

Guillermo Parada González

Postdoctoral Researcher in Molecular and Computational Biology

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EDUCATION

2022 PhD, Biological Sciences, University of Cambridge.

2015–2021 Doctoral research, Wellcome Sanger Institute and The Gurdon Institute, University of Cambridge.

2021 PhD thesis: *Computational analyses of non-canonical architectural and structural features associated with alternative splicing.*

2007–2012 Professional Degree and Licentiate in Biochemistry, Pontificia Universidad Católica de Chile.

2012 Undergraduate thesis: *Bioinformatics analysis of non-canonical introns in the human transcriptome.*

Early training

2003–2005 Explora CONICYT scientific training programme for secondary-school students, Chile; completed advanced courses in microbiology and biotechnology hosted by the Universidad Metropolitana de Ciencias de la Educación and Universidad de Chile.

RESEARCH EXPERIENCE

2025 (Sep)–Present – Postdoctoral Researcher, Centre for Developmental Neurobiology, King's College London, and Brain RNA Regulatory Networks Laboratory, The Francis Crick Institute (co-led by Ben Blencowe and Jernej Ule).

Completing projects initiated in the Blencowe laboratory in Toronto and carrying out large-scale computational analyses to identify shared molecular signatures across neurodevelopmental disorders.

2021 (Aug)–2025 (Aug) Postdoctoral Fellow, Blencowe Laboratory, Donnelly Centre, University of Toronto.

Lead and co-lead computational genomics and machine-learning projects on neuronal microexons, splicing code modelling, RNA duplex-mediated exon skipping, and variant effect prediction in neurodevelopmental disease. Co-first author on a major study integrating machine learning with statistical genomics analyses to link predicted microexon-disrupting variants to autism. Co-supervise and mentor trainees across multiple projects, including conceiving and co-leading a Genome Biology study with Hyunbeen Lee as co-first and co-corresponding author, and mentoring Jacob Fine on a manuscript under consideration at Nature Communications. Also co-authored additional collaborative studies published in high-impact journals, including Nature Communications and Molecular Cell.

2021 (Apr)–2021 (May) Research Associate, Hollfelder Laboratory, Department of Biochemistry, University of Cambridge.

Completed a longer-term contribution to a collaborative single-cell total RNA sequencing study initiated during my PhD, leading alternative splicing analyses for the resulting publication in Nature Biotechnology.

2020 (Apr)–2020 (Oct) Research Associate, Hemberg Laboratory, Wellcome Sanger Institute.

Contributed to the completion of multiple collaborative research projects, including computational analyses and manuscript preparation that led to co-author peer-reviewed publications.

2015 (Jul)–2015 (Sep) Visitor Worker, Miska Laboratory, Gurdon Institute, University of Cambridge.

Worked on RNA-focused computational analyses during the transition into doctoral research.

2014 (May)–2015 (Mar) Research Assistant, Andrés Laboratory, Department of Cellular and Molecular Biology, Pontificia Universidad Católica de Chile.

Contributed to gene regulation and neuronal biology projects, leading to co-authored peer-reviewed publications.

2012 (Nov)–2014 (Apr) Research Assistant, Gysling Laboratory, Department of Cellular and Molecular Biology, Pontificia Universidad Católica de Chile.

Completed and extended the computational analyses from my undergraduate thesis on non-canonical splice sites in the human transcriptome, leading to a first-author publication in Nucleic Acids Research.

FELLOWSHIPS AND STUDENTSHIPS

2022 Charles H. Best Postdoctoral Fellowship, University of Toronto. Competitive fellowship supporting postdoctoral research in RNA biology and computational genomics.

2015 Wellcome Trust Four-Year Doctoral Studentship, University of Cambridge. Competitive doctoral studentship covering tuition fees and stipend.

GRANT DEVELOPMENT CONTRIBUTIONS

2023 Simons Foundation Autism Research Initiative (SFARI) grant, Blencowe laboratory. Contributed substantially to the preparation of a successful grant application by providing critical feedback throughout the application process, as well as generating preliminary analyses and figures.

2021 McLaughlin Centre Accelerator Grants in Genomic Medicine, Blencowe laboratory. Contributed to the preparation of a successful grant application by providing critical feedback throughout the application process.

