Issei Imoto

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4383173/publications.pdf

Version: 2024-02-01

198 papers	10,450 citations	28274 55 h-index	40979 93 g-index
199 all docs	199 docs citations	199 times ranked	16681 citing authors

#	Article	IF	Citations
1	Exploration of Tumor-Suppressive MicroRNAs Silenced by DNA Hypermethylation in Oral Cancer. Cancer Research, 2008, 68, 2094-2105.	0.9	559
2	miR-124 and miR-203 are epigenetically silenced tumor-suppressive microRNAs in hepatocellular carcinoma. Carcinogenesis, 2010, 31, 766-776.	2.8	538
3	Clinical heterogeneity of Î±â€synuclein gene duplication in Parkinson's disease. Annals of Neurology, 2006, 59, 298-309.	5.3	308
4	Large-scale genome-wide association study in a Japanese population identifies novel susceptibility loci across different diseases. Nature Genetics, 2020, 52, 669-679.	21.4	304
5	Sex hormone-dependent tRNA halves enhance cell proliferation in breast and prostate cancers. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E3816-25.	7.1	295
6	The Tumor Suppressive MicroRNAmiR-218Targets the mTOR ComponentRictorand Inhibits AKT Phosphorylation in Oral Cancer. Cancer Research, 2011, 71, 5765-5778.	0.9	235
7	miR-152 Is a Tumor Suppressor microRNA That Is Silenced by DNA Hypermethylation in Endometrial Cancer. Cancer Research, 2011, 71, 6450-6462.	0.9	211
8	Obesity-induced DNA released from adipocytes stimulates chronic adipose tissue inflammation and insulin resistance. Science Advances, 2016, 2, e1501332.	10.3	209
9	YAP is a candidate oncogene for esophageal squamous cell carcinoma. Carcinogenesis, 2011, 32, 389-398.	2.8	207
10	Alteration in Copy Numbers of Genes as a Mechanism for Acquired Drug Resistance. Cancer Research, 2004, 64, 1403-1410.	0.9	199
11	PPM1D is a potential target for 17q gain in neuroblastoma. Cancer Research, 2003, 63, 1876-83.	0.9	197
12	Overexpression of SMYD2 relates to tumor cell proliferation and malignant outcome of esophageal squamous cell carcinoma. Carcinogenesis, 2009, 30, 1139-1146.	2.8	154
13	TFDP1, CUL4A, and CDC16 identified as targets for amplification at 13q34 in hepatocellular carcinomas. Hepatology, 2002, 35, 1476-1484.	7.3	148
14	Genome-wide array-based comparative genomic hybridization analysis of pancreatic adenocarcinoma: Identification of genetic indicators that predict patient outcome. Cancer Science, 2007, 98, 392-400.	3.9	147
15	Association of 17q21-q24 gain in ovarian clear cell adenocarcinomas with poor prognosis and identification of PPM1D and APPBP2 as likely amplification targets. Clinical Cancer Research, 2003, 9, 1995-2004.	7.0	139
16	PIK3CA mutation is an oncogenic aberration at advanced stages of oral squamous cell carcinoma. Cancer Science, 2006, 97, 1351-1358.	3.9	137
17	Frequent Silencing of Low Density Lipoprotein Receptor-Related Protein 1B (LRP1B) Expression by Genetic and Epigenetic Mechanisms in Esophageal Squamous Cell Carcinoma. Cancer Research, 2004, 64, 3741-3747.	0.9	132
18	Comparative genomic hybridization (CGH)-arrays pave the way for identification of novel cancer-related genes. Cancer Science, 2004, 95, 559-563.	3.9	130

#	Article	IF	Citations
19	Expression of cIAP1, a target for 11q22 amplification, correlates with resistance of cervical cancers to radiotherapy. Cancer Research, 2002, 62, 4860-6.	0.9	124
20	ASK1 and ASK2 differentially regulate the counteracting roles of apoptosis and inflammation in tumorigenesis. EMBO Journal, 2009, 28, 843-853.	7.8	119
21	Monitoring the HER2 copy number status in circulating tumor DNA by droplet digital PCR in patients with gastric cancer. Gastric Cancer, 2017, 20, 126-135.	5.3	111
22	Frequent Silencing of the Candidate Tumor Suppressor PCDH20 by Epigenetic Mechanism in Nonâ€“Small-Cell Lung Cancers. Cancer Research, 2006, 66, 4617-4626.	0.9	108
23	Genetic Classification of Lung Adenocarcinoma Based on Array-Based Comparative Genomic Hybridization Analysis: Its Association with Clinicopathologic Features. Clinical Cancer Research, 2005, 11, 6177-6185.	7.0	103
24	SASPase regulates stratum corneum hydration through profilaggrinâ€toâ€filaggrin processing. EMBO Molecular Medicine, 2011, 3, 320-333.	6.9	102
25	Expression and Gene Amplification of Actinin-4 in Invasive Ductal Carcinoma of the Pancreas. Clinical Cancer Research, 2008, 14, 5348-5356.	7.0	101
