

Dr. Carl HERRMANN

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Personal data

- Born 20.12.1971 in Nantes (France)
- French-German citizenship
- Married, four daughters

Scientific Career

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| since 2018 | <ul style="list-style-type: none">▪ Head of the group <i>Biomedical Genomics</i> at the <i>Health Data Science Unit</i> (HDSU) – Medical Faculty Heidelberg and BioQuant▪ Deputy-head of the <i>Health Data Science Unit</i>▪ Lecturer (Akademischer Oberrat) at the Medical Faculty Heidelberg |
| 2013 – 2018 | <ul style="list-style-type: none">▪ Head of the group <i>Cancer Regulatory Genomics</i> in the division of Theoretical Bioinformatics, German Cancer Research Center (DKFZ), Heidelberg▪ Lecturer (Akademischer Rat) at the Institute for Pharmacy and Molecular Biotechnologies (IPMB) – University Heidelberg |
| 2012 – 2013 | <ul style="list-style-type: none">▪ Visiting scientist at EMBL, Heidelberg |
| 2003 – 2012 | <ul style="list-style-type: none">▪ Assistant-professor ("Maître de Conférences") in bioinformatics at Aix-Marseille University (F)▪ Researchers at the <i>Institut Technologies Avancées pour le Génome et la Clinique</i> (TAGC) – Inserm, Marseille (F) |
| 2001 – 2003 | <ul style="list-style-type: none">▪ Postdoc at the Institute for Theoretical Physics, University of Turin |
| 1999 – 2001 | <ul style="list-style-type: none">▪ Postdoc at the Institute for Theoretical Physics, Martin Luther University Halle-Saale |

Studies

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| 1996 - 1999 | <ul style="list-style-type: none">▪ Ph.D. in theoretical physics (Supergravitation and String Theory) at the <i>Centre de Physique Théorique</i>, CNRS and Aix-Marseille, Marseille University (F) |
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- 1994 – 1995 ▪ Master (DEA) in theoretical physics, Ecole Normale Supérieure, Paris
- 1989 - 1994 ▪ Engineering degree in applied mathematics and computer sciences at the *Ecole Nationale des Ponts et Chaussées*, Paris

Research Interests and Expertise

- Computational aspects in regulatory genomics applied to developmental and disease.
- Methods development for the integration of biomedical datasets, using ML approaches.

Scientific duties

- seit 2018: Mitglied des Scientific Boards des *Research and Training Group "Big Data Research in the Biosciences"* (Universität Heidelberg – DBT Indien)
- 2008 – 2012: Leiter des Computerzentrums *Centre de ressources et formation en bioinformatique* (CRFB) am Campus Luminy – Université Aix-Marseille (Organisation von bioinformatischen Workshops und Lehrveranstaltungen)
- 2005-2008: Mitglied des *scientific advisory boards* des Rechenzentrums Vital-IT an der Universität Lausanne (<https://www.vital-it.ch>)
- Seit 2014: Mitglied der Studienkommission Molekulare Biotechnologie – Fakultät für Biowissenschaften
- Seit 2020: associate-editor PLOS Computational Biology
- Mitglied der *Société française de Bioinformatique* (SFBI)

Grants obtained

- 2020 - 2021: DFG - Fokus COVID-19: Immunität und Pathomechanismen "*Identification of the molecular origins of comorbidity in COVID-19 patients*" (47.550 euros – PI)
- 2020 - 2024: DFG – Transregio TRR179 (140.000 euros – co-PI)
- 2020 – 2022: 4EU+ *Network of Bioinformatics Master Programs*
- 2019 – 2020: EIT Health COMETH Projekt "*Innovative benchmarking approaches to improve COmputational METHods for big data analysis in Health*" (78.000 euros - PI)
- 2019 - 2022: BMBF – e:Med COMMITMENT Projekt "*COMorbidity Modeling via Integrative Transfer machine-learning in MENTal illness*" (415.914 euros – co-PI)
- 2019 – 2022: DFG Spatial Genome Architecture in Development and Disease" SPP2202 ; Projekt "*Nukleare Landschaft der HIV Integration in Mikrogliä*" (169.800 euros - PI)
- 2016 – 2020: NCT3.0 Integrative Projects in Basic Cancer Research ENHANCE Projekt "*ENHancers And Non-coding Cancer (Epi-)Mutations*" (280.000 euros - PI)

Teaching (excerpts)

2018: nominated for the *Ars Legendi* teaching prize

Bachelor Molekulare Biotechnologie (Universität Heidelberg)

- Einführung in die Mathematik (Mathe A / Mathe B) (1./2. Semester)
- Einführung in die Datenanalyse – Projektmodul (3./4. Semester)
- Bioinformatik 1/2 (5./6. Semester)

Master Molekulare Biotechnologie (Universität Heidelberg)

- Seminar *Biologische Netzwerke* (mit J. Saez-Rodriguez)
- Meet-Eu Projektmodul (Teil des 4EU+ Bioinformatics Master Network Programms)

Universität Aix-Marseille (2003 – 2013)

- Einführung in die Bioinformatik (Bachelor – 2. Jahr)
- Bioinformatik der transkriptionellen Regulation (Master in Bioinformatik & Biochemie)

Universidad Nacional Autónoma de México (UNAM) (2012)

- Modul „*Bioinformatic approaches for cis-regulation*“, Licenciatura en Ciencias Genómicas (20 Std.)

