

General Information

Name: Prof. Dr. Christoph Plass
Date of Birth: 30.07.1961
Gender: Male
Address: German Cancer Research Center (DKFZ)
Cancer Epigenomics, Im Neuenheimer Feld 280, 69120 Heidelberg
Phone: +49 6221 423300
E-Mail: c.plass@dkfz.de
Current Position: Head, Division of Cancer Epigenomics, DKFZ, Heidelberg

Academic Education

1988-1993 PhD study at Institut für Biologie der Medizinischen Universität, Lübeck
1982-1987 Study of Biology at the Freie Universität Berlin, Berlin

Academic Degrees

1993 Dr rer. nat. (PhD)
1987 Diploma in Biology, Freie Universität Berlin

Professional Experience

Since 2007 German Cancer Research Center (DKFZ), Heidelberg, Germany,
Department of Epigenomics and Cancer Risk Factors, Professor
2005-2007 The Ohio State University, Columbus, USA, Department of Medical
Microbiology and Immunology, Division of Human Cancer Genetics,
Professor
2002-2005 The Ohio State University, Columbus, USA Department of Medical
Microbiology and Immunology, Division of Human Cancer Genetics,
Associate Professor
1997-2002 The Ohio State University, Columbus, USA, Department of Medical
Microbiology and Immunology, Division of Human Cancer Genetics,
Assistant Professor
1996-1997 Roswell Park Cancer Institute, Buffalo, NY, Molecular and Cellular
Biology Department, Cancer Research Scientist II
1993-1996 Roswell Park Cancer Institute, Buffalo, NY, Laboratory of Dr Verne
Chapman, Molecular and Cellular Biology Department, Postdoc

Miscellaneous

Awards and Honors:

2016 Taiwan Tsungming Tu Award
2007 Stohlman Scholar, Leukemia Lymphoma Society of America
2006 Barbara J. Bonner Chair in Lung Cancer
2005 Elected Fellow, American Association for the Advancement of Science
2003 Honorary Faculty of the Mirrors Honors Society
2002-2007 Leukemia Lymphoma Society of America Scholar
2002-2005 V-Foundation Translational Award

Other Activities:

Since 2019 Editor in Chief, International Journal of Cancer
Since 2018 Coordinator of DFG FOR 2674 Program
Since 2005 Member of AAAS
Since 1999 Member of American Society for Human Genetics
Since 1998 Member of Society for Neuro-Oncology

Since 1997
Since 1997

Member of Mammalian Genome Society
Member of American Association for Cancer Research