26	Overexpressed NF-ÎºBâ€“inducing kinase contributes to the tumorigenesis of adult T-cell leukemia and Hodgkin Reed-Sternberg cells. Blood, 2008, 111, 5118-5129.	1.4	97
27	Amplification and Overexpression of TGIF2, a Novel Homeobox Gene of the TALE Superclass, in Ovarian Cancer Cell Lines. Biochemical and Biophysical Research Communications, 2000, 276, 264-270.	2.1	91
28	Involvement of overexpressed wild-type BRAF in the growth of malignant melanoma cell lines. Oncogene, 2004, 23, 8796-8804.	5.9	91
29	Meta-analyses of Blood Homocysteine Levels for Gender and Genetic Association Studies of the MTHFR C677T Polymorphism in Schizophrenia. Schizophrenia Bulletin, 2014, 40, 1154-1163.	4.3	88
30	Overexpression of PDZK1 within the 1q12-q22 Amplicon Is Likely To Be Associated with Drug-Resistance Phenotype in Multiple Myeloma. American Journal of Pathology, 2004, 165, 71-81.	3.8	86
31	Frequent silencing of protocadherin 17 , a candidate tumour suppressor for esophageal squamous cell carcinoma. Carcinogenesis, 2010, 31, 1027-1036.	2.8	86
32	Frequent silencing of a putative tumor suppressor gene melatonin receptor 1 A (MTNR1A) in oral squamousâ€cell carcinoma. Cancer Science, 2008, 99, 1390-1400.	3.9	83
33	Genetically Distinct and Clinically Relevant Classification of Hepatocellular Carcinoma: Putative Therapeutic Targets. Gastroenterology, 2007, 133, 1475-1486.	1.3	80
34	Screening of DNA copyâ€number aberrations in gastric cancer cell lines by arrayâ€based comparative genomic hybridization. Cancer Science, 2005, 96, 100-110.	3.9	79
35	Actinin-4 gene amplification in ovarian cancer: a candidate oncogene associated with poor patient prognosis and tumor chemoresistance. Modern Pathology, 2009, 22, 499-507.	5.5	77
36	Promoter Hypermethylation Contributes to Frequent Inactivation of a Putative Conditional Tumor Suppressor Gene Connective Tissue Growth Factor in Ovarian Cancer. Cancer Research, 2007, 67, 7095-7105.	0.9	76

#	Article	IF	Citations
37	An alternatively spliced isoform of transcriptional repressor ATF3 and its induction by stress stimuli. Nucleic Acids Research, 2002, 30, 2398-2406.	14.5	75
38	SKI and MEL1 Cooperate to Inhibit Transforming Growth Factor-Î² Signal in Gastric Cancer Cells. Journal of Biological Chemistry, 2009, 284, 3334-3344.	3.4	74
39	SNO Is a Probable Target for Gene Amplification at 3q26 in Squamous-Cell Carcinomas of the Esophagus. Biochemical and Biophysical Research Communications, 2001, 286, 559-565.	2.1	71
40	Blood diagnostic biomarkers for major depressive disorder using multiplex DNA methylation profiles: discovery and validation. Epigenetics, 2015, 10, 135-141.	2.7	70
41	Nonrandom Chromosomal Imbalances in Esophageal Squamous Cell Carcinoma Cell Lines: Possible Involvement of theATF3andCENPFGenes in the 1q32 Amplicon. Japanese Journal of Cancer Research, 2000, 91, 1126-1133.	1.7	68
42	DNA Methylation Signatures of Peripheral Leukocytes in Schizophrenia. NeuroMolecular Medicine, 2013, 15, 95-101.	3.4	68
43	The selective continued linkage of centromeres from mitosis to interphase in the absence of mammalian separase. Journal of Cell Biology, 2006, 172, 835-846.	5.2	66
44	Nuclear expression of cIAP-1, an apoptosis inhibiting protein, predicts lymph node metastasis and poor patient prognosis in head and neck squamous cell carcinomas. Cancer Letters, 2005, 224, 141-151.	7.2	65
45	Methylation-Associated Silencing of theNuclear Receptor 1I2Gene in Advanced-Type Neuroblastomas, Identified by Bacterial Artificial Chromosome Array-Based Methylated CpG Island Amplification. Cancer Research, 2005, 65, 10233-10242.	0.9	64
46	Genetic profile of hepatocellular carcinoma revealed by array-based comparative genomic hybridization: Identification of genetic indicators to predict patient outcome. Journal of Hepatology, 2005, 43, 863-874.	3.7	64
47	KrÃ¼ppelâ€like factor 12 plays a significant role in poorly differentiated gastric cancer progression. International Journal of Cancer, 2009, 125, 1859-1867.	5.1	64
48	TERC identified as a probable target within the 3q26 amplicon that is detected frequently in non-small cell lung cancers. Clinical Cancer Research, 2003, 9, 4705-13.	7.0	63
49	ADAM23, a possible tumor suppressor gene, is frequently silenced in gastric cancers by homozygous deletion or aberrant promoter hypermethylation. Oncogene, 2005, 24, 8051-8060.	5.9	62
