

CV

Dr. med. Dr. rer. nat. **Andreas Mock**, M.Sc., M.Phil.

Resident Pathologist & Group Leader Clinical Bioinformatics

Institute of Pathology, LMU Munich

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Education

- 2016-2020 **PhD studies (Dr. rer. nat.)**
German Cancer Research Center (DKFZ) & Heidelberg University Hospital, Germany
- 2008-2017 **Medical studies (Dr. med.)**
University of Heidelberg, Germany
- 2014-2015 **Master studies (M.Phil.) in Computational Biology**
University of Cambridge, UK
- 2012-2013 **Master studies (M.Sc.) in Translational Medical Research**
University of Heidelberg, Germany

Experience

- Apr 2022 – today **Resident in Pathology & Group Leader**
Institute of Pathology, University of Munich
Director: Dr. Prof. Frederick Klauschen
- Jan 2019 – Mar 2022 **Research Associate**
German Cancer Research Center (DKFZ)
Department of Translational Medical Oncology, Director: Prof. Dr. Fröhling
Member of MASTER Precision Oncology trial
- Mar 2019 – Mar 2022 **Medical Advisor**
HiGHmed & EUCANCan Medical Informatics Initiatives
Topic: Variant annotation and prioritization for Precision Oncology
- Aug 2017 – Mar 2022 **Residency in Internal Medicine, Hematology & Oncology**
National Center for Tumor Disease (NCT) Heidelberg
Department of Medical Oncology, Director: Prof. Dr. Jäger
Specialization: Head and Neck Oncology
- Jan 2017 - Feb 2017 **Medical Intern in Pathology**
Massachusetts General Hospital & Harvard Medical School, Boston
Harvard Medical School Exchange Clerkship Program
Department of Pathology, Massachusetts General Hospital
Director: Dr. David Louis
- May 2016 - Apr 2017 **Bioinformatic Trainee**
European Molecular Biology Laboratory (EMBL)
Multi-omics and statistical computing group - PI: Dr. Wolfgang Huber
- May 2015 – Sep 2015 **Research Associate**
Cancer Research UK Cambridge Institute
Molecular and computational diagnostics group - PI: Dr. Nitzan Rosenfeld

Selected Publications

Web of Science Statistics: 04/24

Sum der Citations: 949

H-Index: 18

Klauschen F, Dippel J, Keyl P, Jurmeister P, Bockmayr M, **Mock A**, Buchstab O, Alber M, Ruff L, Montavon G, Müller KR.

Toward Explainable Artificial Intelligence for Precision Pathology

Annu. Rev. Pathol. Mech. Dis. 2024 Jan 24;19:541-570.

IF (2022): **36.2**

Mock A, Teleanu MV, Kreutzfeldt S, Heilig CE, Hülleln J, Möhrmann L, Jahn A, Hanf D, Kerle IA, Singh HM, Hutter B, Uhrig S, Fröhlich M, Neumann O, Hartig A, Brückmann S, Hirsch S, Grund K, Dikow N, Lipka DB, Renner M, Bhatti IA, Apostolidis L, Schlenk RF, Schaaf CP, Stenzinger A, Schröck E, Hübschmann D, Heining C, Horak P, Glimm H, Fröhling S.

NCT/DKFZ MASTER Handbook of Interpreting Whole-Genome, Transcriptome, and Methylome Data for Precision Oncology

NPJ Precis Oncol. 2023 Oct 26;7(1):109

IF (2022): **7.9**

Mock A, Braun M, Scholl C, Fröhling S, Erkut C.

Transcriptome profiling for precision cancer medicine using shallow nanopore cDNA sequencing.

Sci Rep. 2023 Feb 9;13(1):2378.

