INFORMAZIONI PERSONALI

Prof. Giuseppe Matullo

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http://medchirurgia.campusnet.unito.it/do/docenti.pl/Show?_id=gmatullo#profilo;

Sesso M | Data di nascita 07/06/1967 | Nazionalità Italiana

POSIZIONE ATTUALE

- Professore Ordinario di Genetica Medica MED/03 presso il Dipartimento di Scienze Mediche, Scuola di Medicina, Università di Torino (dal 2018; Professore Associato dal 2006)
- Dirigente Biologo Ospedale Molinette, Servizio di Genetica Medica, Città della Salute e della Scienza, Torino (dal 2015)
- Responsabile dell'Unità "Genomic Variation, Complex Diseases and Population Medicine" presso il Dipartimento di Scienze Mediche), Università di Torino (dal 2006)
- Responsabile della Piattaforma di Analisi Genomica presso il DSM (dal 2018)

AREE DI RICERCA

- Genetica delle malattie complesse e interazioni geni-ambiente
- Genetica medica e di popolazioni
- Suscettibilità genetica nelle malattie cardiovascolari e metaboliche
- Genetica ed epidemiologia molecolare dei tumori
- Correlazione genotipo-fenotipo in relazione alla capacità di riparare i danni del DNA
- Polimorfismi e mutazioni nei geni della riparazione del DNA, suscettibilità tumorale e risposta alla terapia
- Genomica delle popolazioni umane e studi di associazione genome-wide nei tumori e in patologie cardiovascolari e metaboliche
- Epigenomica delle malattie complesse e cambiamenti epigenetici dovuti a esposizioni ambientali, dieta e stile di vita
- Analisi di mutazioni e della variabilità genetica umana tramite Next Generation Sequencing (NGS) su piattaforme Illumina (HiScanSQ e MiSeq): exome sequencing, pannelli custom (Agilent / Illumina).
- Whole-genome sequencing in campioni di popolazione ben caratterizzati dell'Italian Genome Project (IGP) e del Network for Italian Genomes (NIG)

SINOSSI DELLA RICERCA

Il prof. Giuseppe Matullo è ordinario di genetica umana presso il Dipartimento di Scienze Mediche, Università di Torino (Italia), Facoltà di Medicina e PI della Unità "Variabilità Genomica, Malattie Complesse e Mecicina di Popolazione". È un esperto riconosciuto a livello internazionale nell'analisi di studi di associazione genome- ed epigenome-wide (GWAS ed EWAS) di tratti complessi, cancro (ad es. vescica e mesotelioma), malattie cardiovascolari (CVD) e altre malattie croniche. Le competenze del Prof. Matullo coprono diversi aspetti della genetica molecolare delle malattie complesse, dalla variazione genomica, alla trascrizione, alla regolazione dell'espressione (metilazione del DNA e miRNA), tutte da indagare congiuntamente con l'esposizione ambientale ed i fattori dello stile di vita (interazioni gene-ambiente). Ha anche indagato la lunghezza dei telomeri e la metilazione del DNA come misura dell'età biologica e come risultato dell'interazione tra fattori genetici e ambientali nello sviluppo di malattie croniche. Il gruppo del prof. Matullo ha una lunga esperienza nell'applicazione di tecniche di genetica molecolare ad alta processività (High-Throughput) per lo studio di ampie popolazioni (ad esempio, lo studio EPIC, 500.000 volontari in tutta Europa). In particolare, il suo gruppo è stato coinvolto per molti anni nell'analisi della correlazione genotipo-fenotipo della riparazione del DNA, nell'identificazione di biomarcatori correlati all'alimentazione e al cancro / CVD (progetto ECNIS, EPIC-CVD). La lunghezza dei telomeri dei leucociti (LTL) è stata misurata in EPIC-CVD (42.000 individui) e in altre malattie croniche in diversi progetti collaborativi in relazione ad esposizioni / stile di vita ambientale, attività di riparazione del DNA, stress ossidativo, invecchiamento. Negli ultimi anni ha utilizzato ampiamente approcci di sequenziamento Next Generations che includono ampi pannelli genici, sequenziamento dell'esoma e dell'intero genoma sia nel campo patologico che negli studi di popolazione. Il suo gruppo ha svolto numerose ricerche nel campo della medicina traslazionale in oncologia (tra i quali il cancro alla vescica e il mesotelioma) per l'identificazione di biomarcatori omici (in particolare la variazione genomica, la metilazione del DNA e il profilo dei miRNA) che possano essere utilizzati per la diagnosi precoce, la stratificazione dei pazienti per la