50	HuR Regulates Alternative Splicing of the TRA2Î² Gene in Human Colon Cancer Cells under Oxidative Stress. Molecular and Cellular Biology, 2014, 34, 2857-2873.	2.3	62
51	microRNA-203 suppresses invasion and epithelial-mesenchymal transition induction via targeting NUAK1 in head and neck cancer. Oncotarget, 2016, 7, 8223-8239.	1.8	61
52	Genomeâ€wide DNA methylation profiles in liver tissue at the precancerous stage and in hepatocellular carcinoma. International Journal of Cancer, 2009, 125, 2854-2862.	5.1	58
53	HER2 amplification detected in the circulating DNA of patients with gastric cancer: a retrospective pilot study. Gastric Cancer, 2015, 18, 698-710.	5.3	58
54	Frequent silencing of DBC1 is by genetic or epigenetic mechanisms in non-small cell lung cancers. Human Molecular Genetics, 2005, 14, 997-1007.	2.9	57

#	Article	IF	Citations
55	Array-based comparative genomic hybridization analysis of high-grade neuroendocrine tumors of the lung. Cancer Science, 2005, 96, 661-667.	3.9	56
56	Identification of PAK4 as a putative target gene for amplification within 19q13.12â€q13.2 in oral squamousâ€cell carcinoma. Cancer Science, 2009, 100, 1908-1916.	3.9	55
57	Copy-number variations on the X chromosome in Japanese patients with mental retardation detected by array-based comparative genomic hybridization analysis. Journal of Human Genetics, 2010, 55, 590-599.	2.3	55
58	Plasma total homocysteine is associated with DNA methylation in patients with schizophrenia. Epigenetics, 2013, 8, 584-590.	2.7	55
59	Sex differences of leukocytes DNA methylation adjusted for estimated cellular proportions. Biology of Sex Differences, 2015, 6, 11.	4.1	55
60	Protease-Activated Receptor-2 Plays a Critical Role in Vascular Inflammation and Atherosclerosis in Apolipoprotein Eâ€“Deficient Mice. Circulation, 2018, 138, 1706-1719.	1.6	55
61	Differentially Regulated Genes as Putative Targets of Amplifications at 20q in Ovarian Cancers. Japanese Journal of Cancer Research, 2002, 93, 1114-1122.	1.7	54
62	Genome-wide DNA methylation profiles in both precancerous conditions and clear cell renal cell carcinomas are correlated with malignant potential and patient outcome. Carcinogenesis, 2009, 30, 214-221.	2.8	53
63	Frequent Inactivation of a Putative Tumor Suppressor, Angiopoietin-Like Protein 2, in Ovarian Cancer. Cancer Research, 2008, 68, 5067-5075.	0.9	51
64	Lysosomal-Associated Protein Multispanning Transmembrane 5 Gene (LAPTM5) Is Associated with Spontaneous Regression of Neuroblastomas. PLoS ONE, 2009, 4, e7099.	2.5	51
65	Genetic or epigenetic silencing of low density lipoprotein receptor-related protein 1B expression in oral squamous cell carcinoma. Cancer Science, 2006, 97, 1070-1074.	3.9	50
66	Identification of a novel fusion gene in a pre-B acute lymphoblastic leukemia with t(1;19)(q23;p13). Cancer Science, 2004, 95, 503-507.	3.9	49
67	Effect of Clozapine on DNA Methylation in Peripheral Leukocytes from Patients with Treatment-Resistant Schizophrenia. International Journal of Molecular Sciences, 2017, 18, 632.	4.1	49
68	Prevalence of pathogenic germline variants detected by multigene sequencing in unselected Japanese patients with ovarian cancer. Oncotarget, 2017, 8, 112258-112267.	1.8	49
69	Genetic Clustering of Clear Cell Renal Cell Carcinoma Based on Array-Comparative Genomic Hybridization: Its Association with DNA Methylation Alteration and Patient Outcome. Clinical Cancer Research, 2008, 14, 5531-5539.	7.0	48
70	Identification and Characterization of Human PKNOX2, a Novel Homeobox-Containing Gene. Biochemical and Biophysical Research Communications, 2001, 287, 270-276.	2.1	46
71	Identification of ZASC1 encoding a KrÃ¼ppel-like zinc finger protein as a novel target for 3q26 amplification in esophageal squamous cell carcinomas. Cancer Research, 2003, 63, 5691-6.	0.9	46
72	CD44 is a potential target of amplification within the 11p13 amplicon detected in gastric cancer cell lines. Genes Chromosomes and Cancer, 2000, 29, 315-324.	2.8	44

#	Article	IF	Citations
73	A Novel Amplification at 17q21-23 in Ovarian Cancer Cell Lines Detected by Comparative Genomic Hybridization. Gynecologic Oncology, 2001, 81, 172-177.	1.4	44
74	A Novel Amplicon at 9p23-24 in Squamous Cell Carcinoma of the Esophagus That Lies Proximal toGASC1and HarborsNFIB. Japanese Journal of Cancer Research, 2001, 92, 423-428.	1.7	44
