

Curriculum Vitae

Manuela Zucknick, PhD

Personal information

Born in Eisenhüttenstadt (Germany) on 31 October 1978

Affiliation Department of Biostatistics
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Areas of work

Statistical analysis of high-dimensional *omics* data; statistical methods for risk prediction modelling (in particular with respect to survival endpoints) and the evaluation of prognostic and predictive markers using computationally intensive resampling methods; exploratory analysis (visualisation) and the development of adequate normalisation methods of *omics data*.

My current focus is on Bayesian methods for integrating different data sources and for incorporating prior biological knowledge in risk prediction models and the efficient implementation of Markov chain Monte Carlo methods as stochastic search algorithms for these models.

Applications are in translational and clinical cancer research, e.g. the development of risk prediction models for clinical endpoints such as patient survival, based on classical clinical and genetic features as well as transcriptomic, genomic and epigenomic high-throughput data.

Research interests

Prognostic models for time-to-event data and their assessment

Statistical modelling of high-dimensional data

Penalised likelihood methods

Bayesian variable selection

Bayesian hierarchical models for integrating data sources and incorporating prior knowledge

Markov chain Monte Carlo methods as stochastic search algorithms for Bayesian hierarchical models for high-dimensional data

Positions and professional experience

- Since 2015 Associated professor at the Department of Biostatistics, Institute of Basic Medical Sciences, University of Oslo, Norway
- Apr-Sep 2014 Visiting lecturer at the Faculty of Statistics, TU Dortmund University, Germany, and acting chair of the Institute of Mathematical Statistics and Industrial Applications (*Lehrstuhlvertretung*)
- 2008–2014 Researcher at the Division of Biostatistics, German Cancer Research Center (DKFZ), Heidelberg, Germany
- 2013–2014 Working group “Bayesian statistics for integrative genomics” (team leader)
- 2008–2013 Working group “Statistics for translational oncology” (postdoc)
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Education

- 2004–2008 PhD in Biostatistics at the Department of Epidemiology and Public Health, Imperial College London, United Kingdom
- Thesis title: *Multivariate Analysis of Tumour Gene Expression Profiles Applying Regularisation and Bayesian Variable Selection Techniques*
Supervisors: Prof. Sylvia Richardson and Prof. Hani Gabra
- 2003–2004 MSc in Bioinformatics at the Centre for Bioinformatics, Imperial College London, United Kingdom
- Individual project: *Approximate Bayesian computation in population genetics and genomics* (Supervisor: Prof. David Balding)
Group project: *Developing a metabolic pathway database and applications for pathway representation* (Supervisor: Prof. Marek Sergot)
- 2001–2002 Enrolled in the MSc Statistics programme at the Department of Statistics, Iowa State University, USA, as a full-time student as part of a student exchange programme with the University of Dortmund, Germany
- 1998–2003 Diplom in Statistics at the Department of Statistics, University of Dortmund, Germany
- Thesis title: *Classifying single nucleotide polymorphism data using support vector machines*
Supervisors: Prof. Katja Ickstadt and Prof. Claus Weihs
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Stipends and Awards

- 2012–2013 Selected participant in the Helmholtz mentoring programme for women *In Führung gehen* (“Preparing for leadership”)
- Jan 2010 Oberwolfach Leibniz Graduate Student; travel stipend for the workshop *Statistical Issues in Prediction: what can be learned for individualized predictive medicine?* at the Mathematisches Forschungsinstitut Oberwolfach, Germany
- Jul 2005 Travel stipend for the European Young Statisticians training camp (StatCamp) in Oslo, Norway
- 2003–2007 Wellcome Trust stipend for a 4-year PhD programme at Imperial College London, United Kingdom

Professional memberships

since 2010	International Society for Bayesian Analysis
since 2009	International Society for Clinical Biostatistics
since 2008	International Biometric Society, German Region
2014–2016	Secretary of the Working Group “Bayes Methods”
2004–2007	International Biometric Society, British Region
2002–2003	American Statistical Association

Review assignments (statistical journals)

BBA - Proteins and Proteomics
Bioinformatics
Biometrical Journal
Computational Statistics
Scandinavian Journal of Statistics
Statistical Applications in Genetics and Molecular Biology
Statistics in Medicine
Statistical Modelling

Review assignments (clinical journals)

