Liewei Wang

List of Publications by Year
in descending order

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163	7,983	57758	60623
papers	citations	44 h-index	81 g-index

177	177	177	13690
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	FKBP51 Affects Cancer Cell Response to Chemotherapy by Negatively Regulating Akt. Cancer Cell, 2009, 16, 259-266.	16.8	643
2	Genomics and Drug Response. New England Journal of Medicine, 2011, 364, 1144-1153.	27.0	552
3	ATP-sensitive K+channel openers prevent Ca2+overload in rat cardiac mitochondria. Journal of Physiology, 1999, 519, 347-360.	2.9	323
4	Effect of Genotype-Guided Oral P2Y12 Inhibitor Selection vs Conventional Clopidogrel Therapy on Ischemic Outcomes After Percutaneous Coronary Intervention. JAMA - Journal of the American Medical Association, 2020, 324, 761.	7.4	257
5	Preemptive Genotyping for Personalized Medicine: Design of the Right Drug, Right Dose, Right Timeâ€"Using Genomic Data to Individualize Treatment Protocol. Mayo Clinic Proceedings, 2014, 89, 25-33.	3.0	250
6	Prostate cancerâ€"associated SPOP mutations confer resistance to BET inhibitors through stabilization of BRD4. Nature Medicine, 2017, 23, 1063-1071.	30.7	240
7	Measure transcript integrity using RNA-seq data. BMC Bioinformatics, 2016, 17, 58.	2.6	187
8	Pharmacogenomics: Precision Medicine and Drug Response. Mayo Clinic Proceedings, 2017, 92, 1711-1722.	3.0	156
9	Gemcitabine and Cytosine Arabinoside Cytotoxicity: Association with Lymphoblastoid Cell Expression. Cancer Research, 2008, 68, 7050-7058.	0.9	155
10	Beta-Poisson model for single-cell RNA-seq data analyses. Bioinformatics, 2016, 32, 2128-2135.	4.1	151
11	Circular RNAs and their associations with breast cancer subtypes. Oncotarget, 2016, 7, 80967-80979.	1.8	140
12	Clopidogrel Pharmacogenetics. Circulation: Cardiovascular Interventions, 2019, 12, e007811.	3.9	139
13	Radiation pharmacogenomics: A genome-wide association approach to identify radiation response biomarkers using human lymphoblastoid cell lines. Genome Research, 2010, 20, 1482-1492.	5.5	135
14	DNA methyltransferase expression in triple-negative breast cancer predicts sensitivity to decitabine. Journal of Clinical Investigation, 2018, 128, 2376-2388.	8.2	134
15	CDK4/6-dependent activation of DUB3 regulates cancer metastasis through SNAIL1. Nature Communications, 2017, 8, 13923.	12.8	119
16	Androgen Receptor Variant AR-V9 Is Coexpressed with AR-V7 in Prostate Cancer Metastases and Predicts Abiraterone Resistance. Clinical Cancer Research, 2017, 23, 4704-4715.	7.0	117
17	A comprehensive analysis of breast cancer microbiota and host gene expression. PLoS ONE, 2017, 12, e0188873.	2.5	111
18	Deubiquitination and Activation of AMPK by USP10. Molecular Cell, 2016, 61, 614-624.	9.7	106

