

Alison A Motsinger-Reif

List of Publications by Year in descending order

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Version: 2024-02-01

204
papers

9,633
citations

43973

48
h-index

46693

89
g-index

214
all docs

214
docs citations

214
times ranked

13774
citing authors

#	ARTICLE	IF	CITATIONS
1	Estimation of the Warfarin Dose with Clinical and Pharmacogenetic Data. <i>New England Journal of Medicine</i> , 2009, 360, 753-764.	13.9	1,375
2	Altered bile acid profile associates with cognitive impairment in Alzheimer's disease—An emerging role for gut microbiome. <i>Alzheimer's and Dementia</i> , 2019, 15, 76-92.	0.4	396
3	Metabolic network failures in Alzheimer's disease: A biochemical roadmap. <i>Alzheimer's and Dementia</i> , 2017, 13, 965-984.	0.4	362
4	A balanced accuracy function for epistasis modeling in imbalanced datasets using multifactor dimensionality reduction. <i>Genetic Epidemiology</i> , 2007, 31, 306-315.	0.6	337
5	Warfarin pharmacogenetics: a single VKORC1 polymorphism is predictive of dose across 3 racial groups. <i>Blood</i> , 2010, 115, 3827-3834.	0.6	331
6	CD1d-restricted Human Natural Killer T Cells Are Highly Susceptible to Human Immunodeficiency Virus 1 Infection. <i>Journal of Experimental Medicine</i> , 2002, 195, 869-879.	4.2	203
7	An Introduction to Terminology and Methodology of Chemical Synergy—Perspectives from Across Disciplines. <i>Frontiers in Pharmacology</i> , 2017, 8, 158.	1.6	185
8	Alterations in metabolic pathways and networks in Alzheimer's disease. <i>Translational Psychiatry</i> , 2013, 3, e244-e244.	2.4	174
9	Variation in the glucose transporter gene SLC2A2 is associated with glycemic response to metformin. <i>Nature Genetics</i> , 2016, 48, 1055-1059.	9.4	165
10	Genome-wide association studies in pharmacogenomics. <i>Pharmacogenetics and Genomics</i> , 2013, 23, 383-394.	0.7	144
11	Auriculotherapy for Pain Management: A Systematic Review and Meta-Analysis of Randomized Controlled Trials. <i>Journal of Alternative and Complementary Medicine</i> , 2010, 16, 1097-1108.	2.1	138
12	Shift Work in Nurses: Contribution of Phenotypes and Genotypes to Adaptation. <i>PLoS ONE</i> , 2011, 6, e18395.	1.1	137
13	Multifactor dimensionality reduction: An analysis strategy for modelling and detecting gene - gene interactions in human genetics and pharmacogenomics studies. <i>Human Genomics</i> , 2006, 2, 318-28.	1.4	132
14	Effect of CYP2B6, ABCB1, and CYP3A5 Polymorphisms on Efavirenz Pharmacokinetics and Treatment Response: An AIDS Clinical Trials Group Study. <i>Journal of Infectious Diseases</i> , 2010, 202, 717-722.	1.9	127
15	Gene Profiling of Canine B-Cell Lymphoma Reveals Germinal Center and Postgerminal Center Subtypes with Different Survival Times, Modeling Human DLBCL. <i>Cancer Research</i> , 2013, 73, 5029-5039.	0.4	118
16	Transcriptional profiling of human placentas from pregnancies complicated by preeclampsia reveals dysregulation of sialic acid acetyltransferase and immune signalling pathways. <i>Placenta</i> , 2011, 32, 175-182.	0.7	117
17	Comparison of approaches for machine learning optimization of neural networks for detecting gene-gene interactions in genetic epidemiology. <i>Genetic Epidemiology</i> , 2008, 32, 325-340.	0.6	103
18	Untargeted metabolomic profiling identifies disease-specific signatures in food allergy and asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 145, 897-906.	1.5	98

