Peter L Nagy

List of Publications by Year
in descending order

48 papers	1,934 citations	331670 21 h-index	276875 41 g-index
51 all docs	51 docs citations	51 times ranked	4202 citing authors

#	Article	IF	Citations
1	A trithorax-group complex purified from Saccharomyces cerevisiae is required for methylation of histone H3. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 90-94.	7.1	297
2	Axonally Synthesized ATF4 Transmits a Neurodegenerative Signal across Brain Regions. Cell, 2014, 158, 1159-1172.	28.9	266
3	Implementation of next generation sequencing into pediatric hematology-oncology practice: moving beyond actionable alterations. Genome Medicine, 2016, 8, 133.	8.2	147
4	Analysis of the ABCA4 genomic locus in Stargardt disease. Human Molecular Genetics, 2014, 23, 6797-6806.	2.9	117
5	The Glc7 Phosphatase Subunit of the Cleavage and Polyadenylation Factor Is Essential for Transcription Termination on snoRNA Genes. Molecular Cell, 2008, 29, 577-587.	9.7	107
6	Genomewide demarcation of RNA polymerase II transcription units revealed by physical fractionation of chromatin. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 6364-6369.	7.1	103
7	LMNA cardiomyopathy: cell biology and genetics meet clinical medicine. DMM Disease Models and Mechanisms, 2011, 4, 562-568.	2.4	85
8	Cognitive-behavioral screening reveals prevalent impairment in a large multicenter ALS cohort. Neurology, 2016, 86, 813-820.	1.1	70
9	Mutation abolishing the ZMPSTE24 cleavage site in prelamin A causes a progeroid disorder. Journal of Cell Science, 2016, 129, 1975-80.	2.0	54
10	The genotypic spectrum of ALDH7A1 mutations resulting in pyridoxine dependent epilepsy: A common epileptic encephalopathy. Journal of Inherited Metabolic Disease, 2019, 42, 353-361.	3.6	54
11	DNA-like class R inhibitory oligonucleotides (INH-ODNs) preferentially block autoantigen-induced B-cell and dendritic cell activation in vitro and autoantibody production in lupus-prone MRL-Faslpr/lpr mice in vivo. Arthritis Research and Therapy, 2009, 11, R79.	3.5	48
12	Phenotypic and molecular analyses of primary lateral sclerosis. Neurology: Genetics, 2015, 1, e3.	1.9	48
13	Comparative Anatomy of Chromosomal Domains with Imprinted and Non-Imprinted Allele-Specific DNA Methylation. PLoS Genetics, 2013, 9, e1003622.	3.5	47
14	LMNA variants cause cytoplasmic distribution of nuclear pore proteins in Drosophila and human muscle. Human Molecular Genetics, 2012, 21, 1544-1556.	2.9	44
15	Expanding the clinical spectrum of hereditary fibrosing poikiloderma with tendon contractures, myopathy and pulmonary fibrosis due to FAM111B mutations. Orphanet Journal of Rare Diseases, 2015, 10, 135.	2.7	42
16	Characterization of a novel fusion gene EML4-NTRK3 in a case of recurrent congenital fibrosarcoma. Journal of Physical Education and Sports Management, 2015, 1, a000471.	1.2	39
17	A histone H3K9M mutation traps histone methyltransferase Clr4 to prevent heterochromatin spreading. ELife, 2016, 5, .	6.0	36
18	Discovery of the BMPR1A promoter and germline mutations that cause juvenile polyposis. Human Molecular Genetics, 2010, 19, 4654-4662.	2.9	32

