

# PD Dr. Marc Beyer, MD

Life and Medical Sciences Institute (LIMES)



new Member since 2015

Rheinische Friedrich-Wilhelms-Universität Bonn

Life and Medical Sciences Institute (LIMES)

Genomics & Immunoregulation, Group leader

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## Research Expertise

Marc Beyer's scientific focus is on the characterization of immunoregulatory mechanisms in myeloid and T cells. Based on transcriptomic and epigenetic discovery his group uses genetic engineering to study fundamental molecular mechanisms of immunoregulation.

## Education / Training

University of Bonn, Germany, Life & Medical Sciences, Habilitation, 2015

University of Cologne, Germany, Medicine, MD thesis, 2005

University of Heidelberg, Germany, Bioinformatics, Postgraduate program, 2004

University of Cologne, Germany, Medicine, Medicine Fellow 2002 - 2004

University of Cologne, Germany, Medicine, MD, 2002

## Appointments / Positions Held

Since 2014

Group leader, University of Bonn, Germany

2008 - 2013

Senior postdoctoral research fellow, University of Bonn, Germany

2004 - 2007

Postdoctoral research fellow, University of Cologne, Germany

2002 - 2004

Medicine fellow, University of Cologne, Germany

## 10 Most Relevant Publications for PD Dr. Marc Beyer

1. **Beyer M**, Abdullah Z, Chemnitz JM, Maisel D, Sander J, Lehmann C, Thabet Y, Shinde PV, Schmidleithner L, Köhne M, Trebicka J, Schierwagen R, Hofmann A, Popov A, Lang KS, Oxenius A, Buch T, Kurts C, Heikenwalder M, Fätkenheuer G, Lang PA, Hartmann P, Knolle PA, Schultze JL. 1. Tumor-necrosis factor impairs CD4(+) T cell-mediated immunological control in chronic viral infection. *Nat Immunol.* 2016 Mar 7
2. Schmidt SV, Krebs W, Ulas T, Xue J, Baßler K, Günther P, Hardt AL, Schultze H, Sander J, Klee K, Theis H, Kraut M, **Beyer M**, Schultze JL. The transcriptional regulator network of human inflammatory macrophages is defined by open chromatin. *Cell Res.* 2016 Feb.
3. Schultze JL, **Beyer M**. Myelopoiesis Reloaded: Single-Cell Transcriptomics Leads the Way. *Immunity.* 2016 Jan 19.
4. Böttcher JP, **Beyer M**, Meissner F, Abdullah Z, Sander J, Höchst B, Eickhoff S, Rieckmann JC, Russo C, Bauer T, Flecken T, Giesen D, Engel D, Jung S, Busch DH, Protzer U, Thimme R, Mann M, Kurts C, Schultze JL, Kastenmüller W, Knolle PA. Functional classification of memory CD8(+) T cells by CX3CR1 expression. *Nat Commun.* 2015 Sep 25.
5. Krebs W, Schmidt SV, Goren A, De Nardo D, Labzin L, Bovier A, Ulas T, Theis H, Kraut M, Latz E, **Beyer M**, Schultze JL. Optimization of transcription factor binding map accuracy utilizing knockout-mouse models. *Nucleic Acids Res.* 2014 Dec 1;42(21):13051-60.
6. Xue J, Schmidt SV, Sander J, Draffehn A, Krebs W, Quester I, De Nardo D, Gohel TD, Emde M, Schmidleithner L, Ganesan H, Nino-Castro A, Mallmann MR, Labzin L, Theis H, Kraut M, **Beyer M**, Latz E, Freeman TC, Ulas T, Schultze JL. Transcriptome-based network analysis reveals a spectrum model of human macrophage activation. *Immunity.* 2014 Feb 20;40(2):274-88.
7. Sommer D, Peters A, Wirtz T, Mai M, Ackermann J, Thabet Y, Schmidt J, Weighardt H, Wunderlich FT, Degen J, Schultze JL, **Beyer M**. Efficient genome engineering by targeted homologous recombination in mouse embryos using transcription activator-like effector nucleases. *Nat Commun.* 2014 Jan 13;5:3045.
8. **Beyer M**, Mallmann MR, Xue J, Staratschek-Jox A, Vorholt D, Krebs W, Sommer D, Sander J, Mertens C, Nino-Castro A, Schmidt SV, Schultze JL. High-resolution transcriptome of human macrophages. *PLoS One.* 2012;7(9):e45466.
9. **Beyer M**, Schumak B, Weihrauch MR, Andres B, Giese T, Endl E, Knolle PA, Classen S, Limmer A, Schultze JL. In vivo expansion of naïve CD4+ CD25(high) FOXP3+ regulatory T cells in patients with colorectal carcinoma after IL-2 administration. *PLoS One.* 2012;7(1):e30422.
10. **Beyer M**, Thabet Y, Müller RU, Sadlon T, Classen S, Lahl K, Basu S, Zhou X, Bailey-Bucktrout SL, Krebs W, Schönfeld EA, Böttcher J, Golovina T, Mayer CT, Hofmann A, Sommer D, Debey-Pascher S, Endl E, Limmer A, Hippen KL, Blazar BR, Balderas R, Quast T, Waha A, Mayer G, Famulok M, Knolle PA, Wickenhauser C, Kolanus W, Schermer B, Bluestone JA, Barry SC, Sparwasser T, Riley JL, Schultze JL. Repression of the genome organizer SATB1 in regulatory T cells is required for suppressive function and inhibition of effector differentiation. *Nat Immunol.* 2011 Aug 14;12(9):898-907.