prognosi e terapie personalizzate. In particolare, ha prodotto un brevetto basato su miRNA in grado di identificare, mediante un dosaggio urinario non invasivo, pazienti con carcinoma della vescica da controlli sani (brevetto UROMIRNA).
L'analisi dei profili di metilazione del DNA nelle cellule del sangue sta permettendo anche di ottenere informazioni specifiche sul reale invecchiamento biologico individuale, in particolare in relazione all'invecchiamento del sistema immunitario, con nuove evidenze su potenziali interventi di immunoprevenzione e immunoterapia.
Nel 2016 il Prof. Matullo ha fondato, insieme ad altri noti genetisti italiani e con il sostegno della Società Italiana di Genetica Umana (SIGU), il Network dei Genomi Italiani (NIG; http://www.nig.cineca.it/); una partnership che include diverse università e ospedali pubblici (Torino, Milano, Pavia, Bologna, Trieste, Siena, Roma, Napoli) con l'obiettivo di raccogliere migliaia di esomi e genomi prodotti mediante sequenziamento massivo parallelo, e avere un quadro completo della distribuzione di varianti genetiche / aplotipi in Italia per scopi di genetica clinica e di popolazione, applicazioni forensi e di farmacogenetica.
Negli ultimi anni ha svolto un lavoro importante con il suo gruppo di ricerca nel campo della medicina traslazionale in oncologia (es. Cancro alla vescica, mesotelioma e cancro al seno) alla ricerca di biomarcatori omici (in particolare genomica, metilazione del DNA e profilazione di miRNA) finalizzato alla diagnosi precoce, alla stratificazione dei pazienti per la prognosi e alle terapie personalizzate.

ESPERIENZE LAVORATIVE

2018-2020:	Professore Ordinario di Genetica Medica MED/03 presso il Dipartimento di Scienze Mediche, Scuola di Medicina, Università di Torino
2006-2018:	Professore Associato di Genetica Medica MED/03 presso il Dipartimento di Scienze Mediche, Scuola di Medicina, Università di Torino
2010-2018:	Direttore dell'Unità “Genomic Variation and Translational Research” presso l’Italian Institute for Genomic Medicine (IIGM – ex HuGeF), Torino
2006-2010:	Vice-direttore della Sezione Life-Sciences presso la Fondazione I.S.I (Institute for Scientific Interchange), Torino
2000-2010:	Responsabile dei laboratori di Genetica ed Epidemiologia Molecolare della Fondazione I.S.I (Institute for Scientific Interchange), Torino
1998-2006:	Tecnico di ricerca presso il Dip. di Genetica, Biologia e Biochimica, Università di Torino, Facoltà di Medicina e Chirurgia
Ago-Ott 1997:	ricercatore borsista presso il Rangos Research Center (Università di Pittsburgh, PA, USA) nel laboratorio di Genetica Molecolare (Immunogenetica) diretto dal Prof. Massimo Trucco.
Agosto 1991:	ricercatore borsista presso il laboratorio del Prof. L.L. Cavalli-Sforza, Dip. di Genetica, Università di Stanford University, CA.
Sett-Nov 1991:	ricercatore borsista presso il Rangos Research Center (Università di Pittsburgh, PA, USA) nel laboratorio di Genetica Molecolare (Immunogenetica) diretto dal Prof. Massimo Trucco.