FIRST AUTHOR RESEARCH PUBLICATIONS

Manuscripts under review

Parada, G.E.*; Bretschneider, H.*; Li, J.D.; Fine, J.L.; Dupas, S.J.; Ellis, J.D.; ... ; Morris, Q.D.#; Blencowe, B.J.#

An expanded repertoire of brain microexons is directly impacted by autism-associated genetic variation (2026). Revised manuscript under consideration.

- Co-led the study; combined machine learning and family-based statistical genomics across >7,000 families to link rare and ultra-rare predicted microexon-disrupting variants to ASD.

Peer-reviewed publications

Lee, H.*; Cao, X.*; Parada, G.E.*#; Li, J.D.; Iosub, I.A.; Braunschweig, U.; Rebelo, K.; Ule, J.; Wan, Y.#; Blencowe, B.J.#. Alu-mediated RNA duplexes are associated with widespread exon skipping across primate transcriptomes (2026). *Genome Biology* 27, 94.

- Co-first and corresponding author; supervised the project and led key conceptual and analytical components linking Alu-mediated RNA duplexes to exon skipping and primate splicing divergence.

Georgakopoulos-Soares, I.*; Parada, G.E.*; Wong, H.Y.; Medhi, R.; Furlan, G.; Munita, R.; et al. *Alternative splicing modulation by G-quadruplexes* (2022). *Nature Communications* 13, 2404.

- Co-led the study and analyses; demonstrated that RNA G-quadruplex structures can modulate alternative splicing on a transcriptome-wide scale.

Parada, G.E.; Munita, R.; Georgakopoulos-Soares, I.; Fernandez, H.J.R.; Kedlian, V.R.; Metzakopian, E.; et al. *MicroExonator enables systematic discovery and quantification of microexons across mouse embryonic development* (2021). *Genome Biology* 22, 43.

- Developed MicroExonator and led its application to systematically discover and quantify microexons across mouse embryonic development.

Parada, G.E.*; Munita, R.*; Cerda, C.A.; Gysling, K.# *A comprehensive survey of non-canonical splice sites in the human transcriptome* (2014). *Nucleic Acids Research* 42, 10564–10578.

- Led the computational analysis and defined a high-confidence landscape of non-canonical splice sites in the human transcriptome.

***Equal contribution; #Corresponding authors**

SUPERVISION AND MENTORSHIP

Hyunbeen Lee Current supervision in the Blencowe laboratory on Alu-mediated RNA duplexes and exon skipping, with this work already resulting in a *Genome Biology* paper on which I am co-first and co-corresponding author.

Jacob L. Fine Current supervision in the Blencowe laboratory on computational analyses of rare codon patches and RNA regulatory networks, with this work now under consideration at *Nature Communications*.

Yuyao Song Past mentorship in the Hemberg laboratory on alternative splicing analysis in single-cell RNA-seq, culminating in a *Genome Biology* publication on scASfind.

SELECTED PRESENTATIONS

- 2026** The Regulatory Code for Neuronal Microexons: Implications for the Genetics of Autism Spectrum Disorder. Cambridge RNA Club, University of Cambridge, UK (invited talk; scheduled).
- 2026** The Regulatory Code for Neuronal Microexons: Implications for the Genetics of Autism Spectrum Disorder. 31st Annual Meeting of the RNA Society, Montréal, Canada (selected Flash Talk poster presentation; scheduled).
- 2023** The regulatory code for neuronal microexons: implications for the genetics of autism spectrum disorder. Molecular Biosystems Conference on Eukaryotic Gene Regulation & Functional Genomics, Puerto Varas, Chile (selected poster presentation).
- 2021** Uncovering alternative splicing patterns of microexons across mouse development and neuronal cell-types. Neurogenomics Seminar Series, UK DRI Centre at Imperial College London, UK (invited talk).
- 2019** Alternative splicing modulation by G-quadruplexes. Molecular Biosystems Conference on Eukaryotic Gene Regulation & Functional Genomics, Puerto Varas, Chile (selected talk; Best Talk Prize).
- 2018** Micro-exons: from discovery to quantitative analyses using RNA-seq data. Quantitative Genomics, University College London, UK (selected talk).
- 2017** Quantitative analysis of micro-exon inclusion rates in large-scale RNA-seq experiments. Molecular Biosystems Conference on Eukaryotic Gene Regulation & Functional Genomics, Puerto Varas, Chile (selected talk).
- 2017** Micro-exons: from discovery to quantitative analyses using RNA-seq data. Sanger Institute Away Day, Hinxton, UK (selected talk).
- 2012** Analysis of non-canonical introns in the human transcriptome. International Society for Computational Biology Latin America Conference on Bioinformatics, Santiago, Chile (poster presentation; Best Poster Prize).