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19	Molecular cytogenetic characterization of canine histiocytic sarcoma: A spontaneous model for human histiocytic cancer identifies deletion of tumor suppressor genes and highlights influence of genetic background on tumor behavior. <i>BMC Cancer</i> , 2011, 11, 201.	1.1	96
20	CYP2C8*3 increases risk of neuropathy in breast cancer patients treated with paclitaxel. <i>Annals of Oncology</i> , 2013, 24, 1472-1478.	0.6	94
21	An adaptive permutation approach for genome-wide association study: evaluation and recommendations for use. <i>BioData Mining</i> , 2014, 7, 9.	2.2	93
22	Î±-Hydroxybutyric Acid Is a Selective Metabolite Biomarker of Impaired Glucose Tolerance. <i>Diabetes Care</i> , 2016, 39, 988-995.	4.3	93
23	Polymorphism modulates symptomatic response to antiarrhythmic drug therapy in patients with lone atrial fibrillation. <i>Heart Rhythm</i> , 2007, 4, 743-749.	0.3	92
24	Drug Transporter and Metabolizing Enzyme Gene Variants and Nonnucleoside Reverse-Transcriptase Inhibitor Hepatotoxicity. <i>Clinical Infectious Diseases</i> , 2006, 43, 779-782.	2.9	91
25	International collaborative study to assess cardiovascular risk and evaluate long-term health in cats with preclinical hypertrophic cardiomyopathy and apparently healthy cats: The REVEAL Study. <i>Journal of Veterinary Internal Medicine</i> , 2018, 32, 930-943.	0.6	91
26	Refining tumor-associated aneuploidy through "genomic recoding"™ of recurrent DNA copy number aberrations in 150 canine non-Hodgkin lymphomas. <i>Leukemia and Lymphoma</i> , 2011, 52, 1321-1335.	0.6	89
27	Population-Based <i>in Vitro</i> Hazard and Concentration-Response Assessment of Chemicals: The 1000 Genomes High-Throughput Screening Study. <i>Environmental Health Perspectives</i> , 2015, 123, 458-466.	2.8	89
28	Characterization of Conserved and Nonconserved Imprinted Genes in Swine1. <i>Biology of Reproduction</i> , 2009, 81, 906-920.	1.2	88
29	Prediction of human population responses to toxic compounds by a collaborative competition. <i>Nature Biotechnology</i> , 2015, 33, 933-940.	9.4	88
30	CYP2C8*3 predicts benefit/risk profile in breast cancer patients receiving neoadjuvant paclitaxel. <i>Breast Cancer Research and Treatment</i> , 2012, 134, 401-410.	1.1	81
31	Metabolomic signatures of drug response phenotypes for ketamine and esketamine in subjects with refractory major depressive disorder: new mechanistic insights for rapid acting antidepressants. <i>Translational Psychiatry</i> , 2016, 6, e894-e894.	2.4	81
32	Integrated analysis of genetic and proteomic data identifies biomarkers associated with adverse events following smallpox vaccination. <i>Genes and Immunity</i> , 2009, 10, 112-119.	2.2	77
33	GPNN: power studies and applications of a neural network method for detecting gene-gene interactions in studies of human disease. <i>BMC Bioinformatics</i> , 2006, 7, 39.	1.2	75
34	Multifactor dimensionality reduction for detecting gene-gene and gene-environment interactions in pharmacogenomics studies. <i>Pharmacogenomics</i> , 2005, 6, 823-834.	0.6	72
35	Characterization of canine osteosarcoma by array comparative genomic hybridization and RT-qPCR: Signatures of genomic imbalance in canine osteosarcoma parallel the human counterpart. <i>Genes Chromosomes and Cancer</i> , 2011, 50, 859-874.	1.5	69
36	Gene set analysis methods: a systematic comparison. <i>BioData Mining</i> , 2018, 11, 8.	2.2	68

