

Current position

03/2020 - present **Postdoctoral Associate in Computational Biomedicine**, *Institute of Computational Biomedicine, Englander Institute for Precision Medicine, Weill Cornell Medicine, USA.*
Supervisor: Olivier Elemento

Education

09/2014 - 01/2020 **PhD**, *Medical University of Vienna, Austria.*
Supervisor: Christoph Bock, CeMM Research Centre for Molecular Medicine
09/2012 - 06/2014 **'Mestrado' (MSc) in Molecular and Cell Biology**, *University of Aveiro, Portugal.*
09/2008 - 07/2012 **'Licenciatura' (BSc) in Biology**, *University of Aveiro, Portugal.*

Key publications

Rendeiro*, Ravichandran* *et al.*, **The spatial landscape of lung pathology during COVID-19 progression**. *Nature* (2021) doi:10.1038/s41586-021-03475-6

Rendeiro*, Krausgruber* *et al.*, **Chromatin mapping and single-cell immune profiling define the temporal dynamics of ibrutinib drug response in CLL**. *Nature Communications* (2020). doi:10.1038/s41467-019-14081-6

Datlinger*, Rendeiro*, *et al.* **Ultra-high throughput single-cell RNA sequencing by combinatorial fluidic indexing**. *bioRxiv* (2019). doi:10.1101/2019.12.17.879304

Datlinger, Rendeiro*, Schmidl* *et al.*, **Pooled CRISPR screening with single-cell transcriptome readout**. *Nature Methods* (2017) doi:10.1038/nmeth.4177

Rendeiro*, Schmidl*, Strefford* *et al.*, **Chromatin accessibility maps of chronic lymphocytic leukaemia identify subtype-specific epigenome signatures and transcription regulatory networks**. *Nature Communications* (2016). doi:10.1038/ncomms11938

* *equal contributions*

Scholarships/Grants

10/2020 - present **Molecular and Translational Oncology Research, Training Grant**, T32CA203702.
National Cancer Institute, USA
08/2013 - 06/2014 **Erasmus studies mobility program scholarship**.
European Commission
09/2011 - 06/2012 **Erasmus internship mobility program scholarship**.
European Commission
10/2009 - 06/2010 **"Integration into Research" Grant**.
Science and Technology Foundation, Portugal