AWARDS AND DISTINCTIONS

- 2019** Best Talk selected from abstracts, Molecular Biosystems Conference on Eukaryotic Gene Regulation & Functional Genomics, Puerto Varas, Chile.
- 2017 & 2019** Homerton research grants supporting travel to the Molecular Biosystems Conference on Eukaryotic Gene Regulation & Functional Genomics.
- 2012** Awarded professional title of Biochemist with Distinction (Dos votos de Distinción), Pontificia Universidad Católica de Chile.
- 2012** Best Poster Prize, International Society for Computational Biology Latin America Conference on Bioinformatics.

CO-AUTHORED RESEARCH PUBLICATIONS

Manuscripts under review

- **Fine, J.L.; Parada, G.E.; Li, J.D.; Mitina, A.; Rebelo, K.; Yuen, R.; Moses#, A.M.; Blencowe, B.J#.** Rare codon patches coordinate an RNA regulatory network and are impacted by repeat expansions linked to brain disorders. Under consideration.

Peer-reviewed publications

- **Dupas, S.J.; Parada, G.E.; Li, J.D.; Brown, K.R.; Moffat, J.; Blencowe, B.J#.** Splice isoform-perturbation coupled to single cell transcriptome profiling reveals functions of microexons in neurogenesis and autism-linked pathways (2026). *Nature Communications* 17, 1217.
- **Georgakopoulos-Soares, I.; Yizhar-Barnea, O.; Mouratidis, I.; ... Parada, G.E.; et al.** Leveraging sequences missing from the human genome to diagnose cancer (2025). *Communications Medicine* 5, 363.
- **Song, Y.; Parada, G.E.; Lee, J.T.H.; Hemberg, M.#** Mining alternative splicing patterns in scRNA-seq data using scASfind (2024). *Genome Biology* 25, 197.
- **Salmen, F.*; De Jonghe, J.*; Kaminski, T.; Alemany, A.; Parada, G.E.; ... Hemberg, M.; Hollfelder, F.#; van Oudenaarden, A.#.** High-throughput total RNA sequencing in single cells (2022). *Nature Biotechnology*.
- **Han, H.; Best, A.J.; Braunschweig, U.; Mikolajewicz, N.; Li, J.L.; Roth, J.; Chowdhury, F.; Mantica, F.; Shah, S.N.; Parada, G.E.; et al.** Systematic exploration of dynamic splicing networks reveals conserved multistage regulators of neurogenesis (2022). *Molecular Cell* 82(16):2982–2999.e14.
- **Georgakopoulos-Soares, I.; Victorino, J.; Parada, G.E.; Agarwal, V.; Zhao, J.; et al.** High-throughput characterization of the role of non-B DNA motifs on promoter function (2022). *Cell Genomics* 2(4):100111.