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19	UFL1 promotes histone H4 ufmylation and ATM activation. Nature Communications, 2019, 10, 1242.	12.8	104
20	Human thiopurine S-methyltransferase pharmacogenetics: Variant allozyme misfolding and aggresome formation. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 9394-9399.	7.1	103
21	Functional Genetic Polymorphisms in the Aromatase GeneCYP19Vary the Response of Breast Cancer Patients to Neoadjuvant Therapy with Aromatase Inhibitors. Cancer Research, 2010, 70, 319-328.	0.9	102
22	A cell cycle-dependent BRCA1â€“UHRF1 cascade regulates DNA double-strand break repair pathway choice. Nature Communications, 2016, 7, 10201.	12.8	95
23	Regulation of Serine-Threonine Kinase Akt Activation by NAD + -Dependent Deacetylase SIRT7. Cell Reports, 2017, 18, 1229-1240.	6.4	84
24	Androgen receptor splice variants bind to constitutively open chromatin and promote abiraterone-resistant growth of prostate cancer. Nucleic Acids Research, 2018, 46, 1895-1911.	14.5	79
25	Gemcitabine and Arabinosylcytosin Pharmacogenomics: Genome-Wide Association and Drug Response Biomarkers. PLoS ONE, 2009, 4, e7765.	2.5	75
26	Parkin Regulates Mitosis and Genomic Stability through Cdc20/Cdh1. Molecular Cell, 2015, 60, 21-34.	9.7	74
27	Snail Contributes to the Maintenance of Stem Cell-Like Phenotype Cells in Human Pancreatic Cancer. PLoS ONE, 2014, 9, e87409.	2.5	73
28	AMPK regulates histone H2B O-GlcNAcylation. Nucleic Acids Research, 2014, 42, 5594-5604.	14.5	72
29	Genome-Wide Meta-Analysis of Homocysteine and Methionine Metabolism Identifies Five One Carbon Metabolism Loci and a Novel Association of ALDH1L1 with Ischemic Stroke. PLoS Genetics, 2014, 10, e1004214.	3.5	69
30	Pharmacogenomicsâ€Driven Prediction of Antidepressant Treatment Outcomes: A Machineâ€Learning Approach With Multiâ€trial Replication. Clinical Pharmacology and Therapeutics, 2019, 106, 855-865.	4.7	69
31	Systematic review of the evidence on the cost-effectiveness of pharmacogenomics-guided treatment for cardiovascular diseases. Genetics in Medicine, 2020, 22, 475-486.	2.4	67
32	Selective Estrogen Receptor Modulators and Pharmacogenomic Variation in ZNF423 Regulation of BRCA1 Expression: Individualized Breast Cancer Prevention. Cancer Discovery, 2013, 3, 812-825.	9.4	61
33	Tumor Sequencing and Patient-Derived Xenografts in the Neoadjuvant Treatment of Breast Cancer. Journal of the National Cancer Institute, 2017, 109, .	6.3	61
34	Beta-defensin 1, aryl hydrocarbon receptor and plasma kynurenine in major depressive disorder: metabolomics-informed genomics. Translational Psychiatry, 2018, 8, 10.	4.8	59
35	ATR Inhibition Is a Promising Radiosensitizing Strategy for Triple-Negative Breast Cancer. Molecular Cancer Therapeutics, 2018, 17, 2462-2472.	4.1	59
36	NOTCH3 expression is linked to breast cancer seeding and distant metastasis. Breast Cancer Research, 2018, 20, 105.	5.0	58

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37	Regulation of sister chromatid cohesion by nuclear PD-L1. Cell Research, 2020, 30, 590-601.	12.0	58
38	DBC1 Functions as a Tumor Suppressor by Regulating p53 Stability. Cell Reports, 2015, 10, 1324-1334.	6.4	56
39	Pharmacogenomics: a systems approach. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2010, 2, 3-22.	6.6	55
40	FKBP5 genetic variation. Pharmacogenetics and Genomics, 2013, 23, 156-166.	1.5	54
41	Establishing and characterizing patient-derived xenografts using pre-chemotherapy percutaneous biopsy and post-chemotherapy surgical samples from a prospective neoadjuvant breast cancer study. Breast Cancer Research, 2017, 19, 130.	5.0	53
42	Metabolomic signature of exposure and response to citalopram/escitalopram in depressed outpatients. Translational Psychiatry, 2019, 9, 173.	4.8	53
43	WSB1 promotes tumor metastasis by inducing pVHL degradation. Genes and Development, 2015, 29, 2244-2257.	5.9	52
44	TREM2 interacts with TDP-43 and mediates microglial neuroprotection against TDP-43-related neurodegeneration. Nature Neuroscience, 2022, 25, 26-38.	14.8	52
45	Discovery of a Glucocorticoid Receptor (GR) Activity Signature Using Selective GR Antagonism in ER-Negative Breast Cancer. Clinical Cancer Research, 2018, 24, 3433-3446.	7.0	49
46	FOXA1 overexpression suppresses interferon signaling and immune response in cancer. Journal of Clinical Investigation, 2021, 131, .	8.2	48
47	Genetic Polymorphisms in the Long Noncoding RNA MIR2052HG Offer a Pharmacogenomic Basis for the Response of Breast Cancer Patients to Aromatase Inhibitor Therapy. Cancer Research, 2016, 76, 7012-7023.	0.9	47
48	Aromatase Inhibitor-Associated Bone Fractures: A Case-Cohort GWAS and Functional Genomics. Molecular Endocrinology, 2014, 28, 1740-1751.	3.7	46
49	Tyrosine Phosphorylation of Mitochondrial Creatine Kinase 1 Enhances a Druggable Tumor Energy Shuttle Pathway. Cell Metabolism, 2018, 28, 833-847.e8.	16.2	46
50	Differential roles of ERRFI1 in EGFR and AKT pathway regulation affect cancer proliferation. EMBO Reports, 2018, 19, .	4.5	43
51	A noncanonical AR addiction drives enzalutamide resistance in prostate cancer. Nature Communications, 2021, 12, 1521.	12.8	43
52	FKBP51 regulation of AKT/protein kinase B phosphorylation. Current Opinion in Pharmacology, 2011, 11, 360-364.	3.5	41
53	Estrogens and their precursors in postmenopausal women with early breast cancer receiving anastrozole. Steroids, 2015, 99, 32-38.	1.8	38
54	Association of the Polygenic Scores for Personality Traits and Response to Selective Serotonin Reuptake Inhibitors in Patients with Major Depressive Disorder. Frontiers in Psychiatry, 2018, 9, 65.	2.6	38

