Edwin Cuppen
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Biography

Edwin Cuppen is initiator and scientific director of the Hartwig Medical Foundation (part-time since 2015 and full time since 2021), a not-for-profit organisation that aims to improve cancer care by systematic whole genome sequencing analysis of tumors and that also maintains one of the world's largest databases of cancer whole genome sequencing data enriched with clinical patient data. After his undergraduate and PhD training at Wageningen University and Radboud University Nijmegen as a molecular geneticist, he held research and group leader positions at the Netherlands Cancer Institute, the Hubrecht Institute and the UMC Utrecht. His expertise is in cancer genomics and functional genetics.

Profile

Edwin Cuppen (1970) obtained his masters in molecular sciences at the Agricultural University Wageningen in 1994 (cum laude) and his PhD degree in 1999 at the Radboud University in Nijmegen in the group of Prof. Be Wieringa. During his education, he spent half a year in het Jaenish lab at the Whitehead Institute in Boston. From 1999 to 2002 he performed postdoctoral research at the Netherlands Cancer Institute in Amsterdam and the Hubrecht Institute in Utrecht, The Netherlands, in the group of Prof. Ronald Plasterk. In 2002 he became staff scientist at the Hubrecht Institute and in 2007 he was appointed professor of Genome Biology at the Biology department of the Utrecht University. In 2009 he was appointed professor of Human Genetics and head of the research section of the Medical Genetics department of the University Medical Center Utrecht, while continuing his work at the Hubrecht Institute with a split appointment. In 2015, he left the Hubrecht Institute to transfer his research group completely to the UMC Utrecht and to become the director of the Center for Molecular Medicine (23 research groups, ~250 scientists) and member of the management team (portfolio research and education) of the Division of Biomedical Genetics. In 2017, he stepped down from this position and became director of the Hartwig Medical Foundation in Amsterdam, while remaining associated with the UMC Utrecht for his fundamental research activities. In September 2017, he was invited to be one of the inaugural members of the national cancer research organisation Oncode Institute.
As of Sept 2021, Edwin fully focuses on the activities at Hartwig Medical Foundation, employing genomics technologies to improve diagnostics and care for today's and tomorrow's cancer patients. As scientific director, he drives the multi-omics and systematic data integration agenda to enable routine cancer diagnostics and facilitating third party research.
His area of expertise is in genomics and genetics and his scientific interests are in functional and personal genomics. In 2005, Edwin Cuppen was awarded a European Young Investigators Award for his work on naturally occurring and induced genetic variation in the laboratory rat. He was one of the first to generate gene knockout models in the rat and showed the widespread effect of copy number variation on gene expression levels. In 2013, he was awarded a prestigious NWO Vici grant for dissecting the molecular mechanisms behind structural genomic variation and studying the functional consequences using integrated systematic -omics approaches.
In his current work he combines experimental methods, including next-generation sequencing technology and animal model studies, with bioinformatic approaches to understand the effects of genetic variation under normal and disease conditions, with a specific focus on cancer and congenital disease. His research group has a long track record in high-throughput DNA analysis and was among the first to pioneer next-generation sequencing technology. His group developed and improved various NGS-based techniques and is now routinely applying NGS-based techniques in a wide range of systems from human patients to zebrafish and rat models and adult stem cell culturing systems (normal and tumor derived organoids). His group has specialized in studing genomic structural variation and they are using NGS-based techniques like (small) RNA sequencing, ChIP-Seq, and 4C-seq to detect molecular consequences and dissect underlying biological mechanisms. Furthermore, within the Medical Center settings, he is involved in implementing NGS approaches for diagnostic purposes in clinical genetics and personalized cancer treatment.
Edwin is one of the initiators of the nationally operating Center for Personalized Cancer Treatment (www.cpct.nl, established in 2010) for which he coordinated the centralized genome analysis and bioinformatic data integration efforts. This national collaboration aims for the stratification of cancer patients towards targeted treatments based on whole genome sequencing analysis of the tumor and to bring these developments to cancer patients in The Netherlands in a timely and responsible manner.
Edwin is scientific founder and director of the Hartwig Medical Foundation (2015), an independent not-for-profit organisation that is made possible through philanthropy, which operates a large scale cancer whole genome sequencing facility and in which various national clinical and research parties collaborate for improving personalized cancer patient care.
Edwin is also an inventor on various patents and cofounder of the biotech startup company InteRNA Technologies that focuses on miRNA-based diagnostics and therapeutics. He has been advisor for several biotech startups in the area of genomics technology and bioinformatics.

