

Academic Employment

Jan. 2018 -	Principal Investigator at the St. Anna Children's Cancer Research Institute – CCRI (Vienna, Austria) Research Group "Epigenome-based precision medicine for pediatric sarcomas"
April 2016 - Feb. 2021	FWF Elise Richter Fellow at the St. Anna Children's Cancer Research Institute – CCRI (Vienna, Austria)
Mar. 2012 - Mar. 2016	Senior Postdoctoral Fellow, working with Prof. Heinrich Kovar at the St. Anna Children's Cancer Research Institute – CCRI (Vienna, Austria)
Sept. 2010 - Jan. 2012	HLA Scientist, with the prospect of becoming an ASHI (American Society of Histocompatibility and Immunogenetics) qualified director, at the HLA services of the American Red Cross (USA)
Oct. 2008 - Sept. 2010	Postdoctoral fellow, working with Prof. Alex Meissner at the Broad Institute and the Harvard Department of Stem Cell and Regenerative Biology (USA)
Oct. 2004 - Oct. 2008	PhD student at the Wellcome Trust Sanger Institute and the University of Cambridge (UK) Supervisor: Prof. Stephan Beck
Before Oct. 2004	Undergraduate research at the European Molecular Biology Laboratory (EMBL) / Heidelberg University (Germany) and at the Biochemistry Department / University of Glasgow (UK)

Academic Degrees

Oct. 2008	PhD in Biology, University of Cambridge/Wellcome Trust Sanger Institute (UK), Supervisor: Stephan Beck
Jul. 2004	MSci (integrated with BSci) in Molecular & Cellular Biology, University of Glasgow (UK), GPA: 15.12/16

Scholarships, Awards & Research Grants

2019 - 2023	WWTF LS18-049 "Characterizing and targeting the Ewing sarcoma microenvironment to overcome resistance to therapy" – EUR 799,500
2019 - 2022	OeNB Jubiläumsfonds grant entitled "Epigenetic tumor heterogeneity in Ewing sarcoma's response to chemotherapy" - EUR 150,000
2018 - 2019	Kapsch / CCRI Next Generation Sequencing Grant - EUR 85,000
2018	ÖGKJ Wissenschaftspreis – Research award for best publication in 2017
2017	German Sarcoma Conference Prize for best paper in the field of sarcoma tumors
2016 - 2021	FWF Elise Richter Fellowship (career development / "pathway to independence" fellowship for highly qualified female scientists in Austria) - EUR 356,202
2015 - 2016	Kapsch / CCRI Next Generation Sequencing Grant - EUR 39,180
2014 - 2016	OeNB Jubiläumsfonds grant entitled "Development of an epigenetic biomarker for risk stratification in localized Ewing sarcoma" - EUR 109,310
2013 - 2014	Kapsch / CCRI Next Generation Sequencing Grant - EUR 28,000
2012 - 2014	FWF Lise Meitner Fellowship (highly competitive 2-year post-doctoral fellowship given to highly qualified scientist coming to Austria from abroad) - EUR 133,360
2007	Prize for best oral presentation, 2nd Integrative Physiology Post-Graduate Students Conference, University of Aberdeen
2005	Chibnall Travel Award, Clare College, University of Cambridge
2004 - 2008	The Wellcome Trust Sanger Institute PhD Fellowship (highly competitive 4-year PhD program)
2002 - 2003	Leonardo da Vinci Scholarship (1-year research internship funded by the EU). Work was conducted at EMBL and the University of Heidelberg, Germany

Academic Activities

Paper reviewing	Nature Genetics, Nature Communications, Cell Reports, Nature Protocols, Nucleic Acids Research, BMC Genomics, Frontiers in Oncology, The American Journal of Pathology
Grant reviewing	The French Society for Children Cancer and Leukemia (SFCE), Münster Medical School Internal



11.09.19

Research Program (Germany), LMU Research Fellowship Program (Germany)
Conference organization ESMO Congress 2019&2020 Scientific Committee Member (Sarcoma Sub-Committee)