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37	Genetic Basis for Adverse Events after Smallpox Vaccination. <i>Journal of Infectious Diseases</i> , 2008, 198, 16-22.	1.9	67
38	Immunogenetics of CD4 Lymphocyte Count Recovery during Antiretroviral Therapy: An AIDS Clinical Trials Group Study. <i>Journal of Infectious Diseases</i> , 2006, 194, 1098-1107.	1.9	65
39	Differentially expressed microRNAs and affected biological pathways revealed by a modulated modularity clustering (MMC) analysis of human preeclamptic and IUGR placentas. <i>Placenta</i> , 2013, 34, 599-605.	0.7	65
40	The COVID-19 Pandemic Vulnerability Index (PVI) Dashboard: Monitoring County-Level Vulnerability Using Visualization, Statistical Modeling, and Machine Learning. <i>Environmental Health Perspectives</i> , 2021, 129, 17701.	2.8	65
41	Comparison of smoking-related DNA methylation between newborns from prenatal exposure and adults from personal smoking. <i>Epigenomics</i> , 2019, 11, 1487-1500.	1.0	64
42	Novel methods for detecting epistasis in pharmacogenomics studies. <i>Pharmacogenomics</i> , 2007, 8, 1229-1241.	0.6	61
43	Association of Dilated Cardiomyopathy with the Striatin Mutation Genotype in Boxer Dogs. <i>Journal of Veterinary Internal Medicine</i> , 2013, 27, 1437-1440.	0.6	61
44	Genetic programming neural networks: A powerful bioinformatics tool for human genetics. <i>Applied Soft Computing Journal</i> , 2007, 7, 471-479.	4.1	60
45	Multilocus genetic interactions and response to efavirenz-containing regimens: an Adult AIDS Clinical Trials Group study. <i>Pharmacogenetics and Genomics</i> , 2006, 16, 837-845.	0.7	59
46	Maternal smoking impacts key biological pathways in newborns through epigenetic modification in Utero. <i>BMC Genomics</i> , 2016, 17, 976.	1.2	56
47	Polymorphisms in IL-1 β , vitamin D receptor Fok1, and Toll-like receptor 2 are associated with extrapulmonary tuberculosis. <i>BMC Medical Genetics</i> , 2010, 11, 37.	2.1	55
48	Genomic profiling reveals extensive heterogeneity in somatic DNA copy number aberrations of canine hemangiosarcoma. <i>Chromosome Research</i> , 2014, 22, 305-319.	1.0	54
49	Multifactor dimensionality reduction reveals gene-gene interactions associated with multiple sclerosis susceptibility in African Americans. <i>Genes and Immunity</i> , 2006, 7, 310-315.	2.2	52
50	The effect of reduction in cross-validation intervals on the performance of multifactor dimensionality reduction. <i>Genetic Epidemiology</i> , 2006, 30, 546-555.	0.6	52
51	Canine urothelial carcinoma: genomically aberrant and comparatively relevant. <i>Chromosome Research</i> , 2015, 23, 311-331.	1.0	52
52	Comparative cytogenetic characterization of primary canine melanocytic lesions using array CGH and fluorescence in situ hybridization. <i>Chromosome Research</i> , 2015, 23, 171-186.	1.0	51
53	Methylenetetrahydrofolate reductase genetic polymorphisms and toxicity to 5-FU-based chemoradiation in rectal cancer. <i>British Journal of Cancer</i> , 2011, 105, 1654-1662.	2.9	49
54	Evaluation of genetic risk score models in the presence of interaction and linkage disequilibrium. <i>Frontiers in Genetics</i> , 2013, 4, 138.	1.1	49

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55	Targeted metabolomics and medication classification data from participants in the ADNI1 cohort. <i>Scientific Data</i> , 2017, 4, 170140.	2.4	49
56	Identification and Simian Immunodeficiency Virus Infection of CD1d-Restricted Macaque Natural Killer T Cells. <i>Journal of Virology</i> , 2003, 77, 8153-8158.	1.5	47
57	A comparison of analytical methods for genetic association studies. <i>Genetic Epidemiology</i> , 2008, 32, 767-778.	0.6	47
58	Genetic Predictors of Cardiovascular Mortality During Intensive Glycemic Control in Type 2 Diabetes: Findings From the ACCORD Clinical Trial. <i>Diabetes Care</i> , 2016, 39, 1915-1924.	4.3	47
59	Hemochromatosis Gene Polymorphisms, Mitochondrial Haplogroups, and Peripheral Lipotrophy during Antiretroviral Therapy. <i>Journal of Infectious Diseases</i> , 2008, 197, 858-866.	1.9	46
60	Comparing metabolomic and pathologic biomarkers alone and in combination for discriminating Alzheimer's disease from normal cognitive aging. <i>Acta Neuropathologica Communications</i> , 2013, 1, 28.	2.4	45
61	Pharmacogenomic characterization of US FDA-approved cytotoxic drugs. <i>Pharmacogenomics</i> , 2011, 12, 1407-1415.	0.6	44
62	Morphologic and Molecular Analysis of 39 Spontaneous Feline Pulmonary Carcinomas. <i>Veterinary Pathology</i> , 2012, 49, 971-978.	0.8	44
63	Insights into the inhibition of platelet activation by omega-3 polyunsaturated fatty acids: Beyond aspirin and clopidogrel. <i>Thrombosis Research</i> , 2011, 128, 335-340.	0.8	42
64	Genetic heterogeneity beyond CYP2C8*3 does not explain differential sensitivity to paclitaxel-induced neuropathy. <i>Breast Cancer Research and Treatment</i> , 2014, 145, 245-254.	1.1	41
65	Human Natural Killer T Cells Are Heterogeneous in Their Capacity to Reprogram Their Effector Functions. <i>PLoS ONE</i> , 2006, 1, e50.	1.1	40
66	Epigenome-wide association study of DNA methylation and adult asthma in the Agricultural Lung Health Study. <i>European Respiratory Journal</i> , 2020, 56, 2000217.	3.1	40
67	Twice-Daily Application of HIV Microbicides Alters the Vaginal Microbiota. <i>MBio</i> , 2012, 3, .	1.8	38
68	Differences in X-Chromosome Transcriptional Activity and Cholesterol Metabolism between Placentae from Swine Breeds from Asian and Western Origins. <i>PLoS ONE</i> , 2013, 8, e55345.	1.1	37
69	ABCB1 and GST polymorphisms associated with TP53 status in breast cancer. <i>Pharmacogenetics and Genomics</i> , 2007, 17, 127-136.	0.7	35
70	Complex gene-gene interactions in multiple sclerosis: a multifactorial approach reveals associations with inflammatory genes. <i>Neurogenetics</i> , 2007, 8, 11-20.	0.7	35
71	Association of breed and histopathological grade in canine mast cell tumours. <i>Veterinary and Comparative Oncology</i> , 2017, 15, 829-839.	0.8	35
72	Pharmacometabolomic Assessments of Atenolol and Hydrochlorothiazide Treatment Reveal Novel Drug Response Phenotypes. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2015, 4, 669-679.	1.3	34