ISTRUZIONE E FORMAZIONE

Ottobre 1999 **MSc**

Università di Pavia, European Schools for Advanced Studies, Italia

- Statistical Genetics

Aprile 1997 **PhD**

Università di Torino, Italia

- Genetica Umana

Agosto-Ottobre 1997

- Ricercatore borsista presso il Rangos Research Center, Università di Pittsburgh (PA, USA), Prof. Massimo Trucco

March 1991 **BScD**

Università di Torino, Italia

- Scienze Biologiche

Agosto-Novembre 1991

- Ricercatore Borsista, Dipartimento di Genetica, Università di Stanford (CA, USA), Prof. L.L. Cavalli-Sforza.
- Ricercatore Borsista presso il Rangos Research Center, Università di Pittsburgh (PA, USA), Prof. Massimo Trucco

ATTIVITA' ASSISTENZIALE

Dal 2015

Il Prof. Matullo ha contribuito all'allestimento della facility di Next Generation Sequencing (NGS) presso il Servizio di Genetica Medica dell'AOU "Città della salute e della Scienza" (Torino), contribuendo sia alla scelta delle tecnologie di laboratorio, sia a livello bioinformatico, con la messa a punto di pipeline utilizzabili anche da personale non bioinformatico per l'analisi di dati di sequenziamento di pannelli di geni prevalentemente oncologici. In particolare, è attualmente coinvolto nelle analisi bioinformatiche e nella refertazione di test genetici di pazienti con cancro al seno e all'ovaio in qualità di dirigente biologo presso la S.C. Genetica Medica U (Presidio Molinette) Direttore, prof.sa Barbara Pasini. La SC Genetica Medica U (presidio Molinette) e la SS Diagnosi e Consulenza Genetica (presidio OIRM-Sant'Anna) sono state unificate di in un'unica struttura complessa che assolve a quanto previsto dalla DGR n. 30-4855 del 31.10.2012 ovvero l'istituzione del "Centro Regionale di riferimento per la Genetica Medica".
In questo contesto, negli ultimi 6 anni l'attività assistenziale del prof. Matullo si è focalizzata principalmente sull' analisi dei geni di predisposizione allo sviluppo dei tumori della mammella e dell'ovaio in Next generation Sequencing con pannelli multigenici. Il test ha subito un aumento delle richieste nel corso della seconda metà dell'anno 2015, anche in regime urgenza, per le seguenti ragioni: i) le pazienti affette da tumore ovarico platino-sensibile in ripresa di malattia possono giovarsi del nuovo farmaco "Olaparib" se portatrici di mutazione dei geni BRCA1 o BRCA2, ii) le pazienti affette da tumori della mammella-triplo negativi hanno una probabilità di mutazione dei geni BRCA1 e BRCA2 anche a prescindere dalla storia famigliare e pertanto rientrano tra i soggetti eleggibili al test genetico; iii) le pazienti affette da neoplasia della mammella giovanile (< 36 anni), triplo-negativo (< 50 anni) o con spiccata famigliarità devono poter accedere al test genetico prima del trattamento chirurgico al fine di poter offrire in alternativa al trattamento conservativo una eventuale mastectomia bilaterale se portatrici di mutazione dei geni BRCA1 o BRCA2. L'esecuzione dell'analisi con metodica NGS ha consentito quindi di poter far fronte all'aumento della domanda, velocizzando anche con l'analisi di CNV utilizzando kit specifici.
Il prof. Giuseppe Matullo ha maturato negli anni una notevole competenza nell'utilizzo di metodiche di laboratorio ad "alta processività" per l'analisi della variabilità del genoma umano, nell'analisi bio-informatica di varianti genetiche e nell'organizzazione di gruppi e laboratori di ricerca comprovata dal ruolo svolto presso l'Italian Institute for Genomic Medicine (IIGM) come responsabile della linea di ricerca "Variabilità genomica delle popolazioni umane e malattie complesse", oltre che essere responsabile della piattaforma Genomica del Dipartimento di Scienze Mediche, che ha allestito nell'ambito del progetto d'Eccellenza (2018-2022). Tali competenze sono messe a disposizione del Servizio di Genetica Medica per contribuire ad adottare innovazioni tecnologiche all'avanguardia e a velocizzare i processi di analisi, aumentando il numero di geni indagati simultaneamente.

