Allegato 3

Pubblicazioni Human Technopole 2024-2025

2024

Elenco delle pubblicazioni con affiliazione Human Technopole pubblicate nel 2024. I nomi degli autori con affiliazione Human Technopole sono in grassetto. L'asterisco indica gli studi che sono stati evidenziati con la copertina di un giornale.

Titolo	Autori	Giornale
Emerging methods and applications in 3D genomics	**S. Pedrotti**, **I. Castiglioni**, C. Perez-Estrada, L. Zhao, J. P. Chen, **N. Crosetto**, **M. Bienko**	Current Opinion in Cell Biology
Deconwolf enables high-performance deconvolution of widefield fluorescence microscopy images	E. Wernersson, E. Gelali, G. Girelli, S. Wang, ..., **N. Crosetto**, **M. Bienko**	Nature Methods
scCircle-seq unveils the diversity and complexity of extrachromosomal circular DNAs in single cells	J. P. Chen, C. Diekmann, H. Wu, C. Chen, **G. Della Chiara**, …, **M. Virdi**, …, **M. Bienko**, **N. Crosetto**	Nature Communications
High-quality peptide evidence for annotating non-canonical open reading frames as human proteins	E. W. Deutsch, L. W. Kok , J. M. Mudge, J. Ruiz-Orera, I. Fierro-Monti, Z. Sun, ..., **L. Calviello**, et al.	bioRxiv
A ubiquitous GC content signature underlies multimodal mRNA regulation by DDX3X	Z. Jowhar, A. Xu, S. Venkataramanan, **F. Dossena**, M. L. Hoye, D. L. Silver, S. N. Floor, **L. Calviello**	EMBO Molecular Systems Biology
Drosophila Piwi distinguishes transposons from mRNAs by piRNA complementarity and abundance	M. Ariura, T. Solberg, H. Ishizu, H. Takahashi, **P. Carninci**, H. Siomi, Y. W. Iwasaki	Cell Reports
RADIP technology comprehensively identifies H3K27me3-associated RNA-chromatin interactions	X. Shu, M. Kato, S. Takizawa, Y. Suzuki, **P. Carninci**	Nucleic Acid Research
The commitment of the human cell atlas to humanity	I. Amit, K. Ardlie, F. Arzuaga, G. Awandare, G. Bader, A. Bernier, **P. Carninci**, et al.	Nature Communications
Widespread 3'UTR capped RNAs derive from G-rich regions in proximity to AGO2 binding sites	N. Haberman, H. Digby, R. Faraway, R. Cheung, A. M. Chakrabarti, A. M. Jobbins, C. Parr, K. Yasuzawa, T. Kasukawa, C. W. Yip, M. Kato, H. Takahashi, **P. Carninci,** et al.	BMC Biology
Biallelic GGGCC repeat expansion leading to NAXE-related mitochondrial encephalopathy	K. Ozaki, Y. Yatsuka, Y. Oyazato, A. Nishiyama, K. R. Nitta, ..., **P. Carninci**, et al.	NPJ Genomic Medicine
Compared to other NHEJ factors, DNA-PK protein and RNA levels are markedly increased in all higher primates, but not in prosimians or other mammals	G. Pascarella, K. N. Conner, N. J. Goff, **P. Carninci**, A. J. Olive, K. Meek	DNA Repair
An atlas of transcribed enhancers across helper T cell diversity for decoding human diseases	A. Oguchi, A. Suzuki, S. Komatsu, H. Yoshitomi, S. Bhagat, …, **P. Carninci**, et al.	Science
Systematic assessment of long-read RNA-seq methods for transcript identification and quantification	F. J. Pardo-Palacios, D. Wang, F. Reese, M. Diekhans, S. Carbonell-Sala, …, **P. Carninci**, et al.	Nature Methods

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CapTrap-seq: a platform-agnostic and quantitative approach for high-fidelity full-length RNA sequencing	S. Carbonell-Sala, T. Perteghella, J. Lagarde, H. Nishiyori, E. Palumbo, C. Arnan, H. Takahashi, **P. Carninci**, B. Uszczynska-Ratajczak, R. Guigó	Nature Communications
Annotation of nuclear lncRNAs based on chromatin interactions	S. Agrawal, A. Buyan, J. Severin, M. Koido, T. Alam, …, **P. Carninci**, Mi. J. L. de Hoon	PLoS One
Decryption of sequence, structure, and functional features of SINE repeat elements in SINEUP non-coding RNA-mediated post-transcriptional gene regulation	H. Sharma, M. N. Z. Valentine, N. Toki, H. Nishiyori Sueki, S. Gustincich, H. Takahashi, **P. Carninci**	Nature Communications
CFC-seq: identification of full-length capped RNAs unveil enhancer-derived transcription	C. W. Yip, C. Parr, H. Takahashi, K. Yasuzawa, M. Valentine,…**R. Albanese**, **F. Dossena**, …L. Calviello, M. Bienko, I. Legnini, …, **P. Carninci**	bioRxiv
Challenges in Detecting Somatic Recombination of Repeat Elements: Insights from Short and Long Read Datasets	G. Pascarella, M. Frith, **P. Carninci**	bioRxiv
Single-cell analysis of human diversity in circulating immune cells	K. H. Kock, L. M. Tan, K. Y. Han, Y. Ando, …, **P. Carninci**, et al.	bioRxiv
Integrative Transcriptomics Reveals Layer 1 Astrocytes Altered in Schizophrenia	J. Leon, S. Yoshinaga, Mi. Hino, A. Nagaoka, Y. Ando, …, **P. Carninci**, et al.	bioRxiv
Self-supervised learning for characterising histomorphological diversity and spatial RNA expression prediction across 23 human tissue types	**F. Cisternino**, **S. Ometto**, **S. Chatterjee**, **E. Giacopuzzi**, A. P. Levine, **C. A. Glastonbury**	Nature Communications
Unsupervised cardiac MRI phenotyping with 3D diffusion autoencoders reveals novel genetic insights	**S. Ometto**, **S. Chatterjee**, A. M. Vergani, **A. Landini**, **S. Sharapov**, **E. Giacopuzzi, A. Visconti**, **E. Bianchi**, **F. Santonastaso**, **E. M. Soda**, **F. Cisternino**, **F. Ieva**, **E. Di Angelantonio**, **N. Pirastu**, and **C. A. Glastonbury**	medRxiv
Mutant huntingtin impairs neurodevelopment in human brain organoids through CHCHD2-mediated neurometabolic failure	P. Lisowski, S. Lickfett, A. Rybak-Wolf, C. Menacho, …, **I. Legnini**, et al.	Nature Communications
Recurrent evolution and selection shape structural diversity at the amylase locus	**D. Bolognini**, A. Halgren, R. N. Lou , **A. Raveane**, J. L. Rocha, A. Guarracino, **N. Soranzo**, C. Chin, E. Garrison, P. H. Sudmant	Nature
Inherited polygenic effects on common hematological traits influence clonal selection on JAK2V617F and the development of myeloproliferative neoplasms	J. Guo, K. Walter, P. M. Quiros, M. Gu, E. J. Baxter, J. Danesh, **E. Di Angelantonio**, …, **N. Soranzo**	Nature Genetics
Building pangenome graphs	E. Garrison, **A. Guarracino**, S. Heumos, F. Villani, Z. Bao, L. Tattini, …, **N. Soranzo**, V. Colonna, R. W. Williams, P. Prins	Nature Methods

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Misexpression of inactive genes in whole blood is associated with nearby rare structural variants	T. Vanderstichele, K. L. Burnham, N. de Klein, **M. Tardaguila**, …, **E. Di Angelantonio**, …, **N. Soranzo**, L. Parts, M. Inouye, D. S. Paul, E. E. Davenport	AJHG
CDK12 controls transcription at damaged genes and prevents MYC-induced transcription-replication conflicts	L. Curti, S. Rohban, N. Bianchi, O. Croci, A. Andronache, …, **N. Crosetto**, M. Wade, D. Parazzoli, S. Campaner	Nature Communications
High clonal diversity and spatial genetic admixture in early prostate cancer and surrounding normal tissue	N. Zhang, L. Harbers, M. Simonetti, C. Diekmann, …, **M. Bienko**, **N. Crosetto**	Nature Communications
X-chromosome and kidney function: evidence from a multi-trait genetic analysis of 908,697 individuals reveals sex-specific and sex-differential findings in genes regulated by androgen response elements	M. Scholz, K. Horn, J. Pott, M. Wuttke, …, **N. Pirastu**, et al.	Nature Communications
Opportunities and tradeoffs in single-cell transcriptomic technologies	**M. I. Conte**, **A. Fuentes-Trillo**, **C. Domínguez Conde**	Trends in Genetics
Novel Endogenous Engineering Platform for Robust Loading and Delivery of Functional mRNA by Extracellular Vesicles	A. M. Zickler, X. Liang, D. Gupta, D. R. Mamand, **M. De Luca**, et al.	Advanced Science
MedShapeNet - a large-scale dataset of 3D medical shapes for computer vision	J. Li , Z. Zhou, J. Yang, A. Pepe, C. Gsaxner, …., **S. Chatterjee**, et al.	Biomedical Engineering / Biomedizinische Technik
Beyond Nyquist: A Comparative Analysis of 3D Deep Learning Models Enhancing MRI Resolution	**S. Chatterjee**, A. Sciarra, M. Dünnwald, A. Bhat Talagini Ashoka, et al.	Journal of imaging
VesselBoost: A Python Toolbox for Small Blood Vessel Segmentation in Human Magnetic Resonance Angiography Data	M. Xu, F. L. Ribeiro, M. Barth, M. Bernier, S. Bollmann, **S. Chatterjee**, et al.	bioRxiv
HSP and CD279 gene expression as candidate biomarkers in symptomatic LGLL patients	G. Talarico, A. Franceschin, **A. Raveane**, P. Falvo, S. Mazzara, F. Melle, G. Motta, S. Orecchioni, A. Tenore, G. Gregato, C. Poletti, R. Chiarle, S. Pileri, P.Mancuso, F. Bertolini	Discover Oncology
Clinical and genetic characterization of a progressive RBL2-associated neurodevelopmental disorder	G. N. Aughey, E. Cali, R. Maroofian, M. S. Zaki, A. T. Pagnamenta, …, **E. Giacopuzzi**, et al.	Brain
Bi-allelic genetic variants in the translational GTPases GTPBP1 and GTPBP2 cause a distinct identical neurodevelopmental syndrome	V. Salpietro, R. Maroofian, M. S. Zaki, J. Wangen, A. Ciolfi, …, **E. Giacopuzzi**, …, **A. T. Pagnamenta**, et al.	AJHG
Phage-resistance alters Lipid A reactogenicity: a new strategy for LPS-based conjugate vaccines against Salmonella Rissen	P. Cuomo, **C. Medaglia**, A. Casillo, A. Gentile, C. Fruggiero, M. M. Corsaro, R. Capparelli	Frontiers in Immunology

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Impact of radiotherapy dose, fractionation and immunotherapeutic partner in a mouse model of HR+ mammary carcinogenesis	A. Buqué, N. Bloy, G. Petroni, C. Jiménez-Cortegana, A.Sato, C. Iribarren, T. Yamazaki, C. Galassi, M. Hensler, B. Bhinder, **A. Guarracino**, et al.	Journal of the National Cancer Institute
High-coverage nanopore sequencing of samples from the 1000 Genomes Project to build a comprehensive catalog of human genetic variation	J. A. Gustafson, S. B. Gibson, N. Damaraju, M. P.G. Zalusky, K. Hoekzema, ..., **A. Guarracino**, et al.	Genome Research
Cluster-efficient pangenome graph construction with nf-core/pangenome	S. Heumos, M.L. Heuer, F. Hanssen, L. Heumos, **A. Guarracino**, P. Heringer, P. Ehmele, P. Prins, E. Garrison, S. Nahnsen	Bioinformatics
Pangenome graph layout by Path-Guided Stochastic Gradient Descent	S. Heumos, **A. Guarracino**, J. M. Schmelzle, J. Li, Z. Zhang, J. Hagmann, S. Nahnsen, P. Prins, E. Garrison	Bioinformatics
A proinflammatory stem cell niche drives myelofibrosis through a targetable galectin-1 axis	R. Li , **M. Colombo**, G. Wang, A. Rodriguez-Romera, C. Benlabiod	Science Translational Medicine
Single-cell multiregion dissection of Alzheimer's disease	H. Mathys, C. A. Boix, L. A. Akay, Z. Xia, **J. Davila-Velderrain**, et al.	Nature
Single-cell multi-cohort dissection of the schizophrenia transcriptome	W. B. Ruzicka, S. Mohammadi, J. F Fullard, **J. Davila-Velderrain**, …, P. Roussos, M. Kellis; PsychENCODE Consortium	Science
WWOX deficiency impairs neurogenesis and neuronal function in human organoids	D. Steinberg, **A. Zonca**, I.Rosh, I. Kustanovich, K. Maroun, S. Stern, **J. Davila-Velderrain**, R. Aqeilan	bioRxiv
SARS-CoV-2 brainstem encephalitis in human inherited DBR1 deficiency	Y. Chan, V. Lundberg, J. Le Pen, J. Yuan, D. Lee, **F. Pinci**, …, **O. Harschnitz**, C. M. Rice, L. Studer, J. Casanova, O. Ekwall, S. Zhang	Journal of Experimental Medicine
Human TMEFF1 is a restriction factor for herpes simplex virus in the brain	Y. Chan, Z. Liu, P. Bastard, N. Khobrekar, K. M. Hutchison, Y. Yamazaki, Q. Fan, D. Matuozzo, **O. Harschnitz**, et al.	Nature
SARS-CoV-2 infection causes dopaminergic neuron senescence	L. Yang, T. W. Kim, Y. Han, M. S. Nair, **O. Harschnitz**, J. Zhu, et al.	Cell Stem Cell
Morphoregulatory ADD3 underlies glioblastoma growth and formation of tumor-tumor connections	**C. Barelli**, **F. K. Don**, **R. M. Iannuzzi**, **S. Faletti**, **I. Bertani**, **I. Osei**, S. Sorrentino, **G. Villa**, **V. Sokolova**, **A. Campione**, M. R. Minotti, G. M. Sicuri, R. Stefini, **F. Iorio**, **N. Kalebic**	bioRxiv
Adducins regulate morphology and fate of neural progenitors during neocortical neurogenesis	**C. Ossola**, **N. Cokorac**, **S. Faletti**, **E. Capra**, **I. Bertani**, **C. Ambrosini**, **G. Faga**, **N. Kalebic**	bioRxiv
A framework for neural organoids, assembloids and transplantation studies	S. P. Pașca, P. Arlotta, H. S. Bateup, J. G. Camp, S. Cappello, …, **G. Testa**, et al.	Nature