75	MYEOV, a gene at 11q13, is coamplified with CCND1, but epigenetically inactivated in a subset of esophageal squamous cell carcinomas. Journal of Human Genetics, 2002, 47, 460-464.	2.3	44
76	Genomeâ€wide DNA methylation profiles in urothelial carcinomas and urothelia at the precancerous stage. Cancer Science, 2010, 101, 231-240.	3.9	44
77	Hypomethylation of Long Interspersed Nuclear Element-1 (LINE-1) is Associated with Poor Prognosis via Activation of c-MET in Hepatocellular Carcinoma. Annals of Surgical Oncology, 2014, 21, 729-735.	1.5	44
78	Evaluation of an association between plasma total homocysteine and schizophrenia by a Mendelian randomization analysis. BMC Medical Genetics, 2015, 16, 54.	2.1	44
79	Involvement of cyclin D3 in liver metastasis of colorectal cancer, revealed by genome-wide copy-number analysis. Laboratory Investigation, 2005, 85, 1118-1129.	3.7	43
80	Promoter Analysis and Chromosomal Mapping of Human EBAG9 Gene. Biochemical and Biophysical Research Communications, 2000, 273, 654-660.	2.1	42
81	Novel targets for the 18p11.3 amplification frequently observed in esophageal squamous cell carcinomas. Carcinogenesis, 2002, 23, 19-24.	2.8	41
82	Early G2/M checkpoint failure as a molecular mechanism underlying etoposide-induced chromosomal aberrations. Journal of Clinical Investigation, 2005, 116, 80-89.	8.2	41
83	22q13 microduplication in two patients with common clinical manifestations: A recognizable syndrome?. American Journal of Medical Genetics, Part A, 2007, 143A, 2804-2809.	1.2	40
84	Novel intragenic duplications and mutations of CASK in patients with mental retardation and microcephaly with pontine and cerebellar hypoplasia (MICPCH). Human Genetics, 2012, 131, 99-110.	3.8	40
85	NF90 in Posttranscriptional Gene Regulation and MicroRNA Biogenesis. International Journal of Molecular Sciences, 2013, 14, 17111-17121.	4.1	40
86	Frequent silencing of the candidate tumor suppressor TRIM58 by promoter methylation in early-stage lung adenocarcinoma. Oncotarget, 2017, 8, 2890-2905.	1.8	40
87	Genomeâ€wide association study identifies gastric cancer susceptibility loci at 12q24.11â€12 and 20q11.21. Cancer Science, 2018, 109, 4015-4024.	3.9	39
88	Clinical utility of circulating cell-free Epstein-Barr virus DNA in patients with gastric cancer. Oncotarget, 2017, 8, 28796-28804.	1.8	39
89	The CASK gene harbored in a deletion detected by arrayâ€CGH as a potential candidate for a gene causative of Xâ€linked dominant mental retardation. American Journal of Medical Genetics, Part A, 2008, 146A, 2145-2151.	1.2	38
90	Resequencing and copy number analysis of the human tyrosine kinase gene family in poorly differentiated gastric cancer. Carcinogenesis, 2009, 30, 1857-1864.	2.8	38

#	Article	IF	Citations
91	Genomic Structure and Mapping of Human Orphan Receptor LXR Alpha : Upregulation of LXRa mRNA During Monocyte to Macrophage Differentiation. Journal of Atherosclerosis and Thrombosis, 2000, 7, 145-151.	2.0	37
92	The Xq22 Inversion Breakpoint Interrupted a Novel Ras-Like GTPase Gene in a Patient with Duchenne Muscular Dystrophy and Profound Mental Retardation. American Journal of Human Genetics, 2002, 71, 637-645.	6.2	37
93	Metabolic abnormalities in the genetically obese and diabetic Otsuka Long-Evans Tokushima fatty rat can be prevented and reversed by Î±-glucosidase inhibitor. Metabolism: Clinical and Experimental, 1999, 48, 347-354.	3.4	36
94	Association of KLK5 overexpression with invasiveness of urinary bladder carcinoma cells. Cancer Science, 2007, 98, 1078-1086.	3.9	36
95	NF-ÎºB Inducing Kinase, a Central Signaling Component of the Non-Canonical Pathway of NF-ÎºB, Contributes to Ovarian Cancer Progression. PLoS ONE, 2014, 9, e88347.	2.5	36
96	Aberrant DNA Methylation of Blood in Schizophrenia by Adjusting for Estimated Cellular Proportions. NeuroMolecular Medicine, 2014, 16, 697-703.	3.4	36
97	Overexpressed Skp2 within 5p amplification detected by array-based comparative genomic hybridization is associated with poor prognosis of glioblastomas. Cancer Science, 2005, 96, 676-683.	3.9	35
98	Identification of SMURF1 as a possible target for 7q21.3â€22.1 amplification detected in a pancreatic cancer cell line by inâ€house arrayâ€based comparative genomic hybridization. Cancer Science, 2008, 99, 986-994.	3.9	35
