Sergio Cocozza

List of Publications by Year
in descending order

57 papers	2,580 citations	257101 24 h-index	189595 50 g-index
57 all docs	57 docs citations	57 times ranked	3116 citing authors

#	Article	IF	Citations
1	Spastic Paraplegia and OXPHOS Impairment Caused by Mutations in Paraplegin, a Nuclear-Encoded Mitochondrial Metalloprotease. Cell, 1998, 93, 973-983.	13.5	784
2	The Friedreich ataxia GAA triplet repeat: premutation and normal alleles. Human Molecular Genetics, 1997, 6, 1261-1266.	1.4	188
3	A New Locus for Autosomal Recessive Hereditary Spastic Paraplegia Maps to Chromosome 16q24.3. American Journal of Human Genetics, 1998, 63, 135-139.	2.6	147
4	Functional genomic analysis of frataxin deficiency reveals tissue-specific alterations and identifies the PPARÎ³ pathway as a therapeutic target in Friedreichâ€™s ataxia. Human Molecular Genetics, 2009, 18, 2452-2461.	1.4	109
5	Progressive gaa expansions in dorsal root ganglia of Friedreich's ataxia patients. Annals of Neurology, 2007, 61, 55-60.	2.8	106
6	Genome-wide mapping of 8-oxo-7,8-dihydro-2â€²-deoxyguanosine reveals accumulation of oxidatively-generated damage at DNA replication origins within transcribed long genes of mammalian cells. Nucleic Acids Research, 2019, 47, 221-236.	6.5	94
7	Frataxin fracas. Nature Genetics, 1997, 15, 337-338.	9.4	78
8	Somatic instability of the expanded GAA triplet-repeat sequence in Friedreich ataxia progresses throughout life. Genomics, 2007, 90, 1-5.	1.3	74
9	Recombinant Human Erythropoietin Increases Frataxin Protein Expression Without Increasing mRNA Expression. Cerebellum, 2008, 7, 360-365.	1.4	68
10	Extra-mitochondrial localisation of frataxin and its association with IscU1 during enterocyte-like differentiation of the human colon adenocarcinoma cell line Caco-2. Journal of Cell Science, 2005, 118, 3917-3924.	1.2	61
11	Nucleotide distance influences co-methylation between nearby CpG sites. Genomics, 2020, 112, 144-150.	1.3	58
12	A Combined Nucleic Acid and Protein Analysis in Friedreich Ataxia: Implications for Diagnosis, Pathogenesis and Clinical Trial Design. PLoS ONE, 2011, 6, e17627.	1.1	55
13	PPAR-Î³ Agonist Azelaoyl PAF Increases Frataxin Protein and mRNA Expression. New Implications for the Friedreichâ€™s Ataxia Therapy. Cerebellum, 2009, 8, 98-103.	1.4	46
14	Autosomal dominant cerebellar ataxia type I. Clinical and molecular study in 36 Italian families including a comparison between SCA1 and SCA2 phenotypes. Journal of the Neurological Sciences, 1996, 142, 140-147.	0.3	40
15	Influence of GAA expansion size and disease duration on central nervous system impairment in Friedreich's ataxia: contribution to the understanding of the pathophysiology of the disease. Clinical Neurophysiology, 2000, 111, 1023-1030.	0.7	40
16	Epoetin alfa increases frataxin production in Friedreich's ataxia without affecting hematocrit. Movement Disorders, 2011, 26, 739-742.	2.2	38
17	Genome-Wide Scan for Signatures of Human Population Differentiation and Their Relationship with Natural Selection, Functional Pathways and Diseases. PLoS ONE, 2009, 4, e7927.	1.1	36
18	The genomic landscape of 8-oxodG reveals enrichment at specific inherently fragile promoters. Nucleic Acids Research, 2020, 48, 4309-4324.	6.5	36

#	Article	IF	Citations
19	Determinants of onset age in Friedreichâ€™s ataxia. Journal of Neurology, 1998, 245, 166-168.	1.8	35
20	Identification of Candidate Children for Maturity-Onset Diabetes of the Young Type 2 (MODY2) Gene Testing: A Seven-Item Clinical Flowchart (7-iF). PLoS ONE, 2013, 8, e79933.	1.1	33
21	Pro12Ala Polymorphism of the PPARÂ2 Locus Modulates the Relationship Between Energy Intake and Body Weight in Type 2 Diabetic Patients. Diabetes Care, 2007, 30, 1156-1161.	4.3	32
22	Up-regulation of c-Jun N-terminal kinase pathway in Friedreich's ataxia cells. Human Molecular Genetics, 2002, 11, 2989-2996.	1.4	29
23	DNA methylation landscape of the genes regulating D-serine and D-aspartate metabolism in post-mortem brain from controls and subjects with schizophrenia. Scientific Reports, 2018, 8, 10163.	1.6	29
24	A pathogenetic classification of hereditary ataxias: Is the time ripe?. Journal of Neurology, 2004, 251, 913-22.	1.8	28
25	Improving the Estimation of Celiac Disease Sibling Risk by Non-HLA Genes. PLoS ONE, 2011, 6, e26920.	1.1	24
26	Tracking the evolution of epialleles during neural differentiation and brain development: D-Aspartate oxidase as a model gene. Epigenetics, 2017, 12, 41-54.	1.3	21
27	DNA Methylation Profiles of Tph1A and BDNF in Gut and Brain of L. Rhamnosus-Treated Zebrafish. Biomolecules, 2021, 11, 142.	1.8	21
28	Identification of a novel transcript of X25, the human gene involved in Friedreich ataxia. Neuroscience Letters, 2002, 320, 137-140.	1.0	19
29	New clues on the origin of the Friedreich ataxia expanded alleles from the analysis of new polymorphisms closely linked to the mutation. Human Genetics, 2004, 114, 458-463.	1.8	19
30	DNA Methylation variability among individuals is related to CpGs cluster density and evolutionary signatures. BMC Genomics, 2018, 19, 229.	1.2	19
31	Restriction fragment length polymorphism in the 3? flanking region of the rabbit ?1-globin gene. Biochemical Genetics, 1984, 22, 883-891.	0.8	18
32	Candidate genes and pathways downstream of PAX8 involved in ovarian high-grade serous carcinoma. Oncotarget, 0, 7, 41929-41947.	0.8	18
33	3-Nitropropionic acid increases frataxin expression in human lymphoblasts and in transgenic rat PC12 cells. Neuroscience Letters, 2003, 350, 184-186.	1.0	17
34	CpG Islands Undermethylation in Human Genomic Regions under Selective Pressure. PLoS ONE, 2011, 6, e23156.	1.1	16
35	Modeling DNA methylation by analyzing the individual configurations of single molecules. Epigenetics, 2016, 11, 881-888.	1.3	14
36	DNA sequence context as a marker of CpG methylation instability in normal and cancer tissues. Scientific Reports, 2020, 10, 1721.	1.6	13

