# Mid-Career Research Fellowships

Curriculum Vitae

## Qualifications

**Doctor of Philosophy (PhD) (2008–2012)** | University of Cambridge & EMBL-European Bioinformatics Institute, United Kingdom | *Field of study:* Computational Biology | *Thesis:* Computational Studies on the Biogenesis and Function of Small Non-coding RNAs |*Conferred:* 23/07/13| EMBL PhD Fellowship.

**Bachelor and Master of Science in Pharmacy (2001–2006)** | Faculty of Pharmacy, University of Zagreb, Croatia | *Field of study:* Pharmacy |*Thesis:* Construction, expression, and characterization of chimeric proteins LCK and ZAP-70; Conferred: 31/8/2006; *Grade:* 4.55 / 5 | Dean Award for Highest Grade 2006.

**Bachelor and Master of Science in Molecular Biology (1999–2004)** | Faculty of Science, University of Zagreb, Croatia | *Field of study:* Molecular Biology | *Thesis:* MADNet: Microarray Database Network web server for analysis and interactive visualization of microarray data; Conferred: 29/11/2004; *Grade:* 4.96 / 5 | Dean award for Highest Grade 2004.

**International Baccalaureate (1997–1999)** | United World College – USA, Montezuma, NM, USA  
*Grade:* 42 / 45. | UWC Fellowship.

## Positions

**Senior Research Officer (2023–now)** – Gene Regulation / Prof. Ricky Johnstone, Peter MacCallum Cancer Centre | Melbourne, Australia

* Dysregulated transcription as a mutagen

**Senior Scientist (2021–2023)** – EnviroDNA and Cesar Australia (biotech) | Melbourne, Australia

* Environmental DNA processing and population genetics workflows for conservation projects

**Senior Research Officer (2017–2021)** – Tumour Progression / Prof. Alex Swarbrick and Prof. Chris Ormandy, Garvan Institute of Medical Research | Sydney, Australia

* Computational analyses of cellular genomics across cancer and immunology projects
* Multi-omics, single-cell, spatial transcriptomics, and long-read sequencing in tumour progression studies
* PhD student supervisor: James Torpy (Thesis: An investigation of genomic instability and its impact on cancer development and heterogeneity, 2018-2021)

**Research Officer (2013–2017)** – Genome Biology / Prof. Marcel Dinger, Garvan Institute of Medical Research | Sydney, Australia

* Non-coding transcriptomes, GWAS integration, cancer genomics, ; cloud computing development in prostate cancer consortium
* Co-supervision of 4 PhD students

**PhD Student (2008–2012)** – Functional Genomics and RNA / Prof. Anton Enright, University of Cambridge & EMBL-European Bioinformatics Institute | UK

* Computational methods for research of non-coding RNAs

**Junior scientist (2006–2008)** – GlaxoSmithKline Research Centre | Zagreb, Croatia

* Transcriptomic and proteomic response to immunosuppressive compounds

## Awards and grants

**Peter MacCallum Cancer Foundation Grant (2024)** | Project title: *Preventing transcription-driven evolution of drug resistance*; Principal Investigator; Amount: $55,000; Dates: 1/12/2024-31/11/2025.  
  
**NHMRC Ideas Grant (2020)** | Project title: *The role of LINE-encoded natural antisense transcripts in immune regulation*; Associate Investigator; Amount: 669,095; Period: 2021–2025.

**Croatian Science Foundation (2018)** | Project title: *Differential regulation of the GLI code in BRAF/NRAS-driven tumours*;Chief Investigator B; Amount: $200,000; Period: 2019-2023.  
  
**Garvan Institute Palmer Innovation Prize (2017)** | Project title: *Diagnostic test for microbial infections using real-time DNA sequencing*; Principal investigator; Amount: $15,000; 2017-2018.

## Awards

**Small Technologies Cluster (STC) MedTech Got Talent, Startup Finalist (2017) |** Project title: *Diagnostic test for microbial infections using real-time DNA sequencing*; Organisation: Principal investigator; Amount: $20,000; 2017-2018.

## Publications and outputs

Total number of publications in the last 8 years (or full time equivalent): 24

List your major publications and outputs over the last 8 years (or full time equivalent) and highlight those that relate to your application. Applicants can adapt the subheadings to suit their outputs. Provide full citation including title, authors (in order), publication, issue, year and DOI. Applicants may only include preprint publications (under the relevant subheading) where a manuscript is submitted for peer review and is listed on a pre-print server. Applicants may include other details such as type of publication (e.g., original research, invited review) as well as impact and citation metrics. If listing patents, please provide the status of the patent.