22. Johannes C. Melms*, Jana Biermann*, Huachao Huang*, Yiping Wang*, Ajay Nair*, Somnath Tagore*, Igor Katsyv*, André F. Rendeiro*, Amit Dipak Amin*, Denis Schapiro, Chris J. Frangieh, Adrienne M. Luoma, Aveline Filliol, Yinshan Fang, Hiranmayi Ravichandran, Mariano G. Clausi, George A. Alba, Meri Rogava, Sean W. Chen, Patricia Ho, Daniel T. Montoro, Adam E. Kornberg, Arnold S. Han, Mathieu F. Bakhoun, Niroshana Anandasabapathy, Mayte Suárez-Fariñas, Samuel F. Bakhoun, Yaron Bram, Alain Borczuk, Xinzhen V.Guo, Jay H. Lefkowitz, Charles Marboe, Stephen. M. Lagana, Armando Del Portillo, Emmanuel Zorn, Glen S. Markowitz, Robert F. Schwabe, Robert E. Schwartz, Olivier Elemento, Anjali Saqi, Hanina Hibshoosh, Jianwen Que, Benjamin Izar. **A molecular single-cell lung atlas of lethal COVID-19.** Nature (2021). doi:10.1038/s41586-021-03569-1
21. André F. Rendeiro*, Hiranmayi Ravichandran*, Yaron Bram, Vasuretha Chandar, Junbum Kim, Cem Meydan, Jiwoon Park, Jonathan Foox, Tyler Hether, Sarah Warren, Youngmi Kim, Jason Reeves, Steven Salvatore, Christopher E. Mason, Eric C. Swanson, Alain C. Borczuk, Olivier Elemento, Robert E. Schwartz. **The spatial landscape of lung pathology during COVID-19 progression.** Nature (2021). doi:10.1038/s41586-021-03475-6
20. Sandra Schick, Sarah Grosche, Katharina Eva Kohl, Danica Drpic, Martin G. Jaeger, Nara C. Marella, Hana Imrichova, Jung-Ming G. Lin, Gerald Hofstätter, Michael Schuster, André F. Rendeiro, Anna Koren, Mark Petronczki, Christoph Bock, André C. Müller, Georg E. Winter, Stefan Kubicek. **Acute BAF perturbation causes immediate changes in chromatin accessibility.** Nature Genetics (2021). doi:10.1038/s41588-021-00777-3
19. André F. Rendeiro, Joseph Casano, Charles Kyriakos Vorkas, Harjot Singh, Ayana Morales, Robert A DeSimone, Grant B Ellsworth, Rosemary Soave, Shashi N Kapadia, Kohta Saito, Christopher D Brown, JingMei Hsu, Christopher Kyriakides, Steven Chui, Luca Cappelli, Maria Teresa Cacciapuoti, Wayne Tam, Lorenzo Galluzzi, Paul D Simonson, Olivier Elemento, Mirella Salvatore, Giorgio Inghirami. **Profiling of immune dysfunction in COVID-19 patients allows early prediction of disease progression.** Life Science Alliance (2020). doi:10.26508/lsa.202000955
18. Alexander Swoboda, Robert Soukup, Oliver Eckel, Katharina Kinslechner, Bettina Wingelhofer, David Schörghofer, Christina Sternberg, Ha T T Pham, Maria Vallianou, Jaqueline Horvath, Dagmar Stoiber, Lukas Kenner, Lionel Larue, Valeria Poli, Friedrich Beermann, Takashi Yokota, Stefan Kubicek, Thomas Krausgruber, André F. Rendeiro, Christoph Bock, Rainer Zenz, Boris Kovacic, Fritz Aberger, Markus Hengstschlager, Peter Petzelbauer, Mario Mikula, Richard Moriggl. **STAT3 promotes melanoma metastasis by CEBP-induced repression of the MITF pathway.** Nature (2020). doi:10.1038/s41388-020-01584-6
17. Thomas Krausgruber, Nikolaus Fortelny, Victoria Fife-Gernedl, Martin Senekowitsch, Linda C. Schuster, Alexander Lercher, Amelie Nemc, Christian Schmidl, André F. Rendeiro, Andreas Bergthaler, Christoph Bock. **Structural cells are key regulators of organ-specific immune responses.** Nature (2020). doi:10.1038/s41586-020-2424-4
16. Rainer Hubmann, Susanne Schnabl, Mohammad Araghi, Christian Schmidl, André F. Rendeiro, Martin Hilgarth, Dita Demirtas, Farghaly Ali, Philipp B. Staber, Peter Valent, Christoph Zielinski, Ulrich Jäger, Medhat Shehata. **Targeting Nuclear NOTCH2 by Gliotoxin Recovers a Tumor-Suppressor NOTCH3 Activity in CLL.** Cells (2020). doi:10.3390/cells9061484
15. Elizabeth C Rosser, Christopher J.M. Piper, Diana E Matei, Paul A. Blair, André F. Rendeiro, Michael Orford, Dagmar G. Alber, Thomas Krausgruber, Diego Catalan, Nigel Klein, Jessica J. Manson, Ignat Drozdov, Christoph Bock, Lucy R Wedderburn, Simon Eaton, Claudia Mauri. **Microbiota-Derived Metabolites Suppress Arthritis by Amplifying Aryl-Hydrocarbon Receptor Activation in Regulatory B Cells.** Cell Metabolism (2020). doi:10.1016/j.cmet.2020.03.003
14. André F. Rendeiro*, Thomas Krausgruber*, Nikolaus Fortelny, Fangwen Zhao, Thomas Penz, Matthias Farlik, Linda C. Schuster, Amelie Nemc, Szabolcs Tasnády, Marienn Réti, Zoltán Mátrai, Donat Alpar, Csaba Bódör, Christian Schmidl, Christoph Bock, **Chromatin mapping and single-cell immune profiling define the temporal dynamics of ibrutinib drug response in CLL.** Nature Communications (2020). doi:10.1038/s41467-019-14081-6
13. Michael Delacher, Charles D Imbusch, Agnes Hotz-Wagenblatt, Jan-Philipp Mallm, Katharina Bauer, Malte Simon, Dania Riegel, André F. Rendeiro, Sebastian Bittner, Lieke Sanderink, Asmita Pant, Lisa Schmidlei-