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A polarized FGF8 source specifies frontotemporal signatures in spatially oriented cell populations of cortical assembloids	C. Bosone, **D. Castaldi**, T. R. Burkard, S. J. Guzman, T. Wyatt, **C. Cheroni**, N. Caporale, S. Bajaj, J. A. Bagley, C. Li, B. Sorre, **C. E. Villa**, **G. Testa**, V. Krenn, J. A. Knoblich	Nature Methods
A multi-layered integrative analysis reveals a cholesterol metabolic program in outer radial glia with implications for human brain evolution	J. Moriano, O. Leonardi, **A. Vitriolo**, **G. Testa**, C. Boeckx	Development
Engineering Toxoplasma gondii secretion systems for intracellular delivery of multiple large therapeutic proteins to neurons	S. Bracha, H. J. Johnson, N. A. Pranckevicius, F. Catto, ..., **M. T. Rigoli**, **C. Cheroni**, **M. Bonfanti**, **A. Valenti**, **S. Stucchi**, ..., **N. Caporale**, G. Testa, A. Aguzzi, A. A. Koshy, L. Sheiner, Oded Rechavi	Nature Microbiology
miRNA-mediated inhibition of an actomyosin network in hippocampal pyramidal neurons restricts sociability in adult male mice	R. Narayanan, B. Rocha Levone, J. Winterer, P. Nanda, A. Müller, T. Lobriglio, R. Fiore, P. Germain, **M. Mihailovich**, **G. Testa**, G. Schratt	Cell Reports
Multiscale modeling uncovers 7q11.23 copy number variation-dependent changes in ribosomal biogenesis and neuronal maturation and excitability	**M. Mihailovich**, P. Germain, **R. Shyti**, D. Pozzi, R. Noberini, Y. Liu, **D. Aprile**, E. Tenderini, **F. Troglio**, **S. Trattaro**, S. Fabris, U. Ciptasari, **M. T. Rigoli**, **N. Caporale**, G. D'Agostino, **F. Mirabella**, **A. Vitriolo**, **D. Capocefalo**, **A. Skaros**, A. V. Franchini, S. Ricciardi, I. Biunno, A. Neri, N. N. Kasri, T. Bonaldi, R. Aebersold, M. Matteoli, **G. Testa**	Journal of Clinical Investigation
Tracing the invisible mutant ADNP protein in Helsmoortel-Van der Aa syndrome patients	C. P. D'Incal, E. Cappuyns, K. Choukri, K. De Man, K. Szrama, …, **A. Vitriolo**, **G. Testa**, et al.	Scientific Reports
In and out: Benchmarking in vitro, in vivo, ex vivo, and xenografting approaches for an integrative brain disease modeling pipeline	M. F. Pereira, R. Shyti, **G. Testa**	Stem Cell Reports
YY1 mutations disrupt corticogenesis through a cell-type specific rewiring of cell-autonomous and non-cell-autonomous transcriptional programs	**M. F. Pereira**, **V. Finazzi**, **L. Rizzuti**, **D. Aprile**, **V. Aiello**, L. Mollica, M. Riva, C. Soriani, **F. Dossena**, **R. Shyti**, **D. Castaldi**, E. Tenderini, M. T. Carminho-Rodrigues, J. F. Bally, B. B. A. de Vries, M. Gabriele, **A. Vitriolo**, **G. Testa**	bioRxiv
Curation of causal interactions mediated by genes associated with autism accelerates the understanding of gene-phenotype relationships underlying neurodevelopmental disorders	M. Iannuccelli, **A. Vitriolo**, **L. Licata**, **P. Lo Surdo**, S. Contino, **C. Cheroni**, **D. Capocefalo**, L. Castagnoli, **G. Testa**, G. Cesareni, **L. Perfetto**	Molecular Psychiatry
An integrated transcriptomic cell atlas of human neural organoids	Z. He, L. Dony, J. S. Fleck, A.r Szałata, K. X. Li, I. Slišković, H. Lin, Ma.Santel, A. Atamian, G. Quadrato, J. Sun, S. P. Pașca, **Human Cell Atlas Organoid Biological Network***, J. Gray Camp, F. J. Theis, B. Treutlein	Nature

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Different Names for the Same Thing? Novelty, Expectations, and Performative Nominalism in Personalized and Precision Medicine	I. Galasso, S. Erikainen, M. Pickersgill and **G. Testa**	Social Theory and Health
TBC1D24 interacts with the v-ATPase and regulates intraorganellar pH in neurons	S. Pepe, **D. Aprile**, E. Castroflorio, A. Marte, S. Giubbolini, S. Hopestone, A. Parsons , T. Soares, F. Benfenati, P. L. Oliver, A. Fassio	iScience
Tumor microenvironment-induced FOXM1 regulates ovarian cancer stemness	C. Battistini, H. A. Kenny, M. Zambuto, V. Nieddu, V. Melocchi, A. Decio, P. Lo Riso, **C. E. Villa**, et al.	Cell Death & Disease
Genetic barriers more than environmental associations explain Serratia marcescens population structure	L. Sterzi, R. Nodari, F. Di Marco, M. L. Ferrando, F. Saluzzo, **A. Spitaleri**, et al.	Communications Biology
The Microbiome-Genetics Axis in Autism Spectrum Disorders: A Probiotic Perspective	**M. Mihailovich**, M. Tolinački, S. Soković Bajić, S. Lestarevic, M. Pejovic-Milovancevic, N. Golić	International Jpurnal of Molecular Sciences
Cutting-Edge iPSC-Based Approaches in Studying Host-Microbe Interactions in Neuropsychiatric Disorders	**M. Mihailovich**, S. Soković Bajić, M. Dinić, J. Đokić, M. Živković, D. Radojević, N. Golić	International Journal of Molecular Sciences
Cryo-EM structure of bacterial nitrilase reveals insight into oligomerization, substrate recognition, and catalysis	S. Aguirre-Sampieri, **A. Casañal**, P. Emsley, G. Garza-Ramos	Journal of Structural Biology
Molecular mechanism of thyroxine transport by monocarboxylate transporters	**M. Tassinari**, **G. Tanzi**, **F. Maggiore**, S. Groeneweg, F. S. van Geest, M. Freund, C. J. Stavast, I. Boniardi, **S. Pasqualato**, W. E. Visser, **F. Coscia**	bioRxiv
TOMOMAN: a software package for large-scale cryo-electron tomography data preprocessing, community data sharing and collaborative computing	S. Khavnekar, **P. S. Erdmann**, W. Wan	Journal of Applied Cristallography
Serialized on-grid lift-in sectioning for tomography (SOLIST) enables a biopsy at the nanoscale	**H. T. D. Nguyen**, **G. Perone**, **N. Klena**, **R. Vazzana**, **F. K. Don**, **M. Silva**, **S. Sorrentino**, **P. Swuec**, F. Leroux, **N. Kalebic**, **F. Coscia**, **P. S. Erdmann**	Nature Methods
The intraflagellar transport cycle	**S. E. Lacey**, **G. Pigino**	Nature Reviews Molecular Cell Biology
Structure, interaction and nervous connectivity of beta cell primary cilia	A. Müller, **N. Klena**, S. Pang, L. E. Galicia Garcia, …, **G. Pigino**, M. Solimena	Nature Communications
Protofilament-specific nanopatterns of tubulin post-translational modifications regulate the mechanics of ciliary beating	**G. Alvarez Viar**, **N. Klena**, **F. Martino**, A. P. Nievergelt, **D. Bolognini**, **P. Capasso**, **G. Pigino**	Current Biology

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Extensive structural rearrangement of intraflagellar transport trains underpins bidirectional cargo transport	**S. E. Lacey**, **A. Graziadei**, **G. Pigino**	Cell
Tubulin posttranslational modifications through the lens of new technologies	**G. Alvarez Viar, G. Pigino**	Current Opinion in Cell Biology
Protocol for precision editing of endogenous Chlamydomonas reinhardtii genes with CRISPR-Cas	**A. P. Nievergelt**, D. R. Diener, A. Bogdanova, T. Brown, **G. Pigino**	STAR Protocol
Condensin II activation by M18BP1	A. Borsellini, D. Conti, E. Cutts, R. J. Harris, K. Walstein, **A. Graziadei**, **V. Cecatiello**, …, **A. Vannini**	bioRxiv
Structural insights into distinct mechanisms of RNA polymerase II and III recruitment to snRNA promoters	**S. Zawar Shah**, **T. N. Perry**, **A. Graziadei**, **V. Cecatiello**,T. Kaliyappan, A. D. Misiaszek, C. W. Müller,E. P. Ramsay, **A. Vannini**	bioRxiv
A substrate-interacting region of Parkin directs ubiquitination of the mitochondrial GTPase Miro1	J. Koszela, A. Rintala-Dempsey, **G. Salzano**, V. Pimenta, O. Kamarainen, M. Gabrielsen, A. L. Parui, G. S. Shaw, H. Walden	bioRxiv
System-wide analysis of RNA and protein subcellular localization dynamics	E. Villanueva, T. Smith, **M. Pizzinga**, M. Elzek, R. M. L Queiroz	Nature Methods
Benchmark Software and Data for Evaluating CRISPR-Cas9 Experimental Pipelines Through the Assessment of a Calibration Screen	**R. M. Iannuzzi**, I. Manipur, C. Pacini, F. M. Behan, M. R. Guarracino, M. J. Garnett, **A. Savino**, **F. Iorio**	The CRISPR Journal
Integrative ensemble modelling of cetuximab sensitivity in colorectal cancer patient-derived xenografts	**U. Perron**, E. Grassi, A. Chatzipli, M. Viviani, E. Karakoc, **L. Trastulla**, **L. M. Brochier**, …, **F. Iorio**	Nature Communications
An unbiased lncRNA dropout CRISPR-Cas9 screen reveals RP11-350G8.5 as a novel therapeutic target for multiple myeloma	K. Grillone, S. Ascrizzi, **P. Cremaschi**, J. Amato, N. Polerà, O. Croci, R. Rocca, C. Riillo, F. Conforti, R. Graziano, D. Brancaccio, D. Caracciolo, S. Alcaro, B. Pagano, A. Randazzo, P. Tagliaferri, **F. Iorio**, P. Tassone	Blood*
A benchmark of computational methods for correcting biases of established and unknown origin in CRISPR-Cas9 screening data	**A. Vinceti**, **R. M. Iannuzzi**, I. Boyle, **L. Trastulla**, C. D. Campbell, F. Vazquez, J. M. Dempster, **F. Iorio**	Genome Biology
Distinct genetic liability profiles define clinically relevant patient strata across common diseases	**L. Trastulla**, G. Dolgalev, S. Moser, L. T. Jiménez-Barrón, …, **F. Iorio**, B. Müller-Myhsok, H. Schunkert, M. J. Ziller	Nature Communications
A comprehensive clinically informed map of dependencies in cancer cells and framework for target prioritization	C. Pacini, E. Duncan, E. Gonçalves, J. Gilbert, S. Bhosle, …, **F. Iorio**, M. J. Garnett	Cancer Cell
The crucial role of bioimage analysts in scientific research and publication	B. A. Cimini, P. Bankhead, R. D'Antuono, E. Fazeli, J. Fernandez-Rodriguez, …, **F. Jug**, et al.	Journal of Cell Science
Mechanical and biochemical feedback combine to generate complex contractile oscillations in cytokinesis	M. E. Werner, D. D. Ray, C. Breen, M. F. Staddon, **F. Jug**, S. Banerjee, A. Shaub Maddox	Current Biology

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Live-cell imaging powered by computation	H. Shroff, I. Testa, **F. Jug**, S. Manley	Nature Reviews Molecular Cell Biology
Bioprinting Soft 3D Models of Hematopoiesis using Natural Silk Fibroin-Based Bioink Efficiently Supports Platelet Differentiation	C. A. Di Buduo, M. Lunghi, V. Kuzmenko, P Laurent, G. Della Rosa, C. Del Fante, **D. E. Dalle Nogare**, **F. Jug**, et al.	Advanced Science
MicroSSIM: Improved Structural Similarity for Comparing Microscopy Data	**Ashesh, J. Deschamps, F. Jug**	ECV 2024 Workshops
denoiSplit: A Method for Joint Microscopy Image Splitting and Unsupervised Denoising	**Ashesh, F. Jug**	ECCV 2024
Community-developed checklists for publishing images and image analyses	**C. Schmied**, M. S. Nelson, S. Avilov, G. Bakker, …, **F. Jug**, et al.	Nature Methods
Enabling Global Image Data Sharing in the Life Sciences	P. Bajcsy, S. Bhattiprolu, K. Boerner, B. A. Cimini, L. Collinson, J. Ellenberg, R. Fiolka, M. Giger, W. Goscinski, M. Hartley, N. Hotaling, R. Horwitz, **F. Jug**, et al.	arxiv
CALIPERS: Cell cycle-aware live imaging for phenotyping experiments and regeneration studies	M. Di Sante, M. Pezzotti, J. Zimmermann, A. Enrico, **J. Deschamps**, E. Balmas, S. Becca, A. Reali, A. Bertero, **F. Jug**, F. S. Pasqualini	bioRxiv
FeatureForest: the power of foundation models, the usability of random forests	M. Seifi, **D. Dalle Nogare**, **J. Battagliotti**, V. Galinova, A. K. Rao, AI4Life Horizon Europe Programme Consortium4, J. Decelle, **F. Jug**, and **J. Deschamps**	bioRxiv
Hijacking and Integration of Algal Plastids and Mitochondria in a Polar Planktonic Host	A. K. Rao, D. Yee1, F. Chevalier, C. LeKieffre, M. Pavie, Marine Olivetta, O. Dudin, B. Gallet, E. Hehenberger, **M. Seifi**, **F. Jug**, **J. Deschamps**, T. Wu, R. Gast, P. Jouneau, J. Decelle	bioRxiv
Local DNA compaction creates TF-DNA clusters that enable transcription	N. M. Chabot, R. Purkanti, A. Del Panta Ridolfi, **D. Dalle Nogare**, H. Oda, H. Kimura, **F. Jug**, A. Dal Co, Nadine L. Vastenhouw	bioRxiv
Predicting the evolution of antibiotic resistance	**F. Pinheiro**	Current Opinion in Microbiology
Resource allocation in biochemically structured metabolic networks	L. Seegera**, F. Pinheiro,** M. Lassiga	bioRxiv
Kinbiont: From time series to ecological and evolutionary responses in microbial systems	**F. Angaroni, A. Peruzzi,** E. Z. Alvarenga**,** and **F. Pinheiro**	bioRxiv
Stratified Medicine Paediatrics: Cell free DNA and serial tumour sequencing identifies subtype specific cancer evolution and epigenetic states	S. L. George, C. Lynn, R. Stankunaite, D. Hughes, C. M. Sauer, J. Chalker, …, **A. Sottoriva**, L. Chesler	Cancer Discovery
Circulating tumor DNA dynamics and clinical outcome in metastatic colorectal cancer patients undergoing front-line chemotherapy	M. Ghidini, J. C. Hahne, C. Senti, T. Heide, P. Z. Proszek, …, **A. Sottoriva**, R. Passalacqua, N. Valeri	Clinical Cancer Research

