

PERSONAL INFORMATION

Family name, First name: **Carninci, Piero**

Researcher unique identifiers: ORCID: 0000-0001-7202-7243; Researcher ID: K-1568-2014.

Date of birth: 07 August 1965

Nationality: Italian (in Japan since March 1995)

URL for web site: <https://humantechnopole.it/en/research-centres/genomics/>;
https://www.riken.jp/en/research/labs/ims/transcript_tech/#member

• EDUCATION

- 1990 **National Examination for the profession of Biologist**
University of Ferrara, IT
- 1989 **Doctor in Biological Science**
University of Trieste, IT.

• CURRENT POSITIONS

- 2020-present **Head of Genomics Research Centre - Functional Genomics Programme**
Research Group Leader
Fondazione Human Technopole, Milan, IT
- 2018-present **Team Leader of the Laboratory for Transcriptome Technology**
Center for Integrative Medical Sciences (IMS), RIKEN, Yokohama, JP

• PREVIOUS POSITIONS

- 2018-2022 **Deputy Director**
Center for Integrative Medical Sciences (IMS), RIKEN, Yokohama, JP
- 2013-2021 **Visiting Professor** in Functional Genomics, Graduate School of Medical Life Science,
Yokohama City University, JP.
- 2013-2018 **Director of Division of Genomics Technologies**
Deputy Director of the Center for Life Science Technologies
Leader of the Transcriptome Research Team
RIKEN, Yokohama, JP
- 2008-2013 **Leader of the Functional Genomics Technology Team**
Deputy Project Director of the LSA Technology Development Group and the Omics
Science Center
RIKEN, Yokohama, JP

• FELLOWSHIPS AND AWARDS

- 2018 **Commendation for Science and Technology** received from the Ministry of Education, Culture,
Sports, Science and Technology, Research Category, JP.
- 2014 **Chen Award for Excellence** received from the Human Genome Organization, US.
- 2012 **NISTEP Researchers Award** from the National Institute of Science and Technology Policy for
significant contributions in science and technology, JP.
- 2010 **RIKEN Omics Science Center Award** for the successful completion of FANTOM4 project, JP.
- 2009 **RIKEN Omics Science Center Award** for the development of the Cap Analysis of Gene Expression
(CAGE) method, JP.
- 2007 **Yamazaki-Teiichi Prize** for the development of the cap-trapper technology and its use for the annotation
of the transcriptional output of the genome, JP.
- 2001 **Biotec Award** for scientists under 40 for the construction of full-length cDNA encyclopedia, IT.

• SUPERVISION OF GRADUATE STUDENTS AND POSTDOCTORAL FELLOWS

- 2003-present 50 Postdocs/ 20 PhD/ 20 Master Students
RIKEN, Yokohama, JP; Fondazione Human Technopole, Milan, IT.

• TEACHING ACTIVITIES

- 2022-present **Professor in Molecular Biology**, PhD in Complex System for Quantitative Medicine,
Doctoral School, University of Turin, IT.
- 2016-present **Foreign Adjunct Professor in Genome Analysis**, Dept. of Bioscience and Nutrition,

- Karolinska Institutet, SE.
 2013-2021 **Visiting Professor**, Graduate School of Medical Life Science, Yokohama City University, JP.
 2017-2020 **Visiting Professor**, Faculdade de Medicina Universidade de Sao Paulo, BR.
 2006-2017 **Adjunct Professor**, Dept. of Molecular Biochemistry, Gunma University Graduate School of Medicine, JP.

- **ORGANISATION OF SCIENTIFIC MEETINGS**

- 2016-present Organising Committee of the **International Workshop on Advanced Genomics**, 500 participants, JP.
 2014-present Scientific Coordinator and Organiser of **FANTOM meetings**, 100 participants, JP.
 2013-present Organiser of the **Karolinska Institutet - RIKEN Joint International Doctoral Course**, 25 participants/year, SE/JP.
 2019 Meeting Planning Committee, Program Committee and Organiser of the **Human Cell Atlas General Meetings**, 150 participants, JP/ES.
 2019 Organiser of the **EMBO Workshop, Single cell biology**, 350 participants, JP.
 2019 Organiser of the **Human Genome Meeting (HUGO)**, 470 participants, JP.
 2017 Organiser of the **Human Cell Atlas Asia**, 150 participants, JP.

