

The NHGRI GWAS Catalog, a curated resource of SNP-tr

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Genome-wide Association Studies. , 2013, , 93-100.		1
2	Patterns of Genome-Wide VDR Locations. PLoS ONE, 2014, 9, e96105.	1.1	120
3	Association between Expression Quantitative Trait Loci and Metabolic Traits in Two Korean Populations. PLoS ONE, 2014, 9, e114128.	1.1	4
4	The Impact of the Human Genome Project on Complex Disease. Genes, 2014, 5, 518-535.	1.0	16
5	MicroRNA-138 is a potential regulator of memory performance in humans. Frontiers in Human Neuroscience, 2014, 8, 501.	1.0	49
6	Neuroinformatic analyses of common and distinct genetic components associated with major neuropsychiatric disorders. Frontiers in Neuroscience, 2014, 8, 331.	1.4	73
7	Assessment of Subnetwork Detection Methods for Breast Cancer. Cancer Informatics, 2014, 13s6, CIN.S17641.	0.9	8
8	Molecular genetic psychophysiology: A perspective on the Minnesota contribution. Psychophysiology, 2014, 51, 1203-1204.	1.2	4
9	The HLA-DRB1 amino acid positions 11-13-26 explain the majority of SLE-MHC associations. Nature Communications, 2014, 5, 5902.	5.8	80
10	Measuring missing heritability: Inferring the contribution of common variants. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5272-81.	3.3	279
11	VAS: a convenient web portal for efficient integration of genomic features with millions of genetic variants. BMC Genomics, 2014, 15, 886.	1.2	1
12	Prioritizing causal disease genes using unbiased genomic features. Genome Biology, 2014, 15, 534.	3.8	40
13	Human germline and pan-cancer variomes and their distinct functional profiles. Nucleic Acids Research, 2014, 42, 11570-11588.	6.5	22
14	Personalized sequencing and the future of medicine: discovery, diagnosis and defeat of disease. Pharmacogenomics, 2014, 15, 1771-1790.	0.6	66
15	VSEAMS: a pipeline for variant set enrichment analysis using summary GWAS data identifies IKZF3, BATF and ESRRB as key transcription factors in type 1 diabetes. Bioinformatics, 2014, 30, 3342-3348.	1.8	14
16	eMERGEing progress in genomics—the first seven years. Frontiers in Genetics, 2014, 5, 184.	1.1	79
17	Genome-Wide Discovery of Drug-Dependent Human Liver Regulatory Elements. PLoS Genetics, 2014, 10, e1004648.	1.5	36
18	Genetic-based prediction of disease traits: prediction is very difficult, especially about the future. Frontiers in Genetics, 2014, 5, 162.	1.1	53

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19	Phenome-wide association studies demonstrating pleiotropy of genetic variants within FTO with and without adjustment for body mass index. <i>Frontiers in Genetics</i> , 2014, 5, 250.	1.1	66
20	SecureMA: protecting participant privacy in genetic association meta-analysis. <i>Bioinformatics</i> , 2014, 30, 3334-3341.	1.8	32
21	Beyond the Single SNP: Emerging Developments in Mendelian Randomization in the "Omics" Era. <i>Current Epidemiology Reports</i> , 2014, 1, 228-236.	1.1	18
22	Use of Contemporary Genetics in Cardiovascular Diagnosis. <i>Circulation</i> , 2014, 130, 1971-1980.	1.6	7
23	Expression QTL-based analyses reveal the mechanisms underlying colorectal cancer predisposition. <i>Tumor Biology</i> , 2014, 35, 12607-12611.	0.8	2
24	CardioCxE, a catalog of gene-environment interactions for cardiometabolic traits. <i>BioData Mining</i> , 2014, 7, 21.	2.2	54
25	Characterizing the genetic basis of bacterial phenotypes using genome-wide association studies: a new direction for bacteriology. <i>Genome Medicine</i> , 2014, 6, 109.	3.6	105
26	Approaches to uncovering cancer diagnostic and prognostic molecular signatures. <i>Molecular and Cellular Oncology</i> , 2014, 1, e957981.	0.3	1
27	The study of severe cutaneous drug hypersensitivity reactions from a systems biology perspective. <i>Current Opinion in Allergy and Clinical Immunology</i> , 2014, 14, 301-306.	1.1	6
28	Study of Exonic Variation Identifies Incremental Information Regarding Lipid-Related and Coronary Heart Disease Genes. <i>Circulation Research</i> , 2014, 115, 478-480.	2.0	2
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30	DiseaseConnect: a comprehensive web server for mechanism-based disease-disease connections. <i>Nucleic Acids Research</i> , 2014, 42, W137-W146.	6.5	106
31	Implementation and utilization of genetic testing in personalized medicine. <i>Pharmacogenomics and Personalized Medicine</i> , 2014, 7, 227.	0.4	63
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35	Recent Advances and Future Challenges in the Genetics of Multiple Sclerosis. <i>Frontiers in Neurology</i> , 2014, 5, 130.	1.1	46
36	A genome-wide association analysis for porcine serum lipid traits reveals the existence of age-specific genetic determinants. <i>BMC Genomics</i> , 2014, 15, 758.	1.2	24