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55	Human histamine N-methyltransferase pharmacogenetics: gene resequencing, promoter characterization, and functional studies of a common 5â€²-flanking region single nucleotide polymorphism (SNP). Biochemical Pharmacology, 2002, 64, 699-710.	4.4	37
56	Targeting B7-H1 (PD-L1) sensitizes cancer cells to chemotherapy. Heliyon, 2018, 4, e01039.	3.2	37
57	The lncRNA MIR2052HG regulates ERÎ± levels and aromatase inhibitor resistance through LMTK3 by recruiting EGR1. Breast Cancer Research, 2019, 21, 47.	5.0	36
58	Acylcarnitine metabolomic profiles inform clinically-defined major depressive phenotypes. Journal of Affective Disorders, 2020, 264, 90-97.	4.1	36
59	Proteasome Î² Subunit Pharmacogenomics: Gene Resequencing and Functional Genomics. Clinical Cancer Research, 2008, 14, 3503-3513.	7.0	35
60	Ketamine and ketamine metabolites as novel estrogen receptor ligands: Induction of cytochrome P450 and AMPA glutamate receptor gene expression. Biochemical Pharmacology, 2018, 152, 279-292.	4.4	35
61	Augmentation of Physician Assessments with Multi-Omics Enhances Predictability of Drug Response: A Case Study of Major Depressive Disorder. IEEE Computational Intelligence Magazine, 2018, 13, 20-31.	3.2	34
62	Cell-level somatic mutation detection from single-cell RNA sequencing. Bioinformatics, 2019, 35, 4679-4687.	4.1	34
63	Cohort Profile: The Right Drug, Right Dose, Right Time: Using Genomic Data to Individualize Treatment Protocol (RIGHT Protocol). International Journal of Epidemiology, 2020, 49, 23-24k.	1.9	34
64	Knowledge-guided analysis of "omics" data using the KnowEnG cloud platform. PLoS Biology, 2020, 18, e3000583.	5.6	34
65	A model-based cost-effectiveness analysis of pharmacogenomic panel testing in cardiovascular disease management: preemptive, reactive, or none?. Genetics in Medicine, 2021, 23, 461-470.	2.4	34
66	Aurora-A kinase oncogenic signaling mediates TGF-Î²-induced triple-negative breast cancer plasticity and chemoresistance. Oncogene, 2021, 40, 2509-2523.	5.9	34
67	The eSNV-detect: a computational system to identify expressed single nucleotide variants from transcriptome sequencing data. Nucleic Acids Research, 2014, 42, e172-e172.	14.5	33
68	Knowledge-guided gene prioritization reveals new insights into the mechanisms of chemoresistance. Genome Biology, 2017, 18, 153.	8.8	33
69	CYP2C9 and CYP2C19: Deep Mutational Scanning and Functional Characterization of Genomic Missense Variants. Clinical and Translational Science, 2020, 13, 727-742.	3.1	33
70	Thiopurine S-methyltransferase pharmacogenetics: chaperone protein association and allozyme degradation. Pharmacogenetics and Genomics, 2003, 13, 555-64.	5.7	33
71	Determining the frequency of pathogenic germline variants from exome sequencing in patients with castrate-resistant prostate cancer. BMJ Open, 2016, 6, e010332.	1.9	32
72	Clonal expansion of antitumor T cells in breast cancer correlates with response to neoadjuvant chemotherapy. International Journal of Oncology, 2016, 49, 471-478.	3.3	32