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The genomic landscape of 2,023 colorectal cancers	A. J. Cornish, A. J. Gruber, B. Kinnersley, …, **A. Sottoriva**, T. A. Graham, D. C. Wedge, R. S. Houlston	Nature
Tumor evolution metrics predict recurrence beyond 10 years in locally advanced prostate cancer	J. Fernandez-Mateos, G. D. Cresswell, N. Trahearn, …, **T. Heide**, …, **A. Sottoriva**	Nature Cancer
Homopolymer switches mediate adaptive mutability in mismatch repair-deficient colorectal cancer	H. Kayhanian, W. Cross, S. E. M. van der Horst, P. Barmpoutis, …, **A. Sottoriva**, T. A. Graham, M. Rodriguez-Justo, K. Shiu, H. J. G. Snippert, M. Jansen	Nature Genetics
Immune evasion impacts the landscape of driver genes during cancer evolution	L. Gourmet, **A. Sottoriva**, S. Walker-Samuel, M. Secrier, L. Zapata	Genome Biology
Phenotypic noise and plasticity in cancer evolution	F. J. H. Whiting, J. Househam, A. Baker, **A. Sottoriva**, T. A. Graham	Trends in Cell Biology
Long-term Multimodal Recording Reveals Epigenetic Adaptation Routes in Dormant Breast Cancer Cells	D. Rosano, E. Sofyali, H. Dhiman, C. Ghirardi, D. Ivanoiu, **T. Heide**, ..., **C. James**, ..., **A. Sottoriva**, L. Magnani	Cancer Discovery
Epigenome and early selection determine the tumour-immune evolutionary trajectory of colorectal cancer	E. Lakatos, V. Gunasri, L. Zapata, J. Househam, **T. Heide**, …, **A. Sottoriva**, T. A. Graham	bioRxiv
Cancer Evolution: A Multifaceted Affair	Ciriello G, Magnani L, Aitken SJ, Akkari L, …, **Sottoriva A,** Swarbrick A, Tonon G, Vanharanta S, Zuber J	Cancer Discovery
NeuroVelo: interpretable learning of temporal cellular dynamics from single-cell data	I. K. Boudjelthia, **S. Milite**, N. El Kazwini, Y. Huang, **A. Sottoriva**, G. Sanguinetti	Research Square
Deep Archetypal Analysis for interpretable multi-omic data integration based on biological principles	**S. Milite**, G. Caravagna, **A. Sottoriva**	bioRxiv
Long deletion signatures in repetitive genomic regions track somatic evolution and enable sensitive detection of microsatellite instability	Q. Guo, J. Househam, E.Lakatos, S. Nowinski, I. Al Bakir, …, **A. Sottoriva**, et al.	bioRxiv
Heterogeneity and evolution of DNA mutation rates in microsatellite stable colorectal cancer	E. Grassi, V. Vurchio, G. D. Cresswell, I. Catalano, …, **A. Sottoriva**, et al.	bioRxiv
Differential activity of MAPK signalling defines fibroblast subtypes in pancreatic cancer	L. Veghini, D. Pasini, R. Fang, P. Delfino, D. Filippini, C. Neander, …, **S. D'Agosto**, et al.	Nature Communications
Computational validation of clonal and subclonal copy number alterations from bulk tumor sequencing using CNAqc	A. Antonello, R. Bergamin, N. Calonaci, J. Househam, **S. Milite**, et al.	Genome Biology
Clinical application of tumour-in-normal contamination assessment from whole genome sequencing	J. Mitchell, **S. Milite**, J. Bartram, S. Walker, et al.	Nature Communications

Titolo	Autori	Giornale
Risks of major arterial and venous thrombotic diseases after hospitalisation for influenza, pneumonia, and COVID-19: A population-wide cohort in 2.6 million people in Wales	S. Keene, H. Abbasizanjani, F. Torabi, R. Knight, V. Walker, E. Raffetti, G. Cezard, S. Ip 7, A. Sampri, T. Bolton, R. Denholm, K. Khunti, A. Akbari, J. Quint, S. Denaxas, C. Sudlow**, E. Di Angelantonio**, J. A. C. Sterne, A. Wood, W. N. Whiteley; CVD-COVID-UK/COVID-IMPACT Consortium and the Longitudinal Health and Wellbeing COVID-19 National Core Study	Thrombosis Research
Leucocyte telomere length and conduction system ageing	S. van Duijvenboden, C. P. Nelson, Z. Raisi-Estabragh, J. Ramirez, M. Orini, Q. Wang, N. Aung, V. Codd, S. Stoma, E. Allara, A. M. Wood, **E. Di Angelantonio**, J. Danesh, N. C. Harvey, S. E. Petersen, P. B. Munroe, N. J. Samani	Heart
Assessing the kinetics of oxygen-unloading from red cells using FlowScore, a flow-cytometric proxy of the functional quality of blood	J. Rabcuka, P. A. Smethurst, K. Dammert, J. Saker, G. Aran, G. M. Walsh 5,..., **E. Di Angelantonio**, D. J. Roberts, S. Blonski, P. M. Korczyk, A. Shirakami, R. Cardigan, P. Swietach	eBioMedicine
Novel loci and biomedical consequences of iron homoeostasis variation	E. Allara, S. Bell, R. Smith, S. J. Keene, …, **N. Pirastu**, …, **E. Di Angelantonio**	Communications Biology
Polygenic Prediction of Recurrent Events After Early-Onset Myocardial Infarction	M. Ardissino, E. M. Paraboschi, S. A. Lambert, L. G. Kim, …, **E. Di Angelantonio**, R. Asselta, D. Ardissino, A. S. Butterworth	Circulation: Genomics and Precision Medicine
Risk factors for vasovagal reactions in blood donors: A systematic review and meta-analysis	Y. Wu, H. Qi, **E. Di Angelantonio**, S. Kaptoge, A. M. Wood, L. G. Kim	Trasfusion
Contemporary epidemiology of hospitalised heart failure with reduced versus preserved ejection fraction in England: a retrospective, cohort study of whole-population electronic health records	R. A. Fletcher, P. Rockenschaub, B. L. Neuen, I. J. Walter, N. Conrad, ..., **E. Di Angelantonio**, et al.	The Lancet Public Health
The power of arts-based film interventions to encourage Black blood donors	R. Mills, A. Okubanjo, N. Acheampong, M. Croucher, N. Eaton, A. Kazi, **E. Di Angelantonio**, A. Wood, B. Masser, E. Ferguson	Transfusion
The European Health Data Space can be a boost for research beyond borders	A. Ganna, A. Carracedo, C. F. Christiansen, **E. Di Angelantonio**, Pearl A Dykstra, A. M. Dzhambov, R. Eils, S. Green, K. L. Schneider, T. V. Varga, A. Vuorinen, L. Zuccolo, N. H. Rod, K. Hoeyer	Nature Medicine

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Association of circulating fatty acids with cardiovascular disease risk: Analysis of individual-level data in three large prospective cohorts and updated meta-analysis	F. Shi, R. Chowdhury, E. Sofianopoulou, A. Koulman, …, **E. Di Angelantonio**, et al.	European Journal of Preventive Cardiology
Integrated clinical risk prediction of type 2 diabetes with a multifactorial polygenic risk score	S. C. Ritchie, H. J. Taylor, Y. Liang, H. D. Manikpurage, …, **E. Di Angelantonio**, M. Inouye	medRxiv
Age and sex specific thresholds for risk stratification of cardiovascular disease and clinical decision making: prospective open cohort study	Z. Xu, J. Usher-Smith, L. Pennells, R. Chung, M. Arnold, L. Kim, S. Kaptoge, M. Sperrin, **E. Di Angelantonio**, A. M. Wood	BMJ Medicine
Risk estimation for the primary prevention of cardiovascular disease: considerations for appropriate risk prediction model selection	K. R. van Daalen, D. Zhang, S. Kaptoge, E. Paige, **E. Di Angelantonio**, L. Pennells	The Lancet Global Health
Genome-wide meta-analyses of restless legs syndrome yield insights into genetic architecture, disease biology and risk prediction	B. Schormair, C. Zhao, S. Bell, M. Didriksen, …, **E. Di Angelantonio**, K. Oexle, J. Winkelmann	Nature Genetics
Patent Foramen Ovale Closure in Older Patients With Stroke: Patient Selection for Trial Feasibility	A. Y. Wang, P. M. Rothwell, J. Nelson, J. L. Saver, S. E. Kasner, …, **E. Di Angelantonio**, et al.	Neurology
Genetically predicted plasma cortisol and common chronic diseases: A Mendelian randomization study	W. Lee, S. C. Larsson, A. Wood, **E. Di Angelantonio**, A. S. Butterworth, S. Burgess, E. Allara	Clinical Endocrinology
The value of genetic data from 665,460 individuals in managing iron deficiency anaemia and suitability to donate blood	J. Toivonen, E. Allara; FinnGen; J. Castrén, E. Di Angelantonio, M. Arvas	Vox Sanguinis
Cardiovascular safety of assisted reproductive technology: a meta-analysis	C. A. Pivato., A. Inversetti, G. Condorelli, A. Chieffo, P. E. Levi-Setti, A. C. Latini, A. Busnelli, M. Messa, M. Cristodoro, R. M. Bragato, M. Francone, **L. Zuccolo**, **F. Ieva**, **E. Di Angelantonio**, G. Stefanini, N. Di Simone	European Heart Journal
Estimating dose-response relationships for vitamin D with coronary heart disease, stroke, and all-cause mortality: observational and Mendelian randomisation analyses	E Sofianopoulou, S K Kaptoge, S Afzal, T Jiang, D Gill, TE Gundersen, ..., **E. Di Angelantonio**, J Danesh, AS Butterworth, S Burgess	The Lancet Diabetes & Endocrinology
Association of circulating fatty acids with cardiovascular disease risk: Analysis of individual-level data in three large prospective cohorts and updated meta-analysis	F Shi, R Chowdhury, E Sofianopoulou, A Koulman, L Sun, M Steur, K Aleksandrova, CC Dahm, MB Schulze, YT van der Schouw, C Agnoli, P Amiano, ..., **E. Di Angelantonio**, NG Forouhi, J Danesh, AS Butterworth, S Kaptoge	European Journal of Preventive Cardiology

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Misexpression of inactive genes in whole blood is associated with nearby rare structural variants	T Vanderstichele, KL Burnham, N de Klein, M Tardaguila, B Howell, K Walter, K Kundu, J Koeppel, …, **E. Di Angelantonio**, J Danesh, A Berton, A Platt, AS Butterworth, N Soranzo, L Parts, M Inouye, DS Paul, EE Davenport	Am J Hum Genet
CT-based radiogenomics of intrahepatic cholangiocarcinoma	L. Viganò, V. Zanuso, F. Fiz, L. Cerri, M. E. Laino, A. Ammirabile, E. M. Ragaini, S. Viganò, L. M. Terracciano, M. Francone, **F. Ieva**, L. Di Tommaso, L. Rimassa	Digestive and Liver Disease
Causal effect of chemotherapy received dose intensity on survival outcome: a retrospective study in osteosarcoma	M. Spreafico, **F. Ieva**, M. Fiocco	BMC Medical Research Methodology
Unveiling the biological side of PET-derived biomarkers: a simulation-based approach applied to PDAC assessment	L. Cavinato, J. Hong, M. Wartenberg, S. Reinhard, R. Seifert, P. Zunino, A. Manzoni, **F. Ieva**, A. Chiti, A. Rominger, K. Shi	European Journal of Nuclear Medicine and Molecular Imaging
Radiomics of Intrahepatic Cholangiocarcinoma and Peritumoral Tissue Predicts Postoperative Survival: Development of a CT-Based Clinical-Radiomic Model	F. Fiz, N. Rossi, S. Langella, S. Conci, M. Serenari, …, **F. Ieva**, L. Viganò	Annals of Surgical Oncology
Clinical and Genomic-Based Decision Support System to Define the Optimal Timing of Allogeneic Hematopoietic Stem-Cell Transplantation in Patients With Myelodysplastic Syndromes	C. A. Tentori, C. Gregorio, M. Robin, N. Gagelmann, C. Gurnari, …, **F. Ieva**, M. G. Della Porta; GenoMed4all and Synthema Consortiums	Journal of Clinical Oncology
Cost-effectiveness of single-pill and separate-pill administration of antihypertensive triple combination therapy: a population-based microsimulation study	G. Morabito, C. Gregorio, **F. Ieva**, G. Barbati, G. Mancia, G. Corrao, F. Rea	BMC Public Health
Flexible Approaches Based on Multistate Models and Microsimulation to Perform Real-World Cost-Effectiveness Analyses: An Application to Proprotein Convertase Subtilisin-Kexin Type 9 Inhibitors	C. Gregorio, F. Rea, **F. Ieva**, A. Scagnetto, C. Indennidate, C. Cappelletto, A. Di Lenarda, G. Barbati	Value in Health
Personalized Timing for Allogeneic Stem-Cell Transplantation in Hematologic Neoplasms: A Target Trial Emulation Approach Using Multistate Modeling and Microsimulation	C. Gregorio, M. Spreafico, S. D'Amico, E. Sauta, …, **F. Ieva**	JCO Clinical Cancer Informatics
A NLP-based semi-automatic identification system for delays in follow-up examinations: an Italian case study on clinical referrals	V. Torri, M. Ercolanoni, F. Bortolan, O. Leoni, **F. Ieva**	BMC Medical Informatics and Decision Making
Patients' Radiation Exposure During Endovascular Abdominal Aortic Aneurysm Repair	T. J. Mandigers, I. Fulgheri, G. Pugliese, D. Bissacco, **L. Savarè**, **F. Ieva**, M. Campoleoni, J. A. van Herwaarden, S. Trimarchi, M. Domanin	Annals of Vascular Surgery