- **INSTITUTIONAL RESPONSIBILITIES**

- 2020-present **Head of Genomics Research Centre**, Fondazione Human Technopole, IT.
 2013-present **Chief Scientist and member of the Science Council**, RIKEN, JP.
 2019-2020 **Scientific Advisor**, Fondazione Human Technopole, IT.
 2018-2022 **Deputy Director**, Center for Integrative Medical Sciences, RIKEN, JP.
 2013-2018 **Director of Division of Genomics Technologies**, RIKEN, JP.
Deputy Director of the Center for Life Science Technologie, RIKEN, JP.

- **REVIEWING ACTIVITIES**

- 2022-present **Chair of the Scientific Advisory Board, Steering Group and Management Group** of the *National Genomics Infrastructure and the Genomics Platform of Science for Life Laboratory (SciLifeLab)*, SE.
 2022-present **Reviewer** for the European Research Council (BE), the Natural Sciences and Engineering Research Council of Canada (CA), the French National Research Agency (FR).
 2010-present **Editorial Board**, *Genome Research* (2015-present), *Cell Systems* (2015-2019), *Scientific Data* (2015-2019), *BioEssays* (2010-2019), *Nature Communications* (2010-2016).

- **MEMBERSHIPS OF SCIENTIFIC SOCIETIES**

- 2018-present Executive Board Member, Human Genome Organization, US.
 2017-present EMBO Associate Member, DE.
 2016-present Steering Committee Member, Genome technology “Committee 164” of the Japan Society for the Promotion of Science (JSPS), JP.
 2011-present Member of the Genetics Society of Japan, JP.
 2013-2018 Director of the Japan Association for Omics-based Medicine, JP.

- **MAJOR COLLABORATIONS**

Scientific Coordinator/Organiser of the [FANTOM](#) (Functional ANnotation Of the Mammalian genome) worldwide consortium with over 70 scientific groups. Organising Committee of the [Human Cell Atlas](#), a global partnership to create an exhaustive guidebook of the types and properties of all human cells.

Ten years track-record

Piero Carninci has published over **420 original papers** in peer-reviewed journals with **105K+ citations** in Google Scholar. H-index: **Scopus =99, Google Scholar=119.**

