Alison A Motsinger-Reif

List of Publications by Year
in descending order

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	ToxPi*GIS Toolkit: creating, viewing, and sharing integrative visualizations for geospatial data using ArcGIS. Journal of Exposure Science and Environmental Epidemiology, 2022, 32, 900-907.	1.8	4
2	Comparison of National Vulnerability Indices Used by the Centers for Disease Control and Prevention for the COVID-19 Response. Public Health Reports, 2022, 137, 803-812.	1.3	10
3	Pulmonary Function and Blood DNA Methylation: A Multiancestry Epigenome-Wide Association Meta-analysis. American Journal of Respiratory and Critical Care Medicine, 2022, 206, 321-336.	2.5	15
4	Questionnaire-based exposome-wide association studies (ExWAS) reveal expected and novel risk factors associated with cardiovascular outcomes in the Personalized Environment and Genes Study. Environmental Research, 2022, 212, 113463.	3.7	5
5	Genomic map of candidate human imprint control regions: the imprintome. Epigenetics, 2022, 17, 1920-1943.	1.3	24
6	In vitro iatrogenic hemolysis of canine packed red blood cells during various rapid transfusion techniques. Journal of Veterinary Emergency and Critical Care, 2021, 31, 25-31.	0.4	3
7	Knockoff boosted tree for model-free variable selection. Bioinformatics, 2021, 37, 976-983.	1.8	7
8	The COVID-19 Pandemic Vulnerability Index (PVI) Dashboard: Monitoring County-Level Vulnerability Using Visualization, Statistical Modeling, and Machine Learning. Environmental Health Perspectives, 2021, 129, 17701.	2.8	65
9	The Role of Hepatic Vagal Tone in Ozone-Induced Metabolic Dysfunction in the Liver. Toxicological Sciences, 2021, 181, 229-245.	1.4	7
10	A Type 2 Diabetes Subtype Responsive to ACCORD Intensive Glycemia Treatment. Diabetes Care, 2021, 44, 1410-1418.	4.3	10
11	Interaction between Genetic Risk Scores for reduced pulmonary function and smoking, asthma and endotoxin. Thorax, 2021, 76, 1219-1226.	2.7	7
12	Extending the lymphoblastoid cell line model for drug combination pharmacogenomics. Pharmacogenomics, 2021, 22, 543-551.	0.6	2
13	Adverse Cardiovascular Outcomes and Antihypertensive Treatment: A Genomeâ€Wide Interaction Metaâ€Analysis in the International Consortium for Antihypertensive Pharmacogenomics Studies. Clinical Pharmacology and Therapeutics, 2021, 110, 723-732.	2.3	6
14	High-throughput screening and genome-wide analyses of 44 anticancer drugs in the 1000 Genomes cell lines reveals an association of the NQO1 gene with the response of multiple anticancer drugs. PLoS Genetics, 2021, 17, e1009732.	1.5	6
15	Genome-Wide Meta-analysis Identifies Genetic Variants Associated With Glycemic Response to Sulfonylureas. Diabetes Care, 2021, 44, 2673-2682.	4.3	23
16	Prediction of synergistic drug combinations using PCA-initialized deep learning. BioData Mining, 2021, 14, 46.	2.2	9
17	Race and smoking status associated with paclitaxel drug response in patient-derived lymphoblastoid cell lines. Pharmacogenetics and Genomics, 2021, 31, 48-52.	0.7	0
18	Untargeted metabolomic profiling identifies disease-specific signatures in food allergy and asthma. Journal of Allergy and Clinical Immunology, 2020, 145, 897-906.	1.5	98

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19	Genetic and environmental risk for lymphoma in boxer dogs. Journal of Veterinary Internal Medicine, 2020, 34, 2068-2077.	0.6	8
20	Nonlinear Doseâ€“Response Modeling of High-Throughput Screening Data Using an Evolutionary Algorithm. Dose-Response, 2020, 18, 155932582092673.	0.7	4
