Shiwei Duan

List of Publications by Year
in descending order

257 papers	7,533 citations	71102 41 h-index	82547 72 g-index
262 all docs	262 docs citations	262 times ranked	12316 citing authors

#	Article	IF	Citations
1	Trait-Associated SNPs Are More Likely to Be eQTLs: Annotation to Enhance Discovery from GWAS. PLoS Genetics, 2010, 6, e1000888.	3.5	1,161
2	SCAN: SNP and copy number annotation. Bioinformatics, 2010, 26, 259-262.	4.1	214
3	A genome-wide approach to identify genetic variants that contribute to etoposide-induced cytotoxicity. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 9758-9763.	7.1	195
4	Evaluation of Genetic Variation Contributing to Differences in Gene Expression between Populations. American Journal of Human Genetics, 2008, 82, 631-640.	6.2	192
5	Identification of Genetic Variants Contributing to Cisplatin-Induced Cytotoxicity by Use of a Genomewide Approach. American Journal of Human Genetics, 2007, 81, 427-437.	6.2	173
6	Genetic Architecture of Transcript-Level Variation in Humans. American Journal of Human Genetics, 2008, 82, 1101-1113.	6.2	142
7	Population differences in microRNA expression and biological implications. RNA Biology, 2011, 8, 692-701.	3.1	138
8	The Processing, Gene Regulation, Biological Functions, and Clinical Relevance of N4-Acetylcytidine on RNA: A Systematic Review. Molecular Therapy - Nucleic Acids, 2020, 20, 13-24.	5.1	123
9	Meta-analysis of DNA methylation biomarkers in hepatocellular carcinoma. Oncotarget, 2016, 7, 81255-81267.	1.8	87
10	Population-specific genetic variants important in susceptibility to cytarabine arabinoside cytotoxicity. Blood, 2009, 113, 2145-2153.	1.4	81
11	microRNA-137 promotes apoptosis in ovarian cancer cells via the regulation of XIAP. British Journal of Cancer, 2017, 116, 66-76.	6.4	81
12	Mapping Genes that Contribute to Daunorubicin-Induced Cytotoxicity. Cancer Research, 2007, 67, 5425-5433.	0.9	80
13	ExprTarget: An Integrative Approach to Predicting Human MicroRNA Targets. PLoS ONE, 2010, 5, e13534.	2.5	80
14	Polymorphisms of theABCB1gene are associated with the therapeutic response to risperidone in Chinese schizophrenia patients. Pharmacogenomics, 2006, 7, 987-993.	1.3	79
15	Elevation of Peripheral BDNF Promoter Methylation Links to the Risk of Alzheimer's Disease. PLoS ONE, 2014, 9, e110773.	2.5	79
16	Positive association of the DIO2 (deiodinase type 2) gene with mental retardation in the iodine-deficient areas of China. Journal of Medical Genetics, 2004, 41, 585-590.	3.2	78
17	Homocysteine, Ischemic Stroke, and Coronary Heart Disease in Hypertensive Patients. Stroke, 2015, 46, 1777-1786.	2.0	78
18	Identification of common genetic variants that account for transcript isoform variation between human populations. Human Genetics, 2009, 125, 81-93.	3.8	75

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19	Genetic Variants Contributing to Daunorubicin-Induced Cytotoxicity. Cancer Research, 2008, 68, 3161-3168.	0.9	74
20	Elevated PLA2G7 Gene Promoter Methylation as a Gender-Specific Marker of Aging Increases the Risk of Coronary Heart Disease in Females. PLoS ONE, 2013, 8, e59752.	2.5	73
21	National Trends in American Heart Association Revised Life's Simple 7 Metrics Associated With Risk of Mortality Among US Adults. JAMA Network Open, 2019, 2, e1913131.	5.9	73
22	Genetic variants associated with carboplatin-induced cytotoxicity in cell lines derived from Africans. Molecular Cancer Therapeutics, 2008, 7, 3038-3046.	4.1	66
23	Further evidence for the association between G72/G30 genes and schizophrenia in two ethnically distinct populations. Molecular Psychiatry, 2006, 11, 479-487.	7.9	64