Publications

1. Mansouri L, Wierzbinska JA, [Plass C](#), Rosenquist R. Epigenetic deregulation in chronic lymphocytic leukemia: Clinical and biological impact. Review. **Semin Cancer Biol.** 2018;51:1-11.
2. Lipka DB, Lutsik P, [Plass C](#). From basic knowledge to effective therapies. **Cancer Cell.** 2018; 34(6):871-73.
3. Dietrich S, Oleś M, Lu J, Sellner L, Anders S, Velten B, Wu B, Hüllein J, da Silva Liberio M, Walther T, Wagner L, Rabe S, Ghidelli-Disse S, Bantscheff M, Oleś AK, Słabicki 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, Zirlik 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;128(1):427-45.
4. Lipka DB, Witte T, Toth R, Yang J, Wiesenfarth M, Nöllke P, Fischer A, Brocks D, Gu Z, Park J, Strahm B, Wlodarski M, Yoshimi A, Claus R, Lübbert M, Busch H, Boerries M, Hartmann M, Schönung M, Kilik U, Langstein J, Wierzbinska JA, Pabst C, Garg S, Catalá A, De Moerloose B, Dworzak M, Hasle H, Locatelli F, Masetti R, Schmutz M, Smith O, Stary J, Ussowicz M, van den Heuvel-Eibrink MM, Assenov Y, Schlesner M, Niemeyer C, Flotho C, [Plass C](#). RAS-pathway mutation patterns define epigenetic subclasses in juvenile myelomonocytic leukemia. **Nat Commun.** 2017;8(1):2126.
5. Jäkel C, Bergmann F, Toth R, Assenov Y, van der Duin D, Strobel O, Hank T, Klöppel G, Dorrell C, Grompe M, Moss J, Dor Y, Schirmacher P, [Plass C](#), Popanda O, Schmezer P. Genome-wide genetic and epigenetic analyses of pancreatic acinar cell carcinomas reveal aberrations in genome stability. **Nat Commun.** 2017;8(1):1323.
6. Delacher M, Imbusch CD, Weichenhan D, Breiling A, Hotz-Wagenblatt A, Träger U, Hofer AC, Kägebein D, Wang Q, Frauhammer F, Mallm JP, Bauer K, Herrmann C, Lang PA, Brors B, [Plass C](#), Feuerer M. Genome-wide DNA-methylation landscape defines specialization of regulatory T cells in tissues. **Nat Immunol.** 2017;18(10):1160-72.
7. Brocks D, Schmidt CR, Daskalakis M, Jang HS, Shah NM, Li D, Li J, Zhang B, Hou Y, Laudato S, Lipka DB, Schott J, Bierhoff H, Assenov Y, Helf M, Ressenrova A, Islam MS, Lindroth AM, Haas S, Essers M, Imbusch CD, Brors B, Oehme I, Witt O, Lübbert M, Mallm JP, Rippe K, Will R, Weichenhan D, Stoecklin G, Gerhäuser C, Oakes CC, Wang T, [Plass C](#). DNMT and HDAC inhibitors induce cryptic transcription start sites encoded in long terminal repeats. **Nat Genet.** 2017;49(7):1052-60. Erratum: Nat Genet. 2017;49(7):1661.
8. Oakes CC, Seifert M, Assenov Y, Gu L, Przekopowicz M, Ruppert AS, Wang Q, Serva A, Koser S, Brocks D, Lipka D, Bogatyrova O, Mertens D, Zapatka M, Lichter P, Döhner H, Küppers R, Zenz T, Stilgenbauer S, Byrd JC and [Plass C](#). Progressive epigenetic programming during B cell maturation yields a continuum of disease phenotypes in chronic lymphocytic leukemia. **Nat Genet.** 2016;48(3):253-64.
9. Bock C, Halbritter F, Carmona FJ, Tierling S, Datlinger P, Assenov Y, Berdasco M, Bergmann AK, Booher K, Busato F, Campan M, Dahl C, Dahmcke CM, Diep D, Fernandez AF, Gerhaeuser C, Haake A, Heilmann K, Holcomb T, Hussmann D, Ito M, Klaver R, Kreutz M, Kulis M, Lopez V, Nair SS, Paul DS, Plongthongkum N, Qu WJ, Queiros AC, Reinicke F, Sauter G, Schlomm T, Statham A, Stirzaker C, Strogantsev R, Urduingio RG, Walter K, Weichenhan D, Weisenberger DJ, Beck S, Clark SJ, Esteller M, Ferguson-Smith AC, Fraga MF, Guldborg P, Hansen LL, Laird PW, Martin-Subero JI, Nygren AOH, Peist R, [Plass C](#), Shames DS, Siebert R, Sun XG, Tost J, Walter J, Zhang K, BLUEPRINT consortium, Collaborators (58): Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. **Nat Biotech.** 2016;34(7):726-37.
10. Gu L, Frommel SC, Oakes CC, Simon R, Grupp K, Gerig CY, Bär D, Robinson MD, Baer C, Weiss M, Gu Z, Schapira M, Kuner R, Sülthmann H, Provenzano M; ICGC Project on Early Onset Prostate Cancer, Yaspo ML, Brors B, Korb J, Schlomm T, Sauter G, Eils R, [Plass C](#), Santoro R. BAZ2A (TIP5) is involved in epigenetic alterations in prostate cancer and its overexpression predicts disease recurrence. **Nat Genet.** 2015;47(1):22-30.