10 Selected publications as corresponding author

1. Pascarella G, Hon CC, Hashimoto K, Busch A, Luginbühl J, Parr C, Hin Yip W, Abe K, Kratz A, Bonetti A, Agostini F, Severin J, Murayama S, Suzuki Y, Gustinich S, Frith M, **Carninci P***. Recombination of repeat elements generates somatic complexity in human genomes. *Cell*. 2022 Aug 4;185(16):3025-3040.e6. doi: 10.1016/j.cell.2022.06.032. Epub 2022 Jul 25. PMID: 35882231.
2. Gimenez J, Guler R, Handoko L, Harshbarger J, Hasegawa A, Hasegawa Y, Hashimoto K, Hayatsu N, Heutink P, Hirose T, Imada EL, Itoh M, Kaczkowski B, Kanhere A, Kawabata E, Kawaji H, Kawashima T, Kelly ST, Kojima M, Kondo N, Koseki H, Kouno T, Kratz A, Kurowska-Stolarska M, Kwon ATJ, Leek J, Lennartsson A, Lizio M, López-Redondo F, Luginbühl J, Maeda S, Makeev VJ, Marchionni L, Medvedeva YA, Minoda A, Müller F, Muñoz-Aguirre M, Murata M, Nishiyori H, Nitta KR, Noguchi S, Noro Y, Nurtdinov R, Okazaki Y, Orlando V, Paquette D, Parr CJC, Rackham OJL, Rizzu P, Sánchez Martínez DF, Sandelin A, Sanjana P, Semple CAM, Shibayama Y, Sivaraman DM, Suzuki T, Szumowski SC, Tagami M, Taylor MS, Terao C, Thodberg M, Thongjuea S, Tripathi V, Ulitsky I, Verardo R, Vorontsov IE, Yamamoto C, Young RS, Baillie JK, Forrest ARR, Guigó R, Hoffman MM, Hon CC, Kasukawa T, Kauppinen S, Kere J, Lenhard B, Schneider C, Suzuki H, Yagi K, de Hoon MJL, Shin JW, **Carninci P***. Functional annotation of human long noncoding RNAs via molecular phenotyping. *Genome Res*. 2020 Jul;30(7):1060-1072. doi: 10.1101/gr.254219.119. Epub 2020 Jul 27. PMID: 32718982; PMCID: PMC7397864.
3. Bonetti A, Agostini F, Suzuki AM, Hashimoto K, Pascarella G, Gimenez J, Roos L, Nash AJ, Ghilotti M, Cameron CJF, Valentine M, Medvedeva YA, Noguchi S, Agirre E, Kashi K, Samudyata, Luginbühl J, Cazzoli R, Agrawal S, Luscombe NM, Blanchette M, Kasukawa T, Hoon M, Arner E, Lenhard B, Plessy C, Castelo-Branco G, Orlando V, **Carninci P***. RADICL-seq identifies general and cell type-specific principles of genome-wide RNA-chromatin interactions. *Nat Commun*. 2020 Feb 24;11(1):1018. doi: 10.1038/s41467-020-14337-6. PMID: 32094342; PMCID: PMC7039879.
4. Hashimoto K, Kouno T, Ikawa T, Hayatsu N, Miyajima Y, Yabukami H, Terooatea T, Sasaki T, Suzuki T, Valentine M, Pascarella G, Okazaki Y, Suzuki H, Shin JW, Minoda A, Taniuchi I, Okano H, Arai Y, Hirose N, **Carninci P***. Single-cell transcriptomics reveals expansion of cytotoxic CD4 T cells in supercentenarians. *Proc Natl Acad Sci USA*. 2019 Nov 26;116(48):24242-24251. doi: 10.1073/pnas.1907883116. Epub 2019 Nov 12. PMID: 31719197; PMCID: PMC6883788.
5. Hashimoto K, Suzuki AM, Dos Santos A, Desterke C, Collino A, Ghisletti S, Braun E, Bonetti A, Fort A, Qin XY, Radaelli E, Kaczkowski B, Forrest AR, Kojima S, Samuel D, Natoli G, Buendia MA, Faivre J, **Carninci P***. CAGE profiling of ncRNAs in hepatocellular carcinoma reveals widespread activation of retroviral LTR promoters in virus-induced tumors. *Genome Res*. 2015 Dec;25(12):1812-24. doi: 10.1101/gr.191031.115. Epub 2015 Oct 28. PMID: 26510915; PMCID: PMC4665003.
6. Arner E, Daub CO, Vitting-Seerup K, Andersson R, Lilje B, Drabløs F, Lennartsson A, Rønnerblad M, Hrydziuszko O, Vitezic M, Freeman TC, Alhendi AM, Arner P, Axton R, Baillie JK, Beckhouse A, Bodega B, Briggs J, Brombacher F, Davis M, Detmar M, Ehrlund A, Endoh M, Eslami A, Fagiolini M, Fairbairn L, Faulkner GJ, Ferrai C, Fisher ME, Forrester L, Goldowitz D, Guler R, Ha T, Hara M, Herlyn M, Ikawa T, Kai C, Kawamoto H, Khachigian LM, Klinken SP, Kojima S, Koseki H, Klein S, Mejhert N, Miyaguchi K, Mizuno Y, Morimoto M, Morris KJ, Mummery C, Nakachi Y, Ogishima S, Okada-Hatakeyama M, Okazaki Y, Orlando V, Ovchinnikov D, Passier R, Patrikakis M, Pombo A, Qin XY, Roy S, Sato H, Savvi S, Saxena A, Schwegmann A, Sugiyama D, Swoboda R, Tanaka H, Tomoiu A, Winteringham LN, Wolvetang E, Yanagi-Mizuochi C, Yoneda M, Zabierowski S, Zhang P, Abugessaisa I, Bertin N, Diehl AD, Fukuda S, Furuno M, Harshbarger J, Hasegawa A, Hori F, Ishikawa-Kato S, Ishizu Y, Itoh M, Kawashima T, Kojima M, Kondo N, Lizio M, Meehan TF, Mungall CJ, Murata M, Nishiyori-Sueki H, Sahin S, Nagao-Sato S, Severin J, de Hoon MJ, Kawai J, Kasukawa T, Lassmann T, Suzuki H, Kawaji H, Summers KM, Wells C; FANTOM Consortium, Hume DA, Forrest AR, Sandelin A, **Carninci P***, Hayashizaki Y. Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. *Science*. 2015 Feb 27;347(6225):1010-4. doi: 10.1126/science.1259418. Epub 2015 Feb 12. PMID: 25678556; PMCID: PMC4681433.
7. FANTOM Consortium and the RIKEN PMI and CLST (DGT), Forrest AR, Kawaji H, et al. (**Carninci P***260th of 261 authors) A promoter-level mammalian expression atlas. *Nature*. 2014;507(7493):462-470. doi:10.1038/nature13182. PMID: 24670764; PMCID: PMC4529748.
8. Andersson R, Gebhard C, Miguel-Escalada I, Hoof I, Bornholdt J, Boyd M, Chen Y, Zhao X, Schmidl C, Suzuki T, Ntini E, Arner E, Valen E, Li K, Schwarzfischer L, Glatz D, Raitel J, Lilje B, Rapin N, Bagger

