Eleonora Em Mangano

List of Publications by Citations

20 papers	760 citations	14 h-index	22 g-index
22 ext. papers	891 ext. citations	5.9 avg, IF	3.07 L-index

#	Paper	IF	Citations
20	EXCAVATOR: detecting copy number variants from whole-exome sequencing data. *Genome Biology*, **2013**, 14, R120	18.3	167
19	Gene expression profiling of A549 cells exposed to Milan PM2.5. *Toxicology Letters*, **2012**, 209, 136-45	4.4	114
18	Health risk assessment for air pollutants: alterations in lung and cardiac gene expression in mice exposed to Milano winter fine particulate matter (PM2.5). *PLoS ONE*, **2014**, 9, e109685	3.7	68
17	Integrative transcriptomic and protein analysis of human bronchial BEAS-2B exposed to seasonal urban particulate matter. *Environmental Pollution*, **2016**, 209, 87-98	9.3	59
16	Next Generation Sequencing of Pooled Samples: Guideline for Variants Filtering. *Scientific Reports*, **2016**, 6, 33735	4.9	58
15	The glucose and lipid metabolism reprogramming is grade-dependent in clear cell renal cell carcinoma primary cultures and is targetable to modulate cell viability and proliferation. *Oncotarget* , **2017**, 8, 113502-113515	3.3	50
14	Whole-exome sequencing of primary plasma cell leukemia discloses heterogeneous mutational patterns. *Oncotarget*, **2015**, 6, 17543-58	3.3	45
13	Strategies for comparing gene expression profiles from different microarray platforms: application to a case-control experiment. *Analytical Biochemistry*, **2006**, 353, 43-56	3.1	37
12	Comprehensive genomic characterization of cutaneous malignant melanoma cell lines derived from metastatic lesions by whole-exome sequencing and SNP array profiling. *PLoS ONE*, **2013**, 8, e63597	3.7	27
11	Major Action of Endogenous Lysyl Oxidase in Clear Cell Renal Cell Carcinoma Progression and Collagen Stiffness Revealed by Primary Cell Cultures. *American Journal of Pathology*, **2016**, 186, 2473-85	5.8	25
10	A computational procedure to identify significant overlap of differentially expressed and genomic imbalanced regions in cancer datasets. *Nucleic Acids Research*, **2009**, 37, 5057-70	20.1	24
9	Whole genome SNP genotyping and exome sequencing reveal novel genetic variants and putative causative genes in congenital hyperinsulinism. *PLoS ONE*, **2013**, 8, e68740	3.7	21
8	Renal cell carcinoma primary cultures maintain genomic and phenotypic profile of parental tumor tissues. *BMC Cancer*, **2011**, 11, 244	4.8	20
7	Identification of a diffuse form of hyperinsulinemic hypoglycemia by 18-fluoro-L-3,4 dihydroxyphenylalanine positron emission tomography/CT in a patient carrying a novel mutation of the HADH gene. *European Journal of Endocrinology*, **2009**, 160, 1019-23	6.5	17
6	Genetic analysis of Italian patients with congenital hyperinsulinism of infancy. *Hormone Research in Paediatrics*, **2013**, 79, 236-42	3.3	14
5	A Census of Tandemly Repeated Polymorphic Loci in Genic Regions Through the Comparative Integration of Human Genome Assemblies. *Frontiers in Genetics*, **2018**, 9, 155	4.5	7
4	INTEGRATE: Model-based multi-omics data integration to characterize multi-level metabolic regulation.. *PLoS Computational Biology*, **2022**, 18, e1009337	5	2

3	Contribution of Rare and Low-Frequency Variants to Multiple Sclerosis Susceptibility in the Italian Continental Population.. *Frontiers in Genetics*, **2021**, 12, 800262	4.5	1
2	Genomic and functional evaluation of TNFSF14 in multiple sclerosis susceptibility. *Journal of Genetics and Genomics*, **2021**, 48, 497-507	4	0
1	A multi-step genomic approach prioritized TBKBP1 gene as relevant for multiple sclerosis susceptibility.. *Journal of Neurology*, **2022**, 1	5.5	0