IF (2021): **4.996**

Möhrmann L*, Werner M*, Oleś M*, **Mock A***, Uhrig S*, Jahn A, Kreutzfeldt S, Fröhlich M, Hutter B, Paramasivam N, Richter D, Beck K, Winter U, Pfütze K, Heilig CE, Teleanu MV, Lipka DB, Zapatka M, Hanf D, List C, Allgäuer M, Penzel R, Rüter G, Jelas I, Hamacher R, Falkenhorst J, Wagner S, Brandts CH, Boerries M, Illert AL, Metzeler KH, Westphalen CB, Desuki A, Kindler T, Folprecht G, Weichert W, Brors B, Stenzinger A, Schröck E, Hübschmann D, Horak P, Heining C, Fröhling S, Glimm H.

Comprehensive genomic and epigenomic analysis in cancer of unknown primary guides molecularly-informed therapies despite heterogeneity.

Nat Commun. 2022 Aug 2;13(1):4485.

IF (2021): **17.694**

Jahn A, Rump A, Widmann TJ, Heining C, Horak P, Hutter B, Paramasivam N, Uhrig S, Geldon L, Drukewitz S, Kübler A, Bermudez M, Hackmann K, Porrmann J, Wagner J, Arlt M, Franke M, Fischer J, Kowalzyk Z, William D, Weth V, Oster S, Fröhlich M, Hülleln J, Valle González C, Kreutzfeldt S, **Mock A**, Heilig CE, Lipka DB, Möhrmann L, Hanf D, Oleś M, Teleanu V, Allgäuer M, Ruhnke L, Kutz O, Knurr A, Laßmann A, Endris V, Neumann O, Penzel R, Beck K, Richter D, Winter U, Wolf S, Pfütze K, Geörg C, Meißburger B, Buchhalter I, Augustin M, Aulitzky WE, Hohenberger P, Kroiss M, Schirmacher P, Schlenk RF, Keilholz U, Klauschen F, Folprecht G, Bauer S, Siveke JT, Brandts CH, Kindler T, Boerries M, Illert AL, von Bubnoff N, Jost PJ, Metzeler KH, Bitzer M, Schulze-Osthoff K, von Kalle C, Brors B, Stenzinger A, Weichert W, Hübschmann D, Fröhling S, Glimm H, Schröck E, Klink B.

Comprehensive cancer predisposition testing within the prospective MASTER trial identifies hereditary cancer patients and supports treatment decisions for rare cancers.

Ann Oncol. 2022 Nov;33(11):1186-1199.

IF (2021): **51.769**

Walle T, Bajaj S, Kraske JA, Rösner T, Cussigh CS, Kälber KA, Müller LJ, Strobel SB, Burghaus J, Kallenberger SM, Stein-Thöringer CK, Jenzer M, Schubert A, Kahle S, Williams A, Hoyler B, Zielske L, Skatula R, Sawall S, Leber MF, Kunes RZ, Krisam J, Fremd C, Schneeweiss A, Krauss J, Apostolidis L, Berger AK, Haag GM, Zschäbitz S, Halama N, Springfield C, Kirsten R, Hassel JC, Jäger D; **NCT ANTICIPATE Investigators**; Ungerechts G.

Cytokine release syndrome-like serum responses after COVID-19 vaccination are frequent and clinically inapparent under cancer immunotherapy.

Nat Cancer. 2022 Sept;3(9):1039-1051.

IF (2021): **23.177**

Horak P*, Heining C*, Kreutzfeldt S*, Hutter B*, **Mock A****, Hüllelein J**, Fröhlich M**, Uhrig S**, Jahn A, Rump A, Geldon L, Möhrmann L, Hanf D, Teleanu V, Heilig CE, Lipka DB, Allgäuer M, Ruhnke L, Laßmann A, Endris V, Neumann O, Penzel R, Beck K, Richter D, Winter U, Wolf S, Pfüzte K, Geörg C, Meißburger B, Buchhalter I, Augustin M, Aulitzky WE, Hohenberger P, Kroiss M, Schirmacher P, Schlenk RF, Keilholz U, Klauschen F, Folprecht G, Bauer S, Siveke JT, Brandts CH, Kindler T, Boerries M, Illert AL, von Bubnoff N, Jost PJ, Spiekermann K, Bitzer M, Schulze-Osthoff K, von Kalle C, Klink B, Brors B, Stenzinger A, Schröck E, Hübschmann D, Weichert W, Glimm H, Fröhling S.