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73	Initial evaluation of nighttime restlessness in a naturally occurring canine model of osteoarthritis pain. <i>PeerJ</i> , 2015, 3, e772.	0.9	34
74	Genetic variation in the mitochondrial enzyme carbamyl-phosphate synthetase I predisposes children to increased pulmonary artery pressure following surgical repair of congenital heart defects: A validated genetic association study. <i>Mitochondrion</i> , 2007, 7, 204-210.	1.6	33
75	Novel human genetic variants associated with extrapulmonary tuberculosis: a pilot genome wide association study. <i>BMC Research Notes</i> , 2011, 4, 28.	0.6	33
76	Canine Hereditary Ataxia in Old English Sheepdogs and Gordon Setters Is Associated with a Defect in the Autophagy Gene Encoding RAB24. <i>PLoS Genetics</i> , 2014, 10, e1003991.	1.5	33
77	Relationship Between Mechanical Thresholds and Limb Use in Dogs With Coxofemoral Joint OA—Associated Pain and the Modulating Effects of Pain Alleviation From Total Hip Replacement on Mechanical Thresholds. <i>Veterinary Surgery</i> , 2014, 43, 542-548.	0.5	33
78	A genome-wide association analysis of temozolomide response using lymphoblastoid cell lines shows a clinically relevant association with MGMT. <i>Pharmacogenetics and Genomics</i> , 2012, 22, 796-802.	0.7	32
79	Genetic Variants in <i>CPA6</i> and <i>PRPF31</i> Are Associated With Variation in Response to Metformin in Individuals With Type 2 Diabetes. <i>Diabetes</i> , 2018, 67, 1428-1440.	0.3	32
80	Genetic Tools for Coronary Risk Assessment in Type 2 Diabetes: A Cohort Study From the ACCORD Clinical Trial. <i>Diabetes Care</i> , 2018, 41, 2404-2413.	4.3	32
81	ALFAXALONE ANESTHESIA IN BULLFROGS (<i>LITHOBATES CATESBEIANA</i>) BY INJECTION OR IMMERSION. <i>Journal of Zoo and Wildlife Medicine</i> , 2013, 44, 965-971.	0.3	31
82	Genetic Variants in <i>HSD17B3</i> , <i>SMAD3</i> , and <i>IPO11</i> Impact Circulating Lipids in Response to Fenofibrate in Individuals With Type 2 Diabetes. <i>Clinical Pharmacology and Therapeutics</i> , 2018, 103, 712-721.	2.3	30
83	Loss of Power in Two-Stage Residual Outcome Regression Analysis in Genetic Association Studies. <i>Genetic Epidemiology</i> , 2012, 36, 890-894.	0.6	28
84	Pharmacometabolomic Assessment of Metformin in Non-diabetic, African Americans. <i>Frontiers in Pharmacology</i> , 2016, 7, 135.	1.6	28
85	<i>PPARA</i> Polymorphism Influences the Cardiovascular Benefit of Fenofibrate in Type 2 Diabetes: Findings From ACCORD-Lipid. <i>Diabetes</i> , 2020, 69, 771-783.	0.3	28
86	Cumulative Genetic Risk Predicts Platinum/Taxane-Induced Neurotoxicity. <i>Clinical Cancer Research</i> , 2013, 19, 5769-5776.	3.2	27
87	Genome-wide association and pharmacological profiling of 29 anticancer agents using lymphoblastoid cell lines. <i>Pharmacogenomics</i> , 2014, 15, 137-146.	0.6	27
88	An R package implementation of multifactor dimensionality reduction. <i>BioData Mining</i> , 2011, 4, 24.	2.2	26
89	Genome-wide assessment of recurrent genomic imbalances in canine leukemia identifies evolutionarily conserved regions for subtype differentiation. <i>Chromosome Research</i> , 2015, 23, 681-708.	1.0	26
90	Comparative Exposure Assessment Using Silicone Passive Samplers Indicates That Domestic Dogs Are Sentinels To Support Human Health Research. <i>Environmental Science & Technology</i> , 2020, 54, 7409-7419.	4.6	26

