

**MODELLO PER IL
CURRICULUM VITAE**

INFORMAZIONI PERSONALI

Nome	Salvi Erika
Data di nascita	
Qualifica	Ricercatore sanitario
Amministrazione	Fondazione IRCCS Istituto Neurologico Carlo Besta, Milano
Incarico attuale	Responsabile di Ricerca Data Science Center
Numero telefonico dell'ufficio	0223944655
Fax dell'ufficio	-
E-mail istituzionale	erika.salvi@istituto-besta.it

**TITOLI DI STUDIO E
PROFESSIONALI ED ESPERIENZE
LAVORATIVE**

Titolo di studio	Laurea specialistica in Bioinformatica
Altri titoli di studio e professionali	Dottorato di ricerca in Medicina Molecolare. Curriculum: Genomica Proteomica e Tecnologie correlate, Università degli studi di Milano, Milano Master di II livello, Epidemiologia Genetica Molecolare, Università degli Studi di Pavia, Pavia
Esperienze professionali (incarichi ricoperti)	01/11/2024 – oggi Dipendente con qualifica di Ricercatore Sanitario (disciplina Bioinformatica) presso la Fondazione IRCCS Istituto Neurologico Carlo Besta, UOC Neurologia 3 – Neuroalgologia, Milano. Rapporto di lavoro a tempo indeterminato e tempo pieno. Dicembre 2023 - oggi Responsabile del laboratorio congiunto con il Politecnico di Milano, Computational multi-Omics of Neurological Disorders (MIND Lab). 16/04/2022 – 31/10/2024 Dipendente con qualifica di Ricercatore Sanitario (disciplina Bioinformatica) presso la Fondazione IRCCS Istituto Neurologico Carlo Besta, UOC Neurologia 3 – Neuroalgologia, Milano. Rapporto di lavoro a tempo determinato e tempo pieno. 05/09/2018 – 31/12/2021 Ricercatore (disciplina Bioinformatica) con rapporto di collaborazione coordinata e continuativa (Co.Co.Co.) presso la Fondazione IRCCS Istituto Neurologico Carlo Besta, UOC Neurologia 3 – Neuroalgologia, Milano. 01/03/2010 – 30/03/2018 Ricercatore con rapporto di assegno di ricerca presso il Dipartimento di Scienze della Salute, Università degli Studi di Milano, Milano 01/10/2006 – 15/12/2009 Dottorato di Ricerca in Medicina Molecolare presso il Dipartimento di Scienze e Tecnologie Biomediche, Università degli Studi di Milano, Milano 01/09/2006 – 30/11/2007 Contratto di collaborazione a progetto presso l'Istituto di tecnologie biomediche (ITB), Consiglio Nazionale delle Ricerche(CNR), Segrate (MI)

	01/12/2005 – 31/08/2006 Borsa di Studio presso il Dipartimento di Scienze dell'ambiente e del territorio (DISAT), Università degli Studi di Milano-Bicocca, Milano
Capacità linguistiche	Lingua Italiano: lingua madre Lingua Inglese: livello professionale
Capacità nell'uso delle tecnologie	Utilizzo avanzato di ambienti Linux e Windows. Esperienza nella gestione e analisi di big data su cluster HPC Linux e nello sviluppo di pipeline bioinformatiche per dati NGS di genomica e trascrittomica. Competenze in programmazione e analisi statistica in R, scripting Unix/Linux e uso di strumenti open-source per la bioinformatica.