Academic advisory activities

- 2013 – 2019: member 'wetenschappelijke raad KiKa' (scientific council foundation Children Cancer Free)
- (current) Reviewer for various journals, including Nucleic Acids Research, Genomics, Bioinformatics, BMC Genomics, BMC Bioinformatics, Bioinformatics, Genome Biology, Genome Research, PNAS, Nature Genetics, Nature, Nature Methods, Cell.
- (current) Reviewer and committee member for various national and international funding agencies (NWO, KWF, KiKa, BBSRC, Wellcome Trust, CR-UK, CNRS)
- 2015: Department Evaluation Board Flemisch Institute for Biotechnology (VIB)
- 2013 – 2016: Member and chair of the NWO study group Nucleic Acids
- 2012 – 2014: Expert panel member Finnish Academy of Sciences
- 2010 – 2014 Advisory Board Liverpool Centre for Genomic Research
- 2010 – 2015: Advisory Board Knockout Rat Consortium
- 2009 – 2012: Member FWO expert panel, Belgium
- 2007/2008: Member Scientific Advisory Board ELSYS (Young European Scientists in Life Science)
- 2008: Member scientific site visit committee CGM, Paris, France
- 2007: Expert reviewer FP6 panel
- 2005: Member scientific site visit committee Roslin Institute, Edinburg, UK

Commercial advisory activities

- (current) 2006 – present: Scientific Advisory Board InteRNA Technologies BV (miRNA-based therapeutics)
- 2019 – present: Global WGTS advisory board Illumina
- 2014 – 2017 : Scientific Advisor BlueBee (hardware acceleration genomics)
- 2012 – 2017: Scientific Advisory Board Cergentis BV (targeted sequencing technology)
- 2012 – 2017: Scientific Advisory Board Genalice (high volume data analysis)
- 2013 – 2014: Scientific Advisor Elly Lilly (rat genomics)
- 2008 – 2012: Scientific Advisor Philips Research (DNA analysis technology)

Other national and international activities

- 2020 - current: Strategic management board national branch of EU 1 million+ genome project (MG-NL)
- 2018 - 2021: Steering committee NWO national large scale research infrastructure X-omics
- 2013: Scientific committee 2nd International Conference on Genomics, Ghent, Belgium
- 2013: Chair program committee Federa Dag Next-generation sequencing 2013
- 2007 – 2014: Organizer annual Cold Spring Harbor/Wellcome Trust meeting ‘Rat genomics and models’
- 2010 – 2015: Steering Committee member Center for Personalized Cancer Treatment (www.CPCT.nl)
- 2010 – 2015: Steering Committee member EU FP7 program EURATRANS (www.euratrans.eu)
- 2012 – 2014: Mentor Steyn Parve coaching program UMC Utrecht
- 2011 – 2013: Director Netherlands Center for Genome Diagnostics (CGD)
- 2008 – 2012: Organizer annual Dutch Next-Generation Sequencing Users Meeting
- 2009 – 2012: Chair Jury X-track Honors Program
- 2010: Co-organizer first European (ESF) next-generation sequencing meeting
- 2007 – 2009: Member program committee NWO Computational Life Sciences II.

Patent (applications)

-Weijzen, S., Schaapveld, R., Bourajjaj, M., van Haastert, R., Griffioen, A., van Beijnum, J., Cuppen, E., Berezikov, E., van Puijenbroek, A., Gommans, W., Negar, B., (2011). Mir-190b for treating neo-angiogenesis. US application no 61/521,917 and 61/522,346
-Weijzen, S., Schaapveld, R., Bourajjaj, M., van Haastert, R., Griffioen, A., van Beijnum, J., Cuppen, E., Berezikov, E., van Puijenbroek, A., Gommans, W., van Noort, P., Negar, B., (2011). Mir-142 for treating neo-angiogenesis. US application no 61/521,931
-Weijzen, S., Schaapveld, R., Bouraijaj, M., van Haastert, R., Griffioen, A., van Beijnum, J., Cuppen, E., Berezikov, E., van Puijenbroek, A., Gommans, W. (2011). Mir for treating neo-angiogenesis. EPC:11150645.7-1212
-van Boxtel, R. and Cuppen, E. (2007). Animals of the rattus genus wherein msh6 expression is functionally decreased and methods for the generation of specific mutants there from. WO2009072882
-Cuppen, E., Meijer, G., Berezikov, E., Diosdado, B.,(2007). Small RNA molecules, precursors thereof, means and methods for detecting them, and uses thereof in typing samples. WO2009008720
-Berezikov, E., Cuppen, E., Plasterk, R. (2006). Nucleic acid molecules and collections thereof, their application and modification. WO2007081204