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91	Bayesian neural networks for detecting epistasis in genetic association studies. BMC Bioinformatics, 2014, 15, 368.	1.2	25
92	The steroid metabolome in women with premenstrual dysphoric disorder during GnRH agonist-induced ovarian suppression: effects of estradiol and progesterone addback. Translational Psychiatry, 2017, 7, e1193-e1193.	2.4	25
93	Operative factors associated with short-term outcome in horses with large colon volvulus: 47 cases from 2006 to 2013. Equine Veterinary Journal, 2015, 47, 279-284.	0.9	24
94	Genomic map of candidate human imprint control regions: the imprintome. Epigenetics, 2022, 17, 1920-1943.	1.3	24
95	Risk score modeling of multiple gene to gene interactions using aggregated-multifactor dimensionality reduction. BioData Mining, 2013, 6, 1.	2.2	23
96	Genome-Wide Meta-analysis Identifies Genetic Variants Associated With Glycemic Response to Sulfonylureas. Diabetes Care, 2021, 44, 2673-2682.	4.3	23
97	Comparison of venous sampling methods for thromboelastography in clinically normal dogs. American Journal of Veterinary Research, 2012, 73, 1864-1870.	0.3	22
98	A Genetic Locus on Chromosome 2q24 Predicting Peripheral Neuropathy Risk in Type 2 Diabetes: Results From the ACCORD and BARI 2D Studies. Diabetes, 2019, 68, 1649-1662.	0.3	22
99	Lymphoblastoid Cell Lines Models of Drug Response: Successes and Lessons from this Pharmacogenomic Model. Current Molecular Medicine, 2014, 14, 833-840.	0.6	22
100	A Genetic Response Score for Hydrochlorothiazide Use. Hypertension, 2016, 68, 621-629.	1.3	21
101	Neural networks for genetic epidemiology: past, present, and future. BioData Mining, 2008, 1, 3.	2.2	20
102	Power of grammatical evolution neural networks to detect gene-gene interactions in the presence of error. BMC Research Notes, 2008, 1, 65.	0.6	20
103	A comparison of internal validation techniques for multifactor dimensionality reduction. BMC Bioinformatics, 2010, 11, 394.	1.2	20
104	Evaluation of polymorphisms in the sulfonamide detoxification genes NAT2, CYB5A, and CYB5R3 in patients with sulfonamide hypersensitivity. Pharmacogenetics and Genomics, 2012, 22, 733-740.	0.7	20
105	Understanding the Evolutionary Process of Grammatical Evolution Neural Networks for Feature Selection in Genetic Epidemiology. , 2006, 2006, 1-8.		19
106	Effects of acepromazine maleate on platelet function assessed by use of adenosine diphosphate activated and arachidonic acid activated modified thromboelastography in healthy dogs. American Journal of Veterinary Research, 2012, 73, 595-601.	0.3	19
107	Sphingolipid Metabolic Pathway Impacts Thiazide Diuretics Blood Pressure Response: Insights From Genomics, Metabolomics, and Lipidomics. Journal of the American Heart Association, 2018, 7, .	1.6	19
108	Clinical applications of whole-genome association studies: future applications at the bedside. Expert Review of Molecular Diagnostics, 2006, 6, 551-565.	1.5	18