24	Genetic regulatory subnetworks and key regulating genes in rat hippocampus perturbed by prenatal malnutrition: implications for major brain disorders. Aging, 2020, 12, 8434-8458.	3.1	63
25	The biological role of arachidonic acid 12-lipoxygenase (ALOX12) in various human diseases. Biomedicine and Pharmacotherapy, 2020, 129, 110354.	5.6	61
26	A family-based study of the association between the G72/G30 genes and schizophrenia in the Chinese population. Schizophrenia Research, 2005, 73, 257-261.	2.0	59
27	Meta-analyses of gene methylation and smoking behavior in non-small cell lung cancer patients. Scientific Reports, 2015, 5, 8897.	3.3	59
28	Comprehensive analysis of the impact of SNPs and CNVs on human microRNAs and their regulatory genes. RNA Biology, 2009, 6, 412-425.	3.1	58
29	Platinum Sensitivityâ€“Related Germline Polymorphism Discovered via a Cell-Based Approach and Analysis of Its Association with Outcome in Ovarian Cancer Patients. Clinical Cancer Research, 2011, 17, 5490-5500.	7.0	57
30	LEPR hypomethylation is significantly associated with gastric cancer in males. Experimental and Molecular Pathology, 2020, 116, 104493.	2.1	57
31	Co-expression network analysis identified hub genes critical to triglyceride and free fatty acid metabolism as key regulators of age-related vascular dysfunction in mice. Aging, 2019, 11, 7620-7638.	3.1	56
32	Hypermethylation of EDNRB promoter contributes to the risk of colorectal cancer. Diagnostic Pathology, 2013, 8, 199.	2.0	53
33	The relationship between the therapeutic response to risperidone and the dopamine D2 receptor polymorphism in Chinese schizophrenia patients. International Journal of Neuropsychopharmacology, 2007, 10, 631-7.	2.1	52
34	Identification of genomic regions contributing to etoposide-induced cytotoxicity. Human Genetics, 2009, 125, 173-180.	3.8	51
35	Lower ADD1 Gene Promoter DNA Methylation Increases the Risk of Essential Hypertension. PLoS ONE, 2013, 8, e63455.	2.5	51
36	Unintentional injuries and violence among adolescents aged 12â€“15 years in 68 low-income and middle-income countries: a secondary analysis of data from the Global School-Based Student Health Survey. The Lancet Child and Adolescent Health, 2019, 3, 616-626.	5.6	50

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37	Male-Specific Association between Dopamine Receptor D4 Gene Methylation and Schizophrenia. PLoS ONE, 2014, 9, e89128.	2.5	49
38	A significant association between BDNF promoter methylation and the risk of drug addiction. Gene, 2016, 584, 54-59.	2.2	48
39	miRConnect: Identifying Effector Genes of miRNAs and miRNA Families in Cancer Cells. PLoS ONE, 2011, 6, e26521.	2.5	46
40	Family-Based Association Study of Synapsin II and Schizophrenia. American Journal of Human Genetics, 2004, 75, 873-877.	6.2	44
41	The Diagnostic Value of DNA Methylation in Leukemia: A Systematic Review and Meta-Analysis. PLoS ONE, 2014, 9, e96822.	2.5	44
42	Improved reduced representation bisulfite sequencing for epigenomic profiling of clinical samples. Biological Procedures Online, 2014, 16, 1.	2.9	44
43	Heritable and non-genetic factors as variables of pharmacologic phenotypes in lymphoblastoid cell lines. Pharmacogenomics Journal, 2010, 10, 505-512.	2.0	43
44	A family-based association study of schizophrenia with polymorphisms at three candidate genes. Neuroscience Letters, 2005, 379, 32-36.	2.1	41
45	Susceptibility loci involved in cisplatin-induced cytotoxicity and apoptosis. Pharmacogenetics and Genomics, 2008, 18, 253-262.	1.5	41