Research funding

-Hannarth Foundation (2021-2023): Cancer of Unknown Primary classifier
-NWO roadmap large infrastructure (2018-2023): X-omics
-KWF infrastructure (2018-2021): GENONCO: GENomics portal for precision medicine research in ONCOlogy
-KWF FOOTPRINT (2017-2020): Finding OncOgenic muTational PRocesses IN liver Tumorigenesis

-Oncode Institute (2017-2022): Fundamental and tranlsational cancer research
-ZonMW (2017-2020): Technology Assessment of Next Generation Sequencing in Personalized Oncology
-NWO Vici (2014-2020): Dissecting structural variation
-KWF Stand up to cancer (2013-2017): Cancer organoid genomics
-NWO Zwaartekracht (2013-2022): Cancer Genomics Netherlands
-NGI Zenith (2012-2016): Genetic integrity of adult stem cells
-Center for Genome Diagnostics (CGD), Netherlands Genomics Initiative (2011-2013): Next-generation sequencing in diagnostics
-Center for Personalized Cancer Treatment (CPCT), KWF/Alpe d'huzes (2011)
-NWO TOP-CW (2009 – 2013): Rat genomics
-EU FP7 EURATRANS (2010-2015): Rat systems genetics
-EU FP7 ZFHEALTH (2010-2015): Zebrafish genetics
-NBIC (NGI) BioRange-2 and BioAssist (2010 – 2013): Next-generation sequencing data analysis
-CGC-2 (NGI) (2009-2013): Cancer genetics
-Leducq transatlantic network (2009): miRNA in heart
-SMARTMIX (EZ and OCW) consortium (2008 – 2013): Zebrafish knockout models
-NCSB (NGI) (2008 – 2013): Cancer systems genetics
-NBIC (NGI) Biorange-1 (2006-2009): Bioinformatics analysis for mutation analysis
-EU FP6 ZFMODELS (2004-2009): Zebrafish knockout models
-NWO groot (2005): High-throughput mutation discovery
-IOP Genomics (2002-2007): Rat reverse genetics

Research output

Genomics comes of age: From research tool to routine care
Cuppen, E., Oct 2026, In: Journal of Internal Medicine. 300, 4, p. 390-392 3 p.

Systematic identification of genomic nonresponse biomarkers to cancer therapies
Usset, J., de Ligt, J., Roerink, S., Roepman, P., Cuppen, E. & Martínez-Jiménez, F., Sept 2026, In: ESMO Real World Data and Digital Oncology. 13, 100721.

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van Putten, J., Snaebjornsson, P., Bosch, L. J. W., Koster, R., Roepman, P., Usset, J., Boelens, M. C., van Wezel, T., Rosenberg, E. H., Marchetti, S., Vollebergh, M., Lambregts, D. M. J., van der Kolk, L. E., Cuppen, E., Nienhuis, H. H. & Monkhorst, K., Apr 2026, In: Nature medicine. 32, 4, 1 p., 1555.

Real-world clinical utility of tumor whole-genome sequencing in solid cancers
van Putten, J., Snaebjornsson, P., Bosch, L. J. W., Koster, R., Roepman, P., Usset, J., Boelens, M. C., van Wezel, T., Rosenberg, E. H., Marchetti, S., Vollebergh, M., Lambregts, D. M. J., van der Kolk, L. E., Cuppen, E., Nienhuis, H. H. & Monkhorst, K., Apr 2026, In: Nature medicine. 32, 4, p. 1286-1295 10 p.

Clinical implications of whole genome sequencing in metastatic colorectal cancer
Smabers, L. P., Nienhuis, H. H., de Leng, W. W. J., Roepman, P., Ciftcibasi, I. Ö. A., Wensink, G. E., Huismans, M. A., Valkenburg-van Iersel, L. B. J., Cirkel, G. A., Gootjes, E. C., Verheul, H. M. W., Jeurissen, F. J., Bol, G. M., Kranenburg, O., Koopman, M., Cuppen, E. & Roodhart, J. M. L., 15 Dec 2025, In: Oncogene. 44, 48, p. 4686-4698 13 p.

Genomic distinctions in adolescent and young adult cancer: A comprehensive review
van Putten, J., Lankhorst, L. H., de Langen, A. J., van der Wekken, A. J., Roodhart, J., Bolhuis, K., Oosting, S. F., van Dongen, M., Kok, M., Geurts, M., Koekkoek, J. A. F., Cuppen, E., Nienhuis, H. H. & van der Graaf, W. T. A., Nov 2025, In: Cancer Treatment Reviews. 140, 12 p., 103021.

