Curriculum Vitae

PERSONAL INFORMATION Alessia Russo

Sex Female | Date of birth 26/06/1985 | Nationality Italian

alessia.russo@unito.it

WORK EXPERIENCE

From 1st Oct 2019

Research Technician

University of Turin, Department of Medical Sciences, Via Santena, 19, Torino (TO), Italy

Jul 2018 – Sep2019

Post-doc Researcher

University of Turin, Department of Medical Sciences, Via Santena, 19, Torino (TO), Italy

"Assegnista di Ricerca" Project: "Use of Next Generation Sequencing approaches in patients with familial breast cancer and melanoma"

Jan 2016 – Jun 2018

Post-doc Researcher

Italian Institute for Genomic Medicine (IIGM) (FKA HuGeF) Via Nizza 52, Torino (TO), Italy

Application of Next Generation Sequencing approaches in oncology (mainly breast cancer and infant acute lymphoblastic leukemia).

Feb 2016 – Aug 2016

Collaborator for Next Generation Sequencing protocol set-up and introduction in breast and ovarian cancer diagnostics.

AOU Città della Salute e della Scienza – Genetic Unit (Director: Prof. Barbara Pasini), Via Santena, 19 - Torino (TO), Italy

Mutations analysis of breast and ovarian cancer panel genes: protocol set-up for Next Generation Sequencing, library preparation, sequencing on Illumina platform, troubleshooting, data analysis through SureCall software (Agilent) and in-house pipelines, variants prioritization through database and prediction software.

Jan 2015 – Dec 2015

Post-doc Researcher

Human Genetics Foundation (HuGeF) Via Nizza 52, Torino (TO), Italy

Laboratory of Genomic Variation in Human Population and Complex Disease.

Fellowship granted by Fondazione Umberto Veronesi on the project: "Telomere length and epigenetic changes as aging risk biomarkers in myocardial infarction patients".
Analysis and validation of aging biomarkers such as telomere length and DNA methylation profiles.
Exome sequencing library preparation Analysis of next generation sequencing data
Interpretation of next generation sequencing variants.

Jan 2011 – Dec 2014

PhD Student

University of Turin and Human Genetics Foundation (HuGeF) Via Nizza 52, Torino (TO), Italy

Laboratory of Genomic Variation in Human Population and Complex Disease. Principal Investigator: Prof. Giuseppe Matullo

Telomere length analysis in large population studies of bladder cancer, lymphoma and myocardial infarction.
Genome-wide DNA methylation analysis in relation to myocardial infarction.
Next generation sequencing of cancer genes panels in patients with multiple tumors.
Elaboration and interpretation of data.
Writing and revision of scientific articles.
Collaboration to scientific projects writing.
Poster and oral presentation of data in both national and international conferences.

Nov 2009 – Dec 2010

Post-graduate Fellow

Italian Institute for Scientific Interchange (ISI Foundation) Former address: Viale Settimio Severo 63 - Torino (TO) Italy. Current address: Via Alassio, 11/C, 10126 Torino, Italy.

Laboratory of Molecular Epidemiology. Project: “DNA repair gene expression profiles and polymorphisms in cancer patients: chemotherapy responsiveness and prognostic factors.”

Project: “DNA repair gene expression profiles and polymorphisms in cancer patients: chemotherapy responsiveness and prognostic factors”.
Genotyping and expression profiles in DNA repair genes using Taqman assays
Comet assay to test Nucleotide Excision Repair pathway
Genotype-phenotype correlation

EDUCATION AND TRAINING

January 27th 2015

PhD in Biological Sciences and Human Oncology

University of Study of Turin, TORINO (TO) ITALIA

Medical Genetics, Scientific English, Medical Statistics, journal club activity on Medical Genetics issues. Laboratory activity aimed at the compilation of the experimental thesis. Ability to elaborate and present, graphically and verbally, scientific data in both Italian and English language.

March 2008 – Oct 2009

Molecular Epidemiology Laboratory Trainee

Italian Institute for Scientific Interchange (ISI Foundation). Former address: Viale Settimio Severo 63 - Torino (TO) Italy. Current address: Via Alassio, 11/C, 10126 Torino, Italy.