Publications

<i>Research Articles (*shared first author, #corresponding author)</i>	
1.	Selvanathan SP, Graham GT, Grego AR, Baker TM, Hogg JR, Simpson M, Batish M, Crompton B, Stegmaier K, Tomazou EM , Kovar H, Üren A, Toretsky JA. EWS-FLI1 modulated alternative splicing of ARID1A reveals novel oncogenic function through the BAF complex. <i>Nucleic Acids Res.</i> 2019 Aug 8. doi: 10.1093/nar/gkz699
2.	Grünewald TGP, Cidre-Aranaz F, Surdez D, Tomazou EM , de Álava E, Kovar H, Sorensen PH, Delattre O, Dirksen U. Ewing sarcoma. <i>Nat. Rev. Dis. Primers</i> 4, xxx (2018)
3.	Lawson J, Tomazou EM , Bock C, Sheffield NC. MIRA: An R package for DNA methylation-based inference of regulatory activity. <i>Bioinformatics.</i> 2018 Mar 1. doi: 10.1093/bioinformatics/bty083
4.	Katschnig AM, Kauer MO, Schwentner R, Tomazou EM , Mutz CN, Linder M, Sibilia M, Alonso J, Aryee DNT, Kovar H. EWS-FLI1 perturbs MRTFB/YAP-1/TEAD target gene regulation inhibiting cytoskeletal autoregulatory feedback in Ewing sarcoma. <i>Oncogene.</i> 2017 Jul 3. doi: 10.1038/onc.2017.202
5.	Sheffield NC, Pierron G, Klughammer J, Datlinger P, Schönegger A, Schuster M, Hadler J, Guillemot D, Lapouble E, Freneaux P, Champigneulle J, Bouvier R, Walder D, Ambros IM, Hutter C, Sorz E, Amaral AT, Álava Ed, Schallmoser K, Strunk D, Rinner B, Liegl-Atzwanger B, Huppertz B, Leithner A, Pinieux Gd, Terrier P, Laurence V, Michon J, Ladenstein R, Holter W, Windhager R, Dirksen U, Ambros PF, Delattre O, Kovar H, Bock C#, Tomazou EM# . DNA methylation heterogeneity defines a disease spectrum in Ewing sarcoma. <i>Nature Medicine.</i> 2017 Mar;23(3):386-395
6.	He T, Surdez D, Rantala JK, Haapa-Paananen S, Ban J, Kauer M, Tomazou E , Fey V, Alonso J, Kovar H, Delattre O, Iljin K. High-throughput RNAi screen in Ewing sarcoma cells identifies leucine rich repeats and WD repeat domain containing 1 (LRWD1) as a regulator of EWS-FLI1 driven cell viability. <i>Gene.</i> 2017 Jan 5;596:137-146
7.	Tomazou EM* , Sheffield NC*, Schmidl C, Schuster M, Schönegger A, Datlinger P, Kubicek S, Bock C, and Kovar H. Epigenome mapping reveals distinct modes of gene regulation and widespread enhancer reprogramming by the oncogenic fusion protein EWS-FLI1. <i>Cell Reports.</i> 2015 Feb 24;10(7):1082-95
8.	Svoboda LK, Harris A, Bailey NJ, Schwentner R, Tomazou EM , von Levetzow C, Magnuson B, Ljungman M, Kovar H, and Lawlor ER. Overexpression of HOX genes is prevalent in Ewing sarcoma and is associated with altered epigenetic regulation of developmental transcription programs. <i>Epigenetics.</i> 2014 Dec 2;9(12):1613-25
9.	Bock C*, Tomazou EM* , Müller F, Gu H, Jäger N, Brinkman A, Simmer F, Stunnenberg H, Meissner A. Genome-wide mapping of DNA methylation: a quantitative technology comparison. <i>Nature Biotechnology.</i> 2010 Oct;28(10): 1106-14
10.	Gu H*, Bock C*, Mikkelsen TS, Jäger N, Smith ZD, Tomazou EM , Gnirke A, Lander ES, Meissner A. Genome-scale DNA methylation mapping of clinical samples at single-nucleotide resolution. <i>Nature Methods.</i> 2010 Feb;7(2):133-6
11.	Ottaviani D, Lever E, Mitter R, Jones T, Forshew T, Christova R, Tomazou EM , Rakyen VK, Krawetz SA, Platts AE, Segarane B, Beck S, and Sheer D. Reconfiguration of genomic anchors upon transcriptional activation of the human major histocompatibility complex. <i>Genome Research.</i> 2008 Nov; 18(11):1778-86
12.	Rakyen, VK*, Down TA*, Thorne NP, Flicek P, Kulesha E, Gräf S, Tomazou EM , Bäckdahl L, Johnson N, Herberth M, Howe KL, Jackson DK, Miretti MM, Fiegler H, Marioni JC, Birney E, Hubbard TJP, Carter P, Tavare S, and Beck S. An integrated resource for genome-wide identification and analysis of human tissue-specific differentially methylated regions (tDMRs). <i>Genome Research.</i> 2008 Sep; 18(9): 18-29
13.	Down TA*, Rakyen VK*, Turner DJ, Flicek P, Li H, Thorne NP, Kulesha E, Gräf S, Tomazou EM , Bäckdahl L, Johnson N, Herberth M, Howe KL, Jackson DK, Miretti MM, Marioni JC, Birney E, Hubbard TJP, Durbin R, Tavare S, and Beck S. A Bayesian de-convolution strategy for immunoprecipitation based DNA methylation analysis. <i>Nature Biotechnology.</i> 2008 Jul; 26(7):779-785
14.	Tomazou EM , Rakyen VK, Lefebvre G, Andrews R, Ellis P, Jackson DK, Langford C, Francis MD, Bäckdahl L, Miretti M, Coggill P, Ottaviani D, Sheer D, Murrell A, and Beck S. Generation of a genomic tiling array of the human Major Histocompatibility Complex (MHC) and its application for DNA methylation analysis. <i>BMC Medical Genomics.</i> 2008 May 30;1:19



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