Altro (partecipazione a convegni e seminari, pubblicazioni, collaborazione a riviste, ecc., ed ogni altra informazione che il dirigente ritiene di dover pubblicare)	ORCID ID: 0000-0002-2724-2291 SCOPUS ID: 57860926600 Partecipazioni a convegni e conferenze nazionali ed internazionali come discente e presenting author (ESHG, ASHG, SIGU, ASNP, CIBB). Attività editoriale: - Attività editoriale come revisore in riviste peer-reviewed: Frontiers in neurology, Frontiers in genetics, Journal of the Peripheral Nervous System, Ophthalmic Research, Neurological Sciences, Scientific reports, Journal of hypertension, Gene reports - Topic Editor di Frontiers in genetics 2025: Bioinformatics and Statistical Genetics Approaches for Omics-Based Dissection of Complex Traits Brevetti: - Co-Inventore del brevetto di invenzione nr. 102023000009462 del 11/5/2023- miRNA SLA, microRNA come strumento diagnostico e per lo sviluppo di terapie avanzate nella sclerosi laterale amiotrofica con esordio bulbare - Co-Inventore del brevetto di invenzione nr. 102023000013221 del 27/06/2023, MicroRNA come biomarcatori diagnostici e agenti terapeutici per la neuropatia delle piccole fibre Finanziamenti: - Fondi 5XMILLE 2018 – RC 2018 progetto PAIN RISK - Risk stratification of painful peripheral neuropathies - (Rif. Int. RC18.4), 1/10/2021-30/09/2025, Principal Investigator - Fondazione Regionale per la Ricerca Biomedica "Spinal Muscular Atrophy Translating Customized Health Innovations to Newborn and Grown-up patients". BANDO GIOVANI "EARLY CAREER AWARD - II EDIZIONE" 2023, anno di inizio 2024, responsabile di WP - AriSLA, "Bulbar onset ALS clustering by clinical informed multi-omics (BULB-OMICS)", Bando Arisla 2023, responsabile di WP - PNRR, "Disease biosignatures in ALS/FTD spectrum: new impactful biological perspectives beyond clinical approaches", PNRR: M6/C2_CALL 2023, Collaborator responsabile di WP. - PNRR, "Comprehensive in vitro approach to unravel the pathogenetic mechanisms underlying the novel family of PLIN4 gene expansion-related myopathy and identify biomarkers for early diagnosis". PNRR: M6/C2_CALL 2023. Collaborator responsabile di WP. - COST Action CA24166 INFLAMomx 2025 - Pan-European Network for Inflammaging: A Multi-omics Integration Approach. Secondary proposer. Pubblicazioni h-index: 41 (fonte Scopus) - D'Amato I, Ganguzza E, Basilisco G, Strippoli A, Salvi E, Mehmeti E, Chiappori F, Devigili G, Vecchi M, Lauria G and Marchi M (2025) A unique case of late-onset CIP0 caused by a missense mutation in the long isoform of FLNA. Front. Genet. 16:1611614. doi: 10.3389/fgene.2025.1611614 - Galluzzo A, Maffezzini M, Fumagalli ML, Sambruni I, Musio S, Patanè M, Paterra R, Salvi E, et al. The anti-aging Klotho protects glioblastoma macrophages from radiotherapy-induced inflammation and predicts immunotherapy response. Int J Cancer. 2025 Nov 15;157(10):2156-2172. doi: 10.1002/ijc.70038. Epub 2025 Jul 21. PMID: 40686387; PMCID: PMC12439078. - Singh AK, Bernabucci M, Dvorak NM, Haghighijoo Z, Di Re J, Goode NA, Kadakia FK, Maile LA, Folorunso OO, Wadsworth PA, Tapia CM, Wang P, Wang J, Chen H, Xue Y, Singh J, Hankerd K, Gamez IJ, Kager M, Truong V, Walsh P, Shiers SI, Kuttanna N, Liao H, Marchi M, Salvi E, et al. Sensory neuron-expressed FGF13 controls nociceptive signaling in diabetic neuropathy models. J Clin Invest. 2025 Jul 15;135(14):e183749. doi: 10.1172/JCI183749. PMID: 40662354 - Brugnoni R, Salvi E, Moresco E, Gallone A, Tufano L, Garibaldi M, Filosto M, Grandis M, Maggi L. Pharmacogenetic pilot study of CYP2D6 and CYP1A2 genes in Italian patients with non-dystrophic myotonia and myotonic dystrophy treated with mexiletine. Gene. 2025 Aug 10;960:149536. doi: 10.1016/j.gene.2025.149536. Epub 2025 May 3. PMID: 40324568.