ATTIVITA' DIDATTICA

Dal 1998	Insegnamento di Genetica umana e medica nel corso di Tecnico di laboratorio, Tecnico di Riabilitazione, Fisioterapista, Ortopedico e Logopedista presso la Scuola di Medicina dell'Università di Torino, Italia.
Dal 1998	Insegnamento di Genetica Medica nei corsi di specializzazione in Genetica Medica e Cardiologia, Università di Torino, Italia.
2001 e 2003	Organizzazione e insegnamento nel "Corso Internazionale di Epidemiologia Molecolare", I.S.I. Fondazione, Villa Gualino, Torino, Italia, quarta e sesta edizione.
2002-2010	Organizzazione e insegnamento nel corso di Epidemiologia molecolare presso il Dipartimento di Scienze Biomediche e Oncologia Umana dell'Università di Torino, Italia.
Dal 2003	Consiglio della Scuola di Dottorato in Scienze Biomediche e Oncologia Umana, Università di Torino, Italia.
Dal 2006	Insegnamento di Genetica umana e medica, Facoltà di Medicina e Scuola di Medicina, Università di Torino, Italia.
Dal 2011	Coordinatore del programma di genetica umana nell'ambito della scuola di dottorato in oncologia e scienze biomediche
Dal 2011	Insegnamento di genetica medica presso la Scuola di scienze alimentari e nutrizione umana, Università di Torino, Italia.
Dal 2014	Insegnamento di genetica medica presso il Corso di Laurea in Dietistica, Università di Torino, Italia.
Dal 2017	Comitato didattico e di facoltà del Master in Immunogenetica e biologia dei trapianti
Dal 2017	Insegnamento al Master of Psico-Neuro-Endocrino-Immunologia (PNEI)
Dal 2017	Insegnamento di Genetica Medica nei corsi di specializzazione in Statistica Sanitaria e Biometria, Università di Torino, Italia.

Alla presente anno accademico, le ore di didattica frontale del prof Matullo superano le 120 ore come richiesto da contratto universitario.

ALTRI IMPEGNI ISTITUZIONALI

1) Commissione Ricerca Dipartimento di Scienze Mediche (DSM)
2) Coordinatore del curriculum di Genetica Umana della Scuola di dottorato in Scienze Biomediche e Oncologia Umana (SBO)
3) Membro del collegio dei docenti della scuola di dottorato SBO
4) Commissioni di Laurea e tesi di dottorato
5) Commissioni di concorso
6) Commissione progetto strategico d'Eccellenza
7) Gruppi di lavoro DSM per piattaforma Genomica e Bioinformatica
8) Commissione convalida esami CCL Fisioterapia
9) Commissione Tecnici di Ricerca
10) Consiglio della Scuola di Medicina
11) Commissione di Giunta del DSM