### Journal articles (peer reviewed)

**MAJOR CONTRIBUTION**

-**Bartonicek N**, Rouet R, Warren J, Loetsch C, Rodriguez GS, Walters S, Lin F, Zahra D, Blackburn J, Hammond JM, Reis ALM, Deveson IW, Zammit N, Zeraati M, Grey S, Christ D, Mattick JS, Chtanova T, Brink R, Dinger ME, Weatheritt RJ, Sprent J, King C. The retroelement Lx9 puts a brake on the immune response to virus infection. **Nature**. 2022 Aug;608(7924):757-765. doi: 10.1038/s41586-022-05054-9.

-Baldwin LA, **Bartonicek N**, Yang J, Wu SZ, Deng N, Roden DL, Chan CL, Al-Eryani G, Zanker DJ, Parker BS, Swarbrick A, Junankar S. DNA barcoding reveals ongoing immunoediting of clonal cancer populations during metastatic progression and immunotherapy response. **Nat Commun.** 2022 Nov 7;13(1):6539. doi: 10.1038/s41467-022-34041-x.

-Piggin CL, Roden DL, Law AMK, Molloy MP, Krisp C, Swarbrick A, Naylor MJ, Kalyuga M, Kaplan W, Oakes SR, Gallego-Ortega D, Clark SJ, Carroll JS, **Bartonicek N**, Ormandy CJ. (2020) ELF5 modulates the estrogen receptor cistrome in breast cancer. **PLoS Genet**. 2020 Jan 2;16(1):e1008531. doi: 10.1371/journal.pgen.1008531.

**-Bartonicek N**, Clark MB, Quek XB, Torpy J, Pritchard AL, Maag JL, et al. (2017) Intergenic disease-associated regions are abundant in novel transcripts. **Genome Biology**. 2017 Dec 28;18(1):241. doi: 10.1186/s13059-017-1363-3.

**COLLABORATIONS**

JOHNSTONE LAB (2023-)

-Djajawi TM, Pijpers L, Srivaths A, Chisanga D, Chan KF, Hogg SJ, Neil L, Rivera SM, Bartonicek N, Ellis SL, Lim Kam Sian TCC, Faridi P, Liao Y, Pal B, Behren A, Shi W, Vervoort SJ, Johnstone RW, Kearney CJ. PRMT1 acts as a suppressor of MHC-I and anti-tumor immunity. Cell Rep. 2024 Mar 26;43(3):113831. doi: 10.1016/j.celrep.2024.113831.

ROLE OF NONCODING RNA IN NEUROBLASTOMA

-Mondal S, Liu PY, Seneviratne J, De Weck A, Venkat P, Mayoh C, Wu J, Maag J, Chen J, Wong M, Bartonicek N, Khoo P, Jin L, Ludlow LE, Ziegler DS, Trahair T, Mestdagh P, Cheung BB, Li J, Dinger ME, Street I, Zhang XD, Marshall GM, Liu T. The Super Enhancer-Driven Long Noncoding RNA PRKCQ-AS1 Promotes Neuroblastoma Tumorigenesis by Interacting With MSI2 Protein and Is Targetable by Small Molecule Compounds. **Adv Sci (Weinh)**. 2025 May;12(18):e2412520. doi: 10.1002/advs.202412520. Epub 2025 Mar 18.

-Liu PY, Tee AE, Milazzo G, Hannan KM, Maag J, Mondal S, Atmadibrata B, Bartonicek N, Peng H, Ho N, Mayoh C, Ciaccio R, Sun Y, Henderson MJ, Gao J, Everaert C, Hulme AJ, Wong M, Lan Q, Cheung BB, Shi L, Wang JY, Simon T, Fischer M, Zhang XD, Marshall GM, Norris MD, Haber M, Vandesompele J, Li J, Mestdagh P, Hannan RD, Dinger ME, Perini G, Liu T. The long noncoding RNA lncNB1 promotes tumorigenesis by interacting with ribosomal protein RPL35. Nat Commun. 2019 Nov 5;10(1):5026. doi: 10.1038/s41467-019-12971-3.

SWARBRICK LAB

-Quek C, Pratapa A, Bai X, Al-Eryani G, Pires da Silva I, Mayer A, Bartonicek N, Harvey K, Maher NG, Conway JW, Kasalo RJ, Ben Cheikh B, Braubach O, Palendira U, Saw RPM, Stretch JR, Shannon KF, Menzies AM, Scolyer RA, Long GV, Swarbrick A, Wilmott JS. Single-cell spatial multiomics reveals tumor microenvironment vulnerabilities in cancer resistance to immunotherapy. Cell Rep. 2024 Jul 23;43(7):114392. doi: 10.1016/j.celrep.2024.114392.