46	Association of CDKN2BAS Polymorphism rs4977574 with Coronary Heart Disease: A Case-Control Study and a Meta-Analysis. International Journal of Molecular Sciences, 2014, 15, 17478-17492.	4.1	40
47	Diagnostic role of Wnt pathway gene promoter methylation in non small cell lung cancer. Oncotarget, 2017, 8, 36354-36367.	1.8	40
48	PACdb: a database for cell-based pharmacogenomics. Pharmacogenetics and Genomics, 2010, 20, 269-273.	1.5	40
49	A caseâ€“control study provides evidence of association for a functional polymorphism â^'197C/G in XBP1 to schizophrenia and suggests a sex-dependent effect. Biochemical and Biophysical Research Communications, 2004, 319, 866-870.	2.1	39
50	No association between the promoter variants of tumor necrosis factor alpha (TNF-Î±) and schizophrenia in Chinese Han population. Neuroscience Letters, 2004, 366, 139-143.	2.1	39
51	A case-control study provides evidence of association for a common SNP rs974819 in PDGFD to coronary heart disease and suggests a sex-dependent effect. Thrombosis Research, 2012, 130, 602-606.	1.7	38
52	DNA methylation of CMTM3 , SSTR2 , and MDFI genes in colorectal cancer. Gene, 2017, 630, 1-7.	2.2	38
53	Trends in Self-perceived Weight Status, Weight Loss Attempts, and Weight Loss Strategies Among Adults in the United States, 1999-2016. JAMA Network Open, 2019, 2, e1915219.	5.9	35
54	Population-specific GSTM1 copy number variation. Human Molecular Genetics, 2009, 18, 366-372.	2.9	34

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55	Meta-Analyses of 8 Polymorphisms Associated with the Risk of the Alzheimerâ€™s Disease. PLoS ONE, 2013, 8, e73129.	2.5	34
56	Elevated CpG island methylation of GCK gene predicts the risk of type 2 diabetes in Chinese males. Gene, 2014, 547, 329-333.	2.2	34
57	Determinants of hyperhomocysteinemia in healthy and hypertensive subjects: A population-based study and systematic review. Clinical Nutrition, 2017, 36, 1215-1230.	5.0	34
58	CCL2 promoter hypomethylation is associated with gout risk in Chinese Han male population. Immunology Letters, 2017, 190, 15-19.	2.5	34
59	Distinguishing Lung Adenocarcinoma from Lung Squamous Cell Carcinoma by Two Hypomethylated and Three Hypermethylated Genes: A Meta-Analysis. PLoS ONE, 2016, 11, e0149088.	2.5	34
60	Association between PCSK9 and LDLR gene polymorphisms with coronary heart disease: Case-control study and meta-analysis. Clinical Biochemistry, 2013, 46, 727-732.	1.9	33
61	SNPinProbe_1.0: A database for filtering out probes in the Affymetrix GeneChipÂ® Human Exon 1.0 ST array potentially affected by SNPs. Bioinformation, 2008, 2, 469-470.	0.5	33
62	GCKGene-Body Hypomethylation Is Associated with the Risk of Coronary Heart Disease. BioMed Research International, 2014, 2014, 1-7.	1.9	32
63	The role of TFPI2 hypermethylation in the detection of gastric and colorectal cancer. Oncotarget, 2017, 8, 84054-84065.	1.8	32
64	FstSNP-HapMap3: a database of SNPs with high population differentiation for HapMap3. Bioinformation, 2008, 3, 139-141.	0.5	32
65	Association of BDNF and BCHE with Alzheimer's disease: Meta-analysis based on 56 genetic case-control studies of 12,563 cases and 12,622 controls. Experimental and Therapeutic Medicine, 2015, 9, 1831-1840.	1.8	31
66	Circulating miR-3197 and miR-2116-5p as novel biomarkers for diabetic retinopathy. Clinica Chimica Acta, 2020, 501, 147-153.	1.1	31
67	Positive association between â˜’1021TT genotype of dopamine beta hydroxylase gene and progressive behavior of injection heroin users. Neuroscience Letters, 2013, 541, 258-262.	2.1	30