Journal of Clinical Oncology
Journal of Toxicology and Environmental Health, Part A
Leukemia

Review assignments (funding agencies)

Medical Research Council (United Kingdom)

Software

BVS	MATLAB toolbox for binary Bayesian variable selection (logistic and probit regression) suitable for high-dimensional data, including block MCMC samplers and a parallel tempering algorithm to speed up the sampling process. (http://www.bgx.org.uk/software.html)
BVSflex	R package for Bayesian variable selection allowing for the integration of a second data source via a flexible prior setup (http://bvsflex.r-forge.r-project.org)
c060	R package for extended inference with lasso and elastic-net regularized Cox and generalized linear models (http://c060.r-forge.r-project.org)

Patent applications

International patent application (Nr. PCT/EP2013/062994, International Filing Date: 21-06-2013) with the title *Circulating miRNAs as markers for breast cancer* (one of four inventors with equal shares)

Research funding

- 2013–2015 Else Kröner-Fresenius-Stiftung, *Integrated genome, methylome and transcriptome analyses of CLL: identification of pathomechanisms, prognostic and predictive markers as well as potential therapeutic targets*, co-applicant (EUR 90,000 for Biostatistics)
- 2012–2014 DKFZ - Bayer HealthCare Alliance, Joint project *Statistical methods for early detection of predictive biomarkers based on integrative analysis of omics data for cancer cell lines*, co-applicant (EUR 120,000 plus cloud computing costs, all for Biostatistics)
- 2011–2016 Helmholtz-Gemeinschaft Virtual Institute *Understanding and overcoming resistance to apoptosis and therapy in leukemia*, co-applicant (EUR 150,000 for Biostatistics)
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Student supervision

Regine Meunier (MSc Medical Biometry/Biostatistics, University of Heidelberg), since 10/2014
Integration of multiple genomic data sources in Bayesian variable selection models

Tabea Treppmann (MSc Statistics, TU Dortmund University), 2014
Integration of multiple genomic data sources in a Bayesian proportional hazard model with variable selection (with K. Ickstadt)

Stephan Lücke (MSc Medical Biometry/Biostatistics, University of Heidelberg), 2013
Identification of predictive biomarker signatures based on high-dimensional genomic data

Lars Ismail (MSc Statistics and Operational Research, University of Edinburgh), 2011
Statistical analysis of allogeneic stem-cell transplants in acute myeloid leukemia (AML): a case study for the analysis of time-dependent intervening events with focus on graphical methods

Lisa Bast (BSc Biomathematics, Fachhochschule Koblenz, RheinAhrCampus Remagen), 2011
Validierung von genexpressionsbasierten Prognosemodellen für das Überleben von Patienten mit multiplem Myelom (with A. Benner and M. Berres)

Teaching (lectures and courses)

Faculty of Statistics, TU Dortmund University, Germany (for students in MSc Statistics and MSc Data Sciences programmes)

- Advanced-level class on sampling theory (*Stichprobenverfahren*) (summer semester 2014)
- Practicals on advanced data analysis (*Fallstudien II*) (summer semester 2014)

German Cancer Research Center, Heidelberg, Germany

- Lecture series on *Biostatistical Case Studies using R and Bioconductor* (summer semester 2014)
- Lectures on *Statistical issues in Bioinformatics* as part of the lecture series *Advanced Topics in Biostatistics* (Jan 2012, Feb 2013, Jan 2014)

MSc *Medical Biometry/ Biostatistics* programme at the University of Heidelberg, Germany

- *Molecular Medicine*, lectures in three-day course (Feb 2010, Mar 2012 Feb 2014); organisation of this course (Feb 2014)
- *Preclinical Statistics*, lectures in three-day course (Sep 2011, Sep 2013)

Faculty of Medicine, University of Heidelberg, Germany (teaching for medical students)

- Cross-sectional module Q1 *Epidemiology, Medical Biometry and Medical Informatics* (Querschnittsbereich 1 *Epidemiologie, Medizinische Biometrie und Medizinische Informatik*), Biostatistics lectures in two-week course (Apr 2014)
- *Introduction to biostatistics and the methodology of evidence-based medicine* (*Propädeutik Medizinische Biometrie*), three-day course (Dec 2010)