5. Tadros R, Zheng SL, Grace C, Jordà P, Francis C, West DM, Jurgens SJ, Thomson KL, Harper AR, Ormondroyd E, Xu X, Theotokis PI, Buchan RJ, McGurk KA, Mazzarotto F, Boschi B, Pelo E, Lee M, Nosedà M, Varnava A, Vermeer AMC, Walsh R, Amin AS, van Slegtenhorst MA, Roslin NM, Strug LJ, **Salvi E**, Lanzani C, et al. Large-scale genome-wide association analyses identify novel genetic loci and mechanisms in hypertrophic cardiomyopathy. *Nat Genet.* 2025 Mar;57(3):530-538. doi: 10.1038/s41588-025-02087-4. Epub 2025 Feb 18. PMID: 39966646; PMCID: PMC11906354.
6. Kwiatkowska KM, Garagnani P, Bonafé M, Bacalini MG, Calzari L, Gentilini D, Ziegler D, Gerrits MM, Faber CG, Malik RA, Marchi M, **Salvi E**, Lauria G, Pirazzini C. Painful diabetic neuropathy is associated with accelerated epigenetic aging. *Geroscience.* 2025 Jun;47(3):4041-4054. doi: 10.1007/s11357-025-01516-w. Epub 2025 Jan 23. PMID: 39847262; PMCID: PMC12181573.
7. Catania M, Battipaglia C, Perego A, **Salvi E**, Maderna E, Cazzaniga FA, Rossini PM, Marra C, Vanacore N, Redolfi A, Perani D, Spadin P, Cotelli M, Cappa S, Caraglia N, Tiraboschi P, Tagliavini F, Di Fede G. Exploring the ability of plasma pTau217, pTau181 and beta-amyloid in mirroring cerebrospinal fluid biomarker profile of Mild Cognitive Impairment by the fully automated Lumipulse® platform. *Fluids Barriers CNS.* 2025 Jan 21;22(1):9. doi: 10.1186/s12987-025-00620-5. PMID: 39838411; PMCID: PMC11748262.
8. Kwiatkowska KM, Garagnani P, Bonafé M, Bacalini MG, Sala C, Castellani G, Gentilini D, Calzari L, Ziegler D, Gerrits MM, Faber CG, Malik RA, Marchi M, **Salvi E**, Lauria G, Pirazzini C. High-Resolution Whole-Genome DNA Methylation Revealed Unique Signatures of Painful Diabetic Neuropathy. *Diabetes.* 2025 Apr 1;74(4):640-650. doi: 10.2337/db24-0930. PMID: 39774670; PMCID: PMC11926268.
9. Misra K, Ślęczkowska M, Santoro S, Gerrits MM, Mascia E, Marchi M, **Salvi E**, Smeets HJM, et al. Broadening the Genetic Spectrum of Painful Small-Fiber Neuropathy through Whole-Exome Study in Early-Onset Cases. *Int J Mol Sci.* 2024 Jun 30;25(13):7248. doi: 10.3390/ijms25137248. PMID: 39000354; PMCID: PMC11242789.
10. Claudia Manzoni et al. Genome-wide analyses reveal a potential role for the MAPT, MOBP, and APOE loci in sporadic frontotemporal dementia. *American Journal of Human GeneticsOpen Access* Volume 111, Issue 7, Pages 1316 - 1329 11 July 2024.
11. Almomani R, Sopacua M, Marchi M, Ślęczkowska M, Lindsey P, de Greef BTA, Hoeijmakers JGJ, **Salvi E**, Merkies ISJ, et al. Genetic Profiling of Sodium Channels in Diabetic Painful and Painless and Idiopathic Painful and Painless Neuropathies. *Int J Mol Sci.* 2023 May 5;24(9):8278. doi: 10.3390/ijms24098278. PMID: 37175987; PMCID: PMC10179245.
12. Longobardi A, Catania M, Geviti A, **Salvi E**, Vecchi ER, et al. Autophagy Markers Are Altered in Alzheimer's Disease, Dementia with Lewy Bodies and Frontotemporal Dementia. *Int J Mol Sci.* 2024 Jan 17;25(2):1125. doi: 10.3390/ijms25021125. PMID: 38256197; PMCID: PMC10816165.
13. Andelic M, Marchi M, Marcuzzo S, Lombardi R, Faber CG, Lauria G, **Salvi E***. Archival skin biopsy specimens as a tool for miRNA-based diagnosis: Technical and post-analytical considerations. *Mol Ther Methods Clin Dev.* 2023 Sep 16;31:101116. doi: 10.1016/j.omtm.2023.101116. PMID: 37808256; PMCID: PMC10550798.
14. Hess T, et al. Dissecting the genetic heterogeneity of gastric cancer. *EBioMedicine.* 2023 Jun;92:104616. doi: 10.1016/j.ebiom.2023.104616. Epub 2023 May 18. PMID: 37209533
15. Almomani R, Sopacua M, Marchi M, Ślęczkowska M, Lindsey P, de Greef BTA, Hoeijmakers JGJ, **Salvi E**, et al. Genetic Profiling of Sodium Channels in Diabetic Painful and Painless and Idiopathic Painful and Painless Neuropathies. *Int J Mol Sci.* 2023 May 5;24(9):8278. doi: 10.3390/ijms24098278. PMID: 37175987; PMCID: PMC10179245.
16. * Marchi M, **Salvi E**, Andelic M, Mehmeti E, D'Amato I, et al. TRPA1 gene rare variants in chronic neuropathic and nociplastic pain patients. 2023 Apr 19. doi: 10.1097/j.pain.0000000000002905. Epub ahead of print. PMID: 37079850.
17. Iacomino N, Scandiffio L, Conforti F, **Salvi E**, Tarasco MC, Bortone F, et al. Muscle and Muscle-like Autoantigen Expression in Myasthenia Gravis Thymus: Possible Molecular Hint for Autosensitization. *Biomedicines.* 2023 Feb 28;11(3):732. doi: 10.3390/biomedicines11030732. PMID: 36979710; PMCID: PMC10045167.
18. Andelic M, **Salvi E**, Marcuzzo S, Marchi M, Lombardi R, Cartelli D, et al. Integrative miRNA-mRNA profiling of human epidermis: unique signature of SCN9A painful neuropathy. *Brain.* 2023 Jul 3;146(7):3049-3062. doi: 10.1093/brain/awad025. PMID: 36730021
19. Kyrlyuk K, et al. Genome-wide association analyses define pathogenic signaling pathways and prioritize drug targets for IgA nephropathy. *Nat Genet.* 2023 Jul;55(7):1091-1105. doi: 10.1038/s41588-023-01422-x. Epub 2023 Jun 19. PMID: 37337107.
20. Rossi G, **Salvi E**, Mehmeti E, Ricci M, Villa C, Prioni S, Moda F, et al. Semantic and right temporal variant of FTD: Next generation sequencing genetic analysis on a single-center cohort. *Front Aging Neurosci.* 2022 Dec. PMID: 36570531 PMCID: PMC9773257 DOI: 10.3389/fnagi.2022.1085406
21. Ślęczkowska M, Almomani R, Marchi M, **Salvi E**, de Greef BTA et al. Peripheral Ion Channel Genes Screening in Painful Small Fiber Neuropathy. *Int J Mol Sci.* 2022 Nov 15;23(22):14095. doi: 10.3390/ijms232214095. PMID: 36430572

