Arijit Mukhopadhyay

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/2916956/publications.pdf

Version: 2024-02-01

50	1,589	361413 20	330143 37
papers	citations	h-index	g-index

51	51	51	2605
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Diagnostic and Prognostic Potential of MiR-379/656 MicroRNA Cluster in Molecular Subtypes of Breast Cancer. Journal of Clinical Medicine, 2021, 10, 4071.	2.4	3
2	Human Brain Shows Recurrent Non-Canonical MicroRNA Editing Events Enriched for Seed Sequence with Possible Functional Consequence. Non-coding RNA, 2020, 6, 21.	2.6	5
3	Fusion transcripts in normal human cortex increase with age and show distinct genomic features for single cells and tissues. Scientific Reports, 2020, 10, 1368.	3.3	8
4	Genomic Applications and Insights in Unravelling Cancer Signalling Pathways. , 2019, , 471-511.		0
5	Novel internal regulators and candidate miRNAs within miR-379/miR-656 miRNA cluster can alter cellular phenotype of human glioblastoma. Scientific Reports, 2018, 8, 7673.	3.3	25
6	Identification of miR-379/miR-656 (C14MC) cluster downregulation and associated epigenetic and transcription regulatory mechanism in oligodendrogliomas. Journal of Neuro-Oncology, 2018, 139, 23-31.	2.9	17
7	A-to-I editing in human miRNAs is enriched in seed sequence, influenced by sequence contexts and significantly hypoedited in glioblastoma multiforme. Scientific Reports, 2017, 7, 2466.	3.3	58
8	TBK1 duplication is found in normal tension and not in high tension glaucoma patients of Indian origin. Journal of Genetics, 2016, 95, 459-461.	0.7	12
9	Genetic association and stress mediated down-regulation in trabecular meshwork implicates MPP7 as a novel candidate gene in primary open angle glaucoma. BMC Medical Genomics, 2016, 9, 15.	1.5	15
10	Human brain harbors single nucleotide somatic variations in functionally relevant genes possibly mediated by oxidative stress. F1000Research, 2016, 5, 2520.	1.6	4
11	EPIG-08DOWNREGULATION OF miR-379/miR-656 CLUSTER (C14MC) IN OLIGODENDROGLIOMAS WITH POSSIBLE MECHANISTIC AND CLINICOPATHOLOGICAL IMPLICATIONS. Neuro-Oncology, 2015, 17, v87.4-v88.	1.2	0
12	Altered expression and editing of miRNA-100 regulates iTreg differentiation. Nucleic Acids Research, 2015, 43, 8057-8065.	14.5	44
13	Gene-Rich Large Deletions Are Overrepresented in POAG Patients of Indian and Caucasian Origins. , 2014, 55, 3258.		9
14	Genome-wide analysis identifies common CNVs associated with primary open angle glaucoma. Molecular Cytogenetics, 2014, 7, P131.	0.9	0
15	Genomic copy number variations in glaucomatous neurodegeneration. Molecular Cytogenetics, 2014, 7, I33.	0.9	0
16	Evaluation of Genetic Association of the INK4 Locus with Primary Open Angle Glaucoma in East Indian Population. Scientific Reports, 2014, 4, 5115.	3.3	10
17	Genome-wide analysis reveals downregulation of miR-379/miR-656 cluster in human cancers. Biology Direct, 2013, 8, 10.	4.6	69
18	Mitochondrial Genome Analysis of Primary Open Angle Glaucoma Patients. PLoS ONE, 2013, 8, e70760.	2.5	34