68	Apolipoprotein A5 gene variants and the risk of coronary heart disease: A case-control study and meta-analysis. Molecular Medicine Reports, 2013, 8, 1175-1182.	2.4	29
69	OPRK1 promoter hypermethylation increases the risk of Alzheimerâ€™s disease. Neuroscience Letters, 2015, 606, 24-29.	2.1	28
70	Comprehensive analysis of polymorphisms throughout GAD1 gene: a family-based association study in schizophrenia. Journal of Neural Transmission, 2008, 115, 513-519.	2.8	27
71	Polymorphisms of DRD2 and DRD3 genes and Parkinsonâ€™s disease: A meta-analysis. Biomedical Reports, 2014, 2, 275-281.	2.0	27
72	Catechol-O-methyltransferase gene promoter methylation as a peripheral biomarker in male schizophrenia. European Psychiatry, 2017, 44, 39-46.	0.2	27

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73	Lectin binding of human sperm associates with DEFB126 mutation and serves as a potential biomarker for subfertility. Scientific Reports, 2016, 6, 20249.	3.3	25
74	NDRG4 hypermethylation is a potential biomarker for diagnosis and prognosis of gastric cancer in Chinese population. Oncotarget, 2017, 8, 8105-8119.	1.8	25
75	Failure to find association between TRAR4 and schizophrenia in the Chinese Han population. Journal of Neural Transmission, 2006, 113, 381-385.	2.8	24
76	Association Between Six Genetic Polymorphisms and Colorectal Cancer: A Meta-Analysis. Genetic Testing and Molecular Biomarkers, 2014, 18, 187-195.	0.7	24
77	Meta-Analyses of KIF6 Trp719Arg in Coronary Heart Disease and Statin Therapeutic Effect. PLoS ONE, 2012, 7, e50126.	2.5	24
78	Four Genetic Polymorphisms of Lymphotoxin-Alpha Gene and Cancer Risk: A Systematic Review and Meta-Analysis. PLoS ONE, 2013, 8, e82519.	2.5	24
79	Whole-genome approach implicates CD44 in cellular resistance to carboplatin. Human Genomics, 2009, 3, 128.	2.9	23
80	The PADI4 gene does not contribute to genetic susceptibility to rheumatoid arthritis in Chinese Han population. Rheumatology International, 2011, 31, 1631-1634.	3.0	23
81	Aberrant methylation of the GCK gene body is associated with the risk of essential hypertension. Molecular Medicine Reports, 2015, 12, 2390-2394.	2.4	23
82	Identification of genetic variants and gene expression relationships associated with pharmacogenes in humans. Pharmacogenetics and Genomics, 2008, 18, 545-549.	1.5	22
83	Gene Set Enrichment Analyses Revealed Differences in Gene Expression Patterns between Males and Females. In Silico Biology, 2009, 9, 55-63.	0.9	22
84	An association study between genetic polymorphisms related to lipoprotein-associated phospholipase A2 and coronary heart disease. Experimental and Therapeutic Medicine, 2013, 5, 742-750.	1.8	22
85	Meta-Analysis of Low Density Lipoprotein Receptor (LDLR) rs2228671 Polymorphism and Coronary Heart Disease. BioMed Research International, 2014, 2014, 1-6.	1.9	22
86	Association of six CpG-SNPs in the inflammation-related genes with coronary heart disease. Human Genomics, 2016, 10, 21.	2.9	22
87	GPX3 hypermethylation in gastric cancer and its prognostic value in patients aged over 60. Future Oncology, 2019, 15, 1279-1289.	2.4	21
88	Epigenetic Changes Associated With Interleukin-10. Frontiers in Immunology, 2020, 11, 1105.	4.8	21
89	Meta-analyses of 10 polymorphisms associated with the risk of schizophrenia. Biomedical Reports, 2014, 2, 729-736.	2.0	20
90	Positive Association between APOA5 rs662799 Polymorphism and Coronary Heart Disease: A Case-Control Study and Meta-Analysis. PLoS ONE, 2015, 10, e0135683.	2.5	20