FINANZIAMENTI

Progetti

- Italian Association of Cancer Research (AIRC) grant (2004-2007): "EPIC-Italy: a molecular epidemiology prospective project on diet, genetic susceptibility and cancer risk".
- Italian Association of Cancer Research (AIRC) grant (2004-2007): "Network of molecular epidemiology of cancer in Italy"
- European Community grant "ECNIS" (2005-2010): ECNIS (Environmental Cancer Risk, Nutrition and Individual Susceptibility) is a Network of Excellence operating in the context of the 6th EU Framework Programme for Research and Development (FP6).
- Italian Association of Cancer Research (AIRC) grant (2006-2008): "DNA repair genotype-phenotype correlation and cancer-risk". (P.I.)
- Grant "Progetti di ricerca sanitaria finalizzata anno 2007" (2007-2008), Direzione di Sanità Pubblica: "Identification of functional polymorphisms in DNA repair genes in lymphoblastoid cell lines: cancer risk and response to therapy". (P.I.)
- MIUR ex60% (2007): "DNA repair capacity interindividual variability in relation to prognosis and chemosensitivity". (P.I.)
- Grant "Progetti di ricerca sanitaria finalizzata anno 2008" (2008-2009), Direzione di Sanità Pubblica: "Mutation detection in exfoliated bladder cells in urine for the diagnosis and the monitoring of bladder cancer". (P.I.)
- Grant "Progetti di ricerca sanitaria finalizzata anno 2008bis" (2008-2009), Direzione di Sanità Pubblica: "Identification of genes/polymorphisms involved in bladder cancer through replication of genome-wide association studies". (P.I.)
- Grant "Progetti di ricerca sanitaria finalizzata anno 2008bis" (2008-2009), Direzione di Sanità Pubblica: "Replication of genome-wide association studies on an independent sample of young AMI patients".
- Grant "Progetti di ricerca sanitaria finalizzata anno 2009" (2009-2010), Direzione di Sanità Pubblica: "Endometrial cancer and diet risk factors. A case-control study in the Turin population". (P.I.)
- Grant "Progetti di ricerca sanitaria finalizzata anno 2009" (2009-2010), Direzione di Sanità Pubblica: "Association between leucocyte telomere length and AMI in young patients".
- Grant Project EPICOR2 San Paolo (2008-2010): Risk of cardiovascular events associated to life style, biomarkers and genetic susceptibility in the frame of the EPICOR Italian and European collaboration. (P.I.)
- European Community grant "ECNIS2" (2011-2013): ECNIS (Environmental Cancer Risk, Nutrition and Individual Susceptibility) (FP7).
- Grant Medical Research Council (MRC) and the British Heart Foundation (BHF): "EPIC-Heart" (2010-2012), Cambridge, UK
- European Community grant "EPIC-CVD 7th EU Framework Programme (FP7).
- MIUR ex60% (2012): "Analisi epigenomica nell'infarto del miocardio in relazione a stile di vita, indicatori biologici e di suscettibilità genetica nell'ambito dello studio prospettico EPIC-Italia". (P.I.)
- Grant Hugef to the Unit "Genomic Variation of Human Population and Complex Diseases (2010-2015)"
- Grant Fondazione Veronesi (2013-2015): DNA REPAIR CAPACITY, TELOMERE LENGTH AND EPIGENETIC CHANGES AS AGING BIOMARKERS IN BLADDER CANCER. (P.I.)
- Grant AIRC IG 17464 "Blood DNA methylation changes and plasma microRNA associated to asbestos-exposure and Malignant Pleural Mesothelioma" (2016-2018) (P.I.)
- Grant supported by the Italian Ministry for Education and Research – MIUR project (2018 – 2022), "Departments of Excellence 2018 – 2022" TESEO Traguardi di Eccellenza nelle Scienze mediche Esplorando le Omiche.
- Grant AIRC IG (2019-2023) Non-invasive predictive and prognostic biomarkers in Malignant Pleural Mesothelioma: from preclinical to clinical models (PI)

- Grant H2020-JTI-IMI2-2017-13-two-stage (2019-2023) CARDIATEAM project on Diabetic Cardiomyopathy (P.I. di Unità)
- Grant H2020 INTERVENE, International consortium for integrative genomics prediction. Applicare alla diagnostica clinica Score di Rischio Poligenici nell'ambito del tumore al seno e di patologie cardiovascolari.