22. Rossi G, ***Salvi E**, Benussi L, Mehmeti E, Geviti A, Bellini S, et al. The PINK1 p.Asn521Thr Variant Is Associated with Earlier Disease Onset in GRN/C9orf72 Frontotemporal Lobar Degeneration. *Int J Mol Sci* 2022 Oct 25;23(21):12847. doi: 10.3390/ijms232112847. PMID: 36361641
23. Le Floch E, Cosentino T, Larsen CK, Beuschlein F, Reincke M, Amar L, Rossi GP, De Sousa K, Baron S, Chantalat S, Saintpierre B, Lenzini L, Frouin A, Giscos-Douriez I, Ferey M, Abdellatif AB, Meatchi T, Empana JP, Jouven X, Gieger C, Waldenberger M, Peters A, Cusi D, **Salvi E**, et al, Identification of risk loci for primary aldosteronism in genome-wide association studies. *Nat Commun*. 2022 Sep 3;13(1):5198. doi: 10.1038/s41467-022-32896-8.
24. Bonanno S, Cavalcante P, **Salvi E**, Giagnorio E, Malacarne C, et al. Identification of a cytokine profile in serum and cerebrospinal fluid of pediatric and adult spinal muscular atrophy patients and its modulation upon nusinersen treatment. *Front Cell Neurosci*. 2022 Aug 11;16:982760. doi: 10.3389/fncel.2022.982760. eCollection 2022. PMID: 36035258
25. Marchi M; D'Amato I; Andelic M; Cartelli D; **Salvi E**; Lombardi R; Gumus E; Lauria G. Congenital insensitivity to pain: a novel mutation affecting a U12-type intron causes multiple aberrant splicing of SCN9A. *Pain*. 2022 Jul 1;163(7):e882-e887. doi: 10.1097/j.pain.0000000000002535. Epub 2021 Nov 15. PMID: 34799533
26. Ślęczkowska M, Almomani R, Marchi M, de Greef BTA, Sopacua M, Hoeijmakers JGJ, Lindsey P, **Salvi E**, et al . Peripheral Ion Channel Gene Screening in Painful- and Painless-Diabetic Neuropathy. *Int J Mol Sci*. 2022 Jun 28;23(13):7190. doi: 10.3390/ijms23137190. PMID: 35806193
27. Gorski M, Rasheed H, Teumer A, Thomas LF, Graham SE, Sveinbjornsson G, et al. Genetic loci and prioritization of genes for kidney function decline derived from a meta-analysis of 62 longitudinal genome-wide association studies. *Kidney Int*. 2022 Jun 15:S0085-2538(22)00454-9. doi: 10.1016/j.kint.2022.05.021. PMID: 35716955.
28. Winkler TW, Rasheed H, Teumer A, Gorski M, Rowan BX, Stanzick KJ, Thomas LF, Tin A et al, Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. *Commun Biol*. 2022 Jun 13;5(1):580. doi: 10.1038/s42003-022-03448-z. PMID: 35697829.
29. Sorosina M, Barizzzone N, Clarelli F, Anand S, Lupoli S, **Salvi E**, Mangano E, et al. A multi-step genomic approach prioritized TBKBP1 gene as relevant for multiple sclerosis susceptibility. *J Neurol*. 2022 Aug;269(8):4510-4522. doi: 10.1007/s00415-022-11109-8.
30. Yang WY, Izzi B, Bress AP, Thijs L, Citterio L, Wei FF, **Salvi E**, et al. Association of colorectal cancer with genetic and epigenetic variation in PEAR1-A population-based cohort study. *PLoS One*. 2022 Apr 7;17(4):e0266481. doi: 10.1371/journal.pone.0266481. eCollection 2022.
31. Maj C*, **Salvi E***, Citterio L*, Borisov O, Simonini M, Glorioso V, Barlassina C, Glorioso N, et al. Dissecting the Polygenic Basis of Primary Hypertension: Identification of Key Pathway-Specific Components. *Frontiers in Cardiovascular Medicine* 2022; 9. 10.3389/fcvm.2022.814502.
32. Aysu Okbay, et al. Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. *Nat Genet* 2022 Apr;54(4):437-449. doi: 10.1038/s41588-022-01016-z.
33. Chia, Ruth Et al Genome sequencing analysis identifies new loci associated with Lewy body dementia and provides insights into its genetic architecture. *Nat Genet* 2021 Mar;53(3):294-303
34. Toffano AA, Chiarot G, Zamuner S, Marchi M, **Salvi E**, Waxman SG, et al. Computational pipeline to probe Nav1.7 gain-of-function variants in neuropathic painful syndromes. *Sci Rep* 2020 Oct 21;10(1):17930.
35. Li M, Wang L, Shi DC, Foo JN, Zhong Z, Khor CC, Lanzani C, Citterio L, **Salvi E**, et al. Genome-Wide Meta-Analysis Identifies Three Novel Susceptibility Loci and Reveals Ethnic Heterogeneity of Genetic Susceptibility for IgA Nephropathy. *Journal of the American Society of nephrology* 2020 Dec;31(12):2949-2963.
36. Almomani R, Marchi M, Sopacua M, Lindsey P, **Salvi E**, Koning B, at al. Evaluation of molecular inversion probe versus TruSeq® custom methods for targeted next-generation sequencing. *PLoS One* 2020 Sep 2;15(9):e0238467
37. Clark DW, et al Associations of autozygosity with a broad range of human phenotypes. *Nat Commun*. 2019 Oct 31;10(1):4957.
38. Devigili G, Rinaldo S, Lombardi R, Cazzato D, Marchi M, **Salvi E**, Eleopra R, Lauria G. Diagnostic criteria for small fibre neuropathy in clinical practice and research. *Brain*. 2019 Dec 1;142(12):3728-3736. PubMed PMID: 31665231
39. Tin A, Marten J, et al. Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. *Nat Genet*. 2019 Oct;51(10):1459-1474.
40. Singh S, Warren HR, Hiltunen TP, McDonough CW, El Rouby N, **Salvi E**, et al. Genome-Wide Meta-Analysis of Blood Pressure Response to $\beta(1)$ -Blockers: Results From ICAPS (International Consortium of Antihypertensive Pharmacogenomics Studies). *Journal of the American Heart Association*. 2019 Aug 20;8(16):e013115.
41. Wuttke M, Li Y, Li M, Sieber KB, Feitosa MF et al. A catalog of genetic loci associated with kidney function from analyses of a million individuals. *Nat Genet*. 2019 Jun;51(6):957-972.
42. Damiano S, Lombardi P, **Salvi E**, Papale M, Giordano A, Amenta M, Ballistreri G, Fabroni S, Rapisarda P, Capasso G, Forte IM, Barone D, Ciarcia R. A red orange and lemon by-products