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Estimation of Dynamic Origin-Destination Matrices in a Railway Transportation Network integrating Ticket Sales and Passenger Count Data	G., Galliani, P., Secchi, **F., Ieva**	Transportation Research Part A.
Longitudinal Latent Overall Toxicity (LOTox) profiles in osteosarcoma: a new taxonomy based on latent Markov models	M. Spreafico, **F., Ieva,** M., Fiocco	Statistical Methods and Applications
A Spearman dependence matrix for Multivariate Functional Data	**F., Ieva,** M., Ronzulli, J, Romo, A.M., Paganoni	Journal of Nonparametric Statistics
Inferential tools for assessing dependence across response categories in multinomial models with discrete random effects	C Masci, **F Ieva**, AM Paganoni	Journal of Classification
How much of the past matters? Using dynamic survival models for the monitoring of potassium in heart failure patients using electronic health records	C Gregorio, G Barbati, A Scagnetto, A Di Lenarda, **F Ieva**	arxiv
COVID-19 diagnosis, vaccination during pregnancy, and adverse pregnancy outcomes of 865,654 women in England and Wales: a population-based cohort study	E. Raffetti, T. Bolton, J. Nolan, **L. Zuccolo**, et al.	The Lancet Regional Health - Europe
Trends in fetal alcohol spectrum disorder research: A bibliometric review of original articles published between 2000 and 2023	C. McQuire, N. F. Frennesson, J. Parsonage, M. Van der Heiden, D. Troy, **L. Zuccolo**	Alchohol Clinical & Experimental Research
Analyzing Questions About Alcohol in Pregnancy Using Web-Based Forum Topics: Qualitative Content Analysis	N. F. Frennesson, J. Barnett, Y. Merouani, A. Attwood, **L. Zuccolo**, C.McQuire	JMIR Infodemiology
COVID-19 vaccination and birth outcomes of 186,990 women vaccinated before pregnancy: an England-wide cohort study	A. K. Suseeladevi, R. Denholm, M. Retford, E. Raffetti, C. Burden, K. Birchenall, V. Male, V. Walker, C. Tomlinson, A. M. Wood, and **L. Zuccolo**, on behalf of the CVD-COVID-UK/COVID-IMPACT Consortium	The Lancet Regional Health: Europe
The genetic landscape of neuro-related proteins in human plasma	L. Repetto, J. Chen, Z. Yang, R. Zhai, …, **S. Sharapov**, et al.	Nature Human Behaviour
Socio-demographic and genetic risk factors for drug adherence and persistence across 5 common medication classes	M. Cordioli, **A. Corbetta**, H. M. Kariis, S. Jukarainen, P. Vartiainen, et al.	Nature Communications
Association between plausible genetic factors and weight loss from GLP1-RA and bariatric surgery: a multi-ancestry study in 10 960 individuals from 9 biobanks	J German, M Cordioli, V Tozzo, S Urbut, K Arumäe, R A.J. Smit, J Lee, J H. Li, A Janucik, …, **A Corbetta**, …, H Mbarek, R.J.F. Loos, U. Vainik, A. Ganna	medRxiv
Decoding the epigenetics and chromatin loop dynamics of androgen receptor-mediated transcription	U. Berkay Altıntaş, J. Seo, **C. Giambartolomei**, Do. Ozturan, B. J. Fortunato, G. M. Nelson, et al.	Nature Communications

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Enabling data linkages for rare diseases in a resilient environment with the SERDIF framework	**A. Navarro-Gallinad**, F. Orlandi, J. Scott, E. Havyarimana, N. Basu, M. A. Little, D. O'Sullivan	NPJ Digital Medicine
Time Trends in Liver-Related Mortality in People With and Without Diabetes: Results From a Population-Based Study	S. Ciardullo, G. Morabito, F. Rea, **L. Savaré**, G. Perseghin, G. Corrao	The journal of Clinical Endocrinology & Metabolism
Adherence to GLP1-RA and SGLT2-I affects clinical outcomes and costs in patients with type 2 diabetes	S. Ciardullo, **L. Savaré**, F. Rea, G. Perseghin, G. Corrao	Diabetes Metabolism Research and Review
Machine learning and lean six sigma for targeted patient-specific quality assurance of volumetric modulated arc therapy plans	N. Lambri, D. Dei, G. Goretti, **L. Crespi**, et al.	Physics and Imaging in Radiation Oncology
Deep learning-based optimization of field geometry for total marrow irradiation delivered with volumetric modulated arc therapy	N. Lambri, G. Longari, D. Loiacono, R. Coimbra Brioso, **L. Crespi**,et al.	Medical Physics
Deep learning and atlas-based models to streamline the segmentation workflow of total marrow and lymphoid irradiation	D. Dei, N. Lambri, **L. Crespi**, R. Coimbra Brioso, et al.	La Radiologia Medica
An innovative artificial intelligence-based method to compress complex models into explainable, model-agnostic and reduced decision support systems with application to healthcare (NEAR)	K. Kassem, M. Sperti, A. Cavallo, **A. M. Vergani**, D. Fassino, et al.	Artificial Intelligence in Medicine
Fast and reliable ancestral reconstruction on ancient genotype data with non-negative Least square and Principal Component Analysis	L. de Gennaro, L. Molinaro, **A. Raveane**, **F. Santonastaso**, S.S. Saponetti, **M. C.Massi**, … & F Montinaro	bioRxiv
A multiparametric screen uncovers FDA-approved small molecules that potentiate the nuclear mechano-dysfunctions in ATR-defective cells	M. R. Cera, G. Bastianello, D. Purushothaman, A. Andronache, F. Ascione, M. Robusto, **G. Fagà**, M. Pasi, G. Meroni, Q. Li, R. Choudhary, M. Varasi, M. Foiani, C. Mercurio	Scientific Reports
Optimized and Scalable Precoating-Free Reprogramming of Human Peripheral Blood Mononuclear Cells into iPSCs	**E. Fiacco**, **S. Landi**, **J. Zasso**, **C. Ambrosini**, **G. Faga**	Current Protocols
Human iPSC-derived neural stem cells displaying radial glia signature exhibit long-term safety in mice	M. Luciani, C. Garsia, S. Beretta, I. Cifola, **C. Peano**, I. Merelli, L. Petiti, A. Miccio, V. Meneghini, A. Gritti	Nature Communications
Definition of a Multi-Omics Signature for Esophageal Adenocarcinoma Prognosis Prediction	L. Lambroia, **C. M. Conca Dioguardi**, S. Puccio, A. Pansa, G. Alvisi, G. Basso, **J. Cibella**, F. S. Colombo, S. Marano, S. Basato, R. Alfieri, S. Giudici, C. Castoro, **C. Peano**	Cancers

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(Re)-definition of the holo- and apo-Fur direct regulons of Helicobacter pylori	A. Vannini, E. Pinatel, P. E. Costantini, S. Pelliciari, D. Roncarati, S. Puccio, G. De Bellis, V. Scarlato, **C. Peano**, A. Danielli	Journal of Molecular Biology
Microbial composition associated with biliary stents in patients undergoing pancreatic resection for cancer	A. Blanco-Míguez, S. Carloni, C. Cardenas, C. Conca Dioguardi, …, **C. Peano**, S. Tamburini, R. Rusconi, N. Segata	NPJBiofilms and Microbiomes
Recurrent somatic mutations of FAT family cadherins induce an aggressive phenotype and poor prognosis in anaplastic large cell lymphoma	M. Villa, G. G. Sharma, F. Malighetti, M. Mauri, G. Arosio, …, **S. Bombelli**, et al.	British Journal of Cancer
Multiple cell types including melanocytes contribute to elastogenesis in the developing murine aortic valve	S. Nasim, B. Abdo Abujamra, D. Chaparro, P. Da Silva Nogueira, **A. Riva**, J. D Hutcheson, L. Kos	Scientific Reports
Quinoin, type 1 ribosome inactivating protein alters SARS-CoV-2 viral replication organelle restricting viral replication and spread	S. M. L. Tiano, N. Landi, V. Marano, S. Ragucci, G. Bianco, D. Cacchiarelli, **P. Swuec**, **M. Silva**, R. De Cegli, F. Sacco, A. Di Maro, M. Cortese	International Journal of Biological Macromolecules
Structure-based mechanism of riboregulation of the metabolic enzyme SHMT1	S. Spizzichino, F. Di Fonzo, C. Marabelli, A. Tramonti, A. Chaves-Sanjuan, A. Parroni, G. Boumis, F. R. Liberati, A. Paone, L. C. Montemiglio, M. Ardini, A. J. Jakobi, A. Bharadwaj, **P. Swuec**, et al.	Molecular Cell
IHMCIF: An Extension of the PDBx/mmCIF Data Standard for Integrative Structure Determination Methods	B. Vallat, B. M. Webb, J. D. Westbrook, T. D. Goddard, C. A. Hanke, **A. Graziadei**, et al.	Journal of Molecula Biology
Typical NF2 and LTZR1 mutations are retained in an immortalized human schwann cell model of schwannomatosis	V. Melfi, T. Mohamed, A. Colciago, **A. Fasciani**, R. De Francesco, et al.	Helyion
Castanet: a pipeline for rapid analysis of targeted multi-pathogen genomic data	R. Mayne, S. Secret, C. Geoghegan, A. Trebes, K. Kean, K. Reid, G. Lin, M. A. Ansari, **M. de Cesare**, et al.	Bioinformatics
Targeted metagenomics reveals association between severity and pathogen co-detection in infants with respiratory syncytial virus	G. Lin, S. B. Drysdale, M. D. Snape, D. O'Connor, A. Brown, G. MacIntyre-Cockett, E. Mellado-Gomez, **M. de Cesare**, et al.	Nature Communications
Hydrogel-chitosan and polylactic acid-polycaprolactone bioengineered scaffolds for reconstruction of mandibular defects: a preclinical in vivo study with assessment of translationally relevant aspects	M. Ferrari , S. Taboni, H. H. L. Chan, J. Townson, ..., **M. Ventura**, et al.	Frontiers in Bioenginieering and Biotechnology
Detection of metabolic adaptation in a triple-negative breast cancer animal model with [18F]choline-PET imaging as a surrogate for drug resistance	A. A. Kohan, M. Lupien, D. Cescon, G. Deblois, **M. Ventura**, U. Metser, P. Veit-Haibach	EJNMMI

Titolo	Autori	Giornale
Unveiling the mechanistic link between extracellular amyloid fibrils, mechano-signaling and YAP activation in cancer	F. Farris, A. Elhagh, I. Vigorito, N. Alongi, F. Pisati, M. Giannattasio, **F. Casagrande**, L. Veghini, V. Corbo, C. Tripodo, A. Di Napoli, V. Matafora, A. Bachi	Cell Death & Disease

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Elenco delle pubblicazioni con affiliazione Human Technopole pubblicate nel 2025. I nomi degli autori con affiliazione Human Technopole sono in grassetto. L'asterisco indica gli studi che sono stati evidenziati con la copertina di un giornale.

Titolo	Autori	Giornale
FAIR sharing of Chromatin Tracing datasets using the newly developed 4DN FISH Omics Format	Navelkar R, Cosolo A, Bintu B, Cheng Y, Gardeux V, Gutnik S, Fujimori T, Hafner A, Jay A, Jia BB, Jussila AP, Llimos G, Lioutas A, Martins NMC, Moore WJ, Takei Y, Wong F, Yang K, Zhang H, Zhu Q, **Bienko M**, et al.	arXiv
Translocations can drive expression changes of multiple genes in regulons covering entire chromosome arms	Oncins A, Zaurin R, Toukabri H, Quililan K, Hernández Mora JR, Karpinska MA, …, **Bienko M**, Oudelaar AM, Beekman R	Nucleic Acids Research
Cell type-specific intronic RNAs shape genome architecture during neuronal lineage specification	Kang W, Yip WH, Verron Q, Bouwman BAM, Li-Wang X, Abou Yaghi A, Murata M, Stout M, Salviati L, Shu X, Yasuzawa K, **Gaviraghi M**, **Pracana R**, Lord J, Ballarino R, Falk A, Shin JW, KasukawaT, Yip CW, Kato M, Takahashi H, **Crosetto N**, **Carninci P**, **Bienko M**	bioRxiv
Coupling mechanisms coordinating mRNA translation with stages of the mRNA lifecycle	Famà V, Coscujuela Tarrero L, **Albanese R**, **Calviello L**, Biffo S, Pelizzola M, Furlan M.	RNA Biology
High-quality peptide evidence for annotating non-canonical open reading frames as human proteins	Deutsch EW, Kok LW, Mudge JM, Ruiz-Orera J, Fierro-Monti I, Sun Z, Abelin JG, Alba MM, Aspden JL, Bazzini AA, Bruford EA, Brunet MA, **Calviello L**, et al.	bioRxiv
Ku limits aberrant mRNA splicing promoted by intronic antisense Alu elements	Pascarella G, Mikhova M, Parkhi G, Godfrey J, Heyza J, Janovič T, Olive A, **Carninci P**, Schmidt JC, Meek K.	bioRxiv
Internal ribosome entry sites enhance translation in trans in antisense non-coding SINEUP and circular RNAs	D'Agostino S, Tettey-Matey A, Volpe M, Pierattini B, D'Agostino M, Smělá D, Ansaloni F, …, **Carninci P**, Santoro C, Persichetti F, Pandolfini L, Simonetti A, Espinoza S, Zucchelli S, Sanges R, Bon C, Gustincich S.	Nucleic Acids Research
Asian diversity in human immune cells	Kock KH, Tan LM, Han KY, Ando Y, Jevapatarakul D, Chatterjee A, Lin QXX, …, **Carninci P**, Chambers JC, Hon CC, Matangkasombut P, Charoensawan V, Majumder PP, Shin JW, Park WY, Prabhakar S.	Cell
Systematic evaluation of single-cell multimodal data integration for comprehensive human reference atlas	Acera-Mateos M, Adiconis X, Li JK, Marchese D, Caratù G, Hon CC, Tiwari P, Kojima M, Vieth B, Murphy MA, …, **Carninci P**, Heyn H, Levin JZ, Mereu E.	bioRxiv