Teaching qualifications

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| 2014 | Module I of the “Baden-Württemberg-Zertifikat für Hochschuldidaktik” (training programme required to qualify for a professorship in the German state of Baden-Württemberg) |
| 2001–2002 | <i>English 180D: Advanced speaking for international teaching assistants</i> class and Oral Proficiency Certification Test (OECT) for international teaching assistants at Iowa State University, USA |

Invited talks

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| Oct 2014 | <i>Bayesian models for risk prediction with high-dimensional (integrative) genomics</i> , ZüKoSt (applied seminar), ETH Zürich, Switzerland |
| Sep 2013 | <i>Integrated risk-prediction modelling based on multiple genomic data sources with Bayesian variable selection models</i>
Satellite workshop <i>Statistical Methods in Bioinformatics</i> at the German Conference on Bioinformatics (GCB), Göttingen, Germany |
| Nov 2012 | <i>Integration of multiple genomic data sources in a Bayesian proportional hazards model for variable selection</i>
9th Autumn Symposium of the Research Training Group “Statistical Modelling”, TU Dortmund University, Germany |
| Sep 2012 | <i>Integrated prognostic modelling based on multiple genomic data sources with Bayesian variable selection models</i>
Workshop <i>Building and Evaluating Prognostic Models - Computational Techniques and Strategies</i> , Institut für Medizinische Biometrie, Epidemiologie und Informatik (IMBEI), Johannes Gutenberg University Medical Center, Mainz, Germany |

- Mar 2012 *Integration of multiple genomic data sources in Bayesian regression models for prediction and biomarker selection*
Center for Medical Statistics, Informatics, and Intelligent Systems (CEMSIIS),
Medical University of Vienna, Austria
- Jan 2010 *Independence screening for high-dimensional prognostic Cox models*
Workshop *Statistical Issues in Prediction: what can be learned for individualized predictive medicine?* at Mathematisches Forschungsinstitut Oberwolfach,
Germany
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Publications

Articles

Statistical methodology

- Sill M, Hielscher T, Becker N, Zucknick M (2014). *c060: Extended Inference with Lasso and Elastic-Net Regularized Cox and Generalized Linear Models*. Journal of Statistical Software, accepted
- Zucknick M, Richardson S (2014). *MCMC algorithms for Bayesian variable selection in the logistic regression model for large-scale genomic applications*. Technical report, <http://arxiv.org/abs/1402.2713>
- Sill M, Schröder C, Hoheisel JD, Benner A, Zucknick M (2010). *Assessment and optimisation of normalisation methods for dual-colour antibody microarrays*. BMC Bioinformatics 11:556
- Hielscher T*, Zucknick M*, Werft W, Benner A (2010). *On the prognostic value of survival models with application to gene expression signatures*. Statistics in Medicine 29(7-8):818–829 (* equal contribution)
- Benner A, Zucknick M, Hielscher T, Ittrich C, Mansmann U (2010). *High-Dimensional Cox Models: The Choice of Penalty as Part of the Model Building Process*. Biometrical Journal 52(10):50–69
- Hielscher T*, Zucknick M*, Werft W, Benner A (2009). *On the prognostic value of gene expression signatures for censored data*. In: Advances in Data Analysis, Data Handling and Business Intelligence: Proceedings of the 32nd Annual Conference of the Gesellschaft für Klassifikation e. V., Springer, Heidelberg-Berlin. 663–673 (* equal contribution)
- Zucknick M, Richardson S, Stronach EA (2008). *Comparing stability of gene expression profiles constructed by univariate filtering versus multivariate penalised likelihood methods*. Statistical Applications in Genetics and Molecular Biology, 7:7
- Schwender H, Zucknick M, Ickstadt K, Bolt HM; GENICA network (2004). *A pilot study on the application of statistical classification procedures to molecular epidemiological data*. Toxicology Letters, 151:291–299

Biomedical projects

- Yang R, Pfützte K, Zucknick M, Sutter C, Wappenschmidt B, Marme F, Qu B, Cuk K, Engel C, Schott S, Schneeweiss A, Brenner H, Claus R, Plass C, Bugert P, Hoth M, Sohn C, Schmutzler R, Bartram CR, Burwinkel B (2014). *DNA methylation array analyses identified breast cancer-associated HYAL2 methylation in peripheral blood*. Int J Cancer. [Epub ahead of print]