Whole genome sequencing-based analysis of genetic predisposition to adult glioblastoma
van Opijnen, M. P., van Valkengoed, D. R., de Ligt, J., de Vos, F. Y. F., Broekman, M. L. D., Cuppen, E. & Koster, R., 30 Oct 2025, In: npj Genomic Medicine. 10, 1, 11 p., 70.

Whole genome sequencing of 378 prostate cancer metastases reveals tissue selectivity for mismatch deficiency with potential therapeutic implications
Vis, D. J., Palit, S. A. L., Corradi, M., Cuppen, E., Mehra, N., Lolkema, M. P., Wessels, L. F. A., van der Heijden, M. S., Zwart, W. & Bergman, A. M., 20 Mar 2025, In: Genome Medicine. 17, 1, 13 p., 24.

Patient-derived organoids predict treatment response in metastatic colorectal cancer
Smabers, L. P., Wensink, G. E., Verissimo, C. S., Doorn, M., Yang, T., Voskuilen, T., Huismans, M. A., Valkenburg-van Iersel, L., Cirkel, G. A., Gootjes, E. C., Verheul, H. M. W., Jeurissen, F. J., Bol, G. M., Nienhuis, H. H., Braat, M. N. G. J. A., Cuppen, E., Vries, R. G. J., van der Baan, F. H., Elias, S. G. & Kranenburg, O. & 3 others, Koopman, M., Boj, S. F. & Roodhart, J. M. L., 2025, In: Clinical cancer research : an official journal of the American Association for Cancer Research. 31, 23, p. 5015–5026 12 p.

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The role of molecular biomarkers in recurrent glioblastoma trials: an assessment of the current trial landscape of genome-driven oncology
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Whole genome sequencing in (recurrent) glioblastoma: challenges related to informed consent procedures and data sharing
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Multi-omic analysis identifies hypoalbuminemia as independent biomarker of poor outcome upon PD-1 blockade in metastatic melanoma
Leek, L. V. M., Notohardjo, J. C. L., de Joode, K., Velker, E. L., Haanen, J. B. A. G., Suijkerbuijk, K. P. M., Aarts, M. J. B., de Groot, J. W. B., Kapiteijn, E., van den Berkmortel, F. W. P. J., Westgeest, H. M., de Gruijl, T. D., Retel, V. P., Cuppen, E., van der Veldt, A. A. M., Labots, M., Voest, E. E., van de Haar, J. & van den Eertwegh, A. J. M., 16 May 2024, In: Scientific Reports. 14, 1, 11244.

The 1+Million Genomes Minimal Dataset for Cancer
Riba, M., Sala, C., Culhane, A. C., Flobak, Å., Patocs, A., Boye, K., Plevova, K., Pospíšilová, Š., Gandolfi, G., Morelli, M. J., Bucci, G., Edsjö, A., Lassen, U., Al-Shahrour, F., Lopez-Bigas, N., Hovland, R., Cuppen, E., Valencia, A., Poirel, H. A. & Rosenquist, R. & 7 others, Scollen, S., Arenas Marquez, J., Belien, J., De Nicolo, A., De Maria, R., Torrents, D. & Tonon, G., May 2024, In: Nature Genetics. 56, 5, p. 733-736 4 p.

A pan-cancer analysis of the microbiome in metastatic cancer
Battaglia, T. W., Mimpen, I. L., Traets, J. J. H., van Hoeck, A., Zeverijn, L. J., Geurts, B. S., de Wit, G. F., Noë, M., Hofland, I., Vos, J. L., Cornelissen, S., Alkemade, M., Broeks, A., Zuur, C. L., Cuppen, E., Wessels, L., van de Haar, J. & Voest, E., 25 Apr 2024, In: Cell. 187, 9, p. 2324-2335.e19

Combining Genomic Biomarkers to Guide Immunotherapy in Non-Small Cell Lung Cancer
Van De Haar, J., Mankor, J. M., Hummelink, K., Monkhorst, K., Smit, E. F., Wessels, L. F. A., Cuppen, E., Aerts, J. G. J. V. & Voest, E. E., 1 Apr 2024, In: Clinical Cancer Research. 30, 7, p. 1307-1318 12 p.