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19	Isoform-level brain expression profiling of the spermidine/spermine N1-Acetyltransferase1 (SAT1) gene in major depression and suicide. Neurobiology of Disease, 2015, 79, 123-134.	4.4	28
20	C9ORF72 repeat expansions not detected in a group of patients with schizophrenia. Neurobiology of Aging, 2013, 34, 1309.e9-1309.e10.	3.1	27
21	Tetratricopeptide Repeat Domain 7A (TTC7A) Mutation in a Newborn with Multiple Intestinal Atresia and Combined Immunodeficiency. Journal of Clinical Immunology, 2014, 34, 607-610.	3.8	25
22	The Proper Splicing of RNAi Factors Is Critical for Pericentric Heterochromatin Assembly in Fission Yeast. PLoS Genetics, 2014, 10, e1004334.	3.5	24
23	Allele-specific DNA methylation is increased in cancers and its dense mapping in normal plus neoplastic cells increases the yield of disease-associated regulatory SNPs. Genome Biology, 2020, 21, 153.	8.8	23
24	Whole exome sequencing identifies a homozygous POLG2 missense variant in an infant with fulminant hepatic failure and mitochondrial DNA depletion. European Journal of Medical Genetics, 2016, 59, 540-545.	1.3	21
25	Aerobic exercise elicits clinical adaptations in myotonic dystrophy type 1 patients independently of pathophysiological changes. Journal of Clinical Investigation, 2022, 132, .	8.2	21
26	Determination of the phylogenetic origins of the ÃrpÃ¡d Dynasty based on Y chromosome sequencing of BÃ©la the Third. European Journal of Human Genetics, 2021, 29, 164-172.	2.8	18
27	A case study of an integrative genomic and experimental therapeutic approach for rare tumors: identification of vulnerabilities in a pediatric poorly differentiated carcinoma. Genome Medicine, 2016, 8, 116.	8.2	15
28	Brain-Derived Neurotrophic Factor Elevates Activating Transcription Factor 4 (ATF4) in Neurons and Promotes ATF4-Dependent Induction of Sesn2. Frontiers in Molecular Neuroscience, 2018, 11, 62.	2.9	15
29	Tls1 regulates splicing of shelterin components to control telomeric heterochromatin assembly and telomere length. Nucleic Acids Research, 2014, 42, 11419-11432.	14.5	14
30	Formaldehydeâ€assisted isolation of regulatory elements. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2009, 1, 400-406.	6.6	9
31	Inherited selective cobalamin malabsorption in Komondor dogs associated with a CUBN splice site variant. BMC Veterinary Research, 2018, 14, 418.	1.9	9
32	The role of clinical genomic testing in diagnosis and discovery of pathogenic mutations. Expert Review of Molecular Diagnostics, 2015, 15, 1101-1105.	3.1	8
33	Ultra-rare mutations in SRCAP segregate in Caribbean Hispanic families with Alzheimer disease. Neurology: Genetics, 2017, 3, e178.	1.9	8
34	The histone H3K9M mutation synergizes with H3K14 ubiquitylation to selectively sequester histone H3K9 methyltransferase Clr4 at heterochromatin. Cell Reports, 2021, 35, 109137.	6.4	8
35	Next-Generation Sequencing and Mutational Analysis: Implications for Genes Encoding LINC Complex Proteins. Methods in Molecular Biology, 2018, 1840, 321-336.	0.9	5
36	Editorial. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2008, 647, 1-2.	1.0	4

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37	2q24 deletions: Further characterization of clinical findings and their relation to the SCN cluster. American Journal of Medical Genetics, Part A, 2012, 158A, 2767-2774.	1.2	4
38	Clinical Transcriptome Sequencing Confirms Activation of a Cryptic Splice Site in Suspected SYNGAP1-Related Disorder. Molecular Syndromology, 2018, 9, 295-299.	0.8	4
39	TNFRSF6 (Fas Antigen) Mutations in Patients with Sinus Histiocytosis with Massive Lymphadenopathy (Rosai-Dorfman Disease).. Blood, 2004, 104, 2389-2389.	1.4	3
40	Blood group typing from whole-genome sequencing data. PLoS ONE, 2020, 15, e0242168.	2.5	2
41	A novel noncoding FKRP mutation in early onset limb-girdle muscular dystrophy. Neurology: Genetics, 2020, 6, e388.	1.9	1
42	The Efficacy of Whole Genome Sequencing and RNA-Seq in the Diagnosis of Whole Exome Sequencing Negative Patients with Complex Neurological Phenotypes. Journal of Pediatric Genetics, 0, , .	0.7	0
43	Blood group typing from whole-genome sequencing data. , 2020, 15, e0242168.		0
44	Blood group typing from whole-genome sequencing data. , 2020, 15, e0242168.		0
45	Blood group typing from whole-genome sequencing data. , 2020, 15, e0242168.		0
46	Blood group typing from whole-genome sequencing data. , 2020, 15, e0242168.		0
47	Blood group typing from whole-genome sequencing data. , 2020, 15, e0242168.		0
48	Blood group typing from whole-genome sequencing data. , 2020, 15, e0242168.		0