SEMINARI

Selezione di seminari recenti e comunicazioni ad invito

- GDL SIGU METILAZIONE DNA 18-19 SETTEMBRE Meeting Webinar, Riunione congiunta di tutti i Gruppi di Lavoro SIGU "Analisi della metilazione genome-wide in diagnostica genetica", 18-19 settembre 2020. Presentazione orale Matullo: "Studi di associazione epigenomica e fenotipi complessi".
- Comunicazione orale su invito al 5° Simposio Interregionale di Urologia "Torino Urologicamente Barocca"- Torino, 16-17 novembre 2018. Lecture: Epigenomica delle malattie complesse e tumorali
- 14th International Conference of the International Mesothelioma Interest Group (iMig 2018). Ottawa, 2-5 May 2018. Partecipanti: G. Matullo. Presentazione orale G. Matullo "Peripheral Blood DNA Methylation as Potential Biomarker for Malignant Pleural Mesothelioma in Asbestos-Exposed Subjects".
- The Future of Genetics in Medicine and beyond", Palazzo Carignano, 22-23/06/2017, Torino. Presentazione Orale: G. Matullo: Genomic and epigenomic variability in complex diseases.
- Comunicazione orale su invito su "Le nuove frontiere della genetica: genomica e fattori epigenetici", Lecture inaugurale dell'anno accademicodell'Universita' della Terza Eta' di Moncalieri, Torino, Italia, Istituto Carlo Alberto, Moncalieri, 4 Oct. 2017.
- Comunicazione orale su invito su "Genomic and epigenomic variability in complex diseases",
- Comunicazione orale su invito alla conferenza "First Italian 3i pathways in uro-oncology: Improve, Identify, Individualize "Optimal bladder clancer diagnosis and treatment". 16-17/06// 2017.
- Comunicazione orale su invito su ""The genomic structure of Italian population and the Network for Italian Genomes" alla conferenza "From the genome for all to the genome of all", 19/04/2017, Verona.
- Seminario su invito "Epigenomics of Cardiovascular Diseases" al workshop su "Methylation array meeting", Imperial College London, London, UK, 12/04/2017.
- Seminario "Un database di riferimento dei dati genomici italiani. Discussione, esercitazioni e simulazioni" durante il corso "Geni e test genetici: dal laboratorio alle applicazioni cliniche"(2018), modulo "VARIABILITA' E GENOMA UMANO, Istituto Mendel, Roma, (29/09/ 2017);
- Seminario "Una mappa di riferimento della popolazione italiana" durante il corso "Geni e test genetici: dal laboratorio alle applicazioni cliniche"(2018), modulo "NGS e le sue applicazioni. Strategie di analisi e gestione del risultato. Isolati genetici, NGS e tratti complessi ", Istituto Mendel, Roma, (9-10/6/2016);
- Presentazione orale "Una mappa di riferimento della popolazione italiana" alla conferenza XVII Annual meeting SIGU, Rimini, 21/10/ 2015
- Comunicazione orale su invito "Modificazioni epigenetiche, esposizione ad asbesto e rischio di mesothelioma" durante il workshop congiunto GdL Genetic Oncology e GdL of Epigenetics, Rimini, 21/10/ 2015
- Lecture nel contesto di "Rehbruecke Colloquium", Epigenomic changes and telomere length in chronic diseases, DIFE, 18/02/2015, Postdam, Germania.
- Presentazione orale Completion of telomere length measurements and proposal for statistical plan. EPIC-CVD Meeting, 25/04/ 2014, Cambridge, UK.
- Presentazione orale. Preliminary data on telomere length in EPIC-CVD. EPIC-CVD Meeting, 25/04/ 2014, Cambridge, UK.
- Comunicazione orale su invito Epigenomics of myocardial infarction. 3rd World Genetics & Genomics Online Conference, 20-22/05/2014.
- Comunicazione orale su invito Epigenomics, Environment and complex diseases: myocardial infarction. Istituto Mendel, 16/06/2014, Roma, Italia.
- Presentazione orale Epigenomics of myocardial infarction. XVI Congresso Nazionale

SIGU, 25-27/09/2013 Roma, Italia.
- Presentazione orale Leukocyte telomere length measurements in EPIC-CVD. EPIC-CVD meeting, 23/05/2013, Cambridge, UK.
- Presentazione orale. Leukocyte telomere length in EPIC-CVD: validation, QC and analytical plans. EPIC-CVD meeting, 10/11/2013, Cambridge, UK.
- Comunicazione orale su invito DNA repair genotype-phenotype correlation: from cancer risk to therapy response. Golden Helix Symposia; Genomic Medicine: Translating Genes into Health. 18-21/04/2012, Torino, Italia .
- Presentazione orale. Identificazione di fattori di rischio genetici nello sviluppo del mesotelioma pleurico (MPM): uno studio di associazione caso-controllo genome-wide. XV Congresso Nazionale SIGU, 21-25/11/2012, Sorrento, Italia.
- Presentazione orale Genomic variation in human populations and complex diseases. ESOF, EuroScience Open Forum, 2-7/07/2010, Torino, Italia.