99	ACTN4 gene amplification and actininâ€4 protein overexpression drive tumour development and histological progression in a highâ€grade subset of ovarian clearâ€cell adenocarcinomas. Histopathology, 2012, 60, 1073-1083.	2.9	35
100	Unfavorable prognostic factors associated with high frequency of microsatellite instability and comparative genomic hybridization analysis in endometrial cancer. Clinical Cancer Research, 2003, 9, 5675-82.	7.0	35
101	Claudin-6 is a single prognostic marker and functions as a tumor-promoting gene in a subgroup of intestinal type gastric cancer. Gastric Cancer, 2020, 23, 403-417.	5.3	34
102	GPC5 is a possible target for the 13q31-q32 amplification detected in lymphoma cell lines. Journal of Human Genetics, 2003, 48, 331-335.	2.3	32
103	Dermokine as a novel biomarker for early-stage colorectal cancer. Journal of Gastroenterology, 2010, 45, 1201-1211.	5.1	30
104	Early manifestations of BPAN in a pediatric patient. American Journal of Medical Genetics, Part A, 2014, 164, 3095-3099.	1.2	30
105	Identification of target genes within an amplicon at 14q12-q13 in esophageal squamous cell carcinoma. Genes Chromosomes and Cancer, 2001, 32, 112-118.	2.8	29
106	Detection of cryptic chromosome aberrations in a patient with a balanced t(1;9)(p34.2;p24) by array-based comparative genomic hybridization. American Journal of Medical Genetics, Part A, 2005, 139A, 32-36.	1.2	29
107	Partial tandem duplication ofGRIA3 in a male with mental retardation. American Journal of Medical Genetics, Part A, 2007, 143A, 1448-1455.	1.2	29
108	Non-incidental coamplification of Myc and ERBB2, and Myc and EGFR, in gastric adenocarcinomas. Modern Pathology, 2007, 20, 622-631.	5.5	29

#	Article	IF	Citations
109	A novel PTCH1 mutation in a patient with Gorlin syndrome. Human Genome Variation, 2014, 1, 14022.	0.7	29
110	Heterozygous deletion at 14q22.1â€“q22.3 including the BMP4 gene in a patient with psychomotor retardation, congenital corneal opacity and feet polysyndactyly. American Journal of Medical Genetics, Part A, 2008, 146A, 2905-2910.	1.2	28
111	Overexpression of NF-ÎºB inducing kinase underlies constitutive NF-ÎºB activation in lung cancer cells. Lung Cancer, 2010, 70, 263-270.	2.0	28
112	An association study of four candidate loci for human male fertility traits with male infertility. Human Reproduction, 2015, 30, 1510-1514.	0.9	27
113	Translocation (1;22)(p36;q11.2) with concurrent del(22)(q11.2) resulted in homozygous deletion of SNF5/INI1 in a newly established cell line derived from extrarenal rhabdoid tumor. Journal of Human Genetics, 2004, 49, 586-589.	2.3	26
114	ITCH is a putative target for a novel 20q11.22 amplification detected in anaplastic thyroid carcinoma cells by arrayâ€based comparative genomic hybridization. Cancer Science, 2008, 99, 1940-1949.	3.9	26
115	Deep intronic GPR143 mutation in a Japanese family with ocular albinism. Scientific Reports, 2015, 5, 11334.	3.3	26
116	Novel deletion at Xq24 including the UBE2A gene in a patient with X-linked mental retardation. Journal of Human Genetics, 2010, 55, 244-247.	2.3	25
117	Specific molecular signatures of nonâ€tumor liver tissue may predict a risk of hepatocarcinogenesis. Cancer Science, 2014, 105, 749-754.	3.9	23
118	Gene amplification of Myc and its coamplification with ERBB2 and EGFR in gallbladder adenocarcinoma. Anticancer Research, 2009, 29, 19-26.	1.1	23
119	Skp2 overexpression is a p27Kip1-independent predictor of poor prognosis in patients with biliary tract cancers. Cancer Science, 2004, 95, 969-976.	3.9	22
120	BCL2L2 is a probable target for novel 14q11.2 amplification detected in a non-small cell lung cancer cell line. Cancer Science, 2007, 98, 1070-1077.	3.9	22
121	Clinical application of array-based comparative genomic hybridization by two-stage screening for 536 patients with mental retardation and multiple congenital anomalies. Journal of Human Genetics, 2011, 56, 110-124.	2.3	22
122	Genomic copyâ€number alterations of <scp>MYC</scp> and <scp>FHIT</scp> genes are associated with survival in esophageal squamousâ€cell carcinoma. Cancer Science, 2012, 103, 1558-1566.	3.9	22
123	Conformational plasticity of JRAB/MICAL-L2 provides â€œlaw and orderâ€in collective cell migration. Molecular Biology of the Cell, 2016, 27, 3095-3108.	2.1	22
124	A novel missense mutation of COL5A2 in a patient with Ehlersâ€“Danlos syndrome. Human Genome Variation, 2016, 3, 16030.	0.7	22