extract rich in anthocyanins inhibits the progression of diabetic nephropathy. *J Cell Physiol.* 2019 Dec;234(12):23268-23278.

43. Bandres-Ciga S, et al. Shared polygenic risk and causal inferences in amyotrophic lateral sclerosis. *Ann Neurol.* 2019 Apr;85(4):470-481.
44. Karlsson Linnér R, Biroli P, Kong E, Meddens SFW et al. Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. *Nat Genet.* 2019 Feb;51(2):245-257
45. Arcidiacono T, Simonini M, Lanzani C, Citterio L, **Salvi E**, Barlassina C, Spotti D, Cusi D, Manunta P, Vezzoli G. Claudin-14 Gene Polymorphisms and Urine Calcium Excretion. *Clin J Am Soc Nephrol.* 2018 Oct 8;13(10):1542-1549
46. Lee JJ, et al Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. *Nat Genet.* 2018 Aug;50(8):1112-1121.
47. Marchi M, Provitera V, Nolano M, Romano M, Maccora S, D'Amato I, **Salvi E**, Gerrits M, Santoro L, Lauria G. A novel SCN9A splicing mutation in a compound heterozygous girl with congenital insensitivity to pain, hyposmia and hypogeusia. *J Peripher Nerv Syst.* 2018 Sep;23(3):202-206
48. F. Wei, L. Thijs, Z. Zhang, L. Jacobs, W. Yang, **E. Salvi**, et al (2017). The risk of nephrolithiasis is causally related to inactive matrix Gla protein, a marker of vitamin K status: a Mendelian randomization study in a Flemish population. *Nephrol Dial Transplant.* 2018 Mar 1;33(3):514-522.
49. Palluzzi F, Ferrari R, Graziano F, Novelli V, Rossi G, Galimberti D, Rainero I, Benussi L, Nacmias B, Bruni AC, Cusi D, **Salvi E**, Borroni B, Grassi M. A novel network analysis approach reveals DNA damage, oxidative stress and calcium/cAMP homeostasis-associated biomarkers in frontotemporal dementia. *PLoS One.* 2017 Oct 11;12(10):e0185797. eCollection 2017. PubMed PMID: 29020091
50. Macé A, Tuke MA, Deelen P, Kristiansson K, Mattsson H, Nöukas M, Sapkota Y, Schick U, Porcu E, Rüeger S, McDaid AF, Porteous D, Winkler TW, **Salvi E**, et al Shrine CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. *Nat Commun.* 2017 Sep 29;8(1):744. PubMed PMID: 28963451
51. Nolte IM, Munoz ML, Tragante V, Amare AT, Jansen R, Vaez A, von der Heyde B, Avery CL, Bis JC, Dierckx B, van Dongen J, Gogarten SM, Goyette P, Hernesniemi J, Huikari V, Hwang SJ, Jaju D, Kerr KF, Kluttig A, Krijthe BP, Kumar J, van der Laan SW, Lyytikäinen LP, Maihofer AX, Minassian A, van der Most PJ, Müller-Nurasyid M, Nivard M, **Salvi E**, Stewart JD, Thayer JF, et al. Genetic loci associated with heart rate variability and their effects on cardiac disease risk. *Nat Commun.* 2017 2017 Jun 14;8:15805. doi: 10.1038/ncomms16140. PubMed PMID: 28767105
52. T. Aung, M. et al. (2017) Genetic association study of exfoliation syndrome identifies a protective rare variant at LOXL1 and five new susceptibility loci. *Nat Genet.*;49(7):993-1004. doi: 10.1038/ng.3875. Epub 2017 May 29.
53. N. Bolli, M. Barcella, **E. Salvi**, F. D'Avila, A. Vendramin, C. De Philippis, et al(2017). Next-generation sequencing of a family with a high penetrance of monoclonal gammopathies for the identification of candidate risk alleles. *CANCER*, ISSN: 0008-543X 2017 Oct 1;123(19):3701-3708
54. F. Pasutto, M. Zenkel, U. Hoja, D. Berner, S. Uebe, F. Ferrazzi, J. Schödel, P. Liravi, M. Ozaki, D. Paoli, P. Frezzotti, T. Mizoguchi, S. Nakano, T. Kubota, S. Manabe, **E. Salvi**, et al (2017). Pseudoexfoliation syndrome-associated genetic variants affect transcription factor binding and alternative splicing of LOXL1. *NATURE COMMUNICATIONS*, vol. 8, ISSN: 2041-1723 8:15466
55. W. Yang, T. Petit, N. Cauwenberghs, Z. Zhang, C. Sheng, L. Thijs, **E. Salvi**, et al (2017). PEAR1 is not a major susceptibility gene for cardiovascular disease in a Flemish population. *BMC MEDICAL GENETICS*, vol. 18, p. 1-9, ISSN: 1471-2350, doi: 10.1186/s12881-017-0411-x
56. M. Li, et al (2017). SOS2 and ACP1 Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. *JOURNAL OF THE AMERICAN SOCIETY OF NEPHROLOGY*, vol. 28, p. 981-994, ISSN: 1046-6673, doi: 10.1681/ASN.2016020131
57. **E. Salvi**, Z. Wang, F. Rizzi, Y. Gong, C.W. McDonough, S. Padmanabhan, et al (2017). Genome-Wide and Gene-Based Meta-Analyses Identify Novel Loci Influencing Blood Pressure Response to Hydrochlorothiazide. *HYPERTENSION*, vol. 69, p. 51-59, ISSN: 0194-911X, doi: 10.1161/HYPERTENSIONAHA.116.08267
58. J.S. Ried, et al. (2016). A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. *NATURE COMMUNICATIONS*, vol. 7, 13357, ISSN: 2041-1723, doi: 10.1038/ncomms13357
59. M. Landini, I. Merelli, M.E. Raggi, N. Galluccio, F. Ciceri, A. Bonfanti, S. Camposeo, A. Massagli, L. Villa, **E. Salvi**, D. Cusi, M. Molteni, L. Milanese, A. Marabotti, A. Mezzelani (2016). Association analysis of noncoding variants in neurologins 3 and 4X genes with autism spectrum disorder in an Italian cohort. *INTERNATIONAL JOURNAL OF MOLECULAR SCIENCES*, vol. 17, p. 1-13, ISSN: 1422-0067, doi: 10.3390/ijms17101765
60. E. Koumakis, M. Bouaziz, P. Dieudé, A. Cauvet, B. Ruiz, P. Airò, D. Cusi, M. Matucci-Cerinic, **E. Salvi**, G. Cuomo, et al (2016). A candidate gene study identifies a haplotype of CD2 as novel

susceptibility factor for systemic sclerosis. CLINICAL AND EXPERIMENTAL RHEUMATOLOGY, vol. 34, p. 43-48, ISSN: 0392-856X