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109	Accuracy of SNPs to predict risk of HLA alleles associated with drug-induced hypersensitivity events across racial groups. <i>Pharmacogenomics</i> , 2015, 16, 817-824.	0.6	18
110	Relative Quantification and Higher-Order Modeling of the Plasma Glycan Cancer Burden Ratio in Ovarian Cancer Case-Control Samples. <i>Journal of Proteome Research</i> , 2015, 14, 4394-4401.	1.8	18
111	Embracing Integrative Multiomics Approaches. <i>International Journal of Genomics</i> , 2016, 2016, 1-5.	0.8	18
112	Multivariate methods and software for association mapping in dose-response genome-wide association studies. <i>BioData Mining</i> , 2012, 5, 21.	2.2	17
113	Prevalence of onychectomy in cats presented for veterinary care near Raleigh, NC and educational attitudes toward the procedure. <i>Veterinary Anaesthesia and Analgesia</i> , 2014, 41, 48-53.	0.3	16
114	Modulation of GLP-1 Levels by a Genetic Variant That Regulates the Cardiovascular Effects of Intensive Glycemic Control in ACCORD. <i>Diabetes Care</i> , 2018, 41, 348-355.	4.3	16
115	Genetic heterogeneity is not as threatening as you might think. <i>Genetic Epidemiology</i> , 2007, 31, 797-800.	0.6	15
116	Bile acids targeted metabolomics and medication classification data in the ADNI1 and ADNI2 cohorts. <i>Scientific Data</i> , 2019, 6, 212.	2.4	15
117	Pulmonary Function and Blood DNA Methylation: A Multi-ancestry Epigenome-Wide Association Meta-analysis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2022, 206, 321-336.	2.5	15
118	Grammatical evolution decision trees for detecting gene-gene interactions. <i>BioData Mining</i> , 2010, 3, 8.	2.2	14
119	A comparison of association methods for cytotoxicity mapping in pharmacogenomics. <i>Frontiers in Genetics</i> , 2011, 2, 86.	1.1	14
120	Identification and Replication of Loci Involved in Camptothecin-Induced Cytotoxicity Using CEPH Pedigrees. <i>PLoS ONE</i> , 2011, 6, e17561.	1.1	14
121	Evaluation of thromboelastography for prediction of clinical bleeding in thrombocytopenic dogs after total body irradiation and hematopoietic cell transplantation. <i>American Journal of Veterinary Research</i> , 2014, 75, 425-432.	0.3	14
122	Thromboelastographic monitoring of the effect of unfractionated heparin in healthy dogs. <i>Journal of Veterinary Emergency and Critical Care</i> , 2017, 27, 71-81.	0.4	14
123	Pharmacometabolomics Informs About Pharmacokinetic Profile of Methylphenidate. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2018, 7, 525-533.	1.3	14
124	Long-term incidence and risk of noncardiovascular and all-cause mortality in apparently healthy cats and cats with preclinical hypertrophic cardiomyopathy. <i>Journal of Veterinary Internal Medicine</i> , 2019, 33, 2572-2586.	0.6	14
125	Genome-Wide Association Study in Immunocompetent Patients with Delayed Hypersensitivity to Sulfonamide Antimicrobials. <i>PLoS ONE</i> , 2016, 11, e0156000.	1.1	14
126	A New Explained-Variance Based Genetic Risk Score for Predictive Modeling of Disease Risk. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2012, 11, Article 15.	0.2	13