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91	DNA methylation and hypertension: emerging evidence and challenges. Briefings in Functional Genomics, 2016, 15, elw014.	2.7	20
92	AGTR1 promoter hypermethylation in lung squamous cell carcinoma but not in lung adenocarcinoma. Oncology Letters, 2017, 14, 4989-4994.	1.8	20
93	Elevated UMOD methylation level in peripheral blood is associated with gout risk. Scientific Reports, 2017, 7, 11196.	3.3	20
94	The Alteration of Subtelomeric DNA Methylation in Aging-Related Diseases. Frontiers in Genetics, 2018, 9, 697.	2.3	20
95	Differences in Leukocyte Telomere Length between Coronary Heart Disease and Normal Population: A Multipopulation Meta-Analysis. BioMed Research International, 2019, 2019, 1-9.	1.9	20
96	Elevated OPRD1 promoter methylation in Alzheimerâ€™s disease patients. PLoS ONE, 2017, 12, e0172335.	2.5	20
97	Association between RASSF1A Promoter Hypermethylation and Oncogenic HPV Infection Status in Invasive Cervical Cancer: a Meta-analysis. Asian Pacific Journal of Cancer Prevention, 2015, 16, 5749-5754.	1.2	20
98	Relationship between chemokine (Câ€“Xâ€“C motif) ligand 12 gene variant (rs1746048) and coronary heart disease: Caseâ€“control study and meta-analysis. Gene, 2013, 521, 38-44.	2.2	19
99	Association between TLR2, MTR, MTRR, XPC, TP73, TP53 genetic polymorphisms and gastric cancer: A meta-analysis. Clinics and Research in Hepatology and Gastroenterology, 2014, 38, 346-359.	1.5	19
100	BCL11A gene DNA methylation contributes to the risk of type 2 diabetes in males. Experimental and Therapeutic Medicine, 2014, 8, 459-463.	1.8	19
101	Identification and functional annotation of lncRNA genes with hypermethylation in colorectal cancer. Gene, 2015, 572, 259-265.	2.2	19
102	Association between homocysteine and incidence of ischemic stroke in subjects with essential hypertension: A matched case-control study. Clinical and Experimental Hypertension, 2015, 37, 557-562.	1.3	19
103	APOE hypermethylation is significantly associated with coronary heart disease in males. Gene, 2019, 689, 84-89.	2.2	19
104	Meta-analyses of methylation markers for prostate cancer. Tumor Biology, 2014, 35, 10449-10455.	1.8	18
105	Significant association between DRD3 gene body methylation and schizophrenia. Psychiatry Research, 2014, 220, 772-777.	3.3	18
106	Elevated methylation of CMTM3 promoter in the male laryngeal squamous cell carcinoma patients. Clinical Biochemistry, 2016, 49, 1278-1282.	1.9	18
107	Elevated methylation of OPRM1 and OPRL1 genes in Alzheimer's disease. Molecular Medicine Reports, 2018, 18, 4297-4302.	2.4	18
108	Complete genome sequence of high-yield strain S. lincolnensis B48 and identification of crucial mutations contributing to lincomycin overproduction. Synthetic and Systems Biotechnology, 2020, 5, 37-48.	3.7	18

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109	miR-940 is a new biomarker with tumor diagnostic and prognostic value. Molecular Therapy - Nucleic Acids, 2021, 25, 53-66.	5.1	18
110	Tumor necrosis factor alpha â˜'308 polymorphism is associated with rheumatoid arthritis in Han population of Eastern China. Rheumatology International, 2007, 28, 121-126.	3.0	17
111	Identification of susceptibility modules for coronary artery disease using a genome wide integrated network analysis. Gene, 2013, 531, 347-354.	2.2	17
112	Meta-analyses of HFE variants in coronary heart disease. Gene, 2013, 527, 167-173.	2.2	17
113	Investigation into the promoter DNA methylation of three genes (CAMK1D, CRY2 and CALM2) in the peripheral blood of patients with type 2 diabetes. Experimental and Therapeutic Medicine, 2014, 8, 579-584.	1.8	17