- Poetsch AR, Lipka DB, Witte T, Claus R, Nöllke P, Zucknick M, Olk-Batz C, Fluhr S, Dworzak M, De Moerloose B, Stary J, Zecca M, Hasle H, Schmutz M, van den Heuvel-Eibrink MM, Locatelli F, Niemeyer CM, Flotho C, Plass C (2014). *RASA4 undergoes DNA hypermethylation in resistant juvenile myelomonocytic leukemia*. *Epigenetics*. 9(9):1252–1260
- Brocks D, Assenov Y, Minner S, Bogatyrova O, Simon R, Koop C, Oakes C, Zucknick M, Lipka DB, Weischenfeldt J, Feuerbach L, Cowper-Sal Lari R, Lupien M, Brors B, Korbel J, Schlomm T, Tanay A, Sauter G, Gerhäuser C, Plass C; ICGC Early Onset Prostate Cancer Project (2014). *Intratumor DNA methylation heterogeneity reflects clonal evolution in aggressive prostate cancer*. *Cell Rep*. 8(3):798–806
- Claus R, Lucas DM, Ruppert AS, Williams KE, Weng D, Patterson K, Zucknick M, Oakes CC, Rassenti LZ, Greaves AW, Geyer S, Wierda WG, Brown JR, Gribben JG, Barrientos JC, Rai KR, Kay NE, Kipps TJ, Shields P, Zhao W, Grever MR, Plass C, Byrd JC (2014). *Validation of ZAP-70 methylation and its relative significance in predicting outcome in chronic lymphocytic leukemia*. *Blood* 124(1):42–48. Erratum in: *Blood* 124(11):1848
- Madhavan D, Wallwiener M, Bents K, Zucknick M, Nees J, Schott S, Cuk K, Riethdorf S, Trumpp A, Pantel K, Sohn C, Schneeweiss A, Surowy H, Burwinkel B (2014). *Plasma DNA integrity as a biomarker for primary and metastatic breast cancer and potential marker for early diagnosis*. *Breast Cancer Res Treat*. 146(1):163–174
- Dutruel C, Bergmann F, Rooman I, Zucknick M, Weichenhan D, Geiselhart L, Kaffenberger T, Rachakonda PS, Bauer A, Giese N, Hong C, Xie H, Costello JF, Hoheisel J, Kumar R, Rehli M, Schirmacher P, Werner J, Plass C, Popanda O, Schmezer P (2014). *Early epigenetic downregulation of WNK2 kinase during pancreatic ductal adenocarcinoma development*. *Oncogene*. 33(26):3401–3410
- Oakes CC, Claus R, Gu L, Assenov Y, Hülle J, Zucknick M, Bieg M, Brocks D, Bogatyrova O, Schmidt CR, Rassenti L, Kipps TJ, Mertens D, Lichter P, Döhner H, Stilgenbauer S, Byrd JC, Zenz T, Plass C (2014). *Evolution of DNA methylation is linked to genetic aberrations in chronic lymphocytic leukemia*. *Cancer Discov*. 4(3):348–361
- Goeppert B, Konermann C, Schmidt CR, Bogatyrova O, Geiselhart L, Ernst C, Gu L, Becker N, Zucknick M, Mehrabi A, Hafezi M, Klauschen F, Stenzinger A, Warth A, Breuhahn K, Renner M, Weichert W, Schirmacher P, Plass C, Weichenhan D (2014). *Global alterations of DNA methylation in cholangiocarcinoma target the wnt signaling pathway*. *Hepatology*. 59(2):544–554
- Sonnet M, Claus R, Becker N, Zucknick M, Petersen J, Lipka DB, Oakes CC, Andrulis M, Lier A, Milsom MD, Witte T, Gu L, Kim-Wanner S-Z, Schirmacher P, Wulfert M, Gattermann N, Lübbert M, Rosenbauer F, Rehli M, Bullinger L, Weichenhan D, Plass C (2014). *Early aberrant DNA methylation events in a mouse model of acute myeloid leukemia*. *Genome Medicine*. 6:34
- Allegra D, Bilan V, Garding A, Zucknick M, Döhner H, Stilgenbauer S, Kuchenbauer F, Mertens D (2014). *Defective DROSHA processing contributes to downregulation of MiR-15/-16 in chronic lymphocytic leukemia*. *Leukemia*. 28(1):98–107
- Goeppert B, Frauenschuh L, Zucknick M, Stenzinger A, Andrulis M, Klauschen F, Joehrens K, Warth A, Renner M, Mehrabi A, Hafezi M, Thelen A, Schirmacher P, Weichert W (2013). *Prognostic impact of tumour-infiltrating immune cells on biliary tract cancer*. *Br J Cancer*. 109(10):2665–2674
- Cuk K, Zucknick M, Madhavan D, Schott S, Golatta M, Heil J, Marmé F, Turchinovich A, Sinn P, Sohn C, Junkermann H, Schneeweiss A, Burwinkel B (2013). *Plasma microRNA panel for minimally invasive detection of breast cancer*. *PLoS One*. 8(10):e76729