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127	Alternative cross-over strategies and selection techniques for grammatical evolution optimized neural networks. , 2006, 2006, 947-948.		12
128	Multifactor Dimensionality Reduction as a Filter-Based Approach for Genome Wide Association Studies. <i>Frontiers in Genetics</i> , 2011, 2, 80.	1.1	12
129	Optimization of Nonlinear Dose- and Concentration-Response Models Utilizing Evolutionary Computation. <i>Dose-Response</i> , 2011, 9, dose-response.0.	0.7	12
130	Beyond IC50s: Towards Robust Statistical Methods for in vitro Association Studies. <i>Journal of Pharmacogenomics & Pharmacoproteomics</i> , 2014, 05, 1000121.	0.2	12
131	Positive association between a glutathione <i>S</i> -transferase polymorphism and lymphoma in dogs. <i>Veterinary and Comparative Oncology</i> , 2014, 12, 227-236.	0.8	12
132	A novel canine model of immune thrombocytopenia: has immune thrombocytopenia (ITP) gone to the dogs?. <i>British Journal of Haematology</i> , 2014, 167, 110-120.	1.2	12
133	A genome-wide study of lipid response to fenofibrate in Caucasians. <i>Pharmacogenetics and Genomics</i> , 2016, 26, 324-333.	0.7	12
134	Human Genomic Association Studies: A Primer for the Infectious Diseases Specialist. <i>Journal of Infectious Diseases</i> , 2007, 195, 1737-1744.	1.9	11
135	The effect of alternative permutation testing strategies on the performance of multifactor dimensionality reduction. <i>BMC Research Notes</i> , 2008, 1, 139.	0.6	11
136	Evaluation of calling algorithms for array-CGH. <i>Frontiers in Genetics</i> , 2013, 4, 217.	1.1	11
137	Identifying individual risk rare variants using protein structure guided local tests (POINT). <i>PLoS Computational Biology</i> , 2019, 15, e1006722.	1.5	11
138	Low-Dose Silver Nanoparticle Surface Chemistry and Temporal Effects on Gene Expression in Human Liver Cells. <i>Small</i> , 2020, 16, e2000299.	5.2	11
139	Common and rare genetic markers of lipid variation in subjects with type 2 diabetes from the ACCORD clinical trial. <i>PeerJ</i> , 2017, 5, e3187.	0.9	11
140	Exploring epistasis in candidate genes for rheumatoid arthritis. <i>BMC Proceedings</i> , 2007, 1, S70.	1.8	10
141	Genomic Profiling in CEPH Cell Lines Distinguishes between the Camptothecins and Indenoisoquinolines. <i>Molecular Cancer Therapeutics</i> , 2011, 10, 1839-1845.	1.9	10
142	Eigenvector metabolite analysis reveals dietary effects on the association among metabolite correlation patterns, gene expression, and phenotypes. <i>Metabolomics</i> , 2016, 12, 1.	1.4	10
143	Carboplatin/taxane-induced gastrointestinal toxicity: a pharmacogenomics study on the SCOTROC1 trial. <i>Pharmacogenomics Journal</i> , 2016, 16, 243-248.	0.9	10
144	Cheminformatics approach to exploring and modeling trait-associated metabolite profiles. <i>Journal of Cheminformatics</i> , 2019, 11, 43.	2.8	10

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145	The influence of packed cell volume versus plasma proteins on thromboelastographic variables in canine blood. <i>Journal of Veterinary Emergency and Critical Care</i> , 2020, 30, 418-425.	0.4	10
146	A Type 2 Diabetes Subtype Responsive to ACCORD Intensive Glycemia Treatment. <i>Diabetes Care</i> , 2021, 44, 1410-1418.	4.3	10
147	Comparison of National Vulnerability Indices Used by the Centers for Disease Control and Prevention for the COVID-19 Response. <i>Public Health Reports</i> , 2022, 137, 803-812.	1.3	10
148	Gene selection and cancer type classification of diffuse large-B-cell lymphoma using a bivariate mixture model for two-species data. <i>Human Genomics</i> , 2013, 7, 2.	1.4	9
149	A comparison of DMET Plus microarray and genome-wide technologies by assessing population substructure. <i>Pharmacogenetics and Genomics</i> , 2016, 26, 147-153.	0.7	9
150	Prediction of synergistic drug combinations using PCA-initialized deep learning. <i>BioData Mining</i> , 2021, 14, 46.	2.2	9
151	A Comparison of Multifactor Dimensionality Reduction and L1-Penalized Regression to Identify Gene-Gene Interactions in Genetic Association Studies. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2011, 10, Article 4.	0.2	8
152	Assessing the utility of whole genome amplified DNA as a template for DMET Plus array. <i>Clinical Chemistry and Laboratory Medicine</i> , 2012, 50, 1329-34.	1.4	8
153	Evaluation of Polymorphisms in the Sulfonamide Detoxification Genes <i>CYP2A6</i> and <i>CYP2A7</i> in Dogs with Sulfonamide Hypersensitivity. <i>Journal of Veterinary Internal Medicine</i> , 2012, 26, 1126-1133.	0.6	8
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