

Peter Chovanec, Ph.D.

28th January 2021

Education

- 2014 - 2019 **PhD - University of Cambridge (The Babraham Institute)**
2010 - 2014 **BSc - Genetics with a research Year in Europe – University of York**
2008 - 2010 **International Baccalaureate:** Gymnazium J. Hronca, Bratislava (SK) and UNIS, New York (USA)

Research experience

- 2020 November – present **Postdoctoral scholar – University of California, Los Angeles**
Department of Human Genetics in Prof. Yi Yin laboratory
- Development and application of novel single cell sequencing technologies and computational approaches to enhance our understanding of mitotic recombination
- 2019 March – 2020 November **Postdoctoral scholar – California Institute of Technology**
Division of Biology and Biological Engineering in Prof. Mitchell Guttman laboratory
- Development of a novel scRNA-seq method utilising the SPRITE barcoding scheme for the simultaneous readout of RNA and DNA for CRISPR screens
 - Development of Snakemake pipelines for the analysis of SPRITE chromatin interaction data and general sequencing datasets
 - Cut&Tag revealed the silencing dependent localisation of SHARP to precise regions of the inactive X chromosome in mouse embryonic stem cells
- 2014 October – 2019 February **PhD - University of Cambridge (The Babraham Institute)**
Supervised by Dr. Anne Corcoran - funded by an industrial CASE studentship
- Bioinformatics pipeline for the analysis of our unbiased DNA based repertoire quantification assay (VDJ-seq) utilising unique molecular identifiers (UMIs)
 - Characterisation of human bone marrow B cell repertoire and their niche in aging using VDJ-seq and single cell transcriptomics (sci-RNA-seq)
 - Assembly of the immunoglobulin heavy chain locus of the 129sv mouse strain utilising the Nanoporetech Minion sequencer
 - Comprehensive flow cytometry and epigenetic analysis of B cell development in a humanised immunoglobulin heavy chain mouse model revealed altered developmental trajectory and underlying mechanisms
 - Transgene localisation and sequencing with 4C based targeted locus amplification (TLA)
 - Bioinformatic analysis examining the heterogeneous transition during primed to naïve reprogramming of human pluripotent stem cells in collaboration with Dr. Peter Rugg-Gunn
 - Investigating the 3D genome organisation remodelling between naïve and primed human pluripotent states in collaboration with Dr. Peter Rugg-Gunn and Dr. Peter Fraser (Promoter Capture Hi-C, Hi-C and ChIP-seq)
- 2013 October - 9 months **BSc dissertation - University of York**
Examining the feasibility of using the Genome Analysis Toolkit (GATK) for accurate SNP genotyping in non-model organisms (*Heliconius* butterfly).
- 2012 September - 10 months **Research placement - IGBMC, Strasbourg**
Department of Functional Genomics and Cancer in Dr. Hinrich Gronemeyer's lab
Elucidating the differential effects of the CREB-binding protein (CBP) versus its paralogue p300 in the context of estrogen receptor alpha (ER α) mediated transcription.
- Re-ChIP experiments coupled with the linear amplification method LinDA to analyse co-binding at the co-activator complex
 - Analysis of the functional impact of CPB and/or p300 using siRNA mediated knockdown on gene expression

Publications

Quinodoz, S.A., Bhat, P., **Chovanec, P.**, Jachowicz, J., Ollikainen, N., Detmar, E., Soehalim, E., Guttman, M. (2020) SPRITE: A genome-wide method to map higher-order 3D spatial interactions in the nucleus using combinatorial split-and-pool barcoding. *Nat Protoc* (in review)

Quinodoz, S.A., Bhat, P., Ollikainen, N., Jachowicz, J., Banerjee, A., **Chovanec, P.**, Blanco, M.R., Chow, A., Markaki, Y., Plath, K., Guttman, M., (2021) RNA promotes the formation of spatial compartments in the nucleus. [bioRxiv 2020.08.25.267435v1](https://doi.org/10.1101/2020.08.25.267435v1) (in review)

Chovanec, P.†, Collier, A.J.†, Krueger, C., Várnai, C., Semprich, Cl., Schoenfelder, S., Corcoran, A.E., Rugg-Gunn, P. (2021) Widespread reorganisation of pluripotent factor binding and gene regulatory interactions between human pluripotent states. [bioRxiv 2019.12.13.875286](https://doi.org/10.1101/2019.12.13.875286) (Accepted in principle)

Teng, Y.*, Young, J.L.*, Edwards, B.*, Hayes, P., Thompson, L., Johnston, C., Edwards, C. Sanders, Y., Writer, M., Pinto, D., Zhang, Y., Roode, M., **Chovanec, P.**, Matheson, L., Corcoran, A.E., Fernandez, A., Montoliu, L., Rossi, B., Tosato, V., Gjuracic, K., Nikitin, D., Bruschi, C., McGuinness, B., Sandal, T., and Romanos, M. (2019) Diverse Human VH antibody fragments with bio-therapeutic properties from the Crescendo Mouse. [New Biotechnol 55, 65–76](https://doi.org/10.1016/j.nbt.2019.05.006).