Comprehensive Genomic and Transcriptomic Analysis for Guiding Therapeutic Decisions in Patients with Rare Cancers.

Cancer Discov. 2021 Jun 10;candisc.0126.2021.

IF (2022): **38.27**

Borchert F*, **Mock A***, Tomczak A*, Hügel J, Alkarkoukly S, Knurr A, Volckmar AL, Stenzinger A, Schirmacher P, Debus J, Jäger D, Longerich T, Fröhling S, Eils R, Bougatf N, Sax U, Schapranow MP.

Knowledge bases and software support for variant interpretation in precision oncology.

Brief Bioinform. 2021 Nov 5;22(6):bbab134.

IF (2021): **13.994**

Pocha K*, **Mock A***, Rapp C, Dettling S, Warta R, Geisenberger C, Jungk C, Martins LR, Grabe N, Reuss D, Debus J, von Deimling A, Abdollahi A, Unterberg A, Herold-Mende CC.

Surfactant expression defines an inflamed stratum of lung adenocarcinoma brain metastases.

Clin Cancer Res. 2020 May 1;26(9):2231-2243

IF (2021): **13.801**

Mock A, Heilig CE, Kreutzfeldt S, Huebschmann D, Heining C, Schröck E, Brors B, Stenzinger A, Jäger D, Schlenk R, Glimm H, Fröhling S, Horak P; DTKT MASTER Network.

Community-driven development of a modified progression-free survival ratio for precision oncology.

ESMO Open. 2019 Nov 13;4(6):e000583.

IF (2021): **6.883**

Mock A*, Zschäbitz S*, Kirsten R, Scheffler M, Wolf B, Herold-Mende C, Kramer R, Busch E, Jenzer M, Jäger D, Grüllich C.

Serum very long-chain fatty acid-containing lipids predict response to immune checkpoint inhibitors in urological cancers.

Cancer Immunol Immunother. 2019 Dec;68(12):2005-2014.

IF (2021): **6.630**

Dietrich S, Oleś M, Lu J, Sellner L, Anders S, Velten B, Wu B, Hüllelein J, da Silva Liberio M, Walther T, Wagner L, Rabe S, Ghidelli-Disse S, Bantscheff M, Oleś AK, Stabicki M, **Mock A**, Oakes CC, Wang S, Oppermann S, Lukas M, Kim V, Sill M, Benner A, Jauch A, Sutton LA, Young E, Rosenquist R, Liu X, Jethwa A, Lee KS, Lewis J, Putzker K, Lutz C, Rossi D, Mokhir A, Oellerich T, Zirklik K, Herling M, Nguyen-Khac F, Plass C, Andersson E, Mustjoki S, von Kalle C, Ho AD, Hensel M, Dürig J, Ringshausen I, Zapatka M, Huber W, Zenz T.

Drug-perturbation-based stratification of blood cancer.

J Clin Invest. 2018 Jan 2;128(1):427-445

IF (2021): **19.456**

Mock A, Murphy S, Morris J, Marass F, Rosenfeld N, Massie C.

CVE: an R package for interactive variant prioritisation in precision oncology.

BMC Med Genomics. 2017 May 25;10(1):37.

IF (2021): **3.622**

Geisenberger C*, **Mock A***, Warta R, Rapp C, Schwager C, Korshunov A, Nied AK, Capper D, Brors B, Jungk C, Jones D, Collins VP, Ichimura K, Bäcklund LM, Schnabel E, Mittelbron M, Lahrmann B, Zheng S, Verhaak RG, Grabe N, Pfister SM, Hartmann C, von Deimling A, Debus J, Unterberg A, Abdollahi A, Herold-Mende C.

Molecular profiling of long-term survivors identifies a subgroup of glioblastoma characterized by chromosome 19/20 co-gain.

Acta Neuropathol. 2015 Sep;130(3):419-34.

IF (2021): **15.887**