125	Tumor-promoting function and prognostic significance of the RNA-binding protein T-cell intracellular antigen-1 in esophageal squamous cell carcinoma. Oncotarget, 2016, 7, 17111-17128.	1.8	22
126	DGCR6 at the proximal part of the DiGeorge critical region is involved in conotruncal heart defects. Human Genome Variation, 2015, 2, 15004.	0.7	21

#	Article	IF	Citations
127	Construction of a high-density and high-resolution human chromosome X array for comparative genomic hybridization analysis. Journal of Human Genetics, 2007, 52, 397-405.	2.3	20
128	HECT-type Ubiquitin Ligase ITCH Targets Lysosomal-associated Protein Multispanning Transmembrane 5 (LAPTM5) and Prevents LAPTM5-mediated Cell Death. Journal of Biological Chemistry, 2011, 286, 44086-44094.	3.4	20
129	Concomitant microduplications of MECP2 and ATRX in male patients with severe mental retardation. Journal of Human Genetics, 2012, 57, 73-77.	2.3	20
130	Detection of 1p36 deletion by clinical exome-first diagnostic approach. Human Genome Variation, 2016, 3, 16006.	0.7	20
131	Deletion at chromosome 10p11.23-p12.1 defines characteristic phenotypes with marked midface retrusion. Journal of Human Genetics, 2012, 57, 191-196.	2.3	19
132	De novo non-synonymous TBL1XR1 mutation alters Wnt signaling activity. Scientific Reports, 2017, 7, 2887.	3.3	19
133	Ancestral Y-linked genes were maintained by translocation to the X and Y chromosomes fused to an autosomal pair in the Okinawa spiny rat Tokudaia muenninki. Chromosome Research, 2016, 24, 407-419.	2.2	18
134	Genome-Wide DNA Methylation Profiles in Renal Tumors of Various Histological Subtypes and Non-Tumorous Renal Tissues. Pathobiology, 2011, 78, 1-9.	3.8	17
135	Junctional <scp>R</scp>ab13â€binding protein (<scp>JRAB</scp>) regulates cell spreading via filamins. Genes To Cells, 2013, 18, 810-822.	1.2	17
136	Establishment of a cell line from a malignant rhabdoid tumor of the liver lacking the function of two tumor suppressor genes, hSNF5/INI1 and p16. Cancer Genetics and Cytogenetics, 2005, 158, 172-179.	1.0	16
137	Simultaneous Detection of Both Single Nucleotide Variations and Copy Number Alterations by Next-Generation Sequencing in Gorlin Syndrome. PLoS ONE, 2015, 10, e0140480.	2.5	16
138	The Association of Elastin Gene Variants with Two Angiographic Subtypes of Polypoidal Choroidal Vasculopathy. PLoS ONE, 2015, 10, e0120643.	2.5	16
139	An 8-cM interstitial deletion on 4q21-q22 in DNA from an infant with hepatoblastoma overlaps with a commonly deleted region in adult liver cancers. American Journal of Medical Genetics Part A, 2001, 103, 176-180.	2.4	15
140	Clinical and molecular cytogenetic characterization of two patients with non-mutational aberrations of theFMR2 gene. American Journal of Medical Genetics, Part A, 2007, 143A, 687-693.	1.2	15
141	Three patients with Schaafâ€“Yang syndrome exhibiting arthrogryposis and endocrinological abnormalities. American Journal of Medical Genetics, Part A, 2018, 176, 707-711.	1.2	15
142	KH-type splicing regulatory protein is involved in esophageal squamous cell carcinoma progression. Oncotarget, 2017, 8, 101130-101145.	1.8	15
143	The incidence of hypoplasia of the corpus callosum in patients with dup (X)(q28) involving MECP2 is associated with the location of distal breakpoints. American Journal of Medical Genetics, Part A, 2012, 158A, 1292-1303.	1.2	14
144	Cumulative effect of the plasma total homocysteine-related genetic variants on schizophrenia risk. Psychiatry Research, 2016, 246, 833-837.	3.3	14

#	Article	IF	Citations
145	Copy number alterations in urothelial carcinomas: their clinicopathological significance and correlation with DNA methylation alterations. Carcinogenesis, 2011, 32, 462-469.	2.8	13
146	Actin Cytoskeletal Reorganization Function of JRAB/MICAL-L2 Is Fine-tuned by Intramolecular Interaction between First LIM Zinc Finger and C-terminal Coiled-coil Domains. Scientific Reports, 2019, 9, 12794.	3.3	13
147	Initiation of recombination suppression and PAR formation during the early stages of neo-sex chromosome differentiation in the Okinawa spiny rat, Tokudaia muenninki. BMC Evolutionary Biology, 2015, 15, 234.	3.2	12
148	The first Japanese patient with mandibular hypoplasia, deafness, progeroid features and lipodystrophy diagnosed via POLD1 mutation detection. Human Genome Variation, 2017, 4, 17031.	0.7	12