Koohy, H.†, Bolland, D.J.†, Matheson, L.S.†, Schoenfelder, S., Stellato, C., Dimond, A., Varnai, C., **Chovanec, P.**, Chessa, T., Denizot, J., Garcia, R.M., Wingett, S.W., Freire-Pritchett, P., Nagano, T., Mielczarek, O., Baizan-Edge, A., Stubbs, B.A., Hawkins, P., Stephens, L., Elderkin, S., Spivakov, M., Fraser, P., Corcoran, A.E., and Varga-Weisz, P.D. (2018) Genome organisation and chromatin analysis identifies transcriptional downregulation of insulin-like growth factor signalling as a hallmark of ageing in developing B cells. [Genome Biol. 19, 126](https://doi.org/10.1093/gbe/abz012).

Chovanec, P., Bolland, D.J., Matheson, L.S., Wood, A.L., Corcoran, A.E. (2018). Unbiased quantification of immunoglobulin diversity at the DNA level with VDJ-seq. [Nat. Protoc. 13, 1232–1252](https://doi.org/10.1038/nprot.2018.123).

Collier, A.J.†, Panula, S.P.†, **Chovanec, P.***, Schell, J.P.*, Reyes, A.P., Petropoulos, S., Corcoran, A.E., Walker, R., Douagi, I., Lanner, F., Rugg-Gunn, P.J. (2017). Comprehensive Cell Surface Protein Profiling Identifies Specific Markers of Human Naive and Primed Pluripotent States. [Cell Stem Cell 20, 874–890.e7](https://doi.org/10.1016/j.stem.2017.08.007)

Matheson, L.S., Bolland, D.J., **Chovanec, P.**, Krueger, F., Andrews, S., Koohy, H., and Corcoran, A. (2017). Local chromatin features including PU.1 and IKAROS binding and H3K4 methylation shape the repertoire of immunoglobulin kappa genes chosen for V(D)J recombination. [Front. Immunol. 8, 1550](https://doi.org/10.3389/fimm.2017.00150).

Bolland, D.J., Koohy, H., Wood, A.L., Matheson, L.S., Krueger, F., Stubbington, M.J.T., Baizan-Edge, A., **Chovanec, P.**, Stubbs, B.A., Tabbada, K., Andrews, S.R., Spivakov, M., Corcoran, A.E. (2016). Two Mutually Exclusive Local Chromatin States Drive Efficient V(D)J Recombination. [Cell Rep. 15, 2475–2487](https://doi.org/10.1016/j.ccr.2016.08.010).

Equal contributions: *; Co-first author: †

Honours and awards

2017 Knowledge Exchange Commercialisation travel award

2017 University of Cambridge Sidney Sussex College travel award

Laboratory skills and techniques

- RNA/DNA library preparation and sequencing including single cell sequencing using combinatorial indexing (sci-RNA-seq) and split-pool recognition of interactions by tag extension (SPRITE)
- ATAC-seq and Fast-ATAC library preparation and data analysis including making homemade Tn5 and pA-Tn5
- Cut&Tag and ChIP-seq of transcription factors and histone modifications
- Tissue culture experience with human and mouse pluripotent stem cells, primary and immortalized cell lines
- Extensive experience in antigen receptor repertoire analysis, library preparation and sequencing
- Extensive flow cytometry experience including 9 colour panel design and data analysis
- 3D DNA Fluorescence *In-Situ* Hybridisation (FISH), including chromosome painting and directly labelled probe making

- Extensive bioinformatics experience including writing Snakemake pipelines and analysis of NGS datasets; proficient in R and python (<https://github.com/peterch405>, <https://github.com/GuttmanLab>)
- Completed UK Home office training modules 1-3 for work with small rodent animals

Invited talks and posters

2018	Keystones Chromatin Architecture and Chromosome Organization. <i>Poster</i>
2017	Babraham bioinformatics seminar. <i>Talk</i>
2016	Babraham flow cytometry seminar. <i>Talk</i>
2016	Babraham sequencing seminar. <i>Talk</i>
2016	Single Cell Genomics, Sanger Institute UK. <i>Poster</i>

Other activities

Public engagement: Royal Society Exhibition (2015); Cambridge Science festival (2016); Epigenetics exhibit designer (2017)

Other: Symposium of Biological and Life Sciences (SymBLS) conference coordinator (2016)