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37	From pharmacogenomics to integrated personal omics profiling: a gap in implementation into healthcare. <i>Personalized Medicine</i> , 2014, 11, 625-629.	0.8	5
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41	Unbiased Approaches to Biomarker Discovery in Neurodegenerative Diseases. <i>Neuron</i> , 2014, 84, 594-607.	3.8	51
42	Reâ€defin G A ddi C CH3 T ion: genomics and epigenomics on substance use disorders. <i>Molecular Genetics & Genomic Medicine</i> , 2014, 2, 273-279.	0.6	2
43	Genome-Wide Association Studies: Getting to Pathogenesis, the Role of Inflammation/Complement in Age-Related Macular Degeneration. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2014, 4, a017186-a017186.	2.9	15
44	Strategies for Evaluating Idiopathic Inflammatory Myopathy Disease Susceptibility Genes. <i>Current Rheumatology Reports</i> , 2014, 16, 446.	2.1	5
45	Proteome-wide analysis of human disease mutations in short linear motifs: neglected players in cancer?. <i>Molecular BioSystems</i> , 2014, 10, 2626-2642.	2.9	80
46	NetComm: a network analysis tool based on communicability. <i>Bioinformatics</i> , 2014, 30, 3387-3389.	1.8	2
47	Editorial: Updated Guidance on Human Genome Epidemiology (HuGE) Reviews and Meta-Analyses of Genetic Associations. <i>American Journal of Epidemiology</i> , 2014, 180, 559-561.	1.6	8
48	Literome: PubMed-scale genomic knowledge base in the cloud. <i>Bioinformatics</i> , 2014, 30, 2840-2842.	1.8	61
49	Genetics of immune-mediated disorders: from genome-wide association to molecular mechanism. <i>Current Opinion in Immunology</i> , 2014, 31, 51-57.	2.4	39
50	Dermatologic applications of direct-to-consumer genomic analysis. <i>Journal of the American Academy of Dermatology</i> , 2014, 71, 993-995.	0.6	2
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55	Genome Scans for Detecting Footprints of Local Adaptation Using a Bayesian Factor Model. <i>Molecular Biology and Evolution</i> , 2014, 31, 2483-2495.	3.5	94
56	A bioinformatics method for predicting long noncoding RNAs associated with vascular disease. <i>Science China Life Sciences</i> , 2014, 57, 852-857.	2.3	55
57	<i>HLA</i> SNPs and amino acid variants are associated with nasopharyngeal carcinoma in Malaysian Chinese. <i>International Journal of Cancer</i> , 2015, 136, 678-687.	2.3	48
58	Etiology of Autism Spectrum Disorder: A Genomics Perspective. <i>Current Psychiatry Reports</i> , 2014, 16, 501.	2.1	12
59	<scp>GWAS</scp>-based pathway analysis differentiates between fluid and crystallized intelligence. <i>Genes, Brain and Behavior</i> , 2014, 13, 663-674.	1.1	27
60	Dissecting complex traits using the <i>Drosophila</i> Synthetic Population Resource. <i>Trends in Genetics</i> , 2014, 30, 488-495.	2.9	82
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70	Detecting association of rare and common variants by adaptive combination of P-values. <i>Genetical Research</i> , 2015, 97, e20.	0.3	3
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72	Polygenic Influence on Educational Attainment. <i>AERA Open</i> , 2015, 1, 233285841559997.	1.3	132
73	Progress and promise in understanding the genetic basis of common diseases. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20151684.	1.2	147