Riconoscimenti e Premi

- Membro del Comitato Scientifico e relatore di diversi corsi nell'ambito della Scuola Medica Ospedaliera 2016-2017, 2017-2018, 2018-2019, 2019-2020, 2020-2021 (21 ECM ciascuno); Geni e test genetici: dal laboratorio alle applicazioni cliniche. Istituto Mendel, Roma, Italia
Chairman e organizzatore della sessione "MUTATION AND EPIMUTATION LOAD IN NORMAL TISSUE" al congresso della Società Italiana di Genetica Umana (SIGU) 2019, Roma, Italia.-
Chairman della sessione Concurrent Symposia S05-08 & Educational Sessions E08-E09-S05 | Large-scale genetic studies in complex diseases, European Human Genetics Conference (annual ESHG meeting), Milano, 16-19 Giugno 2018.
- Membro del Comitato Scientifico e Chairman della Società Italiana di Genetica Umana (SIGU) 2016, e organizzatore e chariman della Tavola Rotonda sul Network dei Genomi Italiani, Torino, Italia
- Chairman e organizzatore della Tavola Rotonda sul Network dei Genomi Italiani, al congresso della Società Italiana di Genetica Umana (SIGU) 2015, Rimini, Italia
- Chairman e organizzatore della sessione "Genomica Funzionale" al congresso della Società Italiana di Genetica Umana (SIGU) 2013, Milano, Italia.
- Chairman e organizzatore della sessione "Malattie Complesse" al congresso della Società Italiana di Genetica Umana (SIGU) 2009, Torino, Italia.
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Membro di organizzazini scientifiche

- Membro della Società Italiana di Genetica Umana (SIGU)
- Membro della European Society of Human Genetics (ESHG)
- Membro della American Society of Human Genetics (ASHG)
- Membro della American Association of Cancer Research (AACR)
- Membro Comitato Esecutivo della Società Italiana di Biometria (SIB) (2000-2003)
- Membro dello "Study Group on DNA repair" coordinato dal Prof. Kraemer K. (http://sigs.nih.gov/DNA-repair/Pages/default.aspx)
- Membro dell'International Consortium on Bladder Cancer (ICBC)
- Membro dell'International Mesothelioma Interest Group (IMIG)
- Membro del Centro Interdipartimentale "G. Scansetti" per lo studio dell'asbesto e di altre fibre tossiche.
- Membro e Fondatore del Network for Italian Genomes (NIG; http://www.nig.cineca.it/)

ULTERIORI INFORMAZIONI

Metrica pubblicazioni

IF TOTALE: >1350
IF MEDIO: 6.39
H-INDEX: 54 (Scopus)
Citazioni: 14,735

Pubblicazioni

(N=217; https://pubmed.ncbi.nlm.nih.gov/?term=matullo+g&sort=date&size=200)
(Vedi file completo pubblicazioni allegato)

Pubblicazioni

1. Cugliari G, Allione A, Russo A, Catalano C, Casalone E, Guarrera S, Grosso F, Ferrante D, Sculco M, La Vecchia M, Pirazzini C, Libener R, Mirabelli D, Magnani C, Dianzani I, **MATULLO G**. New DNA Methylation Signals for Malignant Pleural Mesothelioma Risk Assessment. Cancers (Basel). 2021 May 27;13(11):2636. doi: 10.3390/cancers13112636. PMID: 34071989; PMCID: PMC8199167.

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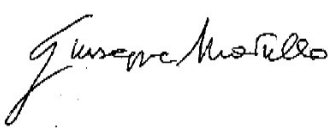

Dati personali Autorizzo il trattamento dei miei dati personali ai sensi del Decreto Legislativo 30 giugno 2003, n. 196 "Codice in materia di protezione dei dati personali".