Titolo	Autori	Giornale
Protocol for direct cDNA cap analysis of gene expression for paired-end patterned flow cell sequencing	Delobel D, Nishiyori-Sueki H, Nisoli I, Kawaji H, Robbe P, **Carninci P**, Takahashi H.	STAR Protocols
Extending cis-regulatory networks using chromatin-RNA interactions	Sahlén P, Carcedo A, Chen YL, Kostic S, Zhigulev A, Petersson Sjögren M, Cordier J, Yip WH, Yip CW, Yasuzawa K, Kasukawa T, Kato M, Lambolez A, Takahashi A, **Bienko M**, Lizana L, **Carninci P**	bioRxiv
Chromatin organizer ASCL1 governs gene programs in thymic epithelial cells, defining immunological self	Akiyama N, Horie K, Namiki K, Chang JC, Miyauchi M, Miyao T, …, **Carninci P**, Hollander GA, Minoda A, Nakajima J, Akiyama T	bioRxiv
Breast cancer identity is defined by specialized enhancer sets via lysine deacetylation	Tachiwana H, Kumegawa K, Matsudo R, Katsuma A, Okabe A, Yoshida N, Shu X, Kato M, Minamisawa T, Ito A, Kimura H, **Carninci P**, Kaneda A, Daigaku Y, Maruyama R, Saitoh N	bioRxiv
ESC models of autism with copy-number variations reveal cell-type-specific translational vulnerability	Nomura J, Zuko A, Kishimoto K, Mutsumine H, Maegawa H, Fukatsu K, Nomura Y, Liu X, Nakai N; **ES Library team**; Takahashi E, Kouno T, Shin JW , Takumi T	Cell Genome
A genome-wide, machine learning-guided exploration of the cis-regulatory code involved in neuronal differentiation	Cassan O, Raynal J, Vroland C, Yasuzawa K, Kouno T, Chang JC, Hon CC, Shin JW, Kato M, Takahashi H, Kasukawa T, Nobusada T, Lagani V, Lehmann R, Yauy K, **Carninci P**, Yip CW, Bréhélin L, Lecellier CH	bioRxiv
Evidence of distal regulations orchestrated by RNAs initiating at short tandem repeats	Grapotte M, Vroland C, Garrido-Martín D, Vignoli A, Calero L, Bouvier Q, Robin M, FANTOM consortium, Yip CW, **Carninci P**, Chatelain C, Bréhélin L, Notredame C, Guigo R, Lecellier CH	bioRxiv
Integrated in silico and in vitro approaches identify SNX.2112 as a drug vulnerability in t(7;12) AML stem-like cells	Cicirò Y., Ragusa E., Johnson E.M., Johns A., Kanannejad S., Gurung R., Oporto Espuelas M., Suen C.W., Torregrosa-Cortes G., **Giustacchini A**., Tosi S., Pina C.	bioRxiv
Intraplaque haemorrhage quantification and molecular characterisation using attention based multiple instance learning	Cisternino F, Song Y, Peters TS, Westerman R, de Borst GJ, Diez Benavente E, van den Dungen NAM, Homoed-van der Kraak P, de Kleijn DPV, Mekke J, Mokry M, Pasterkamp G, den Ruijter HM, Velema E, Miller CL, **Glastonbury CA**, van der Laan SW.	medRxiv
Scalable Deep Learning of Histology Images Reveals Genetic and Phenotypic Determinants of Adipocyte Hypertrophy	Jørsboe E, Kubitz P, Honecker J, Flaccus A, Mvondo D, Raggi M, **Glastonbury CA**, Hansen T, Blüher M, Krag A, Hauner H, Charles PD, Lindgren CM, Nellåker C, Claussnitzer M.	medRxiv

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Quantification of heavy metal exposure in a British population cohort links total mercury levels in plasma with skin tissue-specific changes in mitochondrial-related gene expression	van de Streek M, Ali AT, El-Sayed Moustafa JS, **Glastonbury CA**, Spector TD, Valdes AM, Staff JF, Morton J, Hodgkinson A, Bell JT, Small KS.	Sci Total Environ
Biologically-Inspired Digital Histology for Deep Phenotyping of Placental Composition Changes Across Major Lesion Types	Walker EC, Vanea C, Meir K, Hochner-Celnikier D, Laisk T, Hochner H, Lindgren C, **Glastonbury CA**, Ernst L, Nellaker C	medRxiv
Reasoning Over Pre-training: Evaluating LLM Performance and Augmentation in Women's Health	Imprialou M, Kaltsas N, Oliinyk V, Vigrass T, Schwarzmann J, Rosenthal R, **Glastonbury CA**, Wigley C, Gillam M, Kanani N, Supramaniam P, Granne I, Lindgren CM	medRxiv
Highly accurate assembly polishing with DeepPolisher	Mastoras M, Asri M, Brambrink L, Hebbar P, Kolesnikov A, Cook DE, Nattestad M, Lucas J, Won TS, Chang PC, Carroll A, Paten B, Shafin K; and the **Human Pangenome Reference Consortium**	Genome Res
Leveraging transdiagnostic genetic liability to psychiatric disorders to dissect clinical outcomes of anorexia nervosa	Lu ZA, Ploner A, Birgegård A; **Eating Disorders Working Group of the Psychiatric Genomics Consortium**; Landén M, Bulik CM, Bergen SE.	Mol Psychiatry
Dissecting the Cellular Genetics of Cardiovascular Disease Through Endothelial and Immune Compartments Profiling	Watt S, Ozols M, **Landini A**, Liu B, **Sharapov S**, **Zanotti D**, Ivanova G, Solomon C, Yang XD, Balogun T, Staudt N, Li W, Al-Janabi F, Webb TR, McVey DG, Morrell N, Bennett M, Samani NJ, Gräf S, Ye S, **Pirastu N**, **Soranzo N**, Frontini M	bioRxiv
Competing gene regulatory networks drive naive and memory B cell differentiation	**Demela P**, **Esposito L**, **Marchesan P**, **Bolognini D**, **Giacopuzzi E**, **Ricciardelli E**, **Ferrari P**, **Bombelli S**, **Peano C**, Prati D, Valenti L, **Soskic B**	bioRxiv
Genetic composition and evolutionary trajectories of brain metastasis in non-small-cell lung cancer	Nicoś M, Galant N, Kowalczyk A, Pęksa R, Jarosz B, Żuk M, Wasąg B, Duchnowska R, Krawczyk P, Jassem J, **Crosetto N**	Lung Cancer
A novel germline NF1 splicing variant drives the onset of an anorectal mucosal melanoma in a patient with a stable and durable nivolumab response	Berrino E, Bellomo SE, Mastorino L, Morbidoni V, **Crosetto N**, Sapino A, Sarotto I, Chesta A, Gianluca A, Quaglino P, Zampieri D, Senetta R, Trevisson E, Marchiò C, Ribero S.	Pathologica
Senataxin prevents replicative stress induced by the Myc oncogene	Sberna S, Filipuzzi M, Bianchi N, Croci O, Fardella F, Soriani C, Rohban S, Carnevali S, Albertini AA, **Crosetto N**, Rodighiero S, Chiesa A, Curti L, Campaner S.	Cell Death Dis
Delivery of Biomolecules into Individual Cells and Subcellular Compartments by Localized Electroporation via Nanopipette	**Marcuccio F**, Goff PS, Vadukul DM, Raja F, Li Y, Ren R, Saha D, Magnani L, Aprile FA, Anand U, Sviderskaya EV, Edel JB, Ivanov AP, Gorelkin PV, Korchev Y, Shevchuk A.	ACS Nanosci Au

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LUMEN-A deep learning pipeline for analysis of the 3D morphology of the cerebral lenticulostriate arteries from time-of-flight 7T MRI	Li R, **Chatterjee S**, Jiaerken Y, Zhou X, Radhakrishna C, Benjamin P, Nannoni S, Tozer DJ, Markus HS, Rodgers CT.	Neuroimage
PULASki: Learning inter-rater variability using statistical distances to improve probabilistic segmentation	**Chatterjee S**, Gaidzik F, Sciarra A, Mattern H, Janiga G, Speck O, Nürnberger A, Pathiraja S.	Med Image Anal
Complex-valued neural networks to speed-up MR thermometry during hyperthermia using Fourier PD and PDUNet	Khatun R, **Chatterjee S**, Bert C, Wadepohl M, Ott OJ, Semrau S, Fietkau R, Nürnberger A, Gaipl US, Frey B.	Sci Rep
MedShapeNet - a large-scale dataset of 3D medical shapes for computer vision	Li J, Zhou Z, Yang J, Pepe A, Gsaxner C, Luijten G, Qu C, Zhang T, Chen X, Li W, Wodzinski M, Friedrich P, Xie K, Jin Y, Ambigapathy N, … V, **Chatterjee S**, et al.	Biomed Tech (Berl)
Regulation of mRNA metabolism in immune cells	**Negi MS**, **Soskic B**, **Legnini I**	FEBS Lett
Combining spatial transcriptomics and ECM imaging in 3D for mapping cellular interactions in the tumor microenvironment	Pentimalli TM, Schallenberg S, León-Periñán D, **Legnini I**, Theurillat I, Thomas G, Boltengagen A, Fritzsche S, Nimo J, Ruff L, Dernbach G, Jurmeister P, Murphy S, Gregory MT, Liang Y, Cordenonsi M, Piccolo S, Coscia F, Woehler A, Karaiskos N, Klauschen F, Rajewsky N.	Cell Syst
Narrowing Down Key Players in Autoimmunity via Single-Cell Multiomics	**Gjurgjaj A**, **Conde CD**	Eur J Immunol
VCAM1-expressing T cells and systemic autoimmunity in Regnase-1 deficiency	Cuchet-Lourenço D, Conte MI, Chang S, Ten N, Eletto D, Papapietro O, Plagnol V, …, **Dominguez Conde J**, Farela Neves J, Nejentsev	medRxiv
A novel free fatty acid receptor agonist improving metabolic health in Drosophila models	Brunetti K, Catalani E, Del Quondam S, Romano N, Ceci M, **Clerici G**, **Gordin M**, Bianchini G, Brandolini L, Aramini A, Cervia D.	Pharmacol Res
The SIRT1 activator SRT2104 exerts exercise mimetic effects and promotes Duchenne muscular dystrophy recovery	Giovarelli M, Zecchini S, Casati SR, Lociuro L, Gjana O, Mollica L, Pisanu E, Mbissam HD, Cappellari O, De Santis C, Arcari A, Bigot A, **Clerici G**, et al.	Cell Death Dis
Genetic modulation of protein expression in rat brain	Li L, Wu Z, **Guarracino A**, Villani F, Kong D, Mancieri A, Zhang A, Saba L, Chen H, Brozka H, Vales K, Senko AN, et al.	iScience
Impact of radiation therapy dose, fractionation, and immunotherapeutic partner in a mouse model of hormone receptor-positive mammary carcinogenesis	Buqué A, Bloy N, Petroni G, Jiménez-Cortegana C, Sato A, Iribarren C, Yamazaki T, Galassi C, Hensler M, Bhinder B, **Guarracino A**, et al.	J Natl Cancer Inst

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PANE: fast and reliable ancestral reconstruction on ancient genotype data with non-negative least square and principal component analysis	de Gennaro L, Molinaro L, **Raveane A**, **Santonastaso F**, Saponetti SS, **Massi MC**, Pagani L, Metspalu M, Hellenthal G, Kivisild T, Ventura M, Montinaro F.	Genome Biol
Voltage-gated ion channel diversity underlies neuronal excitability and nervous system evolution	**Davila-Velderrain J**, van Giesen L.	Nat Commun
NeuRoDev resolves lifelong temporal and cellular variation in human cortical gene expression	**Zonca A**, **Bot E**, **Davila-Velderrain J**	bioRxiv
Gene specificity landscapes for comparative transcriptomic analysis across tissues, cell types, and species	**Bot E**, **Davila-Velderrain J**	bioRxiv
WWOX deficiency uncovers a cell-autonomous mechanism impairing myelin repair	Abudiab B, **Manenti C**, Repudi S, Abu-Swai S, Akkawi R, Jbara T, **Davila-Velderrain J**, Aqeilan RI	bioRxiv
Developmentally timed sensory integration enables efficient larval dispersal	Lønnum M, Schuldt MM, **Davila-Velderrain J**, van Giesen L	bioRxiv
Genome-wide CRISPR screen identifies Menin and SUZ12 as regulators of human developmental timing	Xu N, Cho HS, Hackland JOS, Benito-Kwiecinski S, Saurat N, **Harschnitz O**, Russo MV, Garippa R, Ciceri G, Studer L.	Nat Cell Biol
Regional differences in progenitor metabolism shape brain growth during development	Baumann N, Wagener RJ, Javed A, **Conti E**, Abe P, Lopes A, Sansevrino R, Lavalley A, Magrinelli E, Szalai T, Fuciec D, Ferreira C, Fièvre S, Fouassier A, D'Amico D, **Harschnitz O**, Jabaudon D.	Cell
Shaping the Neocortex: Radial Glia and Astrocytes in Development and Evolution	Mosti F, Kawasaki H, Babbit C, di Benedetto B, Silver DL, **Kalebic N**, Falcone C.	J Neurosci
Adducins regulate morphology and fate of neural progenitors during neocortical neurogenesis	**Ossola C**, **Cokorac N**, **Capra E**, **Faletti S**, **Bertani I**, **Ambrosini C**, **Restelli E**, **Casagrande F**, **Fasciani A**, **Bosotti R**, **Maghelli N**, **Faga G**, **Taverna E**, **Kalebic N**.	Cell Rep
Morphoregulatory ADD3 underlies glioblastoma growth and formation of tumor-tumor connections	**Barelli C**, **Kaluthantrige Don F**, **Iannuzzi RM**, **Faletti S**, **Bertani I**, **Osei I**, **Sorrentino S**, **Villa G**, **Sokolova V**, **Campione A**, Minotti MR, Sicuri GM, Stefini R, **Iorio F**, **Kalebic N**	Life Sci Alliance
Stem cell morphology defines functional heterogeneity and therapeutic vulnerabilities in glioblastoma	**Barelli C**, **Bonfanti M**, **Mirabella F**, **Ricca D**, **Alizadehmohajer N**, **Bosotti R**, **Bertani I**, **Sokolova V**, **Campione A**, Sicuri GM, **Peano C**, **Faletti S**, Stefini R, **Kalebic N**	bioRxiv
Human-specific morphoregulatory signatures in basal radial glia characterize neocortex evolution	Schütze TM, Ditzer N, Vangelisti S, Kolodziejczyk A, **Capra E**, …, **Kalebic N**, Boyan Bonev, Mareike Albert	bioRxiv