21	Epigenome-wide association study of DNA methylation and adult asthma in the Agricultural Lung Health Study. European Respiratory Journal, 2020, 56, 2000217.	3.1	40
22	Comparative Exposure Assessment Using Silicone Passive Samplers Indicates That Domestic Dogs Are Sentinels To Support Human Health Research. Environmental Science & Technology, 2020, 54, 7409-7419.	4.6	26
23	Fibrate pharmacogenomics: expanding past the genome. Pharmacogenomics, 2020, 21, 293-306.	0.6	7
24	PPARA Polymorphism Influences the Cardiovascular Benefit of Fenofibrate in Type 2 Diabetes: Findings From ACCORD-Lipid. Diabetes, 2020, 69, 771-783.	0.3	28
25	The influence of packed cell volume versus plasma proteins on thromboelastographic variables in canine blood. Journal of Veterinary Emergency and Critical Care, 2020, 30, 418-425.	0.4	10
26	Lowâ€Dose Silver Nanoparticle Surface Chemistry and Temporal Effects on Gene Expression in Human Liver Cells. Small, 2020, 16, e2000299.	5.2	11
27	Cheminformatics approach to exploring and modeling trait-associated metabolite profiles. Journal of Cheminformatics, 2019, 11, 43.	2.8	10
28	Longâ€term incidence and risk of noncardiovascular and allâ€cause mortality in apparently healthy cats and cats with preclinical hypertrophic cardiomyopathy. Journal of Veterinary Internal Medicine, 2019, 33, 2572-2586.	0.6	14
29	Synergistic Chemotherapy Drug Response Is a Genetic Trait in Lymphoblastoid Cell Lines. Frontiers in Genetics, 2019, 10, 829.	1.1	5
30	Bile acids targeted metabolomics and medication classification data in the ADNI1 and ADNIGO/2 cohorts. Scientific Data, 2019, 6, 212.	2.4	15
31	Comparison of smoking-related DNA methylation between newborns from prenatal exposure and adults from personal smoking. Epigenomics, 2019, 11, 1487-1500.	1.0	64
32	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
33	Genome-wide DNA copy number analysis and targeted transcriptional analysis of canine histiocytic malignancies identifies diagnostic signatures and highlights disruption of spindle assembly complex. Chromosome Research, 2019, 27, 179-202.	1.0	7
34	Identifying individual risk rare variants using protein structure guided local tests (POINT). PLoS Computational Biology, 2019, 15, e1006722.	1.5	11
35	Altered bile acid profile associates with cognitive impairment in Alzheimer's diseaseâ€”An emerging role for gut microbiome. Alzheimer's and Dementia, 2019, 15, 76-92.	0.4	396
36	Current Methods for Quantifying Drug Synergism. Proteomics & Bioinformatics, 2019, 1, 43-48.	0.0	2

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37	Genetic Variants in CPA6 and PRPF31 Are Associated With Variation in Response to Metformin in Individuals With Type 2 Diabetes. Diabetes, 2018, 67, 1428-1440.	0.3	32
38	International collaborative study to assess cardiovascular risk and evaluate longâ€term health in cats with preclinical hypertrophic cardiomyopathy and apparently healthy cats: The REVEAL Study. Journal of Veterinary Internal Medicine, 2018, 32, 930-943.	0.6	91
39	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
40	Pharmacogenetic Analysis of the Modelâ€Based Pharmacokinetics of Five Antiâ€HIV Drugs: How Does This Influence the Effect of Aging?. Clinical and Translational Science, 2018, 11, 226-236.	1.5	7
41	Genetic Variants in HSD17B3, SMAD3, and IPO11 Impact Circulating Lipids in Response to Fenofibrate in Individuals With Type 2 Diabetes. Clinical Pharmacology and Therapeutics, 2018, 103, 712-721.	2.3	30