#	Article	IF	Citations
19	Nuclear morphology and c-Jun N-terminal kinase 1 expression differentiate serum-starved oxidative stress signalling from hydrogen peroxide-induced apoptosis in retinal neuronal cell line. Cell Biology International, 2012, 36, 1021-1027.	3.0	4
20	Genetic Association and Gene-gene interaction ofHAS2,HABP1andHYAL3Implicate Hyaluronan Metabolic Genes in Glaucomatous Neurodegeneration. Disease Markers, 2012, 33, 145-154.	1.3	4
21	Evaluation of the Role of LRRK2 Gene in Parkinsonâ€™s Disease in an East Indian Cohort. Disease Markers, 2012, 32, 355-362.	1.3	7
22	Spectrum of large copy number variations in 26 diverse Indian populations: potential involvement in phenotypic diversity. Human Genetics, 2012, 131, 131-143.	3.8	17
23	Evaluation of the role of LRRK2 gene in Parkinson's disease in an East Indian cohort. Disease Markers, 2012, 32, 355-62.	1.3	5
24	Recent Admixture in an Indian Population of African Ancestry. American Journal of Human Genetics, 2011, 89, 111-120.	6.2	32
25	Recent Admixture in an Indian Population of African Ancestry. American Journal of Human Genetics, 2011, 89, 344.	6.2	0
26	miRvar: A comprehensive database for genomic variations in microRNAs. Human Mutation, 2011, 32, E2226-E2245.	2.5	35
27	Next-Generation Sequencing of a 40 Mb Linkage Interval Reveals TSPAN12 Mutations in Patients with Familial Exudative Vitreoretinopathy. American Journal of Human Genetics, 2010, 86, 240-247.	6.2	202
28	CDK19 is disrupted in a female patient with bilateral congenital retinal folds, microcephaly and mild mental retardation. Human Genetics, 2010, 128, 281-291.	3.8	50
29	Overview of the mutation spectrum in familial exudative vitreoretinopathy and Norrie disease with identification of 21 novel variants in FZD4, LRP5, and NDP. Human Mutation, 2010, 31, 656-666.	2.5	126
30	Variable Clinical Spectrum of the Myocilin Gln368X Mutation in a Dutch Family with Primary Open Angle Glaucoma. Current Eye Research, 2010, 35, 31-36.	1.5	5
31	Clinical and Molecular Evaluation of Probands and Family Members with Familial Exudative Vitreoretinopathy. , 2009, 50, 4379.		68
32	Gene delivery to the retina: focus on non-viral approaches. Drug Discovery Today, 2009, 14, 306-315.	6.4	45
33	Complex genetics of glaucoma: defects in CYP1B1, and not MYOC, cause pathogenesis in an early-onset POAG patient with double variants at both loci. Journal of Genetics, 2008, 87, 265-269.	0.7	5
34	L1 retrotransposition can occur early in human embryonic development. Human Molecular Genetics, 2007, 16, 1587-1592.	2.9	174
35	Myocilin Variants in Indian Patients With Open-angle Glaucoma. JAMA Ophthalmology, 2007, 125, 823.	2.4	20
36	Identification and functional characterization of a novel MYOC mutation in two primary open angle glaucoma families from The Netherlands. Molecular Vision, 2007, 13, 1793-801.	1.1	8

#	Article	IF	Citations
37	Novel human pathological mutations. Gene symbol: MYOC. Disease: primary open angle glaucoma. Human Genetics, 2007, 122, 553.	3.8	0
38	Erosive Vitreoretinopathy and Wagner Disease Are Caused by Intronic Mutations inCSPG2/VersicanThat Result in an Imbalance of Splice Variants. , 2006, 47, 3565.		77
39	OCA1 in Different Ethnic Groups of India is Primarily Due to Founder Mutations in the Tyrosinase Gene. Annals of Human Genetics, 2006, 70, 623-630.	0.8	25
40	Myocilin gene implicated in primary congenital glaucoma. Clinical Genetics, 2005, 67, 335-340.	2.0	102
41	Determination of variants in the 3â€²-region of the Tyrosinase gene requires locus specific amplification. Human Mutation, 2005, 26, 53-58.	2.5	24
42	Evaluation of Optineurin as a candidate gene in Indian patients with primary open angle glaucoma. Molecular Vision, 2005, 11, 792-7.	1.1	31
43	Molecular pathology of haemophilia B: identification of five novel mutations including a LINE 1 insertion in Indian patients. Haemophilia, 2004, 10, 259-263.	2.1	45
44	Bioinformatic approaches for identification and characterization of olfactomedin related genes with a potential role in pathogenesis of ocular disorders. Molecular Vision, 2004, 10, 304-14.	1.1	22
45	Recent advances in molecular genetics of glaucoma. Molecular and Cellular Biochemistry, 2003, 253, 223-231.	3.1	51
46	Analysis of haemophilia B database and strategies for identification of common point mutations in the factor IX gene. Haemophilia, 2003, 9, 187-192.	2.1	16
47	Myocilin mutation 1109 C>T (Pro 370 Leu) is the most common gene defect causing early onset primary open angle glaucoma. Indian Journal of Ophthalmology, 2003, 51, 279-81.	1.1	5
48	Did myocilin evolve from two different primordial proteins?. Molecular Vision, 2002, 8, 271-9.	1.1	13
49	Distribution of p53 codon 72 polymorphism in Indian primary open angle glaucoma patients. Molecular Vision, 2002, 8, 367-71.	1.1	20
50	Mutations in MYOC gene of Indian primary open angle glaucoma patients. Molecular Vision, 2002, 8, 442-8.	1.1	38