- thner, Kathrin L Braband, Bernd Echtenachter, Alexander Fischer, Valentina Giunchiglia, Petra Hoffmann, Matthias Edinger, Christoph Bock, Michael Rehli, Benedikt Brors, Christian Schmidl, Markus Feuerer. **Precursors for Nonlymphoid-Tissue Treg Cells Reside in Secondary Lymphoid Organs and Are Programmed by the Transcription Factor BATF**. *Immunity* (2020). doi:10.1016/j.immuni.2019.12.002
12. Christopher JM Piper, Elizabeth C Rosser, Kristine Oleinika, Kiran Nistala, Thomas Krausgruber, André F. Rendeiro, Aggelos Banos, Ignat Drozdov, Matteo Villa, Scott Thomson, Georgina Xanthou, Christoph Bock, Brigitta Stockinger, Claudia Mauri. **Aryl Hydrocarbon Receptor Contributes to the Transcriptional Program of IL-10-Producing Regulatory B Cells**. *Cell Reports* (2019). doi:10.1016/j.celrep.2019.10.018
 11. Florian Puhm, Taras Afonyushkin, Ulrike Resch, Georg Obermayer, Manfred Rohde, Thomas Penz, Michael Schuster, Gabriel Wagner, André F. Rendeiro, Imene Melki, Christoph Kaun, Johann Wojta, Christoph Bock, Bernd Jilma, Nigel Mackman, Eric Boilard, Christoph J Binder. **Mitochondria are a subset of extracellular vesicles released by activated monocytes and induce type I IFN and TNF responses in endothelial cells**. *Circulation Research* (2019). doi:10.1161/CIRCRESAHA.118.314601
 10. Sandra Schick, André F. Rendeiro, Kathrin Runggatscher, Anna Ringler, Bernd Boidol, Melanie Hinkel, Peter Májek, Loan Vulliard, Thomas Penz, Katja Parapatics, Christian Schmidl, Jörg Menche, Guido Boehmelt, Mark Petronczki, André C. Müller, Christoph Bock, Stefan Kubicek. **Systematic characterization of BAF mutations provides insights into intracomplex synthetic lethalties in human cancers**. *Nature Genetics* (2019). doi:10.1038/s41588-019-0477-9
 9. Sara Sdelci, André F. Rendeiro, Philipp Rathert, Wanhui You, Jung-Ming G. Lin, Anna Ringler, Gerald Hofstätter, Herwig P. Moll, Bettina Gürtl, Matthias Farlik, Sandra Schick, Freya Klepsch, Matthew Oldach, Pisanu Buphamalai, Fiorella Schischlik, Peter Májek, Katja Parapatics, Christian Schmidl, Michael Schuster, Thomas Penz, Dennis L. Buckley, Otto Hudecz, Richard Imre, Shuang-Yan Wang, Hans Michael Maric, Robert Kralovics, Keiryn L. Bennett, Andre C. Müller, Karl Mechtler, Jörg Menche, James E. Bradner, Georg E. Winter, Kristaps Klavins, Emilio Casanova, Christoph Bock, Johannes Zuber, Stefan Kubicek. **MTHFD1 interaction with BRD4 links folate metabolism to transcriptional regulation**. *Nature Genetics* (2019). doi:10.1038/s41588-019-0413-z