42	Modulation of GLP-1 Levels by a Genetic Variant That Regulates the Cardiovascular Effects of Intensive Glycemic Control in ACCORD. Diabetes Care, 2018, 41, 348-355.	4.3	16
43	Gene expression and linkage analysis implicate CBLB as a mediator of rituximab resistance. Pharmacogenomics Journal, 2018, 18, 467-473.	0.9	4
44	Genetic Tools for Coronary Risk Assessment in Type 2 Diabetes: A Cohort Study From the ACCORD Clinical Trial. Diabetes Care, 2018, 41, 2404-2413.	4.3	32
45	Pharmacometabolomics Informs About Pharmacokinetic Profile of Methylphenidate. CPT: Pharmacometrics and Systems Pharmacology, 2018, 7, 525-533.	1.3	14
46	Gene set analysis methods: a systematic comparison. BioData Mining, 2018, 11, 8.	2.2	68
47	The influence of Neanderthal alleles on cytotoxic response. PeerJ, 2018, 6, e5691.	0.9	1
48	Blood Lead Toxicity Analysis of Multipurpose Canines and Military Working Dogs. Journal of Special Operations Medicine: A Peer Reviewed Journal for SOF Medical Professionals, 2018, 18, 74-76.	0.1	0
49	Association of breed and histopathological grade in canine mast cell tumours. Veterinary and Comparative Oncology, 2017, 15, 829-839.	0.8	35
50	The Effect of Heart Disease on Anesthetic Complications During Routine Dental Procedures in Dogs. Journal of the American Animal Hospital Association, 2017, 53, 206-213.	0.5	7
51	Metabolic network failures in Alzheimer's disease: A biochemical roadÂmap. Alzheimer's and Dementia, 2017, 13, 965-984.	0.4	362
52	Targeted metabolomics and medication classification data from participants in the ADNI1 cohort. Scientific Data, 2017, 4, 170140.	2.4	49
53	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
54	Thromboelastographic monitoring of the effect of unfractionated heparin in healthy dogs. Journal of Veterinary Emergency and Critical Care, 2017, 27, 71-81.	0.4	14

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55	An Introduction to Terminology and Methodology of Chemical Synergyâ€"Perspectives from Across Disciplines. Frontiers in Pharmacology, 2017, 8, 158.	1.6	185
56	Common and rare genetic markers of lipid variation in subjects with type 2 diabetes from the ACCORD clinical trial. PeerJ, 2017, 5, e3187.	0.9	11
57	Embracing Integrative Multiomics Approaches. International Journal of Genomics, 2016, 2016, 1-5.	0.8	18
58	Incorporating Concomitant Medications into Genome-Wide Analyses for the Study of Complex Disease and Drug Response. Frontiers in Genetics, 2016, 7, 138.	1.1	2
59	Pharmacometabolomic Assessment of Metformin in Non-diabetic, African Americans. Frontiers in Pharmacology, 2016, 7, 135.	1.6	28
60	A Genetic Response Score for Hydrochlorothiazide Use. Hypertension, 2016, 68, 621-629.	1.3	21
61	A genome-wide study of lipid response to fenofibrate in Caucasians. Pharmacogenetics and Genomics, 2016, 26, 324-333.	0.7	12
62	Comprehensive genomic characterization of five canine lymphoid tumor cell lines. BMC Veterinary Research, 2016, 12, 207.	0.7	5
63	Maternal smoking impacts key biological pathways in newborns through epigenetic modification in Utero. BMC Genomics, 2016, 17, 976.	1.2	56
64	Î±-Hydroxybutyric Acid Is a Selective Metabolite Biomarker of Impaired Glucose Tolerance. Diabetes Care, 2016, 39, 988-995.	4.3	93
65	Eigenvector metabolite analysis reveals dietary effects on the association among metabolite correlation patterns, gene expression, and phenotypes. Metabolomics, 2016, 12, 1.	1.4	10
66	Variation in the glucose transporter gene SLC2A2 is associated with glycemic response to metformin. Nature Genetics, 2016, 48, 1055-1059.	9.4	165