Principal Investigator: Prof. Giuseppe Matullo

Single Nucleotide Polymorphisms genotyping using Taqman assays.
DNA repair analysis using Comet assay.
Genotype-phenotype correlation analysis.
DNA isolation from blood and lymphocytes.
Agarose gel electrophoresis.
RNA isolation from blood and gene expression analysis using Taqman assays.
Isolation of human lymphocytes using Ficoll.
Isolation of exfoliated bladder cells from urine.
Basic knowledge of cell cultures.

September 29th 2009

Master Degree in Medical Biotechnology

University of Study of Turin, TORINO (TO) ITALIA

Final mark: 110/110
Oncology, Human Anatomy, Human Pathology, Human Physiology.

Oct 2006 – Oct 2007

Pharmacology Laboratory Trainee

University of Study of Turin, TORINO (TO) ITALIA
Principal Investigator: Prof. Carola Eva

DNA isolation from mice tails.
Agarose gel electrophoresis.
Gene knock-out confirmation through PCR.

October 1st 2007

Bachelor Degree in Biotechnology

University of Study of Turin, TORINO (TO) ITALIA

Final mark: 102/110
Human and Plant Biology, Molecular Biology, Cellular Biology, Microbiology, Human Genetics, Chemistry, Biochemistry, Pharmacology, Immunology, English.

July 2004

Italian Secondary School Diploma: SCIENTIFIC CERTIFICATE

Liceo Scientifico Statale “Galileo Ferraris”, Torino (TO). Italia

School-leaving examination taken in (year): 2004. Final mark: 80/100

PERSONAL SKILLS

Mother tongue(s) Italian

Other language(s)

	UNDERSTANDING		SPEAKING		WRITING
	Listening	Reading	Spoken interaction	Spoken production	
English	B2	B2	B2	B2	B2

Levels: A1/A2: Basic user - B1/B2: Independent user - C1/C2 Proficient user
Common European Framework of Reference for Languages

Communication skills

Excellent ability to work in a team reached through years working together with a range of different professionals, such as Biologists, Laboratory Technicians, Mathematicians, and Bioinformaticians.
Willingness to share information and experiences. Excellent capacity to adapt to different situations and to manage stress. I am very critical of my work and I have a strong motivated work ethic. Good communication skills, obtained through several poster and oral presentations, in both Italian and English, in the frame of many national and international conferences, and during the PhD activities.

Organisational / managerial skills

Excellent organizational abilities and work optimization. Organization and managing of laboratory activities with University and High School students as well as Primary School children. I am hard-working and determined to reach my objectives on schedule and independently.

Job-related skills

DNA/RNA isolation from blood through manual and automated protocols (Qiasymphony, Qiagen, etc.), agarose gel electrophoresis, DNA/RNA spectrophotometric and fluorometric quantification. Creation, optimization, and use of scripts for automated dilution and liquid handling (TECAN Freedom EVO 100 and 150). Excellent ability to handle with a huge number of samples, obtained thanks to the use of large population studies (i.e. EPIC study). RNA retrotranscription.
Genotyping and expression analysis using RealTime-PCR. Isolation of bladder cells from urine. Lymphocyte isolation using Ficoll-Paque PLUS. DNA repair capacity analysis through Comet assay. PCR validation. Telomere length analysis using both singleplex and multiplex RealTime-PCR. Epigenome-wide analysis through Illumina platform. Library preparation for cancer genes panels sequencing on the MiSeq System (Illumina) an for exome sequencing on the NextSeq500 System (Illumina). Sequencing data analysis using the VariantStudio (Illumina) and SureCall (Agilent) software. Basic knowledge of sequence analysis through in-house pipeline. Basic knowledge of Linux operative system and of the R language. Use of on-line databases (i.e. NCBI, UCSC Genome Browser, etc.) and of tools for sequence variants interpretation (IGV, Sift, Polyphen, Annovar, SnpEff, etc.). Pathway enrichment analysis (i.e DAVID and GSEA functional annotation tools). Laboratory validation of splicing variants.
Databases management. Data interpretation. Basic knowledge of Medical Statistics.
Writing and revision of scientific manuscripts and collaboration to the writing of scientific projects.

Digital skills

Excellent command of Office package (word processor, spread sheet, presentation software). Basic knowledge of Linux Operative System and R language

Driving licence B

ADDITIONAL INFORMATION

Telomere length assay validation at the MRC Epidemiology Unit (Prof. Matt Sims), Addenbrooke's Hospital, Cambridge, UK,January 6th-11th 2014.