114	The interactions between alcohol consumption and DNA methylation of the ADD1 gene promoter modulate essential hypertension susceptibility in a population-based, caseâ€“control study. Hypertension Research, 2015, 38, 284-290.	2.7	17
115	SSTR2 promoter hypermethylation is associated with the risk and progression of laryngeal squamous cell carcinoma in males. Diagnostic Pathology, 2016, 11, 10.	2.0	17
116	An eQTL-based method identifies CTTN and ZMAT3 as pemetrexed susceptibility markers. Human Molecular Genetics, 2012, 21, 1470-1480.	2.9	16
117	The Role of Long Non-Coding RNA NNT-AS1 in Neoplastic Disease. Cancers, 2020, 12, 3086.	3.7	16
118	Diagnostic value of WIF1 methylation for colorectal cancer: a meta-analysis. Oncotarget, 2018, 9, 5378-5386.	1.8	16
119	Genetic associations with coronary heart disease: Meta-analyses of 12 candidate genetic variants. Gene, 2013, 531, 71-77.	2.2	15
120	Positive Association Between rs10918859 of the NOS1AP Gene and Coronary Heart Disease in Male Han Chinese. Genetic Testing and Molecular Biomarkers, 2013, 17, 25-29.	0.7	15
121	Genetic Associations with Hypertension: Meta-Analyses of Six Candidate Genetic Variants. Genetic Testing and Molecular Biomarkers, 2013, 17, 736-742.	0.7	15
122	Association between genetic variations of NMDA receptor NR3 subfamily genes and heroin addiction in male Han Chinese. Neuroscience Letters, 2016, 631, 122-125.	2.1	15
123	Promoter hypermethylation of miR-34a contributes to the risk, progression, metastasis and poor survival of laryngeal squamous cell carcinoma. Gene, 2016, 593, 272-276.	2.2	15
124	Elevated DRD4 promoter methylation increases the risk of Alzheimer's disease in males. Molecular Medicine Reports, 2016, 14, 2732-2738.	2.4	15
125	SMYD3 promoter hypomethylation is associated with the risk of colorectal cancer. Future Oncology, 2018, 14, 1825-1834.	2.4	15
126	Gene set enrichment analyses revealed differences in gene expression patterns between males and females. In Silico Biology, 2009, 9, 55-63.	0.9	15

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127	LINC00963: A potential cancer diagnostic and therapeutic target. Biomedicine and Pharmacotherapy, 2022, 150, 113019.	5.6	15
128	LINC00665: An Emerging Biomarker for Cancer Diagnostics and Therapeutics. Cells, 2022, 11, 1540.	4.1	15
129	No association between the serotonin 1B receptor gene and schizophrenia in a caseâ€“control and family-based association study. Neuroscience Letters, 2005, 376, 93-97.	2.1	14
130	No association between IRS-1 promoter methylation and type 2 diabetes. Molecular Medicine Reports, 2013, 8, 949-953.	2.4	14
131	Landscape of the relationship between type 2 diabetes and coronary heart disease through an integrated gene network analysis. Gene, 2014, 539, 30-36.	2.2	14
132	IGF2BP2 rs11705701 polymorphisms are associated with prediabetes in a Chinese population: A population-based case-control study. Experimental and Therapeutic Medicine, 2016, 12, 1849-1856.	1.8	14
133	Association of SCNN1B promoter methylation with essential hypertension. Molecular Medicine Reports, 2016, 14, 5422-5428.	2.4	14
134	FOXF2 promoter methylation is associated with prognosis in esophageal squamous cell carcinoma. Tumor Biology, 2017, 39, 101042831769223.	1.8	14
135	Hypermethylated Promoters of Secreted Frizzled-Related Protein Genes are Associated with Colorectal Cancer. Pathology and Oncology Research, 2019, 25, 567-575.	1.9	14
136	Genetic Associations with Diabetes: Meta-Analyses of 10 Candidate Polymorphisms. PLoS ONE, 2013, 8, e70301.	2.5	14