67	Genetic Predictors of Cardiovascular Mortality During Intensive Glycemic Control in Type 2 Diabetes: Findings From the ACCORD Clinical Trial. Diabetes Care, 2016, 39, 1915-1924.	4.3	47
68	Metabolomic signatures of drug response phenotypes for ketamine and esketamine in subjects with refractory major depressive disorder: new mechanistic insights for rapid acting antidepressants. Translational Psychiatry, 2016, 6, e894-e894.	2.4	81
69	Use of RNA-seq to identify cardiac genes and gene pathways differentially expressed between dogs with and without dilated cardiomyopathy. American Journal of Veterinary Research, 2016, 77, 693-699.	0.3	7
70	A comparison of DMET Plus microarray and genome-wide technologies by assessing population substructure. Pharmacogenetics and Genomics, 2016, 26, 147-153.	0.7	9
71	Carboplatin/taxane-induced gastrointestinal toxicity: a pharmacogenomics study on the SCOTROC1 trial. Pharmacogenomics Journal, 2016, 16, 243-248.	0.9	10
72	Genome-Wide Association Study in Immunocompetent Patients with Delayed Hypersensitivity to Sulfonamide Antimicrobials. PLoS ONE, 2016, 11, e0156000.	1.1	14

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73	Pharmacometabolomic Assessments of Atenolol and Hydrochlorothiazide Treatment Reveal Novel Drug Response Phenotypes. CPT: Pharmacometrics and Systems Pharmacology, 2015, 4, 669-679.	1.3	34
74	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
75	Genome-wide assessment of recurrent genomic imbalances in canine leukemia identifies evolutionarily conserved regions for subtype differentiation. Chromosome Research, 2015, 23, 681-708.	1.0	26
76	Prediction of human population responses to toxic compounds by a collaborative competition. Nature Biotechnology, 2015, 33, 933-940.	9.4	88
77	Comparative cytogenetic characterization of primary canine melanocytic lesions using array CGH and fluorescence in situ hybridization. Chromosome Research, 2015, 23, 171-186.	1.0	51
78	Accuracy of SNPs to predict risk ofHLAalleles associated with drug-induced hypersensitivity events across racial groups. Pharmacogenomics, 2015, 16, 817-824.	0.6	18
79	Population-Based in Vitro Hazard and Concentrationâ€“Response Assessment of Chemicals: The 1000 Genomes High-Throughput Screening Study. Environmental Health Perspectives, 2015, 123, 458-466.	2.8	89
80	An investigation of gene-gene interactions in dose-response studies with Bayesian nonparametrics. BioData Mining, 2015, 8, 6.	2.2	0
81	Canine urothelial carcinoma: genomically aberrant and comparatively relevant. Chromosome Research, 2015, 23, 311-331.	1.0	52
82	Evaluating the role of admixture in cancer therapy viain vitrodrug response and multivariate genome-wide associations. Pharmacogenomics, 2015, 16, 1451-1463.	0.6	8
83	Relative Quantification and Higher-Order Modeling of the Plasma Glycan Cancer Burden Ratio in Ovarian Cancer Case-Control Samples. Journal of Proteome Research, 2015, 14, 4394-4401.	1.8	18
84	Initial evaluation of nighttime restlessness in a naturally occurring canine model of osteoarthritis pain. PeerJ, 2015, 3, e772.	0.9	34
85	Current Study Designs, Methods, and Future Directions of Genetic Association Mapping. Advances in Bioinformatics and Biomedical Engineering Book Series, 2015, , 323-358.	0.2	0
86	Pain relief improves sleep in dogs with osteoarthritis. , 2015, , 512-512.		0
87	Beyond IC50s: Towards Robust Statistical Methods for in vitro Association Studies. Journal of Pharmacogenomics & Pharmacoproteomics, 2014, 05, 1000121.	0.2	12