Laboratory activities with High School students in the frame of the project “PCTO - Percorsi per le Competenze Trasversali e l'Orientamento”. “I segreti degli acidi nucleici”:

- 16/6/2021-25/6/2021. Russo A., Di Gaetano C., Matullo G.
- 27/6/2022 – 1/7/2022. Russo A. Allione A., Matullo G.

Publications

- "Blood cell DNA methylation biomarkers in preclinical malignant pleural mesothelioma: The EPIC prospective cohort". Allione, A. et al. International Journal of Cancer 2023. IF: 7.3
- "Serum Extracellular Vesicle-Derived microRNAs as Potential Biomarkers for Pleural Mesothelioma in a European Prospective Study". Casalone, E. et al. Cancers 2023. IF: 6.6
- "Genetic and epigenetic characterization of a discordant kmt2a/aff1-rearranged infant monozygotic twin pair". **Russo A.** et al; International Journal of Molecular Sciences 2021. IF: 6.2
- "New DNA methylation signals for malignant pleural mesothelioma risk assessment". Cugliari, G. et al. Cancers 2021. IF: 6.6
- "Functional and clinical implications of genetic structure in 1686 Italian exomes"; Birolo G et al; Hum Mutat. 2021. IF: 4.1.
- "DNA Methylation of FKBP5 as Predictor of Overall Survival in Malignant Pleural Mesothelioma"; Cugliari G et al. Cancers (Basel). 2020. IF: 6.1.
- "Genome-wide Association Analysis in Humans Links Nucleotide Metabolism to Leukocyte Telomere Length"; Chen Li et al; Am J Hum Genet. 2020. IF: 10.5.
- "Advances in genetics of hypertension: the effect of rare variants"; **Russo A.** et al; International Journal of Molecular Sciences (2018). IF: 3.687.
- "H2AX phosphorylation level in peripheral blood mononuclear cells as an event-free survival predictor for bladder cancer"; Turinetto V et al ; Molecular Carcinogenesis (2016). IF: 3.851.
- "Gene-specific DNA methylation profiles and LINE-1 hypomethylation are associated with myocardial infarction risk."; Guarrera S et al ; Clin Epigenetics (2015). IF: 6.091.
- "Genome-wide association study yields variants at 20p12.2 that associate with urinary bladder cancer."; Rafnar T et al ; Hum Mol Genet. (2014). IF: 4.902.
- "Shorter leukocyte telomere length is independently associated with poor survival in patients with bladder cancer."; **Russo A** et al ; Cancer Epidemiol Biomarkers Prev. (2014). IF: 4.554.
- "Novel approach identifies SNPs in SLC2A10 and KCNK9 with evidence for parent-of-origin effect on body mass index."; Hoggart CJ et al ; PLoS Genet. (2014). IF: 5.540.
- "Prediagnostic telomere length and risk of B-cell lymphoma-Results from the EPIC cohort study."; Hosnijeh FS et al ; Int J Cancer. (2014). IF: 7.360.
- "B-vitamins intake, DNA-methylation of One Carbon Metabolism and homocysteine pathway genes and myocardial infarction ris"; Fiorito G et al; Nutr Metab Cardiovasc Dis. (2014). IF: 3.318.
- "Validation of the nucleotide excision repair comet assay on cryopreserved PBMCs to measure inter-individual variation in"; Allione A et al; Mutagenesis (2013). IF: 2.840.
- "Genotype-phenotype analysis of S326C OGG1 polymorphism: a risk factor for oxidative pathologies."; Simonelli V et al; Free Radic Biol Med. (2013). IF: 6.020.
- "Polymorphisms in the XRCC1 gene modify survival of bladder cancer patients treated with chemotherapy."; Sacerdote C et al ; Int J Cancer. (2013). IF: 7.360.
- "Effect of blood storage conditions on DNA repair capacity measurements in peripheral blood mononuclear cells."; Allione A et al ; Mutat Res. (2013). IF: 2.398.
- "Inter-individual variation in nucleotide excision repair pathway is modulated by non-synonymous polymorphisms in ERCC4 a"; Allione A et al; Mutat Res (2013). IF: 2.398.
- "Genetic variants associated with increased risk of malignant pleural mesothelioma: a genome-wide association study."; Matullo G et al ; Plos One (2013). IF: 2.766.
- "Telomere length variation in juvenile acute myocardial infarction."; **Russo A** et al ; Plos One (2012). IF: 2.766.
- "Association between total number of deaths, diabetes mellitus, incident cancers, and haplotypes in chromosomal region 8q"; Guarrera S et al ; Am J Epidemiol. (2012). IF: 4.322.

