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GENERAL INFORMATION

Junior Group Leader
German Cancer Research Center (DKFZ)
Junior Research Group Bioinformatics and Omics Data Analytics
Im Neuenheimer Feld 280, 69120 Heidelberg, Germany

D02

ACADEMIC EDUCATION & QUALIFICATION

Year(s)	Education
1998 – 2003	Human Biology, Philipps University of Marburg, Diploma, Prof. Dr. Hans-Dieter Klenk

SCIENTIFIC EDUCATION & QUALIFICATION

Year(s)	Education
2004-2008	Dr. rer. nat., Biochemistry, Ludwig-Maximilian University of Munich, 2008, Prof. Dr. Dieter Oesterhelt (summa cum laude)

PROFESSIONAL EXPERIENCE

Year(s)	Experience
Since 2017	Head of Junior Research Group Bioinformatics and Omics Data Analytics, German Cancer Research Center (DKFZ), Heidelberg, Germany
2013-2017	Group Leader Computational Oncology in the division of Theoretical Bioinformatics, German Cancer Research Center (DKFZ), Heidelberg, Germany
2011-2013	Postdoc, Division of Theoretical Bioinformatics, German Cancer Research Center (DKFZ), Heidelberg, Germany
2009-2011	Postdoc, Department of Membrane Biochemistry, Max Planck Institute for Biochemistry, Martinsried, Germany

OTHER QUALIFICATIONS/ROLES/RESPONSIBILITIES

Year(s)	
Since 2019	Member of the steering committee of the Helmholtz Information & Data Science School for Health
Since 2017	Faculty member of the undergraduate program „Major Cancer Biology" from the DKFZ

SELECTED PUBLICATIONS

1. Paramasivam N, Hübschmann D, Toprak UH, Ishaque N, Neidert M, Schrimpf D, Stichel D, Reuss D, Sievers P, Reinhardt A, Wefers AK, Jones DTW, Gu Z, Werner J, Uhrig S, Wirsching HG, Schick M, Bewerunge-Hudler M, Beck K, Brehmer S, Urbschat S, Seiz-Rosenhagen M, Hänggi D, Herold-Mende C, Ketter R, Eils R, Ram Z,, Pfister SM, Wick W, Weller M, Grossmann R, von Deimling A, Schlesner M#, Sahm F#. Mutational patterns and regulatory networks in epigenetic subgroups of meningioma. **Acta Neuropathol.** 2019; 138(2):295-308 (#shared senior authorship)
2. Northcott PA, Buchhalter I, Morrissy AS, Hovestadt V, Weischenfeldt J, Ehrenberger T, Gröbner S, Segura-Wang M, Zichner T, Rudneva VA, Warnatz HJ, Sidiropoulos N, Phillips AH, Schumacher S, Kleinheinz K, Waszak SM, Erkek S, Jones DTW, Worst BC, Kool M, Zapatka M, Jäger N, Chavez L, Hutter B, Bieg M, Paramasivam N, Heinold M, Gu Z, Ishaque N, Jäger-Schmidt C, Imbusch CD, Jugold A, Hübschmann D, Risch T, Amstislavskiy V, Gonzalez FGR, Weber UD, Wolf S, Robinson GW, Zhou X, Wu G, Finkelstein D, Liu Y, Cavalli FMG, Luu B, Ramaswamy V, Wu X, Koster J,

Ryzhova M, Cho YJ, Pomeroy SL, Herold-Mende C, Schuhmann M, Ebinger M, Liau LM, Mora J, McLendon RE, Jabado N, Kumabe T, Chuah E, Ma Y, Moore RA, Mungall AJ, Mungall KL, Thiessen N, Tse K, Wong T, Jones SJM, Witt O, Milde T, Von Deimling A, Capper D, Korshunov A, Yaspo ML, Kriwacki R, Gajjar A, Zhang J, Beroukhim R, Fraenkel E, Korbel JO, Brors B, Schlesner M, Eils R, Marra MA, Pfister SM, Taylor MD, Lichter P. The whole-genome landscape of medulloblastoma subtypes. **Nature** 2017;19;547(7663):311-317.