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High resolution multi-scale profiling of embryonic germ cell-like cell derivation reveals pluripotent state transitions in humans	**Stucchi S**, Sepulveda-Rincon LP, Dion C, **Matassa G**, **Valenti A**, **Cheroni C**, **Vitriolo A**, **Prazzoli F**, Young G, **Rigoli MT**, **Nagni R**, Ciprietti M, **Muda B**, Heckhausen Z, Hajkova P, **Caporale N**, **Testa G**, Leitch HG.	Stem Cell Reports
The need for a global effort to attend to human neural organoid and assembloid research	Pașca SP, Arlotta P, Campbell P, Charo A, Evans JH, Farahany N, Gage FH, Godfrey-Smith P, Hyun I, Kriegstein AR, Melloni L, Ming GL, Moreno JD, Sugarman J, Temple S, **Testa G**, Greely HT.	Science
From Cells to Selves and Back: Human Neurodiversity at Single-Cell Resolution	**Lessi M**, **Caporale N**, **Testa G**	Physiology (Bethesda)
YY1 mutations disrupt corticogenesis through a cell type specific rewiring of cell-autonomous and non-cell-autonomous transcriptional programs	**Pereira MF**, **Finazzi V**, **Rizzuti L**, **Aprile D**, **Aiello V**, Mollica L, Riva M, Soriani C, **Dossena F**, **Shyti R**, **Castaldi D**, Tenderini E, Carminho-Rodrigues MT, Bally JF, de Vries BBA, Gabriele M, **Vitriolo A**, **Testa G**	Mol Psychiatry
Tile by tile: capturing the evolutionary mosaic of human conditions	**Caporale N**, **Leonardi O**, **Villa CE**, **Vitriolo A**, Boeckx C, **Testa G**	Curr Opin Genet Dev
Multiplexing cortical brain organoids for the longitudinal dissection of developmental traits at single-cell resolution	**Caporale N**, **Castaldi D**, **Rigoli MT**, **Cheroni C**, **Valenti A**, **Stucchi S**, **Lessi M**, **Bulgheresi D**, **Trattaro S**, **Pezzali M**, **Vitriolo A**, **Lopez-Tobon A**, **Bonfanti M**, **Ricca D**, Schmid KT, Heinig M, Theis FJ, **Villa CE**, **Testa G**	Nat Methods*
A framework for neural organoids, assembloids and transplantation studies	Pașca SP, Arlotta P, Bateup HS, Camp JG, Cappello S, Gage FH, Knoblich JA, …, **Testa G**, Treutlein B, Vaccarino FM, Vanderhaeghen P, Young-Pearse T.	Nature
A molecular cell atlas of endocrine signalling in human neural organoids	**Matassa G**, **Rigoli MT**, **Castaldi D**, **Valenti A**, **Lessi M**, **Caporale N**, **Stucchi S**, **Muda B**, **Nagni R**, **Mainardi L**, **Melon A**, **Tintori A**, **Bulgheresi D**, **Kubacki M**, **Trattaro S**, Evangelista S, Leonards P, Human Cell Atlas Organoid Biological Network, **Villa CE**, **Cheroni C**, **Testa G**	bioRxiv
Mapping and reprogramming tissue microenvironments with MintFlow	Akbarnejad A, Steele L, Jafree DJ, Birk S, Sallese MR, Rademaker K, Boxall A, …, **Villa CE**, **Testa G**, Mahil S, Mehrjou A, Smith C, Vakili S, Clatworthy MR, Mitchell T, Bayraktar OA, Haniffa M, Lotfollahi M	bioRxiv
Benchmarking cerebellar organoids to model autism spectrum disorder and human brain evolution	**Aprile D**, **Leonardi O**, **Petrella A**, **Castaldi D**, **Culotta L**, **Cheroni C**, Valente A, **Bonfanti M**, **Vitriolo A**, Moriano J, **Mirabella F**, **Tintori A**, Boeckx C, **Testa G**	bioRxiv

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Regulatory logic of human cortex evolution by combinatorial perturbations	**Skaros A**, **Vitriolo A**, **Leonardi O**, **Finazzi V**, **Pereira MF**, **Prazzoli F**, Trattaro S, Moriano J, **Capocefalo D**, **Villa CE**, Boettcher M, Boeckx C, **Testa G**	bioRxiv
Disruption of ADNP-KDM1A-GTF2I complex drives neural differentiation imbalance in Helsmoortel-Van der Aa syndrome	**Rizzuti L**, **Vitriolo A**, Pelicano de Almeida M, **Pereira MF**, Meert L, **Dossena F**, **Prazzoli F**, Dekker M, Dekkers DHW, Demmers J, van Ijcken WFJ, Soriani C, Gabriele M, Mohiuddin M, Van Dijck A, **Finazzi V**, **Trattaro S**, Pallotta D, Tenderini E, Vulto-van Silfhout AT, de Vries BBA, Eichler E, Pearson CE, Kooy FR, Poot R, **Testa G**	bioRxiv
A harmonized ovarian cancer scRNA-seq atlas to dissect disease heterogeneity underlying metastatization and chemoresistance	Sallese MR, **Aiello V**, **Villa CE**, Lo Riso P, Testa G	bioRxiv
CHD2 Dosage Ties Autolysosomal Pathway to Cortical Maturation in Disease and Evolution	**Leonardi O**, Lewerissa E, **Aprile D**, Barakat TS, **Culotta L**, Deng R, Haazen L, Linda K, Majoie M, Mordelt A, **Ortale A**, Oudakker A, **Prazzoli F**, Puvogel S, Scheefhals N, Schelhaas HJ, Schoenmaker C, van Hugte E, van Bokhoven H, Verhoeven J, **Vitriolo A**, Boeckx C, **Testa G**, Nadif Kasri N	bioRxiv
Intriguing role of the Golgi apparatus in astrocyte function: Implications for disorders	**Polenghi M**, **Restelli E**, **Taverna E**, Tapella L.	Neural Regen Res
Vesicular trafficking and cell-cell communication in neurodevelopment and neurodegeneration	**Amin S**, **Taverna E**	Front Cell Dev Biol
Metabolic traits shape responses to LSD1-directed therapy in glioblastoma tumor-initiating cells	Marotta G, Osti D, Zaccheroni E, Costanza B, **Faletti S**, Marinaro A, Richichi C, Mesa D, Rodighiero S, Soriani C, Migliaccio E, Ruscitto F, Priami C, et al	Sci Adv
AMPK Activation Downregulates TXNIP, Rab5, and Rab7 Within Minutes, Thereby Inhibiting the Endocytosis-Mediated Entry of Human Pathogenic Viruses	Diesendorf V, **La Rocca V**, Teutsch M, Alattar H, Obernolte H, Kenst K, Seibel J, Wörsdörfer P, Sewald K, Steinke M, Schneider-Schaulies S, Lutz MB, Bodem J.	Cells
TBC1D24 interacts with the v-ATPase and regulates intraorganellar pH in neurons	Pepe S, **Aprile D**, Castroflorio E, Marte A, Giubbolini S, Hopestone S, Parsons A, Soares T, Benfenati F, Oliver PL, Fassio A	iScience
Molecular mechanism of thyroxine transport by monocarboxylate transporters	**Tassinari M**, **Tanzi G**, **Maggiore F**, Groeneweg S, van Geest FS, Freund MET, Stavast CJ, **Boniardi I**, **Pasqualato S**, Visser WE, **Coscia F**	Nat Commun
A conserved acidic residue drives thyroxine synthesis within thyroglobulin and other protein precursors	**Stejskalova C**, Arrigoni F, **Albanesi R**, Bertini L, Mollica L, **Coscia F**	J Biol Chem*

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Three-dimensional visualization of tip-vesicles in growing pollen tubes by electron tomography	Liu Z, Liao M, Liang Z, Gao J, Huang Y, Xiang Y, Ni T, **Erdmann PS**, Jiang L.	Sci China Life Sci
Beyond Dimerization: Harnessing Tetrameric Coiled-Coils for Nanostructure Assembly	Vidmar S, Šmidlehner T, Aupič J, Strmšek Ž, Ljubetič A, Xiao F, Hu G, Liu C, Beck F, **Erdmann PS**, Jerala R.	Angew Chem Int Ed Engl
Condensin II activation by M18BP1	**Borsellini A**, Conti D, Cutts EE, Harris RJ, Walstein K, **Graziadei A**, **Cecatiello V**, Aarts TF, …, Musacchio A, **Vannini A**	Mol Cell
Structural insights into distinct mechanisms of RNA polymerase II and III recruitment to snRNA promoters	**Shah SZ**, **Perry TN**, **Graziadei A**, **Cecatiello V**, Kaliyappan T, Misiaszek AD, Müller CW, **Ramsay EP**, **Vannini A**	Nat Commun
A substrate-interacting region of Parkin directs ubiquitination of the mitochondrial GTPase Miro1	Koszela J, Rintala-Dempsey A, **Salzano G**, Pimenta V, Kamarainen O, Gabrielsen M, Parui AL, Shaw GS, Walden H.	J Cell Biol
Unwrapping the Ciliary Coat: High-Resolution Structure and Function of the Ciliary Glycocalyx	Hoepfner LM, Nievergelt AP, **Matrino F**, Scholz M, **Foster HE**, Rodenfels J, von Appen A, Hippler M, **Pigino G**	Adv Sci (Weinh)
Tubulin tyrosination/detyrosination regulate the affinity and sorting of intraflagellar transport trains on axonemal microtubule doublets	Chhatre A, Stepanek L, Nievergelt AP, **Alvarez Viar G**, Diez S, **Pigino G**	Nat Commun
Novel ATOH7 mutation and structural characterization in families with optic nerve hypoplasia	Ullah MI, **Dad R**, Rehman Z, Shakil M, Alsrhani A, Alameen AAM, Ghanem HB, Manni E, Khan MU, Atif M.	Int J Ophthalmol
Identification of mutations in five Pakistani families with Epilepsy	Ahsan N, Ahmad A, Hussain S, Fatima N, Yousafzai IK, Kalsoom UE, **Dad R**, Hassan MJ	Neurogenetics
Tau uptake by human neurons depends on receptor LRP1 and kinase LRRK2	Evans LD, Strano A, Tuck E, Campbell A, Smith J, Hung C, Behr TS, Ghetti B, Ryskeldi-Falcon B, Karakoc E, **Iorio F**, Reith A, Bassett AR, Livesey FJ.	EMBO J
Impact of cell culture transition on adipose-derived mesenchymal stromal cells: Multi-omics analysis of small- vs large-scale production	Galera MR, **Oikonomou A**, Elsborg JD, Harth L, Fischer-Nielsen A, Løvendorf MB, Dyring-Andersen B, **Iorio F**, Fog LM, Woetmann A, Svalgaard JD.	Mol Ther Methods Clin Dev
The synthetic lethal interaction between CDS1 and CDS2 is a vulnerability in uveal melanoma and across multiple tumor types	Chan PY, Alexander D, Mehta I, Matsuyama LSAS, Harle V, Olvera-León R, Park JS, Arriaga-González FG, …, **Iorio F**, Ryan CJ, Adams DJ.	Nat Genet
Cross-tissue gene expression interactions from bulk, single cell and spatial transcriptomics with crossWGCNA	**Savino A**, **Iannuzzi RM**, Avalle L, Lobascio A, **Iorio F**, Provero P, Poli V.	BMC Genomics
Visions of the future of molecular cell biology	Abu-Remaileh M, Chan CJ, Chen L, Demirer GS, Fiszbein A, **Jug F**, Lechuga-Vieco AV, Luisier R, Pagan J, Sabari BR, Shao S, Sun L, Żylicz JJ.	Nat Rev Mol Cell Biol

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MIFA: Metadata, Incentives, Formats and Accessibility guidelines to improve the reuse of AI datasets for bioimage analysis	Zulueta-Coarasa T, **Jug F**, Mathur A, Moore J, Muñoz-Barrutia A, Anita L, Babalola K, Bankhead P, Gilloteaux P, et al	Nat Methods
Clinical Validation of Deep Learning for Image Restoration of Ultra-Low-Count [18F]FDG PET for Dementia Diagnostics	Schiller F, Brumberg J, Frings L, **Deschamps J**, Schmied C, **Jug F**, Mix M, Meyer PT.	J Nucl Med
FeatureForest: the power of foundation models, the usability of random forests	**Seifi M**, **Dalle Nogare D**, **Battagliotti JM**, **Galinova V**, Rao AK, Jouneau PH, Archit A; AI4Life Horizon Europe Programme Consortium; Pape C, Decelle J, **Jug F**, **Deschamps J**	Npj Imaging
Hijacking and integration of algal plastids and mitochondria in a polar planktonic host	Rao AK, Yee D, Chevalier F, LeKieffre C, Pavie M, Olivetta M, Dudin O, Gallet B, Hehenberger E, **Seifi M**, **Jug F**, **Deschamps J**, Wu TD, Gast R, Jouneau PH, Decelle J.	Curr Biol
Enabling global image data sharing in the life sciences	Bajcsy P, Bhattiprolu S, Börner K, Cimini BA, Collinson L, Ellenberg J, Fiolka R, Giger M, Goscinski W, Hartley M, Hotaling N, Horwitz R, **Jug F**, Kemmer I, Kreshuk A, Lundberg E, Mathur A, Narayan K, Onami S, Plant AL, Prior F, Swedlow JR, Taylor A, Keppler A.	Nat Methods
RESOLFT time lapse imaging empowered by deep learning	Testa I, Minet R, **Ray A**, Pennacchietti F, Coceano G, **Jug F**	Research Square
ResMatching: Noise-Resilient Computational Super-Resolution via Guided Conditional Flow Matching	**Ray A**, Galinova V, **Jug F**	arXiv
E-Seg: Sparsely Supervised Semantic Segmentation of Microscopy Data	**RahnamaiKordasiabi S**, **Dalle Nogare D**, **Jug F**	OpenReview.net
HazeMatching: Dehazing Light Microscopy Images with Guided Conditional Flow Matching	**Ray A**, **Jug F**	arXiv
Pattern Matching-Based Denoising for Images with Repeated Sub-Structures	Badarinarayana AKM, Pratsch C, Lunkenbein T, **Jug F**	MAKE (Machine Learning &Knowledge Extraction)
indiSplit: Bringing Severity Cognizance to Image Decomposition in Fluorescence Microscopy	**Ashesh A**, **Jug F**	arXiv
Micro𝕊plit: Semantic Unmixing of Fluorescent Microscopy Data	**Ashesh A**, **Carrara F**, **Zubarev I**, **Galinova V**, **Croft M**, Pezzotti M, Gong D, **Casagrande F**, **Colombo E**, **Giussani S**, **Restelli E**, **Cammarota E**, **Battagliotti JM**, **Klena N**, Di Sante M, Adhikari R, Feliciano D, **Pigino G**, **Taverna E**, **Harschnitz O**, **Maghelli N**, Scherer N, **Dalle Nogare DE**, **Deschamps J**, Pasqualini F, **Jug F**	bioRxiv