Lambert SR, Witt H, Hovestadt V, Zucknick M, Kool M, Pearson DM, Korshunov A, Ryzhova M, Ichimura K, Jabado N, Fontebasso AM, Lichter P, Pfister SM, Collins VP, Jones DT (2013). *Differential expression and methylation of brain developmental genes define location-specific subsets of pilocytic astrocytoma*. *Acta Neuropathol.* 126(2):291–301

Garding A, Bhattacharya N, Claus R, Ruppel M, Tschuch C, Filarsky K, Idler I, Zucknick M, Caudron-Herger M, Oakes C, Fleig V, Keklikoglou I, Allegra D, Serra L, Thakurela S, Tiwari V, Weichenhan D, Benner A, Radlwimmer B, Zentgraf H, Wiemann S, Rippe K, Plass C, Döhner H, Lichter P, Stilgenbauer S, Mertens D (2013). *Epigenetic upregulation of lncRNAs at 13q14.3 in leukemia is linked to the In Cis downregulation of a gene cluster that targets NF-kB*. *PLoS Genet.* 9(4):e1003373

Claus R, Pfeifer D, Almstedt M, Zucknick M, Hackanson B, Plass C, Lübbert M (2013). *Decitabine induces very early in vivo DNA methylation changes in blasts from patients with acute myeloid leukemia*. *Leuk Res.* 37(2):190–196

Cuk K, Zucknick M, Heil J, Madhavan D, Schott S, Turchinovich A, Arlt D, Rath M, Sohn C, Benner A, Junkermann H, Schneeweiss A, Burwinkel B (2013). *Circulating microRNAs in plasma as early detection markers for breast cancer*. *Int J Cancer.* 132(7):1602–1612

Sturm D, Witt H, Hovestadt V, Khuong-Quang DA, Jones DT, Konermann C, Pfaff E, Tönjes M, Sill M, Bender S, Kool M, Zapatka M, Becker N, Zucknick M, Hielscher T, Liu XY, Fontebasso AM, Ryzhova M, Albrecht S, Jacob K, Wolter M, Ebinger M, Schuhmann MU, van Meter T, Frühwald MC, Hauch H, Pekrun A, Radlwimmer B, Niehues T, von Komorowski G, Dürken M, Kulozik AE, Madden J, Donson A, Foreman NK, Drissi R, Fouladi M, Scheurlen W, von Deimling A, Monoranu C, Roggendorf W, Herold-Mende C, Unterberg A, Kramm CM, Felsberg J, Hartmann C, Wiestler B, Wick W, Milde T, Witt O, Lindroth AM, Schwartzentruber J, Faury D, Fleming A, Zakrzewska M, Liberski PP, Zakrzewski K, Hauser P, Garami M, Klekner A, Bogner L, Morrissy S, Cavalli F, Taylor MD, van Sluis P, Koster J, Versteeg R, Volckmann R, Mikkelsen T, Aldape K, Reifemberger G, Collins VP, Majewski J, Korshunov A, Lichter P, Plass C, Jabado N, Pfister SM (2012). *Hotspot Mutations in H3F3A and IDH1 Define Distinct Epigenetic and Biological Subgroups of Glioblastoma*. *Cancer Cell* 22(4):425–437

Madhavan D, Zucknick M, Wallwiener M, Cuk K, Modugno C, Scharpf M, Schott S, Heil J, Turchinovich A, Yang R, Benner A, Riethdorf S, Trumpp A, Sohn C, Pantel K, Schneeweiss A, Burwinkel B (2012). *Circulating microRNAs as Surrogate Markers for Circulating Tumour Cells and Prognostic Markers in Metastatic Breast Cancer*. *Clin Cancer Res.* 18(21):5972–5982