#	Article	IF	Citations
37	Can Telomere Shortening in Human Peripheral Blood Leukocytes Serve as a Disease Biomarker of Friedreich's Ataxia?. Antioxidants and Redox Signaling, 2013, 18, 1303-1306.	2.5	12
38	Participation to Leisure Activities and Well-Being in a Group of Residents of Naples-Italy: The Role of Resilience. International Journal of Environmental Research and Public Health, 2020, 17, 1895.	1.2	11
39	Granulocyte Macrophage-Colony Stimulating Factor receptor expression on human cardiomyocytes from end-stage heart failure patients. European Journal of Heart Failure, 2006, 8, 564-570.	2.9	10
40	Oxidative DNA Damage and Activation of c-Jun N-Terminal Kinase Pathway in Fibroblasts from Patients with Hereditary Spastic Paraplegia. Cellular and Molecular Neurobiology, 2005, 25, 1245-1254.	1.7	9
41	Triplet repeat instability correlates with dinucleotide instability in primary breast cancer. Oncology Reports, 2007, 17, 193-9.	1.2	9
42	Association between DNA methylation profile and malignancy in follicular-patterned thyroid neoplasms. Endocrine-Related Cancer, 2019, 26, 451-462.	1.6	8
43	Ultra-Deep DNA Methylation Analysis of X-Linked Genes: GLA and AR as Model Genes. Genes, 2020, 11, 620.	1.0	7
44	p53 Expression is Decreased in Primary Breast Carcinomas with Microsatellite Instability. Breast Cancer Research and Treatment, 2002, 73, 257-266.	1.1	6
45	Coronary Heart Disease, Echo-Doppler Evidence of Peripheral Arterial Disease and Polymorphism of Apolipoprotein B Gene and Apo AI/CIII Cluster. Angiology, 1993, 44, 785-790.	0.8	5
46	Clinical and molecular studies in five Brazilian cases of Friedreich ataxia. Arquivos De Neuro-Psiquiatria, 1999, 57, 1-5.	0.3	5
47	Friedreich's ataxia: clinical and molecular study of 25 Brazilian cases. Revista Do Hospital Das Clinicas, 2001, 56, 143-148.	0.5	5
48	Down-regulation of otospiralin mRNA in response to acoustic stress in guinea pig. Hearing Research, 2004, 198, 36-40.	0.9	5
49	Signs of Selective Pressure on Genetic Variants Affecting Human Height. PLoS ONE, 2011, 6, e27588.	1.1	5
50	Artificial Intelligence for Epigenetics: Towards Personalized Medicine. Current Medicinal Chemistry, 2021, 28, 6654-6674.	1.2	5
51	Methodological aspects of the assessment of geneâ€“nutrient interactions at the population level. Nutrition, Metabolism and Cardiovascular Diseases, 2007, 17, 82-88.	1.1	4
52	Evidence for Evolutionary and Nonevolutionary Forces Shaping the Distribution of Human Genetic Variants near Transcription Start Sites. PLoS ONE, 2014, 9, e114432.	1.1	4
53	Evidence of a genetic marker associated with early onset in Friedreich's ataxia. Journal of Neurology, 1993, 240, 254-256.	1.8	2
54	Prevalence of GLA gene mutations and polymorphisms in patients with multiple sclerosis: A cross-sectional study. Journal of the Neurological Sciences, 2020, 412, 116782.	0.3	2

#	Article	IF	Citations
55	Epigenetic remodelling of Fxyd1 promoters in developing heart and brain tissues. Scientific Reports, 2022, 12, 6471.	1.6	2
56	The combination of UCP3â€“55CT and PPARÎ³2Pro12Ala polymorphisms affects BMI and substrate oxidation in two diabeticÂpopulations. Nutrition, Metabolism and Cardiovascular Diseases, 2016, 26, 400-406.	1.1	1
57	An improved combinatorial biclustering algorithm. Neural Computing and Applications, 2013, 22, 293-302.	3.2	0