II transcription,” *bioRxiv*, 2025.
- 4 **K. Kuś**[†], L. Carrique, T. Kecman, M. Fournier, S. S. Hassanein, E. Aydin, C. Kilchert, J. M. Grimes, and L. Vasiljeva[†], “DSIF factor Spt5 coordinates transcription, maturation and exoribonucleolysis of RNA polymerase II transcripts,” *Nature Communications*, vol. 16, no. 1, p. 10, 2025.
- 5 **K. Kuś**^{*}, J. Mark Treherne, D. L. Earnshaw, R. Krzykawska, B. Biesaga, M. Statkiewicz, K. Unrug-Bielawska, Z. Sandowska-Markiewicz, M. Mikula, J. A. Alfaro, and M. P. Krzykowski, “3D culture of pancreatic cancer cells *in vitro* recapitulates an aberrant mitochondrial oxidative phosphorylation genotype observed *in vivo*,” *bioRxiv*, 2024.
- 6 **K. Kuś**[†] and L. Vasiljeva[†], “Studying exoribonuclease activity using fluorescence anisotropy assay,” in *mRNA Decay: Methods and Protocols*, Springer, 2024, pp. 71–80.
- 7 A. Birot, **K. Kuś**, E. Priest, A. Al Alwash, A. Castello, S. Mohammed, L. Vasiljeva, and C. Kilchert, “RNA-binding protein Mub1 and the nuclear RNA exosome act to fine-tune environmental stress response,” *Life Science Alliance*, vol. 5, no. 2, e202101111, 2022.

- 8 B. Srinivasan[†], **K. Kus^{†,*}**, and A. Athanasiadis, "Thermodynamic analysis of Z α domain-nucleic acid interactions," *Biochemical Journal*, vol. 479, no. 16, pp. 1727–1741, 2022.
- 9 L. Gabriel, B. Srinivasan, **K. Kus^{*}**, J. F. Mata, M. J. Amorim, L. E. Jansen, and A. Athanasiadis, "Enrichment of Z α domains at cytoplasmic stress granules is due to their innate ability to bind to nucleic acids," *Journal of Cell Science*, vol. 134, no. 10, jcs258446, 2021.
- 10 D.-H. Heo, **K. Kus^{*}**, P. Grzechnik, S. M. Tan-Wong, A. Birot, T. Kecman, S. Nielsen, N. Zenkin, and L. Vasiljeva, "Transcription and chromatin-based surveillance mechanism controls suppression of cryptic antisense transcription," *Cell Reports*, vol. 36, no. 10, p. 109 671, 2021.
- 11 C. Kilchert, T. Kecman, E. Priest, S. Hester, E. Aydin, **K. Kus**, O. Rossbach, A. Castello, S. Mohammed, and L. Vasiljeva, "System-wide analyses of the fission yeast poly (A)+ RNA interactome reveal insights into organization and function of RNA–protein complexes," *Genome Research*, vol. 30, no. 7, pp. 1012–1026, 2020.
- 12 T. Kecman, **K. Kus**, D.-H. Heo, K. Duckett, A. Birot, S. Liberatori, S. Mohammed, L. Geis-Asteggiane, C. V. Robinson, and L. Vasiljeva, "Elongation/termination factor exchange mediated by PP1 phosphatase orchestrates transcription termination," *Cell Reports*, vol. 25, no. 1, pp. 259–269, 2018.
- 13 B. R. Watts, S. Wittmann, M. Wery, C. Gautier, **K. Kus**, A. Birot, D.-H. Heo, C. Kilchert, A. Morillon, and L. Vasiljeva, "Histone deacetylation promotes transcriptional silencing at facultative heterochromatin," *Nucleic Acids Research*, vol. 46, no. 11, pp. 5426–5440, 2018.
- 14 **K. Kus**, K. Rakus, M. Boutier, T. Tsigkri, L. Gabriel, A. Vanderplasschen, and A. Athanasiadis, "The structure of the *Cyprinid herpesvirus 3* ORF112-Z α -Z-DNA complex reveals a mechanism of nucleic acids recognition conserved with E3L, a poxvirus inhibitor of interferon response," *Journal of Biological Chemistry*, vol. 290, no. 52, pp. 30 713–30 725, 2015.
- 15 B. Szelągęk, W. Kabała, **K. Kus**, M. Zdzalik, A. Twarda-Clapa, P. Golik, M. Burmistrz, D. Florek, B. Władyka, K. Pyrc, *et al.*, "Structural characterization of human coronavirus NL63 N protein," *Journal of Virology*, vol. 91, no. 11, e02503–16, 2015.
- 16 A. R. Tomé, **K. Kus^{*}**, S. Correia, L. M. Paulo, S. Zacarias, M. de Rosa, D. Figueiredo, R. M. E. Parkhouse, and A. Athanasiadis, "Crystal structure of a poxvirus-like Z α domain from *Cyprinid herpesvirus 3*," *Journal of Virology*, vol. 87, no. 7, pp. 3998–4004, 2013.