137	MiR-873-5p: A Potential Molecular Marker for Cancer Diagnosis and Prognosis. Frontiers in Oncology, 2021, 11, 743701.	2.8	14
138	No genetic association between polymorphisms in the AMPA receptor subunit GluR4 gene (GRIA4) and schizophrenia in the Chinese population. Neuroscience Letters, 2004, 369, 168-172.	2.1	13
139	Expression and alternative splicing of folate pathway genes in HapMap lymphoblastoid cell lines. Pharmacogenomics, 2009, 10, 549-563.	1.3	13
140	Association of NQO1 and TNF polymorphisms with Parkinsonâ€™s disease: A meta-analysis of 15 genetic association studies. Biomedical Reports, 2014, 2, 713-718.	2.0	13
141	Meta-analyses between 18 candidate genetic markers and overweight/obesity. Diagnostic Pathology, 2014, 9, 56.	2.0	13
142	Meta-analyses of 4 CFTR variants associated with the risk of the congenital bilateral absence of the vas deferens. Journal of Clinical Bioinformatics, 2014, 4, 11.	1.2	13
143	DNA methylation patterns of protein coding genes and long noncoding RNAs in female schizophrenic patients. European Journal of Medical Genetics, 2015, 58, 95-104.	1.3	13
144	Estrogen and promoter methylation in the regulation of PLA2G7 transcription. Gene, 2016, 591, 262-267.	2.2	13

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145	Prognostic value of MLH1 promoter methylation in male patients with esophageal squamous cell carcinoma. Oncology Letters, 2017, 13, 2745-2750.	1.8	13
146	miR-552: an important post-transcriptional regulator that affects human cancer. Journal of Cancer, 2020, 11, 6226-6233.	2.5	13
147	The role of miRâ€543 in human cancerous and noncancerous diseases. Journal of Cellular Physiology, 2021, 236, 15-26.	4.1	13
148	Prevalent false positives of azoospermia factor a (AZFa) microdeletions caused by single-nucleotide polymorphism rs72609647 in the sY84 screening of male infertility. Asian Journal of Andrology, 2011, 13, 877-880.	1.6	13
149	Population Difference in the Associations of KLOTH Promoter Methylation with Mild Cognitive Impairment in Xinjiang Uygur and Han Populations. PLoS ONE, 2015, 10, e0132156.	2.5	13
150	No association between the genetic polymorphisms within RTN4 and schizophrenia in the Chinese population. Neuroscience Letters, 2004, 365, 23-27.	2.1	12
151	Meta-analyses of four eosinophil related gene variants in coronary heart disease. Journal of Thrombosis and Thrombolysis, 2013, 36, 394-401.	2.1	12
152	Discovery and Functional Assessment of Gene Variants in the Vascular Endothelial Growth Factor Pathway. Human Mutation, 2014, 35, 227-235.	2.5	12
153	Another functional frameâ€shift polymorphism of <scp>DEFB</scp>126 (rs11467497) associated with male infertility. Journal of Cellular and Molecular Medicine, 2015, 19, 1077-1084.	3.6	12
154	Population difference in the association of BDNF promoter methylation with mild cognitive impairment in the Xinjiang Uygur and Han populations. Psychiatry Research, 2015, 229, 926-932.	3.3	12
155	Sex-dichotomous effects of NOS1AP promoter DNA methylation on intracranial aneurysm and brain arteriovenous malformation. Neuroscience Letters, 2016, 621, 47-53.	2.1	12
156	Association between the methylation status of the MGMT promoter in bone marrow specimens and chemotherapy outcomes of patients with acute myeloid leukemia. Oncology Letters, 2016, 11, 2851-2856.	1.8	12
157	Alterations of 5-hydroxymethylcytosines in circulating cell-free DNA reflect retinopathy in type 2 diabetes. Genomics, 2021, 113, 79-87.	2.9	12
158	TNFRSF10C methylation is a new epigenetic biomarker for colorectal cancer. PeerJ, 2018, 6, e5336.	2.0	12