3. Sahm F, Toprak UH, Hübschmann D, Kleinheinz K, Buchhalter I, Sill M, Stichel D, Schick M, Bewerunge-Hudler M, Schrimpf D, Zadeh G, Aldape K, Herold-Mende C, Beck K, Staszewski O, Prinz M, Harosh CB, Eils R, Sturm D, Jones DTW, Pfister SM, Paulus W, Ram Z, Schlesner M#, Grossman R#, von Deimling A#. Meningiomas induced by low-dose radiation carry structural variants of NF2 and a distinct mutational signature. **Acta Neuropathol** 2017;134(1):155-158. (#shared senior authorship)
4. Gu Z, Eils R, Schlesner M. Complex heatmaps reveal patterns and correlations in multidimensional genomic data. **Bioinformatics** 2016;32(18):2847-9.
5. Sturm D, Orr BA, Toprak UH, Hovestadt V, Jones DTW, Capper D, Sill M, Buchhalter I, Northcott PA, Leis I, Ryzhova M, Koelsche C, Pfaff E, Allen SJ, Balasubramanian G, Worst BC, Pajtler KW, Brabetz S, Johann PD, Sahm F, Reimand J, Mackay A, Carvalho DM, Remke M, Phillips JJ, Perry A, Cowdrey C, Drissi R, Fouladi M, Giangaspero F, Łastowska M, Grajkowska W, Scheurlen W, Pietsch T, Hagel C, Gojo J, Lötsch D, Berger W, Slavc I, Haberler C, Jouvet A, Holm S, Hofer S, Prinz M, Keohane C, Fried I, Mawrin C, Scheie D, Mobley BC, Schniederjan MJ, Santi M, Buccoliero AM, Dahiya S, Kramm CM, von Bueren AO, von Hoff K, Rutkowski S, Herold-Mende C, Frühwald MC, Milde T, Hasselblatt M, Wesseling P, Rößler J, Schüller U, Ebinger M, Schittenhelm J, Frank S, Grobholz R, Vajtai I, Hans V, Schneppenheim R, Zitterbart K, Collins VP, Aronica E, Varlet P, Puget S, Dufour C, Grill J, Figarella-Branger D, Wolter M, Schuhmann MU, Shalaby T, Grotzer M, van Meter T, Monoranu CM, Felsberg J, Reifenberger G, Snuderl M, Forrester LA, Koster J, Versteeg R, Volckmann R, van Sluis P, Wolf S, Mikkelsen T, Gajjar A, Aldape K, Moore AS, Taylor MD, Jones C, Jabado N, Karajannis MA, Eils R, Schlesner M, Lichter P, von Deimling A, Pfister SM, Ellison DW, Korshunov A, Kool M. New Brain Tumor Entities Emerge from Molecular Classification of CNS-PNETs. **Cell** 2016;164(5):1060-1072.
6. Gu Z, Eils R, Schlesner M. HilbertCurve: an R/Bioconductor package for high-resolution visualization of genomic data. **Bioinformatics** 2016;32(15):2372-4.
7. Gu Z, Eils R, Schlesner M. gtrellis: an R/Bioconductor package for making genome-level Trellis graphics. **BMC Bioinformatics**. 2016; 17:169.
8. Vater I*, Montesinos-Rongen M*, Schlesner M*, Haake A, Purschke F, Sprute R, Mettenmeyer N, Nazzal I, Nagel I, Gutwein J, Richter J, Buchhalter I, Russell RB, Wiestler OD, Eils R, Deckert M, Siebert R. The mutational pattern of primary lymphoma of the central nervous system determined by whole-exome sequencing. **Leukemia** 2015;29(3):677-85. (*shared first authorship)
9. Jäger N, Schlesner M, Jones DT, Raffel S, Mallm JP, Junge KM, Weichenhan D, Bauer T, Ishaque N, Kool M, Northcott PA, Korshunov A, Drews RM, Koster J, Versteeg R, Richter J, Hummel M, Mack SC, Taylor MD, Witt H, Swartman B, Schulte-Bockholt D, Sultan M, Yaspo ML, Lehrach H, Hutter B, Brors B, Wolf S, Plass C, Siebert R, Trumpp A, Rippe K, Lehmann I, Lichter P, Pfister SM, Eils R. Hypermutation of the inactive X chromosome is a frequent event in cancer. **Cell** 2013;155(3):567-81.
10. Richter J*, Schlesner M*, Hoffmann S*, Kreuz M*, Leich E*, Burkhardt B*, Rosolowski M, Ammerpohl O, Wagener R, Bernhart SH, Lenze D, Szczepanowski M, Paulsen M, Lipinski S, Russell RB, Adam-Klages S, Apic G, Claviez A, Hasenclever D, Hovestadt V, Hornig N, Korbel JO, Kube D, Langenberger D, Lawerenz C, Lisfeld J, Meyer K, Picelli S, Pischimarov J, Radlwimmer B, Rausch T, Rohde M, Schilhabel M, Scholtysik R, Spang R, Trautmann H, Zenz T, Borkhardt A, Drexler HG, Möller P, MacLeod RA, Pott C, Schreiber S, Trümper L, Loeffler M, Stadler PF, Lichter P, Eils R, Küppers R, Hummel M, Klapper W, Rosenstiel P, Rosenwald A, Brors B, Siebert R; ICGC MMML-Seq Project. Recurrent mutation of the ID3 gene in Burkitt lymphoma identified by integrated genome, exome and transcriptome sequencing. **Nat Genet** 2012;44(12):1316-20. (*shared first authorship)