University of Science and Technologies Hanoi (USTH - Vietnam) (2011)

- Modul „*Bioinformatic Annotation of Genomics and metagenomic sequences*“ (30 Std.)

Universität Marien N'Gouabi (Brazzaville – Republic of Congo) (2009)

- Modul „*Annotation of metagenomic sequences*“ (30 Std.)

Publications

68 publications, 3188 citations, h-Index = 26 (Source: Scopus June 2021)

81 publications, 4397 citations, h-Index = 32 (Source: Google Scholars June 2021)

Selected publications:

Ramirez C, Kee C, ... , Boulant S*, **Herrmann C***. (2021) The endogenous cellular protease inhibitor SPINT2 controls SARS-CoV-2 viral infection and is associated to disease severity. *PLOS Pathogens* 17(6)
<https://doi.org/10.1371/journal.ppat.1009687>

Wang Q ,..., **Herrmann, C.** (2021). Integrative ranking of enhancer networks facilitates the discovery of epigenetic markers In cancer. *Frontiers in Genetics*, 12, 591.

Jansky S, Sharma AK, Körber V ..., **Herrmann C**, Höfer T, Westermann F. (2021) Single-cell transcriptomic analyses provide insights into the developmental origins of neuroblastoma. *Nature Genetics*.
<https://doi.org/10.1038/s41588-021-00806-1>

Gartlgruber M, Sharma AK, Quintero A, Dreidax D,... , **Herrmann C***, Westermann F* (2020) Super enhancers define regulatory subtypes and cell identity in neuroblastoma, *Nature Cancer*
<https://www.nature.com/articles/s43018-020-00145-w>

Wu Y, Fletcher M, ..., **Herrmann C***, Radlwimmer B* (2020) Glioblastoma epigenome profiling identifies SOX10 as a master regulator of molecular tumour subtype, *Nature Communications* **11**, 6434

Quintero A, Hübschmann D, Kurzawa N, Steinhauser S, Rentzsch P, Krämer S, ... **Herrmann C** (2020). ShinyButchR: interactive NMF-based decomposition workflow of genome-scale datasets. *Biology Methods and Protocols*, 1–18.

Kumar S, Warrell J, Li S, McGillivray PD, Meyerson W, Salichos L, ... **Herrmann C**, Getz G, Khurana E, Gerstein MB. (2020). Passenger Mutations in More Than 2,500 Cancer Genomes: Overall Molecular Functional Impact and Consequences. *Cell*, 1–13.

Chan CW, Gu Z, Bieg M, ..., **Herrmann C**. (2019) Impact of cancer mutational signatures on transcription factor motifs in the human genome *BMC Medical Genomics* 12(1), 64.

Liu L, Liu C, Quintero A, Wu L, Yuan Y, Wang M, ... , **Herrmann C**, Eils R, Shang S, Xu X. (2019). Deconvolution of single-cell multi-omics layers reveals regulatory heterogeneity. *Nature Communications* 10, 470

Raffel S, Falcone M, Kneisel N, Hansson J, Wang W, Lutz C, ... **Herrmann C**, Ho AD, Krijgsveld J, Radlwimmer B, Trumpp A. (2017). BCAT1 restricts aKG levels in AML stem cells leading to IDHmut-like DNA hypermethylation. *Nature*, 551(7680), 384–388.

Bauer T, Trump S, Ishaque N, Thürmann L, Gu L, Bauer M, ... **Herrmann C***, Eils R*, Lehmann I* (2016). Environment-induced epigenetic reprogramming in genomic regulatory elements in smoking mothers and their children. *Molecular Systems Biology*, 12(3), 861–861.

Steinhauser S, Kurzawa N, Eils R, & **Herrmann C**. (2016). A comprehensive comparison of tools for differential ChIP-seq analysis. *Briefings in Bioinformatics*, 17(August), bbv110.

Nolte N, Kurzawa N, Eils R, & **Herrmann, C**. (2015). MapMyFlu: visualizing spatio-temporal relationships between related influenza sequences. *Nucleic Acids Research*, 43(W1), W547–W551.

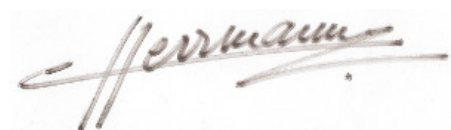
Peifer M, Hertwig F, Roels F, Dreidax D, Gartlgruber M, Menon R, ... , **Herrmann C**, O'Sullivan R, Westermann F, Thomas R, Fischer M. (2015). Telomerase activation by genomic rearrangements in high-risk neuroblastoma. *Nature*, 526(7575), 700–704.

Herrmann C, Van de Sande B, Potier D, & Aerts S. (2012). i-cisTarget: an integrative genomics method for the prediction of regulatory features and cis-regulatory modules. *Nucleic Acids Research*, 40(15), e114–e114.

Thomas-Chollier M, Darbo E, **Herrmann, C**, Defrance M, Thieffry D, & van Helden J. (2012). A complete workflow for the analysis of full-size ChIP-seq (and similar) data sets using peak-motifs. *Nature Protocols*, 7(8), 1551–1568.

Hingamp, P., Brochier, C., Talla, E., Gautheret, D., Thieffry, D., & **Herrmann, C**. (2008). Metagenome Annotation Using a Distributed Grid of Undergraduate Students. *PLOS Biology*, 6(11), e296.

*: Equal contribution or co-corresponding author



Heidelberg, June 9th, 2021