159	Methods for analysis in pharmacogenomics: lessons from the Pharmacogenetics Research Network Analysis Group. Pharmacogenomics, 2009, 10, 243-251.	1.3	11
160	PPARD rs2016520 polymorphism and circulating lipid levels connect with brain diseases in Han Chinese and suggest sex-dependent effects. Biomedicine and Pharmacotherapy, 2015, 70, 7-11.	5.6	11
161	Association of four CpG-SNPs in the vascular-related genes with coronary heart disease. Biomedicine and Pharmacotherapy, 2015, 70, 80-83.	5.6	11
162	Association of human serotonin receptor 4 promoter methylation with autism spectrum disorder. Medicine (United States), 2020, 99, e18838.	1.0	11

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163	IL10 hypomethylation is associated with the risk of gastric cancer. Oncology Letters, 2021, 21, 241.	1.8	11
164	PON1 Hypermethylation and PON3 Hypomethylation are Associated with Risk of Cerebral Infarction. Current Neurovascular Research, 2019, 16, 115-122.	1.1	11
165	Significant interaction of APOE rs4420638 polymorphism with HDL-C and APOA-I levels in coronary heart disease in Han Chinese men. Genetics and Molecular Research, 2015, 14, 13414-13424.	0.2	11
166	Combined moderate and high intensity exercise with dietary restriction improves cardiac autonomic function associated with a reduction in central and systemic arterial stiffness in obese adults: a clinical trial. PeerJ, 2017, 5, e3900.	2.0	11
167	Emerging role of LINC00461 in cancer. Biomedicine and Pharmacotherapy, 2022, 152, 113239.	5.6	11
168	A caseâ€“control association study between the CYP3A4 and CYP3A5 genes and schizophrenia in the Chinese Han population. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2009, 33, 1200-1204.	4.8	10
169	Gender-dependent miR-375 promoter methylation and the risk of type 2 diabetes. Experimental and Therapeutic Medicine, 2013, 5, 1687-1692.	1.8	10
170	Positive association between lymphotoxin-alpha variation rs909253 and cancer risk: a meta-analysis based on 36 caseâ€“control studies. Tumor Biology, 2014, 35, 1973-1983.	1.8	10
171	DNA methylation patterns of protein-coding genes and long non-coding RNAs in males with schizophrenia. Molecular Medicine Reports, 2015, 12, 6568-6576.	2.4	10
172	Elevation of PTPN1 promoter methylation is a significant risk factor of type 2 diabetes in the Chinese population. Experimental and Therapeutic Medicine, 2017, 14, 2976-2982.	1.8	10
173	Differentially methylated regions in patients with rheumatic heart disease and secondary pulmonary arterial hypertension. Experimental and Therapeutic Medicine, 2017, 14, 1367-1372.	1.8	10
174	Significant association of <scp>PRMT</scp>6 hypomethylation with colorectal cancer. Journal of Clinical Laboratory Analysis, 2018, 32, e22590.	2.1	10
175	Association between GPX3 promoter methylation and malignant tumors: A meta-analysis. Pathology Research and Practice, 2019, 215, 152443.	2.3	10
176	An Association Study between Genetic Polymorphism in the Interleukin-6 Receptor Gene and Coronary Heart Disease. BioMed Research International, 2014, 2014, 1-6.	1.9	9
177	Prediabetes Is Associated withHNF-4Î±P2 Promoter Polymorphism rs1884613: A Case-Control Study in Han Chinese Population and an Updated Meta-Analysis. Disease Markers, 2014, 2014, 1-8.	1.3	9
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179	Association of seven thrombotic pathway gene CpG-SNPs with coronary heart disease. Biomedicine and Pharmacotherapy, 2015, 72, 98-102.	5.6	9
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