88	Bayesian neural networks for detecting epistasis in genetic association studies. BMC Bioinformatics, 2014, 15, 368.	1.2	25
89	Single-Nucleotide Polymorphism Data Support the General Unrelatedness of the Males in the Agricultural Health Study. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 2192-2195.	1.1	0
90	Genome-wide association and pharmacological profiling of 29 anticancer agents using lymphoblastoid cell lines. Pharmacogenomics, 2014, 15, 137-146.	0.6	27

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91	Canine Hereditary Ataxia in Old English Sheepdogs and Gordon Setters Is Associated with a Defect in the Autophagy Gene Encoding RAB24. PLoS Genetics, 2014, 10, e1003991.	1.5	33
92	Positive association between a glutathioneâ€Sâ€transferase polymorphism and lymphoma in dogs. Veterinary and Comparative Oncology, 2014, 12, 227-236.	0.8	12
93	A novel canine model of immune thrombocytopenia: has immune thrombocytopenia (ITP) gone to the dogs?. British Journal of Haematology, 2014, 167, 110-120.	1.2	12
94	Relationship Between Mechanical Thresholds and Limb Use in Dogs With Coxofemoral Joint OAâ€Associated Pain and the Modulating Effects of Pain Alleviation From Total Hip Replacement on Mechanical Thresholds. Veterinary Surgery, 2014, 43, 542-548.	0.5	33
95	Evaluation of thromboelastography for prediction of clinical bleeding in thrombocytopenic dogs after total body irradiation and hematopoietic cell transplantation. American Journal of Veterinary Research, 2014, 75, 425-432.	0.3	14
96	VH1-44 gene usage defines a subset of canine B-cell lymphomas associated with better patient survival. Veterinary Immunology and Immunopathology, 2014, 157, 125-130.	0.5	8
97	Genomic profiling reveals extensive heterogeneity in somatic DNA copy number aberrations of canine hemangiosarcoma. Chromosome Research, 2014, 22, 305-319.	1.0	54
98	Prevalence of onychectomy in cats presented for veterinary care near Raleigh, NC and educational attitudes toward the procedure. Veterinary Anaesthesia and Analgesia, 2014, 41, 48-53.	0.3	16
99	An adaptive permutation approach for genome-wide association study: evaluation and recommendations for use. BioData Mining, 2014, 7, 9.	2.2	93
100	Application of next generation sequencing to CEPH cell lines to discover variants associated with FDA approved chemotherapeutics. BMC Research Notes, 2014, 7, 360.	0.6	5
101	Genetic heterogeneity beyond CYP2C8*3 does not explain differential sensitivity to paclitaxel-induced neuropathy. Breast Cancer Research and Treatment, 2014, 145, 245-254.	1.1	41
102	Lymphoblastoid Cell Lines Models of Drug Response: Successes and Lessons from this Pharmacogenomic Model. Current Molecular Medicine, 2014, 14, 833-840.	0.6	22
103	Risk score modeling of multiple gene to gene interactions using aggregated-multifactor dimensionality reduction. BioData Mining, 2013, 6, 1.	2.2	23
104	Differentially expressed microRNAs and affected biological pathways revealed byÂmodulated modularity clustering (MMC) analysis of human preeclamptic and IUGR placentas. Placenta, 2013, 34, 599-605.	0.7	65
105	Comparing metabolomic and pathologic biomarkers alone and in combination for discriminating Alzheimerâ€™s disease from normal cognitive aging. Acta Neuropathologica Communications, 2013, 1, 28.	2.4	45
106	Gene selection and cancer type classification of diffuse large-B-cell lymphoma using a bivariate mixture model for two-species data. Human Genomics, 2013, 7, 2.	1.4	9