-Wu SZ, Al-Eryani G, Roden DL, Junankar S, Harvey K, Andersson A, Thennavan A, Wang C, Torpy JR**, Bartonicek N**, Wang T, Larsson L, Kaczorowski D, Weisenfeld NI, Uytingco CR, Chew JG, Bent ZW, Chan CL, Gnanasambandapillai V, Dutertre CA, Gluch L, Hui MN, Beith J, Parker A, Robbins E, Segara D, Cooper C, Mak C, Chan B, Warrier S, Ginhoux F, Millar E, Powell JE, Williams SR, Liu XS, O'Toole S, Lim E, Lundeberg J, Perou CM, Swarbrick A. A single-cell and spatially resolved atlas of human breast cancers**. Nat Genet.** 2021 Sep;53(9):1334-1347. doi: 10.1038/s41588-021-00911-1.

-Wu SZ, Roden DL, Al-Eryani G, **Bartonicek N**, Harvey K, Cazet AS, Chan CL, Junankar S, Hui MN, Millar EA, Beretov J, Horvath L, Joshua AM, Stricker P, Wilmott JS, Quek C, Long GV, Scolyer RA, Yeung BZ, Segara D, Mak C, Warrier S, Powell JE, O'Toole S, Lim E, Swarbrick A. Cryopreservation of human cancers conserves tumour heterogeneity for single-cell multi-omics analysis. **Genome Med.** 2021 May 10;13(1):81. doi: 10.1186/s13073-021-00885-z.

-Wu SZ, Roden DL, Wang C, Holliday H, Harvey K, Cazet AS, Murphy KJ, Pereira B, Al-Eryani G, **Bartonicek N**, Hou R, Torpy JR, Junankar S, Chan CL, Lam CE, Hui MN, Gluch L, Beith J, Parker A, Robbins E, Segara D, Mak C, Cooper C, Warrier S, Forrest A, Powell J, O'Toole S, Cox TR, Timpson P, Lim E, Liu XS, Swarbrick A. (2020) Stromal cell diversity associated with immune evasion in human triple-negative breast cancer. **EMBO J.** Oct 1;39(19):e104063. doi: 10.15252/embj.2019104063.

DEVELOPMENT OF ANALYTICAL WORKFLOWS FOR SINGLE-CELL TECHNOLOGIES

-Salomon R, Kaczorowski D, Valdes-Mora F, Nordon RE, Neild A, Farbehi N, **Bartonicek N**, Gallego-Ortega D. (2019) Droplet-based single cell RNAseq tools: a practical guide. **Lab Chip.** 2019 May 14;19(10):1706-1727. doi: 10.1039/c8lc01239c.

CROATIAN COLLABORATION

-Piteša N, Kurtović M, Bartoniček N, Gkotsi DS, Čonkaš J, Petrić T, Musani V, Ozretić P, Riobo-Del Galdo NA, Sabol M. Signaling Switching from Hedgehog-GLI to MAPK Signaling Potentially Serves as a Compensatory Mechanism in Melanoma Cell Lines Resistant to GANT-61. Biomedicines. 2023 May 3;11(5):1353. doi: 10.3390/biomedicines11051353.

-Kurtović M, Piteša N, Bartoniček N, Ozretić P, Musani V, Čonkaš J, Petrić T, King C, Sabol M. RNA-seq and ChIP-seq Identification of Unique and Overlapping Targets of GLI Transcription Factors in Melanoma Cell Lines. **Cancers** (Basel). 2022 Sep 19;14(18):4540. doi: 10.3390/cancers14184540.

GARVAN COLLABORATION BONE CANCER

-Youlten SE, Kemp JP, Logan JG, Ghirardello EJ, Sergio CM, Dack MRG, Guilfoyle SE, Leitch VD, Butterfield NC, Komla-Ebri D, Chai RC, Corr AP, Smith JT, Mohanty ST, Morris JA, McDonald MM, Quinn JMW, McGlade AR, Bartonicek N, Jansson M, Hatzikotoulas K, Irving MD, Beleza-Meireles A, Rivadeneira F, Duncan E, Richards JB, Adams DJ, Lelliott CJ, Brink R, Phan TG, Eisman JA, Evans DM, Zeggini E, Baldock PA, Bassett JHD, Williams GR, Croucher PI. Osteocyte transcriptome mapping identifies a molecular landscape controlling skeletal homeostasis and susceptibility to skeletal disease. Nat Commun. 2021 May 5;12(1):2444. doi: 10.1038/s41467-021-22517-1.