Baer C, Claus R, Frenzel LP, Zucknick M, Park YJ, Gu L, Weichenhan D, Fischer M, Pallasch CP, Herpel E, Rehli M, Byrd JC, Wendtner CM, Plass C (2012). *Extensive Promoter DNA Hypermethylation and Hypomethylation Is Associated with Aberrant MicroRNA Expression in Chronic Lymphocytic Leukemia*. *Cancer Res.* 72(15):3775–3785

Claus R, Lucas DM, Stilgenbauer S, Ruppert AS, Yu L, Zucknick M, Mertens D, Bühler A, Oakes CC, Larson RA, Kay NE, Jelinek DF, Kipps TJ, Rassenti LZ, Gribben JG, Döhner H, Heerema NA, Marcucci G, Plass C, Byrd JC (2012). *Quantitative DNA methylation analysis identifies a single CpG dinucleotide important for ZAP-70 expression and predictive of prognosis in chronic lymphocytic leukemia*. *J Clin Oncol.* 30(20):2483–2491

Kayser S, Zucknick M, Döhner K, Krauter J, Köhne CH, Horst HA, Held G, von Lilienfeld-Toal M, Wilhelm S, Rummel M, Germing U, Götze K, Nachbaur D, Schlegelberger B, Göhring G, Späth D, Morlok C, Teleanu V, Ganser A, Döhner H, Schlenk RF; for the German-Austrian AML Study Group (2012). *Monosomal karyotype in adult acute myeloid leukemia: prognostic impact and outcome after different treatment strategies*. *Blood* 119(2):551–558

- Maier P, Heckmann D, Spier I, Laufs S, Zucknick M, Allgayer H, Frühauf S, Zeller WJ, Wenz F. (2012). *F2A sequence linking MGMT(P140K) and MDR1 in a bicistronic lentiviral vector enables efficient chemoprotection of haematopoietic stem cells*. *Cancer Gene Ther.* 19 (11) 802–810
- Heckmann D, Laufs S, Maier P, Zucknick M, Giordano FA, Veldwijk MR, Eckstein V, Wenz F, Zeller WJ, Frühauf S, Allgayer H (2011). *A Lentiviral CXCR4 overexpression and knock-down model in colorectal cancer cell lines reveals plerixafor-dependent suppression of SDF-1 α -induced migration and invasion*. *Onkologie* 34(10):502–508
- Claus R, Hackanson B, Poetsch AR, Zucknick M, Sonnet M, Blagitko-Dorfs N, Hiller J, Wilop S, Brümmendorf TH, Galm O, Platzbecker U, Byrd JC, Döhner K, Döhner H, Lübbert M, Plass C (2012). *Quantitative analyses of DAPK1 methylation in AML and MDS*. *Int J Cancer* 131(2):E138–142
- Olk-Batz C, Poetsch AR, Nöllke P, Claus R, Zucknick M, Sandrock I, Witte T, Strahm B, Hasle H, Zecca M, Stary J, Bergstraesser E, De Moerloose B, Trebo M, van den Heuvel-Eibrink MM, Wojcik D, Locatelli F, Plass C, Niemeyer CM, Flotho C (2011). *Aberrant DNA methylation characterizes juvenile myelomonocytic leukemia (JMML) with poor outcome*. *Blood* 117(18):4871–4880
- Kayser S, Döhner K, Krauter J, Köhne CH, Horst HA, Held G, von Lilienfeld-Toal M, Wilhelm S, Kündgen A, Götze K, Rummel M, Nachbaur D, Schlegelberger B, Göhring G, Späth D, Morlok C, Zucknick M, Ganser A, Döhner H, Schlenk RF (2011). *The impact of therapy-related acute myeloid leukemia (AML) on outcome in 2,853 adult patients with newly diagnosed AML*. *Blood* 117(7):2137–2145
- Krauter J, Wagner K, Stadler M, Dammann E, Zucknick M, Eder M, Buchholz S, Mischak-Weissinger E, Hertenstein B, Ganser A (2011). *Prognostic factors in allo-SCT of elderly patients with AML*. *Bone Marrow Transplant* 46:545–551
- Grund N, Maier P, Giordano FA, Appelt JU, Zucknick M, Li L, Wenz F, Zeller WJ, Frühauf S, Allgayer H, Laufs S (2010). *Analysis of lentiviral SIN vector integration sites and flanking gene expression in human peripheral blood progenitor cells following alkylator chemotherapy*. *Hum Gene Therapy* 21(8):943–956
- Paige AJ, Zucknick M, Janczar S, Paul J, Mein CA, Taylor KJ, Stewart M, Gourley C, Richardson S, Perren T, Ganesan TS, Smyth JF, Brown R, Gabra H (2010). *WWOX tumour suppressor gene polymorphisms and ovarian cancer pathology and prognosis*. *Eur J Cancer* 46(4):818–825
- Schröder C, Jacob A, Tonack S, Radon TP, Sill M, Zucknick M, Ruffer S, Costello E, Neoptolemos JP, Crnogorac-Jurcevic T, Bauer A, Fellenberg K, Hoheisel JD (2010). *Dual-color proteomic profiling of complex samples with a microarray of 810 cancer-specific antibodies*. *Mol Cell Proteomics* 9(6):1271–1280
- Wagner K, Damm F, Göhring G, Görlich K, Heuser M, Schäfer I, Ottmann O, Lübbert M, Heit W, Kanz L, Schlimok G, Raghavachar AA, Fiedler W, Kirchner HH, Brugger W, Zucknick M, Schlegelberger B, Heil G, Ganser A, Krauter J. (2010). *Impact of IDH1 R132 mutations and an IDH1 single nucleotide polymorphism in cytogenetically normal acute myeloid leukemia: SNP rs11554137 is an adverse prognostic factor*. *Journal of Clinical Oncology* 28(14):2356–2364
- Paschka P, Schlenk RF, Gaidzik VI, Habdank M, Krönke J, Bullinger L, Späth D, Kayser S, Zucknick M, Götze K, Horst HA, Germing U, Döhner H, Döhner K. (2010). *IDH1 and IDH2 Mutations are Frequent Genetic Alterations in Acute Myeloid Leukemia (AML) and Confer Adverse Prognosis in Cytogenetically Normal AML with NPM1 Mutation without FLT3-ITD:*

