Matthieu Moisse

List of Publications by Year
in descending order

43	3,614	186265 28	265206 42
papers	citations	h-index	g-index

49	49	49	9411
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	RNF170 mutation causes autosomal dominant sensory ataxia with variable pyramidal involvement. European Journal of Neurology, 2022, 29, 345-349.	3.3	2
2	Structural variation analysis of 6,500 whole genome sequences in amyotrophic lateral sclerosis. Npj Genomic Medicine, 2022, 7, 8.	3.8	23
3	Genome-wide study of DNA methylation shows alterations in metabolic, inflammatory, and cholesterol pathways in ALS. Science Translational Medicine, 2022, 14, eabj0264.	12.4	38
4	Whole-genome sequencing reveals that variants in the Interleukin 18 Receptor Accessory Protein 3â€²UTR protect against ALS. Nature Neuroscience, 2022, 25, 433-445.	14.8	16
5	The Effect of <scp>SMN</scp> Gene Dosage on <scp>ALS</scp> Risk and Disease Severity. Annals of Neurology, 2021, 89, 686-697.	5.3	10
6	HDAC6 inhibition restores TDPâ€43 pathology and axonal transport defects in human motor neurons with TARDBP mutations. EMBO Journal, 2021, 40, e106177.	7.8	51
7	C9orf72 -derived arginine-containing dipeptide repeats associate with axonal transport machinery and impede microtubule-based motility. Science Advances, 2021, 7, .	10.3	57
8	Histone Deacetylase Inhibition Regulates Lipid Homeostasis in a Mouse Model of Amyotrophic Lateral Sclerosis. International Journal of Molecular Sciences, 2021, 22, 11224.	4.1	27
9	Common and rare variant association analyses in amyotrophic lateral sclerosis identify 15 risk loci with distinct genetic architectures and neuron-specific biology. Nature Genetics, 2021, 53, 1636-1648.	21.4	223
10	A Patient with neonatal cholestasis. Medycyna Wieku Rozwojowego, 2021, 24, 31-33.	0.2	1
11	Induction and recovery of CpG site specific methylation changes in human bronchial cells after long-term exposure to carbon nanotubes and asbestos. Environment International, 2020, 137, 105530.	10.0	30
12	ATXN1 repeat expansions confer risk for amyotrophic lateral sclerosis and contribute to TDP-43 mislocalization. Brain Communications, 2020, 2, fcaa064.	3.3	33
13	Restoration of histone acetylation ameliorates disease and metabolic abnormalities in a FUS mouse model. Acta Neuropathologica Communications, 2019, 7, 107.	5.2	61
14	Differentiation but not ALS mutations in FUS rewires motor neuron metabolism. Nature Communications, 2019, 10, 4147.	12.8	41
15	Meta-analysis of epigenome-wide association studies in neonates reveals widespread differential DNA methylation associated with birthweight. Nature Communications, 2019, 10, 1893.	12.8	140
16	Global and gene-specific DNA methylation effects of different asbestos fibres on human bronchial epithelial cells. Environment International, 2018, 115, 301-311.	10.0	10
17	Differences in MWCNT- and SWCNT-induced DNA methylation alterations in association with the nuclear deposition. Particle and Fibre Toxicology, 2018, 15, 11.	6.2	57
18	GLI2 promoter hypermethylation in saliva of children with a respiratory allergy. Clinical Epigenetics, 2018, 10, 50.	4.1	19

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19	Genome-wide Analyses Identify KIF5A as a Novel ALS Gene. Neuron, 2018, 97, 1268-1283.e6.	8.1	517
20	Integrated genome analysis of uterine leiomyosarcoma to identify novel driver genes and targetable pathways. International Journal of Cancer, 2018, 142, 1230-1243.	5.1	59
21	Reconsidering the causality of TIA1 mutations in ALS. Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration, 2018, 19, 1-3.	1.7	22
22	Progranulin reduces insoluble TDP-43 levels, slows down axonal degeneration and prolongs survival in mutant TDP-43 mice. Molecular Neurodegeneration, 2018, 13, 55.	10.8	38
23	Genetic Architecture of Adaptive Immune System Identifies Key Immune Regulators. Cell Reports, 2018, 25, 798-810.e6.	6.4	36
24	Progranulin functions as a cathepsin D chaperone to stimulate axonal outgrowth in vivo. Human Molecular Genetics, 2017, 26, 2850-2863.	2.9	111
25	Defining Y-SNP variation among the Flemish population (Western Europe) by full genome sequencing. Forensic Science International: Genetics, 2017, 31, e12-e16.	3.1	6
26	Amplification of 1q32.1 Refines the Molecular Classification of Endometrial Carcinoma. Clinical Cancer Research, 2017, 23, 7232-7241.	7.0	37
27	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	2.4	67
28	Genetic heterogeneity after first-line chemotherapy in high-grade serous ovarian cancer. European Journal of Cancer, 2016, 53, 51-64.	2.8	45
29	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	2.9	40
30	Candidate locus analysis of the TERTâ€“CLPTM1L cancer risk region on chromosome 5p15 identifies multiple independent variants associated with endometrial cancer risk. Human Genetics, 2015, 134, 231-245.	3.8	34
31	DNA methylation profiling of non-small cell lung cancer reveals a COPD-driven immune-related signature. Thorax, 2015, 70, 1113-1122.	5.6	37
32	Evaluation of efficacy and safety markers in a phase II study of metastatic colorectal cancer treated with aflibercept in the first-line setting. British Journal of Cancer, 2015, 113, 1027-1034.	6.4	34
33	Expression of FOXP1 and Colorectal Cancer Prognosis. Laboratory Medicine, 2015, 46, 299-311.	1.2	17
34	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. Human Molecular Genetics, 2015, 24, 1478-1492.	2.9	50
35	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	2.5	49
36	Somatic copy number alterations predict response to platinum therapy in epithelial ovarian cancer. Gynecologic Oncology, 2014, 135, 415-422.	1.4	38

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37	Genome dynamics of the human embryonic kidney 293 lineage in response to cell biology manipulations. Nature Communications, 2014, 5, 4767.	12.8	421
38	Identification of New Genetic Susceptibility Loci for Breast Cancer Through Consideration of Geneâ€Environment Interactions. Genetic Epidemiology, 2014, 38, 84-93.	1.3	28
39	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. Human Molecular Genetics, 2014, 23, 6034-6046.	2.9	12
40	Mismatch repair deficiency endows tumors with a unique mutation signature and sensitivity to DNA double-strand breaks. ELife, 2014, 3, e02725.	6.0	71
41	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	21.4	960
42	Pipit: visualizing functional impacts of structural variations. Bioinformatics, 2013, 29, 2206-2207.	4.1	1
43	Whole-genome sequencing reveals a coding non-pathogenic variant tagging a non-coding pathogenic hexanucleotide repeat expansion in C9orf72 as cause of amyotrophic lateral sclerosis. Human Molecular Genetics, 2012, 21, 2412-2419.	2.9	33