PROSTATE CANCER CONSORTIUM

-Philp LK, Rockstroh A, Sadowski MC, Taherian Fard A, Lehman M, Tevz G, Libério MS, Bidgood CL, Gunter JH, McPherson S, **Bartonicek N**, Wade JD, Otvos L, Nelson CC. Leptin antagonism inhibits prostate cancer xenograft growth and progression. Endocr Relat Cancer. 2021 Apr 29;28(5):353-375. doi: 10.1530/ERC-20-0405.

-Philp LK, Rockstroh A, Lehman M, Sadowski MC, Bartonicek N, Wade JD, Otvos L, Nelson CC. Adiponectin receptor activation inhibits prostate cancer xenograft growth. Endocr Relat Cancer. 2020 Dec;27(12):711-729. doi: 10.1530/ERC-20-0297.

-Tousignant KD, Rockstroh A, Taherian Fard A, Lehman ML, Wang C, McPherson SJ, Philp LK, **Bartonicek N**, Dinger ME, Nelson CC, Sadowski MC. (2019) Lipid uptake is an androgen-enhanced lipid supply pathway associated with prostate cancer disease progression and bone metastasis. **Mol Cancer Res.** 2019 Feb 26. doi: 10.1158/1541-7786.MCR-18-1147.

BREAST CANCER NONCODING RNA - CAPTURE COLLABORATIONS

-Moradi Marjaneh M, Beesley J, O'Mara TA, Mukhopadhyay P, Koufariotis LT, Kazakoff S, Hussein N, Fachal L, **Bartonicek N**, Hillman KM, Kaufmann S, Sivakumaran H, Smart CE, McCart Reed AE, Ferguson K, Saunus JM, Lakhani SR, Barnes DR, Antoniou AC, Dinger ME, Waddell N, Easton DF, Dunning AM, Chenevix-Trench G, Edwards SL, French JD. (2020) Non-coding RNAs underlie genetic predisposition to breast cancer. **Genome Biol.** 2020 Jan 7;21(1):7. doi: 10.1186/s13059-019-1876-z.

-Betts JA, Moradi Marjaneh M, Al-Ejeh F, Lim YC, Shi W, Sivakumaran H, Tropée R, Patch AM, Clark MB, Bartonicek N, Wiegmans AP, Hillman KM, Kaufmann S, Bain AL, Gloss BS, Crawford J, Kazakoff S, Wani S, Wen SW, Day B, Möller A, Cloonan N, Pearson J, Brown MA, Mercer TR, Waddell N, Khanna KK, Dray E, Dinger ME, Edwards SL, French JD. (2017) Long Noncoding RNAs CUPID1 and CUPID2 Mediate Breast Cancer Risk at 11q13 by Modulating the Response to DNA Damage. Am J Hum Genet. 2017 Aug 3;101(2):255-266. doi: 10.1016/j.ajhg.2017.07.007.

POPULATION GENETICS OF ENDANGERED AUSTRALIAN MAMMALS

-Ahrens, C., Slavenko, A., Kriesner, P., van Rooyen, A., Heinze, D., Bartonicek, N., & Weeks, A. (2025). Stochastic wind-driven migration likely maintains panmixia in the endangered bogong moth, Agrotis infusa. Biological Conservation, doi: 10.1016/j.biocon.2025.110993

-Weeks AR, Kriesner P, Bartonicek N, van Rooyen A, Cairns KM, Ahrens CW. Genetic structure and common ancestry expose the dingo-dog hybrid myth. Evol Lett. 2024 Oct 19;9(1):1-12. doi: 10.1093/evlett/qrae057.

OTHER COLLABORATIONS

-Hardwick SA, Bassett SD, Kaczorowski D, Blackburn J, Barton K, **Bartonicek N**, Carswell SL, Tilgner HU, Loy C, Halliday G, Mercer TR, Smith MA, Mattick JS. (2019) Targeted, High-Resolution RNA Sequencing of Non-coding Genomic Regions Associated With Neuropsychiatric Functions. **Front Genet.** 2019 Apr 12;10:309. doi: 10.3389/fgene.2019.00309.

-Lancaster GI, Langley KG, Berglund NA, Kammoun HL, Reibe S, Estevez E, Weir J, Mellett NA, Pernes G, Conway JRW, Lee MKS, Timpson P, Murphy AJ, Masters SL, Gerondakis S, **Bartonicek N**, Kaczorowski DC, Dinger ME, Meikle PJ, Bond PJ, Febbraio MA. (2018) Evidence that TLR4 Is Not a Receptor for Saturated Fatty Acids but Mediates Lipid-Induced Inflammation by Reprogramming Macrophage Metabolism. **Cell Metab.** 2018 May 1;27(5):1096-1110.e5. doi: 10.1016/j.cmet.2018.03.014.

## Presentations

OZ Single Cell (2019) Workshop: Computational aspects of CITE-seq technology.