149	Functions of Breast Cancer Predisposition Genes: Implications for Clinical Management. International Journal of Molecular Sciences, 2022, 23, 7481.	4.1	12
150	Novel human mutation and CRISPR/Cas genome-edited mice reveal the importance of C-terminal domain of MSX1 in tooth and palate development. Scientific Reports, 2016, 6, 38398.	3.3	11
151	Lack of replication of four candidate SNPs implicated in human male fertility traits: a large-scale population-based study. Human Reproduction, 2015, 30, 1505-1509.	0.9	10
152	Primary microcephaly caused by novel compound heterozygous mutations in ASPM. Human Genome Variation, 2018, 5, 18015.	0.7	10
153	A rare male patient with classic Rett syndrome caused by MeCP2_e1 mutation. American Journal of Medical Genetics, Part A, 2018, 176, 699-702.	1.2	10
154	Array comparative genomic hybridization analysis discloses chromosome copy number alterations as indicators of patient outcome in lymph node-negative breast cancer. BMC Cancer, 2019, 19, 521.	2.6	10
155	Caffeine yields aneuploidy through asymmetrical cell division caused by misalignment of chromosomes. Cancer Science, 2008, 99, 1539-1545.	3.9	9
156	Genome-first approach diagnosed Cabezas syndrome via novel CUL4B mutation detection. Human Genome Variation, 2017, 4, 16045.	0.7	9
157	Frequent silencing of RASSF1A by DNA methylation in thymic neuroendocrine tumours. Lung Cancer, 2017, 111, 116-123.	2.0	9
158	Genome-wide association study identifies ERBB4 on 2q34 as a novel locus associated with sperm motility in Japanese men. Journal of Medical Genetics, 2018, 55, 415-421.	3.2	9
159	Functionally confirmed compound heterozygous ADAM17 missense loss-of-function variants cause neonatal inflammatory skin and bowel disease 1. Scientific Reports, 2021, 11, 9552.	3.3	9
160	Meta-analysis of association studies between DISC1 missense variants and schizophrenia in the Japanese population. Schizophrenia Research, 2012, 141, 271-273.	2.0	8
161	Current status of collaborative relationships between dialysis facilities and dental facilities in Japan: results of a nationwide survey. BMC Nephrology, 2015, 16, 17.	1.8	8
162	A novel frameshift mutation of CHD7 in a Japanese patient with CHARGE syndrome. Human Genome Variation, 2016, 3, 16004.	0.7	8

#	Article	IF	Citations
163	Novel CLCN7 compound heterozygous mutations in intermediate autosomal recessive osteopetrosis. Human Genome Variation, 2017, 4, 17036.	0.7	8
164	Supramaximal CCK and CCh concentrations abolish VIP potentiation by inhibiting adenylyl cyclase activity. American Journal of Physiology - Renal Physiology, 1998, 275, G1202-G1208.	3.4	7
165	Fortuitous detection of a submicroscopic deletion at 1q25 in a girl with Cornelia-de Lange syndrome carrying t(5;13)(p13.1;q12.1) by array-based comparative genomic hybridization. American Journal of Medical Genetics, Part A, 2007, 143A, 1191-1197.	1.2	7
166	Diagnosis and Prognostication of Ductal Adenocarcinomas of the Pancreas Based on Genome-Wide DNA Methylation Profiling by Bacterial Artificial Chromosome Array-Based Methylated CpG Island Amplification. Journal of Biomedicine and Biotechnology, 2011, 2011, 1-10.	3.0	7
167	SNP array screening of cryptic genomic imbalances in 450 Japanese subjects with intellectual disability and multiple congenital anomalies previously negative for large rearrangements. Journal of Human Genetics, 2016, 61, 335-343.	2.3	7
168	Manifestation of recessive combined Dâ€2â€, Lâ€2â€hydroxyglutaric aciduria in combination with 22q11.2 deletion syndrome. American Journal of Medical Genetics, Part A, 2018, 176, 351-358.	1.2	7
169	The expression and clinical significance of connective tissue growth factor in advanced head and neck squamous cell cancer. Human Cell, 2014, 27, 121-128.	2.7	6
170	A novel COL11A1 mutation affecting splicing in a patient with Stickler syndrome. Human Genome Variation, 2015, 2, 15043.	0.7	6
171	Novel compound heterozygous CDH23 variants in a patient with Usher syndrome type I. Human Genome Variation, 2019, 6, 8.	0.7	6
172	Factors associated with regular dental visits among hemodialysis patients. World Journal of Nephrology, 2016, 5, 455.	2.0	6
173	Effect of chronic oral administration of the CCK receptor antagonist loxiglumide on exocrine and endocrine pancreas in normal rats. International Journal of Gastrointestinal Cancer, 1997, 22, 177-185.	0.4	5