Mean IF: 6.6
H-index: 12

Oral Presentations

- "Polymorphisms in DNA Repair Genes, Chemotherapy and Survival in Bladder Cancer". European Environmental Mutagen Society, Barcelona, Spain, July 4th-7th 2011.
- "Polymorphisms in DNA Repair Genes, Chemotherapy and Survival in Bladder Cancer". Italian Society of Human Genetics (SIGU), Milano, Italy, Nov. 13th-16th, 2011
- "Exome Sequencing and Genome–Wide Methylation Analysis in Monozygotic Twins Discordant for Acute Lymphoblastic Leukemia". Italian Society of Human Genetics (SIGU), Turin, Italy, Nov. 23th-25th, 2016.
- "Exome Sequencing and Genome–Wide Methylation Analysis in Monozygotic Twins Discordant for Acute Lymphoblastic Leukemia". EMBO Workshop, Turin, Italy, Sept. 8th-10th, 2017.

Honours and awards

- "2015 Reviewers' Choice Abstract", American Society of Human Genetics, Baltimore, USA, Oct. 6th-10th, 2015.
- "2016 Best E-poster", Italian Society of Human Genetics, Nov. 23th-25th, 2016.
- "2020 Best E-posters", Italian Society of Human Genetics, Nov. 11th-13th, 2020.

Fellowships

- One year Post-graduate Fellowship–year 2009-2010 offered by “ISI Foundation, Institute for Scientific Interchange”. Title of the Project: “DNA repair gene expression profiles and polymorphisms in cancer patients: chemotherapy responsiveness and prognostic factors”.
- One year Post-doctoral Fellowship–year 2015 offered by Fondazione Umberto Veronesi. Title of the Project: “Telomere length and epigenetic changes as aging risk biomarkers in myocardial infarction patients”.
- One year Post-doctoral Fellowship–year 2015 offered by Fondazione Umberto Veronesi. Title of the Project: “Telomere length and epigenetic changes as aging risk biomarkers in myocardial infarction patients”.
- One year Post-doctoral Fellowship–year 2016 offered by the University of Study of Turin. Title of the Project: “Telomere length measurement, DNA methylation, and Next Generation Sequencing in chronic disease”.
- One year Post-doctoral Fellowship–year 2017 offered by the University of Study of Turin. Title of the Project: “Telomere length measurement, DNA methylation, and Next Generation Sequencing in chronic disease”.
- Two years “Assegno di Ricerca”–years 2018-2019 offered by University of Turin. Prof. Barbara Pasini. Project: “Use of Next Generation Sequencing approaches in patients with familial breast cancer and melanoma”.

Courses

- “Molecular Epidemiology”, Cancer Epidemiology Unit, University of Turin, Italy. May 17th-18th and 21st-22nd 2010.
- Scientific English Course in the frame of the 'High Level Education Project' organized by the University of Turin, Italy. Year: 2012. Course duration: 60 hours.
- 26th Course in Medical Genetics organized by the European Genetics Foundation, Bertinoro, Italy, May 12th-16th 2013.
- Training for Illumina MiSeq platform by Illumina Field Application Scientist. May. 7th-8th 2014.
- “NGS Data Analysis and Application in the Diagnostic Field”, Pavia, Italy, Sept. 23th-25th 2015.
- “Practical Course on the Interpretation of Variants in BRCA Genes”, Milano, Italy, Feb. 3rd 2017.
- EMBO Workshop "Integrating genomics and biophysics to comprehend functional genetic variation”, Turin, Italy, Sept. 8-10th 2017.
- Training for Illumina NextSeq550 platform by Illumina Field Application Scientist. Jan. 17th-18th 2019.
- Analisi dei Geni *BRCA1* e *BRCA2* e di Pannelli Multi-Genici nel Percorso Diagnostico dei Tumori Eredo-Familiari della Mammella e dell'Ovaio. Rome, Italy, May 15th-16th 2019.
- L'NGS NELLA DIAGNOSTICA. DALL'ESOMA AL GENOMA. LE TECNOLOGIE OMICS. October 29th-30th 2020.