107	Association of Dilated Cardiomyopathy with the Striatin Mutation Genotype in Boxer Dogs. Journal of Veterinary Internal Medicine, 2013, 27, 1437-1440.	0.6	61
108	ALFAXALONE ANESTHESIA IN BULLFROGS (LITHOBATES CATESBEIANA) BY INJECTION OR IMMERSION. Journal of Zoo and Wildlife Medicine, 2013, 44, 965-971.	0.3	31

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109	Alterations in metabolic pathways and networks in Alzheimerâ€™s disease. Translational Psychiatry, 2013, 3, e244-e244.	2.4	174
110	Naturally occuring canine cancers: powerful models for stimulating pharmacogenomic advancement in human medicine. Pharmacogenomics, 2013, 14, 1929-1931.	0.6	4
111	Gene Profiling of Canine B-Cell Lymphoma Reveals Germinal Center and Postgerminal Center Subtypes with Different Survival Times, Modeling Human DLBCL. Cancer Research, 2013, 73, 5029-5039.	0.4	118
112	CYP2C8*3 increases risk of neuropathy in breast cancer patients treated with paclitaxel. Annals of Oncology, 2013, 24, 1472-1478.	0.6	94
113	Cumulative Genetic Risk Predicts Platinum/Taxane-Induced Neurotoxicity. Clinical Cancer Research, 2013, 19, 5769-5776.	3.2	27
114	Genome-wide association studies in pharmacogenomics. Pharmacogenetics and Genomics, 2013, 23, 383-394.	0.7	144
115	Evaluation of genetic risk score models in the presence of interaction and linkage disequilibrium. Frontiers in Genetics, 2013, 4, 138.	1.1	49
116	Evaluation of calling algorithms for array-CGH. Frontiers in Genetics, 2013, 4, 217.	1.1	11
117	Differences in X-Chromosome Transcriptional Activity and Cholesterol Metabolism between Placentae from Swine Breeds from Asian and Western Origins. PLoS ONE, 2013, 8, e55345.	1.1	37
118	A comparison of GE optimized neural networks and decision trees. , 2012, , .		0
119	Grammatical evolution support vector machines for predicting human genetic disease association. , 2012, , .		5
120	Twice-Daily Application of HIV Microbicides Alters the Vaginal Microbiota. MBio, 2012, 3, .	1.8	38
121	Research Highlights: Highlights from the latest articles in pharmacogenomics of warfarin dosing. Pharmacogenomics, 2012, 13, 861-864.	0.6	2
122	Research Highlights. Pharmacogenomics, 2012, 13, 137-140.	0.6	0
123	Comparison of venous sampling methods for thromboelastography in clinically normal dogs. American Journal of Veterinary Research, 2012, 73, 1864-1870.	0.3	22
124	Assessing the utility of whole genome amplified DNA as a template for DMET Plus array. Clinical Chemistry and Laboratory Medicine, 2012, 50, 1329-34.	1.4	8
125	A genome-wide association analysis of temozolomide response using lymphoblastoid cell lines shows a clinically relevant association with MGMT. Pharmacogenetics and Genomics, 2012, 22, 796-802.	0.7	32
126	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

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127	Morphologic and Molecular Analysis of 39 Spontaneous Feline Pulmonary Carcinomas. Veterinary Pathology, 2012, 49, 971-978.	0.8	44
128	Loss of Power in Twoâ€Stage Residualâ€Outcome Regression Analysis in Genetic Association Studies. Genetic Epidemiology, 2012, 36, 890-894.	0.6	28
129	A New Explained-Variance Based Genetic Risk Score for Predictive Modeling of Disease Risk. Statistical Applications in Genetics and Molecular Biology, 2012, 11, Article 15.	0.2	13
130	Effects of acepromazine maleate on platelet function assessed by use of adenosine diphosphate activatedâ€“ and arachidonic acidâ€“ activated modified thromboelastography in healthy dogs. American Journal of Veterinary Research, 2012, 73, 595-601.	0.3	19