Funding

- 2025 ■ **The Medical Sciences Internal Fund: Pump-Priming , £12,000**, University of Oxford. Project: "Exploring a link between conserved, druggable histone deacetylase complex and RNA polymerase II transcription"
- 2010–2014 ■ **Ph.D. fellowship from Fundação para a Ciência e a Tecnologia, Portugal**
- 2009 ■ **UREKA stipend (Summer Undergraduate Fellowships in a Biomedical Research Network) funded by the Science Foundation Ireland, Galway, Ireland**

Teaching and Mentoring

- Graduate students ■ Niek Schoemaker, Alex Au, Sarah Hassanein, Sum Po Ava Chan, Isobel Jury, Anna Wiecek, Diogo Ribeiro
- Practical ■ "Origins of replication" - bioinformatics class in R environment to analyse genome-wide data, Department of Biochemistry, University of Oxford
- Tutorial ■ "Splicing and 3'-end RNA processing", Department of Biochemistry, University of Oxford

Conferences and courses

- 18-19/03/2024 ■ **35th UK Oxford Annual RNA Polymerase Workshop**, Oxford, UK. Talk: "DSIF factor Spt5 coordinates transcription, maturation and exoribonucleolysis of RNA polymerase II transcripts"
- 25-28/01/2024 ■ **RNA UK meeting**, Windermere, UK. Talk: "DSIF factor Spt5 coordinates transcription, maturation and exoribonucleolysis of RNA polymerase II transcripts"
- 19-23/09/2023 ■ **Regulation of RNA 3' end formation across eukaryotic genomes**, Oxford, UK. Poster: "Investigating interactions between termination factor Xrn2 (torpedo) and the RNA polymerase II transcriptional machinery"
- 5-7/04/2019 ■ **V Polish Conference of Genetics "Genomica"**, Cracow, Poland. Invited speaker
- 26-28/01/2018 ■ **RNA UK meeting**, Windermere, UK. Poster: "Mechanistic insights into the function of the conserved factors that coordinate RNA polymerase II transcription and RNA processing"
- 20-24/09/2017 ■ **Regulation of RNA 3' end formation across eukaryotic genomes**, Oxford, UK. Poster: "Mechanistic insights into function of the conserved essential factors that coordinate RNA polymerase II transcription and RNA processing"
- 11-13/06/2014 ■ **Structural Modeling for Large Macromolecular Complexes**, Oeiras, Portugal
- 1-4/09/2012 ■ **The FEBS workshop on RNA Biology**, Tavira, Portugal. Poster: "Dissecting the specificity determinants of Adenosine to Inosine RNA editing"
- 26-27/01/2012 ■ **Portuguese RNA Meeting 2012**, Lisbon, Portugal
- 9-11/05/2011 ■ **RNA Bioinformatics**, Oeiras, Portugal
- 2-7/05/2011 ■ **Bioinformatics using Python for Biologists**, Oeiras, Portugal
- 20-22/11/2009 ■ **XI Seminar of Biotechnology Students**, Poznań, Poland. Poster: "Predicting the methylation status of CG clusters in mouse germ cells"

Collaborations

- Prof. Jason Schnell, University of Oxford ■ NMR studies on transcriptional factors.
- Dr. Marcin Krzykawski, Real-Research ■ Industry partnership. I take an advisory role and provide bioinformatics expertise.
- Dr. Ewa Chrostek, Jagiellonian University ■ AlphaFold modeling of *Wolbachia-Drosophila* interactors.

Additional Activities

- Advisory board ■ Advisory role and bioinformatics consulting including RNA-seq data analysis for Real-Research, Kraków.
- Reviewing activity ■ Co-peer review for Nature Communications, Molecular Cell, Nature, and NSMB.
- Outreach ■ Open day 2012, Interactive presentation - Instituto Gulbenkian de Ciência, Oeiras

Skills and Expertise

- Bioinformatics ■ $\LaTeX$, Chimera, VMD, machine learning, R, Python, Coot, Linux, Windows, PyMOL, CCP4, Phenix, high-throughput sequencing pipelines, cryoSPARC
- Molecular biology ■ TT-seq, RNA-seq, CHIP-seq, qPCR, mutagenesis, protein expression and purification, Western Blotting, radioactive assays, in vitro transcription, EMSA, ITC, crystallography
- Languages ■ Polish (Native), English (Fluent), Portuguese (Intermediate)