A Study of the German-Austrian AML Study Group (AMLSG). Journal of Clinical Oncology 28(22):3636–3643

Winkler D, Schneider C, Zucknick M, Bogelein D, Schulze K, Zenz T, Mohr J, Philippen A, Huber H, Buhler A, Habermann A, Benner A, Döhner H, Stilgenbauer S, Mertens D (2010). *Protein expression analysis of chronic lymphocytic leukemia defines the effect of genetic aberrations and uncovers a correlation of CDK4, P27 and P53 with hierarchical risk*. Haematologica 95(11):1880–1888

Giordano FA, Appelt JU, Zucknick M, Abba M, Zeller WJ, Fruehauf S, Allgayer H, Laufs S (2009). *Cold spots in hot spots: transcription start sites of active genes are spared from HIV vector integration*. AIDS 23(18):2535–2537

Sharma R, Zucknick M, London R, Kacevska M, Liddle C, Clarke SJ (2008). *Systematic Inflammatory Response Predicts Prognosis in Patients with Advanced-Stage Colorectal Cancer*. Clinical Colorectal Cancer, 7(5):331–337

Sharma R, Hoskins JM, Rivory LP, Zucknick M, London R, Liddle C, Clarke SJ (2008). *Thymidylate Synthase and Methylenetetrahydrofolate Reductase Gene Polymorphisms and Toxicity to Capecitabine in Advanced Colorectal Cancer Patients*. Clinical Cancer Research, 14:817–825

Book chapters

Zucknick M, Hielscher T, Sill M, Benner A (2012). *Graphical Displays for Biomarker Data*. In Eds. Krause A, O’Connell M, A Picture is Worth a Thousand Tables: Graphics in Life Sciences, Springer

Book reviews

Lorenzo Bermejo J, Zucknick M (2013). (Book review) *Bayesian Biostatistics*. Lesaffre E and Lawson AB (2012). John Wiley & Sons, Ltd. ISBN 978-0-470-01823-1, Biometrical Journal 55(6):969–970

Mauda Zucknick

Oslo, 06 January 2015