- FO, Jørgensen M, Andersen PR, Bertin N, Rackham O, Burroughs AM, Baillie JK, Ishizu Y, Shimizu Y, Furuhata E, Maeda S, Negishi Y, Mungall CJ, Meehan TF, Lassmann T, Itoh M, Kawaji H, Kondo N, Kawai J, Lennartsson A, Daub CO, Heutink P, Hume DA, Jensen TH, Suzuki H, Hayashizaki Y, Müller F, Forrest ARR, **Carninci P***, Rehli M, Sandelin A. An atlas of active enhancers across human cell types and tissues. *Nature*. 2014 Mar 27;507(7493):455-461. doi: 10.1038/nature12787. PMID: 24670763; PMCID: PMC5215096.
9. Fort A, Hashimoto K, Yamada D, Salimullah M, Keya CA, Saxena A, Bonetti A, Voineagu I, Bertin N, Kratz A, Noro Y, Wong CH, de Hoon M, Andersson R, Sandelin A, Suzuki H, Wei CL, Koseki H; FANTOM Consortium, Hasegawa Y, Forrest AR, **Carninci P***. Deep transcriptome profiling of mammalian stem cells supports a regulatory role for retrotransposons in pluripotency maintenance. *Nat Genet*. 2014 Jun;46(6):558-66. doi: 10.1038/ng.2965. Epub 2014 Apr 28. PMID: 24777452.
10. Haberle V, Li N, Hadzhiev Y, Plessy C, Previti C, Nepal C, Gehrig J, Dong X, Akalin A, Suzuki AM, van IJcken WFJ, Armant O, Ferg M, Strähle U, **Carninci P***, Müller F, Lenhard B. Two independent transcription initiation codes overlap on vertebrate core promoters. *Nature*. 2014 Mar 20;507(7492):381-385. doi: 10.1038/nature12974. Epub 2014 Feb 16. PMID: 24531765; PMCID: PMC4820030.

Articles and Book Chapters

Book Chapter: Bonetti A, Kwon AT, Arner E, **Carninci P**. Analysis of Enhancer-Promoter Interactions using CAGE and RADICL-Seq Technologies. *Methods Mol Biol*. 2021;2351:201-210. doi: 10.1007/978-1-0716-1597-3_11. PMID: 34382191.

Book Chapter: Takahashi H, Nishiyori-Sueki H, Ramilowski JA, Itoh M, **Carninci P**. Low Quantity Single Strand CAGE (LQ-ssCAGE) Maps Regulatory Enhancers and Promoters. *Methods Mol Biol*. 2021;2351:67-90. doi: 10.1007/978-1-0716-1597-3_4. PMID: 34382184. *News & Views*: Hon CC, **Carninci P**. Expanded ENCODE delivers invaluable genomic encyclopedia. *Nature*. 2020 Jul;583(7818):685-686. doi: 10.1038/d41586-020-02139-1. PMID: 32728235. *News & Views*: **Carninci P**. Genomics: mice in the ENCODE spotlight. *Nature*. 2014 Nov 20;515(7527):346-7. doi: 10.1038/515346a. PMID: 25409821.

Granted patents

Inventor in **59 patents/applications**, including *Structural Domains of Antisense RNA Molecules Up-Regulating Translation* (WO2019150346A1), *Biomarker for cancer and use thereof* (WO2017047102A1), *Functional nucleic acid molecule and use thereof* (WO2012133947A1).

Organisation of international conferences

2017-2019 Chair of organising committee of the **12th & 13th International Workshop on Advanced Genomics**, 500 participants, JP.

2015-2017 Chair of organising committee of the **International Mouse Genome Conference**, 350 participants, JP.

Prizes

2016 Shimadzu Prize for the development of cap-trapper and CAGE and the contribution to understand genome function and regulation, JP.

Leadership in industrial innovation

2018- **Co-founder** of TransSINE Therapeutics, UK. Developing SINEPS, antisense RNA that specifically enhance protein translation, as therapeutics. Seed funding with £13.7M completed in 2022. Role in the **Board**.

2011-2020 **Co-founder** and **Director** of TransSINE Technologies Ltd., a RIKEN Venture, to develop SINEUPs non-coding RNAs, a class of antisense RNAs that specifically enhance protein translation. Activity moved in UK by selling assets and IP to TransSINE Therapeutics, an RNA therapeutics company, Cambridge, UK.

2013 **Scientific Advisory Board** of K.K. DNAform, JP.