131	Multivariate methods and software for association mapping in doseâ€response genomeâ€wide association studies. BioData Mining, 2012, 5, 21.	2.2	17
132	Global tests of P-values for multifactor dimensionality reduction models in selection of optimal number of target genes. BioData Mining, 2012, 5, 3.	2.2	7
133	A comparison of internal model validation methods for multifactor dimensionality reduction in the case of genetic heterogeneity. BMC Research Notes, 2012, 5, 623.	0.6	6
134	CYP2C8*3 predicts benefit/risk profile in breast cancer patients receiving neoadjuvant paclitaxel. Breast Cancer Research and Treatment, 2012, 134, 401-410.	1.1	81
135	Evaluation of Polymorphisms in the Sulfonamide Detoxification Genes <scp>CYB</scp>5A and <scp>CYB</scp>5R3 in Dogs with Sulfonamide Hypersensitivity. Journal of Veterinary Internal Medicine, 2012, 26, 1126-1133.	0.6	8
136	Are plasma level and CYP genotypes predictors of liver injury in an Ethiopian population?. Pharmacogenomics, 2012, 13, 138-9.	0.6	0
137	Do genetic polymorphisms of nevirapine metabolic, transport and antigen recognition enzymes play a role in nevirapine toxicity risk?. Pharmacogenomics, 2012, 13, 139-40.	0.6	0
138	Replication study of CYP4F2 association with warfarin response in an Israeli population. Pharmacogenomics, 2012, 13, 863-4.	0.6	0
139	Refining tumor-associated aneuploidy through â€˜genomic recodingâ€™ of recurrent DNA copy number aberrations in 150 canine non-Hodgkin lymphomas. Leukemia and Lymphoma, 2011, 52, 1321-1335.	0.6	89
140	Insights into the inhibition of platelet activation by omega-3 polyunsaturated fatty acids: Beyond aspirin and clopidogrel. Thrombosis Research, 2011, 128, 335-340.	0.8	42
141	Multifactor Dimensionality Reduction as a Filter-Based Approach for Genome Wide Association Studies. Frontiers in Genetics, 2011, 2, 80.	1.1	12
142	A comparison of association methods for cytotoxicity mapping in pharmacogenomics. Frontiers in Genetics, 2011, 2, 86.	1.1	14
143	Identification and Replication of Loci Involved in Camptothecin-Induced Cytotoxicity Using CEPH Pedigrees. PLoS ONE, 2011, 6, e17561.	1.1	14
144	Shift Work in Nurses: Contribution of Phenotypes and Genotypes to Adaptation. PLoS ONE, 2011, 6, e18395.	1.1	137

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145	The Effect of Retrospective Sampling on Estimates of Prediction Error for Multifactor Dimensionality Reduction. Annals of Human Genetics, 2011, 75, 46-61.	0.3	3
146	Transcriptional profiling of human placentas from pregnancies complicated by preeclampsia reveals disregulation of sialic acid acetylesterase and immune signalling pathways. Placenta, 2011, 32, 175-182.	0.7	117
147	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. BMC Cancer, 2011, 11, 201.	1.1	96
148	An R package implementation of multifactor dimensionality reduction. BioData Mining, 2011, 4, 24.	2.2	26
149	Novel human genetic variants associated with extrapulmonary tuberculosis: a pilot genome wide association study. BMC Research Notes, 2011, 4, 28.	0.6	33
150	Characterization of canine osteosarcoma by array comparative genomic hybridization and RTâ€qPCR: Signatures of genomic imbalance in canine osteosarcoma parallel the human counterpart. Genes Chromosomes and Cancer, 2011, 50, 859-874.	1.5	69
151	Pharmacogenomic characterization of US FDA-approved cytotoxic drugs. Pharmacogenomics, 2011, 12, 1407-1415.	0.6	44