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Translating microbial kinetics into quantitative responses and testable hypotheses using Kinbiont	**Angaroni F**, **Peruzzi A**, Alvarenga EZ, **Pinheiro F**	Nat Commun
Epigenetically driven and early immune evasion in colorectal cancer evolution	Lakatos E, Gunasri V, Zapata L, Househam J, **Heide T**, Trahearn N, Swinyard O, …, **Sottoriva A**, Graham TA	Nat Genet
Quantitative measurement of phenotype dynamics during cancer drug resistance evolution using genetic barcoding	Whiting FJH, Mossner M, Gabbutt C, Kimberley C, Barnes CP, Baker AM, Yara-Romero E, **Sottoriva A**, Nichols RA, Graham TA.	Nat Commun
Epigenetic Heritability of Cell Plasticity Drives Cancer Drug Resistance through a One-to-Many Genotype-to-Phenotype Paradigm	Oliveira EA, **Milite S**, Fernandez-Mateos J, Cresswell GD, Yara-Romero E, Vlachogiannis G, Chen B, **James CT**, Patruno L, Ascolani G, Acar A, **Heide T**, Spiteri I, Graudenzi A, Caravagna G, Bertotti A, Graham TA, Magnani L, Valeri N, **Sottoriva A**	Cancer Res
Heterogeneity and evolution of DNA mutation rates in microsatellite stable colorectal cancer	Grassi E, Vurchio V, Cresswell GD, Catalano I, Lupo B, Sassi F, Galimi F, …, **Sottoriva A**, Trusolino L, Bertotti A.	Sci Transl Med
MIDAA: deep archetypal analysis for interpretable multi-omic data integration based on biological principles	**Milite** S, Caravagna G, **Sottoriva A**	Genome Biol
MYC ecDNA promotes intratumour heterogeneity and plasticity in PDAC	Fiorini E, Malinova A, Schreyer D, Pasini D, Bevere M, Alessio G, Rosa D, **D'Agosto S**, **Azzolin L**, **Milite** S, Andreani S, Lupo F, Veghini L, Grimaldi S, Pedron S, …, **Sottoriva A**, Scarpa A, Tuveson DA, Bailey P, Corbo V.	Nature
Computational pathology applied to clinical colorectal cancer cohorts identifies immune and endothelial cell spatial patterns predictive of outcome	Trahearn N, Sakr C, Banerjee A, Lee SH, Baker AM, Kocher HM, Angerilli V, Morano F, Bergamo F, Maddalena G, Intini R, **Cremolini C**, Caravagna G, Graham T, Pietrantonio F, Lonardi S, Fassan M**, Sottoriva A**	J Pathol
Stratified Medicine Pediatrics: Cell-Free DNA and Serial Tumor Sequencing Identifies Subtype-Specific Cancer Evolution and Epigenetic States	George SL, Lynn C, Stankunaite R, Hughes D, Sauer CM, Chalker J, …, **Sottoriva A**, Chesler L.	Cancer Discov
Circulating Tumor DNA Dynamics and Clinical Outcome in Metastatic Colorectal Cancer Patients Undergoing Front-Line Chemotherapy	Ghidini M, Hahne JC, Senti C**, Heide T**, Proszek PZ, Shaikh R, Carter P, Hubank M, Trevisani F, Garrone O, Cappelletti MR, Generali D, Cattaneo M, Gnocchi N, Donati G, Gobbi A, Grizzi G, Lampis A, Elghadi R, Tanzi G, Tomasello G, Ratti M, Pinato DJ, Fassan M, Vlachogiannis G, **Sottoriva A**, Cortellini A, Passalacqua R, Valeri N.	Clin Cancer Res

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Comparison between germline and somatic loss-of-function RNF43 mutations reveals different genotype-phenotype associations and provides insights into the genetic mechanisms of colorectal tumourigenesis	Palles C, Freeman-Mills L, Arbe-Barnes E, Feeley N, Chegwidden L, Curley H, Galavotti S, Woolley C, Cheadle J, Mouradov D, Sieber O, Salatino S, Thorn S, Goel A, Fernandez-Tajes J, Omwenga S, Biswas S, Maughan T, Leedham SJ; S:CORT Consortium; **UK Colorectal Cancer Genomics Consortium**; et al.	Gut
Single cell multi-omic whole genome sequencing and chromatin accessibility profiling reveals genome-epigenome coevolution in colorectal cancer	Mossner M, Colson C, Guo Q, Whiting F, Grant H, Stafford A, Kyle P, Donato-Brown D, Murphy J, **Sottoriva A**, Baker A, Graham TA	bioRxiv
Mixtures of Neural Cellular Automata: A Stochastic Framework for Growth Modelling and Self-Organization	**Milite S**, **Caravagna G**, **Sottoriva A**	arXiv
BASCULE: bayesian inference and clustering of mutational signatures leveraging biological priors	Buscaroli E, Sadr A, Bergamin R, **Milite S**, Villegas Garcia EN, Tasciotti A, Ansuini A, Ramazzotti D, Calonaci N, Caravagna G.	Genome Biol.
Combined clinical, metabolomic, and polygenic scores for cardiovascular risk prediction	Ritchie SC, Jiang X, Pennells L, Xu Y, Coffey C, Liu Y, Gibson JT, Surendran P, Karthikeyan S, Lambert SA, Danesh J, Butterworth AS, Wood A, Kaptoge S, **Di Angelantonio E**, Inouye M.	Eur Heart J
Large-scale characterisation of the nasal microbiome redefines Staphylococcus aureus colonisation status	Aggarwal D, Bellis KL, Blane B, de Goffau MC, Wagner J, Ng DYK, Raven KE, …, **Di Angelantonio E**, Butterworth AS, Geoghegan JA, Danesh J, Parkhill J, Peacock SJ, Harrison EM.	Nat Commun
Role of pain and anxiety in mediating relationships between donation history and vasovagal reaction symptoms in blood donors in England	Wu Y, **Di Angelantonio E**, Kaptoge S, Wood AM, Gilchrist PT, Walker M, Kingston N, Masser B, Roberts D, Ferguson E, Kim LG.	Transfusion
Burden of cardiovascular diseases in England (2020-24): a national cohort using electronic health records data	Allara E, Shi W, Bolton T, Chalmers F, Brizzi LF, Musto L, Shah ASV, Tomlinson C, Walter I, Conrad N, Danesh J, **Di Angelantonio E**, Petersen SE, Khunti K, Raffetti E, Cezard G, Denaxas S, Wood AM, Whiteley W.	Lancet Public Health
Impact of Valve Frame Height on PCI Outcomes After TAVR	Pivato CA, **Di Angelantonio E**, Tartaglia F, Condorelli G, Fontana N, **Ieva F**, Godino C, Nakase M, Hug K, Rheude T, Munoz-Garcia AJ, et al.	JACC Cardiovasc Interv

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Blood donor populations reveal a clear association between ferritin and change in haemoglobin levels	Meulenbeld A, Turkulainen EV, Li W, Pothast MR, Qi H, Allara E, Di Angelantonio E; INTERVAL Trial Group; Swanevelder R, Brits T, Paalvast Y, van den Hurk K, Matlung HL, Swinkels DW, Russell WA, Arvas M, Janssen MP.	Br J Haematol
Array genotyping of transfusion-relevant blood cell antigens in 6946 ancestrally diverse study participants	Gleadall NS, Koets L, Shamardina O, Gollub J, Gottschalk AJ, Razeghi O, Ochoa-Garay G, Stephens J, Varma R, Martin J, Allara E, Brown CJ, Daly J, **Di Angelantonio E**, et al.	Blood
Cardiac Troponins and Cardiovascular Disease Risk Prediction: An Individual-Participant-Data Meta-Analysis	Shah ASV, Keene SJ, Pennells L, Kaptoge S, Kimenai DM, Walker M, Halley JD, …, **Di Angelantonio E**; CAPRICE Co-Investigators	J Am Coll Cardiol
Metabolic reaction fluxes as amplifiers and buffers of risk alleles for coronary artery disease	Foguet C, Jiang X, Ritchie SC, Persyn E, Xu Y, Ben-Eghan C, Taylor HJ, **Di Angelantonio E**, Danesh J, Butterworth AS, Lambert SA, Inouye M.	Mol Syst Biol
Optimal risk assessment intervals for primary prevention of cardiovascular disease: a population-based two-stage landmarking study	Gu Z, Gasperoni F, Paige E, Sweeting M, Usher-Smith J, Poppe K, Stevens D, Arnold M, **Di Angelantonio E**, Wood AM, Barrett JK.	BMJ Public Health
Key priorities for the implementation of the 2023 ESC Guidelines for the management of cardiovascular disease in patients with diabetes in low-resource settings	Marx N, Schütt K, Müller-Wieland D, **Di Angelantonio E**, Herrington WG, Ajjan RA, Kautzky-Willer A, Rocca B, Sattar N, Fauchier L, Lettino M, Federici M; Members of the Task Force for the 2023 ESC Guidelines for the management of cardiovascular disease in patients with diabetes	Eur Heart J Qual Care Clin Outcomes
UK Longitudinal Linkage Collaboration (UK LLC): The National Trusted Research Environment for Longitudinal Research	Boyd A, Evans KM, Turner EL, Flaig R, Oakley J, Campbell KC, Thomas R, McLachlan S, Crane M, …, **Di Angelantonio E**, et al.	Int J Popul Data Sci
Primary Prevention of Cardiovascular Disease in Asia: Challenges: A Narrative Review	Dalakoti M, Lin NHY, Yap J, Cader A, Dipanker P, Lee D, Raja Shariff RE, Cuenza L, … Lip GYH, Yang E, Virani SS, Hageman S, Liu H, **Di Angelantonio E**, Dorairaj P, Koh AS, Chin C, Al Mahmeed W, Chan MY, Foo R.	JACC Adv
Primary Prevention of Cardiovascular Disease in Asia: Opportunities and Solutions: A Narrative Review	Dalakoti M, Lin NHY, Yap J, Cader A, Dipanker P, Lee D, Raja Shariff RE, Cuenza L, …, **Di Angelantonio E**, Dorairaj P, Koh AS, Chin C, Al Mahmeed W, Chan MY, Foo R.	JACC Adv
2024 Revision of the level of evidence grading system for ESC clinical practice guideline recommendations II: diagnostic tests and prediction models	**Di Angelantonio E**, Pennells L, Abdelhamid M, Aboyans V, Asteggiano R, Čelutkienė J, Grobbee DE, Iung B, Jüni P, McEvoy JW, Rakisheva A, Rossello X, Visseren FLJ, Baigent C, Prescott EB.	Eur Heart J

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The contribution of genetic determinants of blood gene expression and splicing to molecular phenotypes and health outcomes	Tokolyi A, Persyn E, Nath AP, Burnham KL, Marten J, Vanderstichele T, **Tardaguila M**, …, **Di Angelantonio E**, Peters JE, **Soranzo N**, Danesh J, Butterworth AS, Inouye M, Davenport EE, Paul DS.	Nat Genet
Expected outcomes of stratified post-donation testing in whole blood donation in England: A discrete event simulation modeling study	Qi H, Wood AM, Kaptoge S, McMahon A, Mehenny S, Kingston N, Ouwehand WH, Danesh J, Roberts DJ, **Di Angelantonio E**, Kim LG.	Transfusion
Clinical utility and implementation of polygenic risk scores for predicting cardiovascular disease: A clinical consensus statement of the ESC Council on Cardiovascular Genomics, the ESC Cardiovascular Risk Collaboration, and the European Association of Preventive Cardiology	Schunkert H, **Di Angelantonio E**, Inouye M, Patel RS, Ripatti S, Widen E, Sanderson SC, Kaski JP, McEvoy JW, Vardas P, Wood A, Aboyans V, Vassiliou VS, Visseren FLJ, Lopes LR, Elliott P, Kavousi M.	Eur Heart J
Cohort profile: the BangladEsh Longitudinal Investigation of Emerging Vascular and nonvascular Events (BELIEVE) cohort study	Chowdhury R, Khan N, Pennells L, Iurilli MLC, Uddin Miah MT, Monower MM, Rahman KMT, Samin S, Saqeeb KN, Tasmin I, …, **Di Angelantonio E**, Danesh J; BELIEVE Study	BMJ Open
Conventional and regionally distinctive risk factors for first-onset myocardial infarction: the Bangladesh Risk of Acute Vascular Events (BRAVE) case-control study	Chowdhury R, Naheed A, Monower MM, Shahzad S, Raqib R, Tasmin I, Spackman S, Kaptoge S, Pennells L, Butterworth AS, Danesh J, Di Angelantonio E	Lancet Reg Health Southeast Asia
Cardiovascular safety of assisted reproductive technology: a meta-analysis	Pivato CA, Inversetti A, Condorelli G, Chieffo A, Levi-Setti PE, Latini AC, Busnelli A, Messa M, Cristodoro M, Bragato RM, Francone M, **Zuccolo L**, **Ieva F**, **Di Angelantonio E**, Stefanini G, Di Simone N.	Eur Heart J
Leucocyte telomere length and conduction system ageing	van Duijvenboden S, Nelson CP, Raisi-Estabragh Z, Ramirez J, Orini M, Wang Q, Aung N, Codd V, Stoma S, Allara E, Wood AM, **Di Angelantonio E**, Danesh J, Harvey NC, Petersen SE, Munroe PB, Samani NJ.	Heart
Assessing the kinetics of oxygen-unloading from red cells using FlowScore, a flow-cytometric proxy of the functional quality of blood	Rabcuka J, Smethurst PA, Dammert K, Saker J, Aran G, Walsh GM, Tan JCG, Codinach M, McTaggart K, Marks DC, Bakker SJL, McMahon A, **Di Angelantonio E**, Roberts DJ, Blonski S, Korczyk PM, Shirakami A, Cardigan R, Swietach P.	EBioMedicine