61. L.E.J.M. Scheepers, F. Wei, K. Stolarz-Skrzypek, S. Malyutina, V. Tikhonoff, L. Thijs, **E. Salvi**, C. Barlassina, et al (2016). Xanthine oxidase gene variants and their association with blood pressure and incident hypertension: A population study. JOURNAL OF HYPERTENSION, vol. 34, p. 2147-2154, ISSN: 0263-6352, doi: 10.1097/HJH.0000000000001077
62. F. Rizzi, C. Conti, E. Dogliotti, A. Terranegra, **E. Salvi**, D. Braga, F. Ricca, et al (2016). Interaction between polyphenols intake and PON1 gene variants on markers of cardiovascular disease : A nutrigenetic observational study. JOURNAL OF TRANSLATIONAL MEDICINE, vol. 14, 186, ISSN: 1479-5876, doi: 10.1186/s12967-016-0941-6
63. Z.C. Jing, B.X. Wu, J.J. Peng, X.L. Li, L. Pan, S.P. Zhao, D.Y. Li, Z.X. Yu, J.B. Gong, Q.Y. Zhao, J.N. Cao, G.T. Sheng, J. Li, B.J.M.X.Y. Li, S. Jiang, C.F. Liang, **E. Salvi**, V. Carubelli (2016). Effect of intravenous l-carnitine in Chinese patients with chronic heart failure. EUROPEAN HEART JOURNAL SUPPLEMENTS, vol. 18, p. A27-A36, ISSN: 1554-2815, doi: 10.1093/eurheartj/suw008
64. Okbay, J.P. et al (2016). Genome-wide association study identifies 74 loci associated with educational attainment. NATURE, vol. 533, p. 539-542, ISSN: 0028-0836
65. C. Pattaro, et al (2016). Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. NATURE COMMUNICATIONS, vol. 7, 10023, ISSN: 2041-1723, doi: 10.1038/ncomms10023
66. S. Lupoli, **E. Salvi**, M. Barcella, C. Barlassina (2015). Pharmacogenomics considerations in the control of hypertension. PHARMACOGENOMICS, vol. 16, p. 1951-1964, ISSN: 1462-2416, doi: 10.2217/pgs.15.131
67. W. Yang, T. Petit, L. Thijs, Z. Zhang, L. Jacobs, A. Hara, F. Wei, **E. Salvi**, L. Citterio, S. D. Carpini, Y. Gu, J. Knez, N. Cauwenberghs, M. Barcella, C. Barlassina, P. Manunta, G. Coppiello, X.L. Aranguren, T. Kuznetsova, D. Cusi, P. Verhamme, A. Luttun, J.A. Staessen (2015). Coronary risk in relation to genetic variation in MEOX2 and TCF15 in a Flemish population BMC Genetics, vol. 16, 116, ISSN: 1471-2156, doi: 10.1186/s12863-015-0272-2
68. R. Ferrari*, M. Grassi*, **E. Salvi***, B. Borroni*, F. Palluzzi, et al (2015). A genome-wide screening and SNPs-to-genes approach to identify novel genetic risk factors associated with frontotemporal dementia. NEUROBIOLOGY OF AGING, vol. 36, p. 2904.e13-2904.e26, ISSN: 0197-4580, doi: 10.1016/j.neurobiolaging.2015.06.005
69. D. Yu, C.A. et al. (2015). Cross-Disorder Genome-Wide Analyses Suggest a Complex Genetic Relationship Between Tourette's Syndrome and OCD. THE AMERICAN JOURNAL OF PSYCHIATRY, vol. 172, p. 82-93, ISSN: 0002-953X, doi: 10.1176/appi.ajp.2014.13101306
70. K. Männik, R. Mägi, A. Macé, B. Cole, A.L. Guyatt, H.A. Shihab, A.M. Maillard, H. Alavere, A. Kolk, A. Reigo, E. Mihailov, L. Leitsalu, A. Ferreira, M. Nõukas, A. Teumer, **E. Salvi**, D. Cusi, et al (2015). Copy number variations and cognitive phenotypes in unselected populations. JAMA, vol. 313, p. 2044-2054, ISSN: 0098-7484, doi: 10.1001/jama.2015.4845
71. L. Olivi, C. Vandenbriele, Y. Gu, **E. Salvi**, S.D. Carpini, Y. Liu, L. Jacobs, Y. Jin, et al (2015). PEAR1 is not a human hypertension-susceptibility gene. BLOOD PRESSURE, vol. 24, p. 61-64, ISSN: 0803-7051, doi: 10.3109/08037051.2014.986928
72. L. Olivi, Y.M. Gu, **E. Salvi**, Y.P. Liu, L. Thijs, D. Velayutham, Y. Jin, L. Jacobs, F. D'Avila, T. Petit, M. Barcella, C. Lanzani, T. Kuznetsova, P. Manunta, C. Barlassina, D. Cusi, J.A. Staessen (2015). The -665 C>T polymorphism in the eNOS gene predicts cardiovascular mortality and morbidity in white Europeans. JOURNAL OF HUMAN HYPERTENSION, vol. 29, p. 167-172, ISSN: 0950-9240, doi: 10.1038/jhh.2014.66
73. M. Arismendi, M. Giraud, N. Ruzehaji, P. Dieudé, E. Koumakis, B. Ruiz, P. Airo, D. Cusi, M. Matucci-Cerinic, **E. Salvi**, G. Cuomo, et al (2015). Identification of NF-κB and PLCL2 as new susceptibility genes and highlights on a potential role of IRF8 through interferon signature modulation in systemic sclerosis. ARTHRITIS RESEARCH & THERAPY, vol. 17, p. 1-11, ISSN: 1478-6354, doi: 10.1186/s13075-015-0572-y
74. M. Chittani, R. Zaninello, C. Lanzani, F. Frau, M.F. Ortu, **E. Salvi**, G. Fresu, et al (2015). TET2 and CSMD1 genes affect SBP response to hydrochlorothiazide in never-treated essential hypertensives. JOURNAL OF HYPERTENSION, vol. 33, p. 1301-1309, ISSN: 0263-6352, doi: 10.1097/HJH.000000000000005
75. M. Gorski, A. et al. (2015). Genome-wide association study of kidney function decline in individuals of European descent. KIDNEY INTERNATIONAL, vol. 87, p. 1017-1029, ISSN: 0085-2538, doi: 10.1038/ki.2014.361
76. P.K. Joshi, et al. (2015). Directional dominance on stature and cognition in diverse human populations. NATURE, vol. 523, p. 459-462, ISSN: 0028-0836, doi: 10.1038/nature14618
77. T.P. Hiltunen, K.M. Donner, A. Sarin, J. Saarela, S. Ripatti, A.B. Chapman, J.G. Gums, Y. Gong, R.M. Cooper-DeHoff, F. Frau, V. Glorioso, R. Zaninello, **E. Salvi**, N. Glorioso, E. Boerwinkle, S.T.