Improved detection of colibactin-induced mutations by genotoxic E. coli in organoids and colorectal cancer
Rosendahl Huber, A., Pleguezuelos-Manzano, C., Puschhof, J., Ubels, J., Boot, C., Saftien, A., Verheul, M., Trabut, L. T., Groenen, N., van Roosmalen, M., Ouyang, K. S., Wood, H., Quirke, P., Meijer, G., Cuppen, E., Clevers, H. & van Boxtel, R., 11 Mar 2024, In: Cancer Cell. 42, 3, p. 487-496.e6

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Samsom, K. G., Bosch, L. J. W., Schipper, L. J., Schout, D., Roepman, P., Boelens, M. C., Lalezari, F., Klompenhouwer, E. G., de Langen, A. J., Buffart, T. E., van Linder, B. M. H., van Deventer, K., van den Burg, K., Unmehopa, U., Rosenberg, E. H., Koster, R., Hogervorst, F. B. L., van den Berg, J. G., Riethorst, I. & Schoenmaker, L. & 9 others, van Beek, D., de Bruijn, E., van der Hoeven, J. J. M., van Snellenberg, H., van der Kolk, L. E., Cuppen, E., Voest, E. E., Meijer, G. A. & Monkhorst, K., Mar 2024, In: Nature protocols. 19, 3, p. 700-726 27 p.

EXO1 protects BRCA1-deficient cells against toxic DNA lesions
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Impact of genetic counseling strategy on diagnostic yield and workload for genome-sequencing-based tumor diagnostics
Koster, R., Schipper, L. J., Giesbertz, N. A. A., van Beek, D., Mendeville, M., Samsom, K. G., Rosenberg, E. H., Hogervorst, F. B. L., Roepman, P., Boelens, M. C., Bosch, L. J. W., van den Berg, J. G., Meijer, G. A., Voest, E. E., Cuppen, E., Ruijs, M. W. G., van Wezel, T., van der Kolk, L. & Monkhorst, K., Feb 2024, In: Genetics in medicine : official journal of the American College of Medical Genetics. 26, 2, 13 p., 101032.

Next generation sequencing of high-grade adult-type diffuse glioma in the Netherlands: interlaboratory variation in the primary diagnostic and recurrent setting
van Opijnen, M. P., Broekman, M. L. D., Cuppen, E., Dubbink, H. J., Ter Elst, A., van Eijk, R., Mühlebner, A., Jansen, C., van der Geize, R., Speel, E.-J. M., Groenen, P. J. T. A., de Vos, F. Y. F., Wesseling, P., de Leng, W. W. J. & Maas, S. L. N., Feb 2024, In: Journal of Neuro-Oncology. 166, 3, p. 485-492 8 p.

Genomic Alterations Associated with Estrogen Receptor Pathway Activity in Metastatic Breast Cancer Have a Differential Impact on Downstream ER Signaling
Angus, L., Smid, M., Wilting, S. M., Bos, M. K., Steeghs, N., Konings, I. R. H. M., Tjan-Heijnen, V. C. G., van Riel, J. M. G. H., van de Wouw, A. J., Cpct Consortium, Cuppen, E., Lolkema, M. P., Jager, A., Sleijfer, S. & Martens, J. W. M., 4 Sept 2023, In: Cancers. 15, 17, 14 p., 4416.

The genomic and transcriptomic landscape of advanced renal cell cancer for individualized treatment strategies
de Joode, K., van de Geer, W. S., van Leenders, G. J. L. H., Hamberg, P., Westgeest, H. M., Beeker, A., Oosting, S. F., van Rooijen, J. M., Beerepoot, L. V., Labots, M., Mathijssen, R. H. J., Lolkema, M. P., Cuppen, E., Sleijfer, S., van de Werken, H. J. G. & van der Veldt, A. A. M., 3 Jul 2023, In: Scientific Reports. 13, 1, p. 1-15 10720.

Pan-cancer whole-genome comparison of primary and metastatic solid tumours
Martínez-Jiménez, F., Movasati, A., Brunner, S. R., Nguyen, L., Priestley, P., Cuppen, E. & Van Hoeck, A., 8 Jun 2023, In: Nature. 618, 7964, p. 333-341 9 p.

Genetic immune escape landscape in primary and metastatic cancer
Martínez-Jiménez, F., Priestley, P., Shale, C., Baber, J., Rozemuller, E. & Cuppen, E., May 2023, In: Nature Genetics. 55 , 5, p. 820-831 12 p.

The genome-wide mutational consequences of DNA hypomethylation
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Identifying somatic changes in drug transporters using whole genome and transcriptome sequencing data of advanced tumors
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Heritable defects in telomere and mitotic function selectively predispose to sarcomas
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Author Correction: A deep learning system accurately classifies primary and metastatic cancers using passenger mutation patterns (Nature Communications, (2020), 11, 1, (728), 10.1038/s41467-019-13825-8)
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