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Risks of major arterial and venous thrombotic diseases after hospitalisation for influenza, pneumonia, and COVID-19: A population-wide cohort in 2.6 million people in Wales	Keene S, Abbasizanjani H, Torabi F, Knight R, Walker V, Raffetti E, Cezard G, Ip S, Sampri A, Bolton T, Denholm R, Khunti K, Akbari A, Quint J, Denaxas S, Sudlow C, **Di Angelantonio E**, Sterne JAC, Wood A, Whiteley WN; CVD-COVID-UK/COVID-IMPACT Consortium and the Longitudinal Health and Wellbeing COVID-19 National Core Study	Thromb Res
Risk factors for vasovagal reactions in blood donors: A systematic review and meta-analysis	Wu Y, Qi H, **Di Angelantonio E**, Kaptoge S, Wood AM, Kim LG.	Transfusion
The common VTE-protective G haplotype of F5 increases factor V-short, TFPI function, and risk of bleeding	Sims MC, Gierula M, Stephens JC, Tokolyi A, Stefanucci L, Persyn E, Sun L, Collins JH, Davenport EE, **Di Angelantonio E**, Downes K, Inouye M, Paul DS, Thomas W, Tolios A, Ouwehand WH, Gleadall NS, Crawley JTB, Butterworth AS, Frontini M, Ahnström J.	Blood Adv
Association of circulating fatty acids with cardiovascular disease risk: analysis of individual-level data in three large prospective cohorts and updated meta-analysis	Shi F, Chowdhury R, Sofianopoulou E, Koulman A, Sun L, Steur M, Aleksandrova K, Dahm CC, Schulze MB, …, **Di Angelantonio E**, Forouhi NG, Danesh J, Butterworth AS, Kaptoge S.	Eur J Prev Cardiol
Clinical outcomes of percutaneous coronary interventions after transcatheter aortic valve replacement	Pivato CA, Cozzi O, **Fontana N**, **Ieva F**, Condorelli G, Godino C, Reimers B, Nakase M, Hug K, Rheude T, Munoz-Garcia AJ, Jimenez Diaz VA, Ielasi A, Barbanti M, Biasco L, et al.	Eur Heart J Open
Uncovering mortality patterns and hospital effects in COVID-19 heart failure patients: a novel multilevel logistic cluster-weighted modeling approach	Caldera L, Masci C, Cappozzo A, Forlani M, Antonelli B, Leoni O, **Ieva F**	Biometrics
Wavelet-Mixed Landmark Survival Models for the Effect of Short-Term Changes of Potassium in Heart Failure Patients	Gregorio C, Barbati G, Scagnetto A, Lenarda AD, **Ieva F**	Biom J
Real-world effectiveness of influenza vaccination in preventing influenza and influenza-like illness in children	Rigamonti V, Torri V, Morris SK, **Ieva F**, Giaquinto C, Donà D, Di Chiara C, Cantarutti A; CARICE study group	Vaccine
CT-radiomics and pathological tumor response to systemic therapy: A predictive analysis for colorectal liver metastases. Development and internal validation of a clinical-radiomic model	Ammirabile A, Cavinato L, Ferro CAP, Fiz F, Savino MS, Russolillo N, Balbo Mussetto A, …, **Ieva F**, Torzilli G, Viganò L.	Eur J Surg Oncol
Unveiling the biological side of PET-derived biomarkers: a simulation-based approach applied to PDAC assessment	Cavinato L, Hong J, Wartenberg M, Reinhard S, Seifert R, Zunino P, Manzoni A, **Ieva F**, Chiti A, Rominger A, Shi K.	Eur J Nucl Med Mol Imaging

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CT-based radiogenomics of intrahepatic cholangiocarcinoma	Viganò L, Zanuso V, Fiz F, Cerri L, Laino ME, Ammirabile A, Ragaini EM, Viganò S, Terracciano LM, Francone M, **Ieva F**, Di Tommaso L, Rimassa L.	Dig Liver Dis
Unraveling time-varying causal effects of multiple exposures: integrating Functional Data Analysis with Multivariable Mendelian Randomization	**Fontana N**, **Ieva F**, **Zuccolo L**, **Di Angelantonio E**, Secchi P.	arXiv
Multi-state Modeling of Delay Evolution in Suburban Rail Transports	Colombo S, Gimenez Zapiola A, **Ieva F**, Vantini S	arXiv
Cost-effectiveness of first-line osimertinib informed by electronic medical records via text-mining: a real-world Italian case study of EGFR-mutated advanced NSCLC patients	Corso F, Baili P, Scotti F, Mazzeo L, Torri V, Lo Russo G., Proto C, Giani C, Ganzinelli M, di Mauro RM, Cappozzo A, Paganoni AM, Prelaj A & **Ieva F**	ESMO Real World Data and Digital Oncology
A neural-network approach for predicting time to cardiovascular diseases in HIV patients based on real-world data	Lurani Cernuschi A, Masci C, Corso F, Muccini C, Ceccarelli D, Galli L, **Ieva F**, Castagna F, Paganoni AM	Operational Research
SAFE-LD: A novel method for the estimation of linkage disequilibrium from summary statistics	**de Sanctis GE**, **Sharapov S**, **Bolognini D**, **Ieva F**, **Soranzo N**, **Di Angelantonio E**, **Giambartolomei C**, **Pirastu N**	bioRxiv
Interpretable phenotyping of Heart Failure patients with Dutch discharge letters	Torri V, Boonstra MJ, van de Veerdonk MC, Kalkman DN, Uijl A, **Ieva F**, Abu-Hanna A, Asselbergs FW, Calixto I	arXiv
Enhancing Causal Inference in Functional Data: a Method for Estimating Time-Varying Causal Treatment Effects	**Ieva F**, **Fontana N**, Pivato CA, **Di Angelantonio E**, Secchi P	New Trends in Functional Statistics and Related Field
DISARM++: Beyond scanner-free harmonization	Caldera L, Cavinato L, Cirone A, Cama I, Garbarino S, Lodi R, Tagliavini F, Nigri A, De Francesco S, Cappozzo A, Piana M, **Ieva F**	arXiv
A statistical significance-based approach for clustering grouped data via generalized linear model with discrete random effects	Ragni A, Masci C, **Ieva F** , Paganoni AM	Journal of the Royal Statistical Society Series A: Statistics in Society
Data analytics for real-world data integration in TKI-treated NSCLC patients using electronic health records	Mazzeo L, Corso F, Baili P, Scotti F, Torri V, Ganzinelli M, Mišković V, Leporati R, Provenzano L, Spagnoletti A, Silvestri C, Giani C, Cavalli C, di Mauro RM, Meazza Prina M, Proto C, Brambilla M, Occhipinti M, Manglaviti S, Beninato T, Miliziano D, Dumitrascu D, Di Liberti G, Cassano TS , de Braud FGM , Lo Russo G, Cappozzo A, Paganoni AM, **Ieva F**, Prelaj A	ESMO Real World Data and Digital Oncology
An Unsupervised Natural Language Processing Pipeline for Assessing Referral Appropriateness	Torri V, Bottelli A, Ercolanoni M, Leoni O, **Ieva F**	arXiv

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Automatic identification of diagnosis from hospital discharge letters via weakly-supervised Natural Language Processing	Torri, V., Barbieri, E., Cantarutti, A., Giaquinto, C., **Ieva, F**.	arXiv
Dynamics of Influenza Vaccination and Respiratory Virus Infections in Children: A Multistate Model Approach.	Giorcelli, A., Rigamonti, V., Rocchi, M., **Ieva, F**., Torri, V., Cavinato, L., Morris, S.K., Cotugno, N., Palma, P., Nordeng, H., Trinh, N., Donà, D., Giaquinto, C., Di Chiara, C., Cantarutti, A.	medrxiv
NLP-based assessment of prescription appropriateness from Italian referrals.	Torri, V., Bottelli, A, Ercolanoni, M., Leoni, O., **Ieva, F**	arXiv
Prenatal alcohol exposure before pregnancy awareness: a thematic analysis of online forum comments and misinformation	Frennesson NF, Merouani Y, Barnett J, Attwood A, **Zuccolo L**, McQuire C.	Front Public Health
Performance of Large Language Models (LLMs)in the Cognitive Analysis of Misinformation: Evaluation Study	Wojtczak DN, McConville R, McQuire C, **Zuccolo L**, Peersman C	JMIR Infodemiology
Systematic mediation and interaction analyses of kidney function genetic loci in a general population study	**Ghasemi-Semeskandeh D**, Emmert D, König E, Foco L, Gögele M, Sarhan MS, Barin L, Fujii R, Fuchsberger C, Peters DJM, Pramstaller PP, Pattaro C.	PLoS One
Clinical and Metabolic Signatures of FAM47E-SHROOM3 Haplotypes in a General Population Sample	**Ghasemi-Semeskandeh D**, König E, Foco L, Dordevic N, Gögele M, Rainer J, Ralser M, Acoba D, Domingues FS, Peters DJM, Pramstaller PP, Pattaro C.	Kidney Int Rep
Haplomics: A Snakemake pipeline for haplotype-based association analysis in multi-omics studies	**Ghasemi-Semeskandeh D**, Foco L, Fujii R, Rainer J, Feli M, Ralser M, Domingues FS, Pramstaller PP, Pattaro C.	medRxiv
Association between plausible genetic factors and weight loss from GLP1-RA and bariatric surgery	German J, Cordioli M, Tozzo V, Urbut S, Arumäe K, Smit RAJ, Lee J, Li JH, Janucik A, Ding Y, Akinkuolie A, Heyne HO, Eoli A, Saad C, Al-Sarraj Y, Abdel-Latif R, Mohammed S, Hail MA, Barry A, Wang Z, Cajuso T, **Corbetta A**, Natarajan P, Ripatti S, Philippakis A, Szczerbinski L, Pasaniuc B, Kutalik Z, Mbarek H, Loos RJF, Vainik U, Ganna A.	Nat Med
Removing genetic effects on plasma proteins enhances their utility as disease biomarkers	Fusco D, Yang Z, Viippola E, Cajuso T, **Corbetta A**, Caime C, German J, Fu M, Argentieri MA, FinnGen, Nakanishi T, Yang Z, Ganna A.	medrxiv
Large-scale multi-omics identifies drug targets for heart failure with reduced and preserved ejection fraction	Rasooly D, **Giambartolomei C**, Peloso GM, Dashti H, Ferolito BR, Golden D, Horimoto ARVR, et al.	Nat Cardiovasc Res
Automatic base-dose planning for a robust field junction in total marrow irradiation	Lambri N, Dei D, Brioso RC, **Crespi L**, Loiacono D, Scorsetti M, Mancosu P.	Phys Med

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Single-Cell Atlas of Cardiac Endothelial Cell Heterogeneity in Pressure Overload	Demenego G, Puccio S, Cassanmagnago GA, Gianferro F, Carullo P, De Simone G, Colombo FS, Rubino M, Basso G, Lugli E, Greco CM, **Peano C**, Condorelli G.	Circ Res
Tissue-specific antitumor NK cell subsets identified in colorectal cancer liver metastases express candidate therapeutic targets	Mikulak J, Supino D, Marzano P, Terzoli S, Carriero R, Cazzetta V, Piazza R, Bruni E, …, **Peano C**, Donadon M, Costa G, Torzilli G, Mantovani A, Garlanda C, Mavilio D.	J Clin Invest
Reticulated platelets in coronary artery disease: a multidimensional approach unveils prothrombotic signalling and novel therapeutic targets	Kirmes K, Han J, Klug M, Bloxham CJ, Babyak O, Bernett J, Arend L, Manz Q, Raka L, …, **Peano C**, et al.	Eur Heart J
Single-cell RNA sequencing of platelets: challenges and potential	Viggiani G, Kirmes K, Han J, Klug M, Kühne S, Condorelli G, Laugwitz KL, Bloxham CJ, **Peano C**, Raake P, Bernlochner I, Bongiovanni D	J Thromb Thrombolysis
Chemosensor receptors are lipid-detecting regulators of macrophage function in cancer	Marelli G, Morina N, Puccio S, Iovino M, Pandini M, Portale F, Carvetta M, Mishra D, Diana E, Meregalli G, Paraboschi E, **Cibella J**, **Peano C**, et al.	Nat Immunol
Microtubule association induces a Mg-free apo-like ADP pre-release conformation in kinesin-1 that is unaffected by its autoinhibitory tail	Atherton J, Chegkazi MS, Leusciatti M, Di Palma M, Peirano E, Pozzer LS, Meli MVA, **Pasqualato S**, Foran T, Morra G, Steiner RA.	Nat Commun
Intrinsic Alterations of the Inflammatory Pathways in Primary Canine Atopic Keratinocytes	Santoro D, Archer L, Scotti G, Ahrens K, **Riva A**	Allergy
Two FAM134B isoforms differentially regulate ER dynamics during myogenesis	Buonomo V, Lohachova K, Reggio A, Cano-Franco S, Cillo M, Santorelli L, Venditti R, , **Silva M**, De Cegli R, Di Bartolomeo S, Gargioli C, **Swuec P**, et al.	EMBO J
IHMValidation: Assessment of Integrative Structure Models Deposited to the Protein Data Bank	Zalevsky AO, Vallat B, Webb BM, Tangmunarunkit H, Sekharan MR, Shafaeibejestan A, Ganesan S, Sagendorf J, Jeffries CM, Trewhella J, **Graziadei A**, et al.	J Mol Biol
Breaking Boundaries in Histone Modification MS-Based Detection: A Tailored Search Strategy for Unrestricted Identification of Novel Epigenetic Marks	Vai A, Noberini R, **Graziadei A**, Polasky DA, Yu F, Nesvizhskii AI, Bonaldi T	Mol Cell Proteomics
A Roadmap for Improving Reliability and Data Sharing in Crosslinking Mass Spectrometry	Rappsilber J, Bruce J, Combe C, Fried SD, **Graziadei A**, Heck AJR, Iacobucci C, Leitner A, et al.	Mol Cell Proteomics
SUMO-2 activity is inhibited by non-covalent interactions with the Aβ peptide: an exploration of potential pathogenic mechanisms in Alzheimer's disease	Ciaffaglione V, Grasso G, Lanza V, Sciacca MFM, Zimbone S, Giuffrida ML, Iacobucci C, **Di Ianni A**, Calcagno D, Grasso G, Alloni A, Orsini F, Fraser P, Fioriti L, Milardi D.	Int J Biol Macromol

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Development of a 3D ex vivo model of brain-leukemia interaction to study the role of activin A in the central nervous system microenvironment	Dander E, Pischiutta F, Di Marzo N, Pascente R, **Panini N**, Fallati A, Biondi A, Zanier ER, D'Amico G.	Sci Rep
Interphase cell morphology defines the mode, symmetry, and outcome of mitosis	Lovegrove HE, Hulmes GE, Ghadaouia S, Revell C, Giralt-Pujol M, Alhashem Z, Pena A, **Dalle Nogare D**, et al.	Science
Characterization and Clinical Implications of p53 Dysfunction in Patients With Myelodysplastic Syndromes	Zampini M, Riva E, Lanino L, Sauta E, Antunes Dos Reis R, Ejarque RMA, Maggioni G, **Termanini A**, Merlotti A, Campagna A, Dall'Olio L, et al.	J Clin Oncol
Nf-core/crisprseq: a versatile pipeline for comprehensive analysis of CRISPR gene editing and screening assays	Mir-Pedrol J, Kuhlburger L, Sanvicente-García M, Yazar M, Ryan C, Krakau S, Gabernet G, Güell M, **Bonfanti M**, Nahnsen S	NAR Genomics and Bioinformatics
Active and Probe-Free Intracellular Rheology via Phase-Sensitive Thermoviscous Flows	Stoev ID, Bolger-Munro M, Minopoli A, Wagner S, Krishnaswamy VR, Erben E, Weißenbruch K, **Maghelli N**, Bastmeyer M, Heisenberg CP, Kreysing M.	arXiv