- Turner, J.A. Johnson, K.K. Kontula (2015). Pharmacogenomics of hypertension: a genome-wide, placebo-controlled cross-over study, using four classes of antihypertensive drugs. *JOURNAL OF THE AMERICAN HEART ASSOCIATION. CARDIOVASCULAR AND CEREBROVASCULAR DISEASE*, vol. 4, p. 1-26, ISSN: 2047-9980, doi: 10.1161/JAHA.114.001521
78. Y. Liu, Y. Gu, L. Thijs, M.H.J. Knapen, **E. Salvi**, L. Citterio, et al (2015). Inactive matrix gla protein is causally related to adverse health outcomes: a mendelian randomization study in a flemish population. *HYPERTENSION*, vol. 65, p. 463-470, ISSN: 0194-911X, doi: 10.1161/HYPERTENSIONAHA.114.04494
79. C.J. Hoggart, G. Venturini, M. Mangino, F. Gomez, G. Ascari, J.H. Zhao, A. Teumer, T.W. Winkler, N. Tšernikova, J. Luan, E. Mihailov, G.B. Ehret, W. Zhang, D. Lamparter, T. Esko, A. Macé, S. Rüeger, P. Bochud, M. Barcella, Y. Dauvilliers, B. Benyamin, D.M. Evans, C. Hayward, M.F. Lopez, L. Franke, A. Russo, I.M. Heid, **E. Salvi**, S. Vendantam, D.E. Arking, et al. (2014). Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. *PLOS GENETICS*, vol. 10, p. 1-12, ISSN: 1553-7390, doi: 10.1371/journal.pgen.1004508
80. F. Frau, R. Zaninello, **E. Salvi**, M.F. Ortu, D. Braga, D. Velayutham, et al(2014). Genome-wide association study identifies CAMKID variants involved in blood pressure response to losartan : the SOPHIA study. *PHARMACOGENOMICS*, vol. 15, p. 1643-1652, ISSN: 1462-2416, doi: 10.2217/pgs.14.119
81. J. Knez, **E. Salvi**, V. Tikhonoff, K. Stolarz-Skrzypek, et al (2014). Left ventricular diastolic function associated with common genetic variation in ATP12A in a general population. *BMC MEDICAL GENETICS*, vol. 15, p. 1-10, ISSN: 1471-2350, doi: 10.1186/s12881-014-0121-6
82. K. Kiryluk, Y. Li, F. Scolari, S. Sanna-Cherchi, M. Choi, M. Verbitsky, D. Fasel, S. Lata, S. Prakash, S. Shapiro, C. Fischman, H.J. Snyder, G. Appel, C. Izzi, B.F. Viola, N. Dalleria, L. Del Vecchio, C. Barlassina, **E. Salvi**, F.E. Bertinetto, A. Amoroso, et al (2014). Discovery of new risk loci for IgA nephropathy implicates genes involved in immunity against intestinal pathogens. *NATURE GENETICS*, vol. 46, p. 1187-1196, ISSN: 1061-4036, doi: 10.1038/ng.3118
83. E. Koumakis, M. Bouaziz, P. Dieudé, B. Ruiz, G. Riemekasten, P. Airo, M. Müller-Nurasyid, D. Cusi, M. Matucci-Cerinic, I. Melchers, **E. Salvi**, K. Strauch, et al (2013). A regulatory variant in CCR6 is associated with susceptibility to antitopoisomerase-positive systemic sclerosis. *ARTHRITIS AND RHEUMATISM*, vol. 65, p. 3202-3218, ISSN: 0004-3591, doi: 10.1002/art.38136
84. **E. Salvi**, F. Becherucci, A. Bellasi, S. Bruno, G. Castellano, P. Esposito, G. Gentile, S. Netti, M. Papale, D. Ricci, F. Trepiccone, M. Zacchia (2013). L'Accademia delle idee: iniziativa dei giovani per i giovani. Contenitore di progetti innovativi?. *Giornale Italiano di Nefrologia*, vol. 32, p. 1-7, ISSN: 1724-5990
85. **E. Salvi**, T. Kuznetsova, L. Thijs, S. Lupoli, K. Stolarz-Skrzypek, F. D'Avila, V. Tikhonoff, S. De Astis, M. Barcella, J. Seidlerová, P. Benaglio, S. Malyutina, F. Frau, D. Velayutham, R. Benfante, L. Zagato, A. Title, D. Braga, D. Marek, K. Kawecka-Jaszcz, E. Casiglia, J. Filipovsky, Y. Nikitin, C. Rivolta, P. Manunta, J.S. Beckmann, C. Barlassina, D. Cusi, J.A. Staessen (2013). Target sequencing, cell experiments, and a population study establish endothelial nitric oxide synthase (eNOS) gene as hypertension susceptibility gene. *Hypertension*, vol. 62, p. 844-852, ISSN: 0194-911X, doi: 10.1161/HYPERTENSIONAHA.113.01428
86. E. Sommariva, C. Pappone, F. Martinelli Boneschi, C. Di Resta, M.R. Carbone, **E. Salvi**, P. Vergara, S. Sala, D. Cusi, M. Ferrari, S. Benedetti (2013). Genetics can contribute to the prognosis of Brugada syndrome: a pilot model for risk stratification. *EUROPEAN JOURNAL OF HUMAN GENETICS*, vol. 21, p. 911-917, ISSN: 1018-4813, doi: 10.1038/ejhg.2012.289
87. S. Lupoli, **E. Salvi**, C. Barlassina (2013). Dietary Salt Intake, Blood Pressure, and Genes. *Current nutrition reports*, vol. 2, p. 134-141, ISSN: 2161-3311, doi: 10.1007/s13668-013-0047-1
88. **E. Salvi**, D. Cusi (2012). Response to endothelial nitric oxide synthase polymorphism rs3918226 associated with hypertension does not affect plasma nitrite levels in healthy subjects. *Hypertension*, vol. 59, p. [1-2], ISSN: 0194-911X, doi: 10.1161/HYPERTENSIONAHA.112.194894
89. **E. Salvi**, Z. Kutalik, N. Glorioso, P. Benaglio, F. Frau, T. Kuznetsova, H. Arima, et al (2012). Genomewide association study using a high-density single nucleotide polymorphism array and case-control design identifies a novel essential hypertension susceptibility locus in the promoter region of endothelial NO synthase. *Hypertension*, vol. 59, p. 248-255, ISSN: 0194-911X, doi: 10.1161/HYPERTENSIONAHA.111.181990
90. V. Boraska, A. et al (2012). Genome-wide association study to identify common variants associated with brachial circumference: a meta-analysis of 14 cohorts. *PLOS ONE*, vol. 7, p. 1-10, ISSN: 1932-6203, doi: 10.1371/journal.pone.0031369
91. Farkash, H. Neuvirth, Y. Goldschmidt, C. Conti, F. Rizzi, S. Bianchi, **E. Salvi**, D.M. Cusi, A. Shabo (2011). A standard based approach for biomedical knowledge representation. In: *User Centred*