174	Gene amplification of ERBB2 and EGFR in adenocarcinoma in situ and intramucosal adenocarcinoma of Barrett's esophagus. Pathology International, 2010, 60, 466-471.	1.3	5
175	A 590 kb deletion caused by nonâ€allelic homologous recombination between two LINEâ€1 elements in a patient with mesomeliaâ€synostosis syndrome. American Journal of Medical Genetics, Part A, 2017, 173, 1082-1086.	1.2	5
176	Siblings with MAN1B1-CDG Showing Novel Biochemical Profiles. Cells, 2021, 10, 3117.	4.1	5
177	Multiplex PCR/Liquid Chromatography Assay for Screening of Subtelomeric Rearrangements. Genetic Testing and Molecular Biomarkers, 2007, 11, 241-248.	1.7	4
178	Molecular cloning of t(2;7)(p24.3;p14.2), a novel chromosomal translocation in myelodysplastic syndrome-derived acute myeloid leukemia. Journal of Human Genetics, 2009, 54, 355-359.	2.3	4
179	Conservation of the TGFÎ²/Labial Homeobox Signaling Loop in Endoderm-Derived Cells between Drosophila and Mammals. Pancreatology, 2010, 10, 74-84.	1.1	4
180	A novel COL11A1 missense mutation in siblings with non-ocular Stickler syndrome. Human Genome Variation, 2016, 3, 16003.	0.7	4

#	Article	IF	Citations
181	Exome-first approach identified a novel gloss deletion associated with Lowe syndrome. Human Genome Variation, 2016, 3, 16037.	0.7	4
182	The cryptic Y-autosome translocation in the small Indian mongoose, Herpestes auropunctatus, revealed by molecular cytogenetic approaches. Chromosoma, 2016, 125, 807-815.	2.2	4
183	A case with concurrent duplication, triplication, and uniparental isodisomy at 1q42.12-qter supporting microhomology-mediated break-induced replication model for replicative rearrangements. Molecular Cytogenetics, 2017, 10, 15.	0.9	4
184	Targeted exome sequencing and chromosomal microarray for the molecular diagnosis of nevoid basal cell carcinoma syndrome. Journal of Dermatological Science, 2017, 86, 206-211.	1.9	4
185	A 16q22.2-q23.1 deletion identified in a male infant with West syndrome. Brain and Development, 2019, 41, 888-893.	1.1	4
186	A Personal Breast Cancer Risk Stratification Model Using Common Variants and Environmental Risk Factors in Japanese Females. Cancers, 2021, 13, 3796.	3.7	4
187	A FRMD7 variant in a Japanese family causes congenital nystagmus. Human Genome Variation, 2015, 2, 15002.	0.7	3
188	Case of nonâ€mosaic trisomy 20 in amniotic fluid cultures without anomalies in the fetus: Cytogenetic discrepancy between amniocytes and fetal blood. Journal of Obstetrics and Gynaecology Research, 2015, 41, 141-144.	1.3	2
189	Molecular diagnosis of an infant with TSC2/PKD1 contiguous gene syndrome. Human Genome Variation, 2020, 7, 21.	0.7	2
190	TP63 mutation mapping information in TP63 mutation-associated syndromes. Advances in Oral and Maxillofacial Surgery, 2022, 5, 100253.	0.3	2
191	A unique TBX5 microdeletion with microinsertion detected in patient with Holtâ€“Oram syndrome. American Journal of Medical Genetics, Part A, 2015, 167, 3192-3196.	1.2	1
192	Next-generation sequencing for the diagnosis of patients with congenital multiple anomalies andâ€¦/â€¦or intellectual disabilities. Journal of Medical Investigation, 2020, 67, 246-249.	0.5	1
193	Prevalence of Pathogenic Germline BRCA1/2 Variants and Their Association with Clinical Characteristics in Patients with Epithelial Ovarian Cancer in a Rural Area of Japan. Genes, 2022, 13, 1085.	2.4	1
194	Outcomes of 6Âyears of activities by the Tokushima Medical Associationâ€™s Steering Committee for Diabetes Prevention to prevent type 2 diabetes in the general population of Tokushima Prefecture. Diabetology International, 2013, 4, 23-33.	1.4	0
195	Impact of annual body mass index gain on obesity development in <scp>J</scp>apanese 6â€yearâ€old nonâ€obese children. Pediatrics International, 2013, 55, 761-766.	0.5	0
196	Construction of a combinatorial pipeline using two somatic variantÂ callingÂ methodsÂ for whole exome sequence data of gastric cancer. Journal of Medical Investigation, 2017, 64, 233-240.	0.5	0
197	The C-terminal region including the MH6 domain of Msx1 regulates skeletal development. Biochemical and Biophysical Research Communications, 2020, 526, 62-69.	2.1	0
198	Identification of aberrant DNA methylation profiles in non-tumor liver tissues of patients with non-B, non-C hepatocellular carcinoma.. Journal of Clinical Oncology, 2014, 32, 249-249.	1.6	0