152	Genomic Profiling in CEPH Cell Lines Distinguishes between the Camptothecins and Indenoisoquinolines. Molecular Cancer Therapeutics, 2011, 10, 1839-1845.	1.9	10
153	A Comparison of Multifactor Dimensionality Reduction and L1-Penalized Regression to Identify Gene-Gene Interactions in Genetic Association Studies. Statistical Applications in Genetics and Molecular Biology, 2011, 10, Article 4.	0.2	8
154	Optimization of Nonlinear Dose- and Concentration-Response Models Utilizing Evolutionary Computation. Dose-Response, 2011, 9, dose-response.0.	0.7	12
155	Methylenetetrahydrofolate reductase genetic polymorphisms and toxicity to 5-FU-based chemoradiation in rectal cancer. British Journal of Cancer, 2011, 105, 1654-1662.	2.9	49
156	Quality of Reporting on Randomised Controlled Trials of Auriculotherapy for Pain. Acupuncture in Medicine, 2011, 29, 122-126.	0.4	6
157	Characterizing Canine Lymphoma As a Potential Large Animal Model of Human Diffuse Large B-Cell Lymphoma. Blood, 2011, 118, 5193-5193.	0.6	1
158	The Vitamin D Receptor Gene and Disease Severity in Sickle Cell Anemia. Blood, 2011, 118, 2122-2122.	0.6	0
159	Ex-Vivo Modeling for Heritability Assessment and Genetic Mapping in Pharmacogenomics. Proceedings, 2011, 2011, 306-318.	0.3	1
160	Warfarin pharmacogenetics: a single VKORC1 polymorphism is predictive of dose across 3 racial groups. Blood, 2010, 115, 3827-3834.	0.6	331
161	A comparison of internal validation techniques for multifactor dimensionality reduction. BMC Bioinformatics, 2010, 11, 394.	1.2	20
162	Polymorphisms in IL-1Î², vitamin D receptor FokI, and Toll-like receptor 2 are associated with extrapulmonary tuberculosis. BMC Medical Genetics, 2010, 11, 37.	2.1	55

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163	Grammatical evolution decision trees for detecting gene-gene interactions. BioData Mining, 2010, 3, 8.	2.2	14
164	Discussion of a Genomeâ€Wide Association Approach to Determine HIVâ€1 Set Point in African Americans. Journal of Infectious Diseases, 2010, 201, 1118-1120.	1.9	1
165	Effect ofCYP2B6,ABCB1, andCYP3A5Polymorphisms on Efavirenz Pharmacokinetics and Treatment Response: An AIDS Clinical Trials Group Study. Journal of Infectious Diseases, 2010, 202, 717-722.	1.9	127
166	Institutional Profile: UNC Institute for Pharmacogenomics and Individualized Therapy: interdisciplinary research for individual care. Pharmacogenomics, 2010, 11, 13-21.	0.6	1
167	Auriculotherapy for Pain Management: A Systematic Review and Meta-Analysis of Randomized Controlled Trials. Journal of Alternative and Complementary Medicine, 2010, 16, 1097-1108.	2.1	138
168	Grammatical Evolution Decision Trees for Detecting Gene-Gene Interactions. Lecture Notes in Computer Science, 2010, , 98-109.	1.0	3
169	Characterization of Conserved and Nonconserved Imprinted Genes in Swine1. Biology of Reproduction, 2009, 81, 906-920.	1.2	88
170	Integrated analysis of genetic and proteomic data identifies biomarkers associated with adverse events following smallpox vaccination. Genes and Immunity, 2009, 10, 112-119.	2.2	77
171	Estimation of the Warfarin Dose with Clinical and Pharmacogenetic Data. New England Journal of Medicine, 2009, 360, 753-764.	13.9	1,375
172	Neural networks for genetic epidemiology: past, present, and future. BioData Mining, 2008, 1, 3.	2.2	20
173	Comparison of approaches for machineâ€learning optimization of neural networks for detecting geneâ€gene interactions in genetic epidemiology. Genetic Epidemiology, 2008, 32, 325-340.	0.6	103
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