- **Georgakopoulos-Soares, I.; Mouratidis, I.; Parada, G.E.; Matharu, N.; Hemberg, M.; Ahituv, N.** Asymmetron: a toolkit for the identification of strand asymmetry patterns in biological sequences (2021). *Nucleic Acids Research* 49(1):e4.
- **Gapp, K.; Parada, G.E.; Gross, F.; Corcoba, A.; Kaur, J.; Grau, E.; Hemberg, M.; Bohacek, J.; Miska, E.A.** Single paternal dexamethasone challenge programs offspring metabolism and reveals multiple candidates in RNA-mediated inheritance (2021). *iScience* 24, 102870.
- **Urbonaite, G.; Lee, J.T.H.; Liu, P.; Parada, G.E.; Hemberg, M.; Acar, M.** A yeast-optimized single-cell transcriptomics platform elucidates how mycophenolic acid and guanine alter global mRNA levels (2021). *Communications Biology* 4, 822.
- **Akay, A.; Di Domenico, T.; Suen, K.M.; Nabih, A.; Parada, G.E.; et al.** The Helicase Aquarius/EMB-4 Is Required to Overcome Intronic Barriers to Allow Nuclear RNAi Pathways to Heritably Silence Transcription (2017). *Developmental Cell* 42, 241–255.e6.
- **Gómez, A.V.; Córdova, G.; Munita, R.; Parada, G.E.; Barrios, Á.P.; Cancino, G.I.; Álvarez, A.R.; Andrés, M.E.** Characterizing HSF1 Binding and Post-Translational Modifications of hsp70 Promoter in Cultured Cortical Neurons: Implications in the Heat-Shock Response (2015). *PLOS ONE* 10, e0129329.
- **Sáez, J.E.; Gómez, A.V.; Barrios, Á.P.; Parada, G.E.; Galdames, L.; González, M.; Andrés, M.E.** Decreased Expression of CoREST1 and CoREST2 Together with LSD1 and HDAC1/2 during Neuronal Differentiation (2015). *PLOS ONE* 10, e0131760.

OTHER PUBLICATIONS

- **Parada, G.E.; Hemberg, M.** Identification and Quantification of Microexons Using Bulk and Single-Cell RNA-Seq Data. *Methods in Molecular Biology: Alternative Splicing* (2022). 2537:129–147.
- **Parada, G.E.; Hemberg, M.** Bridge over troubled transcripts (2022). *Nature Computational Science* 2, 142–143.
- **Georgakopoulos-Soares, I.; Parada, G.E.; Hemberg, M.** Secondary structures in RNA synthesis, splicing and translation. *Computational and Structural Biotechnology Journal* (2022). 20:2871–2884.
- **von Bernhardt, R.; Cornejo, F.; Parada, G.E.; Eugén, J.** Role of TGFβ signaling in the pathogenesis of Alzheimer's disease (2015). *Frontiers in Cellular Neuroscience* 9, 426.

TEACHING, TRAINING AND COURSE INSTRUCTION

2021 & 2019 Tutor, Wellcome Genome Campus advanced course on Next Generation Sequencing Bioinformatics, Santiago, Chile.

2020 Tutor, Reproducible Bioinformatics Methods, Pontificia Universidad Católica de Chile (invited by the Sjöberg Laboratory).

2017–2019 Tutor on University of Cambridge courses in RNA-seq analysis, Python programming, data science in Python, and computational methods for biological data analysis.

2013 Teaching Assistant, Cell Biology (BIO141c), Pontificia Universidad Católica de Chile.

2012–2013 Teaching Assistant, Molecular Biology of the Cell (BIO238M), Pontificia Universidad Católica de Chile.

TECHNICAL EXPERTISE

Computational genomics and transcriptomics: Bulk and single-cell RNA-seq analysis; alternative splicing, isoform, and microexon discovery and quantification; comparative and evolutionary transcriptomics.

Machine learning for regulatory genomics: Supervised and unsupervised learning; sequence-based splicing code models; genomic foundation-model fine-tuning for variant effect prediction.

Programming and reproducible computing: Python; R; Unix / shell scripting; Snakemake; Git; version-controlled bioinformatics pipelines; HPC and GPU computing environments.

Research themes: RNA biology; regulatory genomics; machine learning for transcriptomics; human genetics and neurodevelopmental disorders.

REFEREES

Prof. Benjamin J. Blencowe — Banbury Chair in Medical Research; Canada Research Chair in RNA Biology and Genomics, University of Toronto. Postdoctoral supervisor. Email: b.blencowe@utoronto.ca

Prof. Martin Hemberg — Associate Professor, Brigham and Women's Hospital and Harvard Medical School. PhD supervisor. Email: mhemberg@bwh.harvard.edu

Prof. Eric A. Miska — Head of the Department of Biochemistry; Herchel Smith Professor of Molecular Genetics, University of Cambridge. PhD supervisor. Email: eam29@cam.ac.uk