	Networked Health Care. STUDIES IN HEALTH TECHNOLOGY AND INFORMATICS, vol. 169, p. 689-693, IOS Press, doi: 10.3233/978-1-60750-806-9-689 92. L. Citterio, M. Simonini, L. Zagato, E. Salvi, S. Delli Carpini, C. Lanzani, E. et al (2011). Genes involved in vasoconstriction and vasodilation system affect salt-sensitive hypertension. PLOS ONE, vol. 6, p. 1-8, ISSN: 1932-6203, doi: 10.1371/journal.pone.00196 93. P. Dieudé, M. Bouaziz, M. Guedj, G. Riemekasten, P. Airo, M. Müller, D.M. Cusi, M. Matucci Cerinic, I. Melchers, W. Koenig, E. Salvi, et al (2011). Evidence for the contribution of the X chromosome to Systemic Sclerosis susceptibility: association with the functional IRAK1 196Phe/532Ser haplotype. ARTHRITIS AND RHEUMATISM, vol. 63, p. 3979-3987, ISSN: 0004-3591, doi: 10.1002/art.30640 94. S. Sawcer, Kim, et al (2011). Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. NATURE, vol. 476, p. 214-219, ISSN: 0028-0836, doi: 10.1038/nature10251 95. T. Johnson, et al (2011). Blood pressure loci identified with a gene-centric array. AMERICAN JOURNAL OF HUMAN GENETICS, vol. 89, p. 688-700, ISSN: 0002-9297, doi: 10.1016/j.ajhg.2011.10.013 96. Y. Allannore, M. Saad, P. Dieudé, J. Avouac, J.H. Distler, P. Amouyel, M. Matucci Cerinic, G. Riemekasten, P. Airo, I. Melchers, E. Hachulla, D.M. Cusi, H.E. Wichmann, J. Wipff, J.C. Lambert, N. Hunzelmann, K. Tiev, P. Caramaschi, E. Diot, O. Kowal-Bielecka, G. Valentini, L. Mouthon, L. Czirájk, N. Damjanov, E. Salvi, C. Conti, M. et al (2011). Genome-wide scan identifies TNIP1, PSORS1C1, and RHOB as novel risk loci for systemic sclerosis. PLOS GENETICS, vol. 7, p. e1002091-1-e1002091-13, ISSN: 1553-7390, doi: 10.1371/journal.pgen.1002091 97. C. Lanzani, L. Citterio, N. Glorioso, P. Manunta, G. Tripodi, E. Salvi, S.D. Carpini, M. et al (2010). Adducin- and ouabain-related gene variants predict the antihypertensive activity of rostafuroxin, part 2 : clinical studies. SCIENCE TRANSLATIONAL MEDICINE, vol. 2, 59ra87, ISSN: 1946-6234, doi: 10.1126/scitranslmed.3001814 98. F. Torri, A. Akelai, S. Lupoli, M. Sironi, D. Amann-Zalcenstein, M. Fumagalli, C. Dal Fiume, E. Ben-Asher, K. Kanyas, R. Cagliani, P. Cozzi, G. Trombetti, L.S. Lievers, E. Salvi, A. Orro, et al (2010). Fine mapping of AH1 as a schizophrenia susceptibility gene: from association to evolutionary evidence. FASEB JOURNAL, vol. 24, p. 3066-3082, ISSN: 0892-6638, doi: 10.1096/fj.09-152611 99. H. Lango Allen, et al (2010). Hundreds of variants clustered in genomic loci and biological pathways affect human height. NATURE, vol. 467, p. 832-838, ISSN: 0028-0836, doi: 10.1038/nature09410 100. S.G. Potkin, G. Guffanti, A. Lakatos, J.A. Turner, F. Kruggel, J.H. Fallon, A.J. Saykin, A. Orro, S. Lupoli, E. Salvi, M. Weiner, F. Macciardi (2009). Hippocampal atrophy as a quantitative trait in a genome-wide association study identifying novel susceptibility genes for Alzheimer's disease. PLOS ONE, ISSN: 1932-6203, doi: 10.1371/journal.pone.0006501 4(8):e6501 101. Orro, G.G. Guffanti Masetti, E. Salvi, F. Macciardi, L. Milanese (2008). SNPLims: a data management system for genome wide association studies. BMC BIOINFORMATICS, ISSN: 1471-2105, doi: 10.1186/1471-2105-9-S2-S13. 102. P. D'Ursi, E. Salvi, P. Fossa, L. Milanese, E. Rovida (2005). Modelling the interaction of steroid receptors with endocrine disrupting chemicals. BMC BIOINFORMATICS, vol. 6, p. 1-8, ISSN: 1471-2105, doi: 10.1186/1471-2105-6-S4-S10
--	---

Il presente CV ha funzione di autocertificazione ai sensi del D.P.R. n. 445 del 28/12/2000. Il sottoscritto è a conoscenza che, ai sensi dell'art. 76 del DPR 445/2000, le dichiarazioni mendaci, la falsità negli atti e l'uso di atti falsi sono puniti ai sensi del codice penale e delle leggi speciali. Inoltre, il sottoscritto autorizza al trattamento dei dati personali ai sensi dell'art. 13 GDPR 679/16 – "Regolamento europeo sulla protezione dei dati personali". Dichiaro altresì di essere informata che i dati personali raccolti saranno trattati, anche con strumenti informatici, esclusivamente nell'ambito del procedimento per il quale la presente dichiarazione viene resa, e che al riguardo competono alla sottoscritta i diritti previsti dall'art. 7 del medesimo provvedimento di legge.

Data: 09 ottobre 2025

F.to
ERIKA SALVI

"Il documento originale, con la sottoscrizione, è conservato agli atti della SC Gestione e Sviluppo delle Risorse Umane"