 8. Christian Schmidl*, Gregory I Vladimer*, André F. Rendeiro*, Susanne Schnabl*, Thomas Krausgruber, Christina Taubert, Nikolaus Krall, Tea Pemovska, Mohammad Araghi, Berend Snijder, Rainer Hubmann, Anna Ringler, Kathrin Runggatscher, Dita Demirtas, Oscar Lopez de la Fuente, Martin Hilgarth, Cathrin Skrabs, Edit Porpacz, Michaela Gruber, Gregor Hoermann, Stefan Kubicek, Philipp B Staber, Medhat Shehata, Giulio Superti-Furga, Ulrich Jäger, Christoph Bock. **Combined chemosensitivity and chromatin profiling prioritizes drug combinations in CLL**. *Nature Chemical Biology* (2019). doi:10.1038/s41589-018-0205-2
 7. Tahsin Stefan Barakat, Florian Halbritter, Man Zhang, André F. Rendeiro, Christoph Bock, Ian Chambers. (2017). **Functional dissection of the enhancer repertoire in human embryonic stem cells**. *Cell Stem Cell* (2018). 10.1016/j.stem.2018.06.014
 6. Paul Datlinger, André F. Rendeiro*, Christian Schmidl*, Thomas Krausgruber, Peter Traxler, Johanna Klughammer, Linda C Schuster, Amelie Kuchler, Donat Alpar, Christoph Bock. **Pooled CRISPR screening with single-cell transcriptome readout**. *Nature Methods* (2017). doi:10.1038/nmeth.4177
 5. Roman A Romanov, Amit Zeisel, Joanne Bakker, Fatima Girach, Arash Hellysaz, Raju Tomer, Alán Alpár, Jan Mulder, Frédéric Clotman, Erik Keimpema, Brian Hsueh, Ailey K Crow, Henrik Martens, Christian Schwindling, Daniela Calvigioni, Jaideep S Bains, Zoltán Máté, Gábor Szabó, Yuchio Yanagawa, Ming-Dong Zhang, André F. Rendeiro, Matthias Farlik, Mathias Uhlén, Peer Wulff, Christoph Bock, Christian Broberger, Karl Deisseroth, Tomas Hökfelt, Sten Linnarsson, Tamas L Horvath, Tibor Harkany. **Molecular interrogation of hypothalamic organization reveals distinct dopamine neuronal subtypes**. *Nature Neuroscience* (2016). doi:10.1038/nn.4462
 4. Clara Jana-Lui Busch, Tim Hendriks, David Weismann, Sven Jäckel, Sofie M. A. Walenbergh, André F. Rendeiro, Juliane Weißer, Florian Puhm, Anastasiya Hladik, Laura Göderle, Nikolina Papac-Milicevic, Gerald Haas, Vincent Millischer, Saravanan Subramaniam, Sylvia Knapp, Keiryn L. Bennett, Christoph Bock, Christoph Reinhardt, Ronit Shiri-Sverdlov, Christoph J. Binder. **Malondialdehyde epitopes are sterile mediators of hepatic inflammation in hypercholesterolemic mice**. *Hepatology* (2017). doi:10.1002/hep.28970
 3. André F. Rendeiro*, Christian Schmidl*, Jonathan C. Strefford*, Renata Walewska, Zadie Davis, Matthias Farlik, David Oscier, Christoph Bock. **Chromatin accessibility maps of chronic lymphocytic**