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74	Genome-Wide Association Studies and Liver Disease. <i>Seminars in Liver Disease</i> , 2015, 35, 355-360.	1.8	1
75	Evaluation of CADD Scores in Curated Mismatch Repair Gene Variants Yields a Model for Clinical Validation and Prioritization. <i>Human Mutation</i> , 2015, 36, 712-719.	1.1	39
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79	MicroRNA-650 in a copy number-variable region regulates the production of interleukin 6 in human osteosarcoma cells. <i>Oncology Letters</i> , 2015, 10, 2603-2609.	0.8	17
80	Recurrent Coding Sequence Variation Explains Only A Small Fraction of the Genetic Architecture of Colorectal Cancer. <i>Scientific Reports</i> , 2015, 5, 16286.	1.6	24
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82	LENS: web-based lens for enrichment and network studies of human proteins. <i>BMC Medical Genomics</i> , 2015, 8, S2.	0.7	27
83	Functional annotation of HOT regions in the human genome: implications for human disease and cancer. <i>Scientific Reports</i> , 2015, 5, 11633.	1.6	24
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85	Synchronized age-related gene expression changes across multiple tissues in human and the link to complex diseases. <i>Scientific Reports</i> , 2015, 5, 15145.	1.6	180
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91	Disease-associated variants in different categories of disease located in distinct regulatory elements. <i>BMC Genomics</i> , 2015, 16, S3.	1.2	41

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92	Extensive Admixture and Selective Pressure Across the Sahel Belt. <i>Genome Biology and Evolution</i> , 2015, 7, 3484-3495.	1.1	68
93	The role of visualization and 3-D printing in biological data mining. <i>BioData Mining</i> , 2015, 8, 22.	2.2	5
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95	Multiple SNP Set Analysis for Genome-Wide Association Studies Through Bayesian Latent Variable Selection. <i>Genetic Epidemiology</i> , 2015, 39, 664-677.	0.6	19
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97	A New Correction for Multiple Testing in Gene-Gene Interaction Studies. <i>Annals of Human Genetics</i> , 2015, 79, 380-384.	0.3	7
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103	Crowdsourced direct-to-consumer genomic analysis of a family quartet. <i>BMC Genomics</i> , 2015, 16, 910.	1.2	20
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117	Introduction to the analysis of next generation sequencing data and its application to venous thromboembolism. <i>Thrombosis and Haemostasis</i> , 2015, 114, 920-932.	1.8	10
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129	Single-Base Pair Genome Editing in Human Cells by Using Site-Specific Endonucleases. <i>International Journal of Molecular Sciences</i> , 2015, 16, 21128-21137.	1.8	10

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130	Implications of pleiotropy: challenges and opportunities for mining Big Data in biomedicine. <i>Frontiers in Genetics</i> , 2015, 6, 229.	1.1	41
131	Mapping asthma-associated variants in admixed populations. <i>Frontiers in Genetics</i> , 2015, 6, 292.	1.1	31
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139	An Efficient Stepwise Statistical Test to Identify Multiple Linked Human Genetic Variants Associated with Specific Phenotypic Traits. <i>PLoS ONE</i> , 2015, 10, e0138700.	1.1	3
140	Genes Regulated by Vitamin D in Bone Cells Are Positively Selected in East Asians. <i>PLoS ONE</i> , 2015, 10, e0146072.	1.1	5
141	Forward Individualized Medicine from Personal Genomes to Interactomes. <i>Frontiers in Physiology</i> , 2015, 6, 364.	1.3	15
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149	Human Enhancers Are Fragile and Prone to Deactivating Mutations. Molecular Biology and Evolution, 2015, 32, 2161-2180.	3.5	17
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151	Gene: a gene-centered information resource at NCBI. Nucleic Acids Research, 2015, 43, D36-D42.	6.5	534
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164	Genomic architecture of asthma differs by sex. Genomics, 2015, 106, 15-22.	1.3	48
165	Drosophila and experimental neurology in the post-genomic era. Experimental Neurology, 2015, 274, 4-13.	2.0	13

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167	A Multipurpose, High-Throughput Single-Nucleotide Polymorphism Chip for the Dengue and Yellow Fever Mosquito, <i>Aedes aegypti</i> . <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 711-718.	0.8	56
168	Extracting research-quality phenotypes from electronic health records to support precision medicine. <i>Genome Medicine</i> , 2015, 7, 41.	3.6	181
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170	MeRP: a high-throughput pipeline for Mendelian randomization analysis. <i>Bioinformatics</i> , 2015, 31, 957-959.	1.8	7
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