leukaemia identify subtype-specific epigenome signatures and transcription regulatory networks. *Nature Communications*. 7:11938 (2016). doi:10.1038/ncomms11938

2. Christian Schmidl*, [André F. Rendeiro](#)*, Nathan C Sheffield, Christoph Bock. 2015. **ChIPmentation: fast, robust, low-input ChIP-seq for histones and transcription factors.** *Nature Methods* (2015). doi:10.1038/nmeth.3542
1. Michaela Schwaiger, Anna Schönauer, [André F. Rendeiro](#), Carina Pribitzer, Alexandra Schauer, Anna Gilles, Johannes Schinko, David Fredman, and Ulrich Technau. **Evolutionary conservation of the eumetazoan gene regulatory landscape.** *Genome Research* (2014). doi:10.1101/gr.162529.113

Preprints (does not include preprints later published in peer-reviewed journals)

4. Nathan C. Sheffield, Michał Stolarczyk, Vincent P. Reuter, [André F. Rendeiro](#). **Linking big biomedical datasets to modular analysis with Portable Encapsulated Projects.** *bioRxiv* (2020). doi:10.1101/2020.10.0
3. Paul Datlinger*, [André F. Rendeiro](#)*, Thorina Boenke, Thomas Krausgruber, Daniele Barreca, Christoph Bock. **Ultra-high throughput single-cell RNA sequencing by combinatorial fluidic indexing.** *bioRxiv* (2019). doi:10.1101/2019.12.17.879304
2. Alexander Swoboda, Robert Soukup, Katharina Kinslechner, Bettina Wingelhofer, David Schoerghofer, Christina Sternberg, Ha Pham, Maria Vallianou, Jaqueline Horvath, Dagmar Stoiber, Lukas Kenner, Lionel Larue, Valeria Poli, Friedrich Beermann, Takashi Yokota, Stefan Kubicek, Thomas Krausgruber, [André F. Rendeiro](#), Christoph Bock, Rainer Zenz, Boris Kovacic, Fritz Aberger, Markus Hengstschaeger, Peter Petzelbauer, Mario Mikula, Richard Moriggl. **STAT3 promotes melanoma metastasis by CEBP-induced repression of the MITF pigmentation pathway.** *BiorXiv* (2018) doi:10.1101/422832
1. [André F. Rendeiro](#), Pavla Navratilova, Eric Thompson (2014). **Chromatin preparation for ChIP-seq in *Oikopleura dioica*.** *figshare*. doi:10.6084/m9.figshare.884562

Communications

Conference talks

7. **Chromatin mapping and single-cell immune profiling define the temporal dynamics of Ibrutinib response in CLL.** *Young Scientist Association of the Medical University of Vienna PhD Symposia*, June 2019, Vienna, Austria.
6. **Chromatin mapping and single-cell immune profiling define the temporal dynamics of Ibrutinib response in CLL.** *Frontiers in Single Cell Genomics Meeting - Cold Spring Harbour Asia*, November 2018, Suzhou, China.
5. **CROP-seq: updates on the single cell CRISPR screening method.** *10X User Group Meeting 2018*, April 2018, EMBL, Heidelberg, Germany.
4. **Pooled CRISPR screening with single-cell transcriptome readout.** *SLAS 2018*, February 2018, San Diego, USA. **Pooled CRISPR screening with single-cell transcriptome readout.** *Illumina User Group Meeting 2017*, February 2018, Bern, Switzerland.
3. **Large-scale ATAC-seq profiling to identify disease subtypes, regulatory networks and monitoring treatment in CLL.** *Illumina User Group Meeting 2017*, February 2018, Cologne, Germany.
2. **Pooled CRISPR screening with single-cell transcriptome readout.** *Ascona Workshop 2017*, May 2017, Ascona, Switzerland.
1. **Evolutionary conservation of the eumetazoan gene regulatory landscape.** *XVIII Portuguese Genetics Society Meeting*, June 2013. Porto, Portugal

Conference posters

5. **Chromatin mapping and single-cell immune profiling define the temporal dynamics of ibrutinib drug response in chronic lymphocytic leukemia.** *SCOG Workshop Computational Single Cell Genomics*, May 2019. Munich, Germany. doi:10.6084/m9.figshare.7892663.v1
4. **Combined chromatin accessibility and chemosensitivity profiling identifies targetable pathways and rational drug combinations in Ibrutinib-treated chronic lymphocytic leukemia.** *Young Scientist Association of the Medical University of Vienna PhD Symposia*, June 2017. Vienna, Austria.
3. **Large-scale chromatin profiling uncovers heterogeneity of molecular phenotypes and gene**

regulatory networks of chronic lymphocytic leukemia. *Young Scientist Association of the Medical University of Vienna PhD Symposia*, June 2016, Vienna, Austria. 10.6084/m9.figshare.3479528.v1 **Best poster award in "Malignant Diseases" category.**

2. **Large-scale chromatin profiling uncovers heterogeneity of molecular phenotypes and gene regulatory networks of chronic lymphocytic leukemia.** *Keystone Symposia on Chromatin and Epigenetics*, March 2016, Whistler, Vancouver, Canada. <https://doi.org/10.6084/m9.figshare.3479528.v1>
1. **Identification of cis-regulatory elements in the sea anemone *Nematostella vectensis*.** *Evonet Symposium*, September 2012, Vienna Austria. doi:10.6084/m9.figshare.107026

Additional experience

Research Activity

- 08/2013 - 06/2014 **The role of E2F regulation and H3K79 methylation in *Oikopleura dioica*'s cell cycle modes**, *Sars International Centre for Marine Molecular Biology*, Bergen, Norway.
Supervisor: Eric Thompson
- 09/2011 - 07/2012 **Identification of cis-regulatory elements in *Nematostella vectensis* using ChIP-seq**, *Dept. of Molecular Evolution and Development, University of Vienna, Austria*.
Supervisor: Ulrich Technau
- 09/2010 - 06/2011 **Tol2-mediated zebrafish transgenesis for studies in protein mistranslation**, *RNA Biology Laboratory, Biology Department, University of Aveiro, Portugal*.
Supervisor: Manuel Santos
- 09/2009 - 06/2010 **Transcriptome studies with microarrays in heat-shocked yeast**, *RNA Biology Laboratory, Biology Department, University of Aveiro, Portugal*.
Supervisor: Manuel Santos

Courses and other scientific activity

- 04/2021 Probabilistic Modeling in Genomics, Virtual meeting - Cold Spring Harbor, NY, USA
- 09/2015 Summer School on Machine Learning for Personalised Medicine - Marie Curie Initial Training Network, Manchester, UK
- 09/2012 Scientific writing course - University of Aveiro, Portugal

Associative/Administrative

- 09/2010 - 06/2012 Member of the Biology department counsel, University of Aveiro, Portugal
- 09/2009 - 06/2011 Member of the undergraduate Biology committee, University of Aveiro, Portugal

Awards

- 06/2016 **Best poster award - "Malignant diseases" category**, *YSA Symposium*.
Young Scientist Association of the Medical University of Vienna
- 06/2016 **Best artwork award - "Illustrations and digital simulations" category**, *ScienceArt Competition of the YSA Symposium*.
Young Scientist Association of the Medical University of Vienna

Skills

Computational Biology

- Programming Experienced in *Python* and *R* programming; Beginner level *Rust* programming;
Competence in software development: version control, testing, continuous integration.
- Data science Development of data processing pipelines; Data-driven unsupervised analysis and visualisation;
Statistical analysis; Application of unsupervised and supervised machine learning models;
Basic experience with Bayesian methods and probabilistic programming
- Applications Image analysis (IMC, IHC, brightfield microscopy); single cell *-seq; flow cytometry; bulk
ATAC-/ChIP-/RNA-seq; CRISPR screens

Molecular Biology

Techniques Chromatin IP, ChIP-seq, NGS libraries, Western blotting, PCR, Cloning
 Additional experience in: Chemical screening, Zebrafish and *Nematostella* handling and microinjection, basic experience in immunohistochemistry, fluorescence and confocal microscopy

Software

IMC A package for the analysis of imaging mass cytometry data:
<https://github.com/ElementoLab/imc>

imcpipeline A pipeline for the preprocessing of imaging mass cytometry data:
<https://github.com/ElementoLab/imcpipeline>

imctransfer Program for the robust, parallel transfer of raw IMC data between machines:
<https://github.com/ElementoLab/imctransfer>

page-enrichment A Python implementation of the Parametric Analysis of Gene Set Enrichment (PAGE):
<https://github.com/afrendeiro/page-enrichment>

ngs-toolkit A toolkit for the analysis of NGS data:
<https://github.com/afrendeiro/toolkit>

peppy A package to work with Portable Encapsulated Projects (PEP) in Python:
<https://github.com/pepkit/peppy>

looper A job controller for Portable Encapsulated Projects (PEP):
<https://github.com/pepkit/looper>

open_pipelines Pipelines for a variety of NGS data:
https://github.com/epigen/open_pipelines

Languages

Portuguese Native speaker
 English Very good
 Spanish Conversational
 German Basic
 French Basic

Basic words and phrases only

Basic words and phrases only

Updated on 2021/04/29