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73	Prognostic association of plasma cell-free DNA-based androgen receptor amplification and circulating tumor cells in pre-chemotherapy metastatic castration-resistant prostate cancer patients. Prostate Cancer and Prostatic Diseases, 2018, 21, 411-418.	3.9	32
74	STK38 promotes ATM activation by acting as a reader of histone H4 ufmylation. Science Advances, 2020, 6, eaax8214.	10.3	32
75	Genetic variants in <scp>VEGF</scp> pathway genes in neoadjuvant breast cancer patients receiving bevacizumab: Results from the randomized phase III <scp>G</scp>epar<scp>Q</scp>uinto study. International Journal of Cancer, 2015, 137, 2981-2988.	5.1	31
76	HEATR1 Negatively Regulates Akt to Help Sensitize Pancreatic Cancer Cells to Chemotherapy. Cancer Research, 2016, 76, 572-581.	0.9	31
77	Discovery of genetic biomarkers contributing to variation in drug response of cytidine analogues using human lymphoblastoid cell lines. BMC Genomics, 2014, 15, 93.	2.8	30
78	Aberrant activation of super enhancer and choline metabolism drive antiandrogen therapy resistance in prostate cancer. Oncogene, 2020, 39, 6556-6571.	5.9	29
79	Mapping depression rating scale phenotypes onto research domain criteria (RDoC) to inform biological research in mood disorders. Journal of Affective Disorders, 2018, 238, 1-7.	4.1	28
80	Implementation of preemptive DNA sequenceâ€“based pharmacogenomics testing across a large academic medical center: The Mayo-Baylor RIGHT 10K Study. Genetics in Medicine, 2022, 24, 1062-1072.	2.4	28
81	Estrogen, SNP-Dependent Chemokine Expression and Selective Estrogen Receptor Modulator Regulation. Molecular Endocrinology, 2016, 30, 382-398.	3.7	27
82	TSPYL Family Regulates CYP17A1 and CYP3A4 Expression: Potential Mechanism Contributing to Abiraterone Response in Metastatic Castrationâ€Resistant Prostate Cancer. Clinical Pharmacology and Therapeutics, 2018, 104, 201-210.	4.7	27
83	The association of obesity and coronary artery disease genes with response to SSRIs treatment in major depression. Journal of Neural Transmission, 2019, 126, 35-45.	2.8	27
84	Mutational Landscapes of Sequential Prostate Metastases and Matched Patient Derived Xenografts during Enzalutamide Therapy. PLoS ONE, 2015, 10, e0145176.	2.5	26
85	Exome sequencing reveals frequent deleterious germline variants in cancer susceptibility genes in women with invasive breast cancer undergoing neoadjuvant chemotherapy. Breast Cancer Research and Treatment, 2015, 153, 435-443.	2.5	26
86	Estimation and inference for the indirect effect in high-dimensional linear mediation models. Biometrika, 2020, 107, 573-589.	2.4	23
87	Calmodulin-like protein 3 is an estrogen receptor alpha coregulator for gene expression and drug response in a SNP, estrogen, and SERM-dependent fashion. Breast Cancer Research, 2017, 19, 95.	5.0	22
88	SNPs near the cysteine proteinase cathepsin O gene (CTSO) determine tamoxifen sensitivity in ERÎ±-positive breast cancer through regulation of BRCA1. PLoS Genetics, 2017, 13, e1007031.	3.5	22
89	Pathway-Based Analysis of Genome-Wide Association Data Identified SNPs in HMMR as Biomarker for Chemotherapy- Induced Neutropenia in Breast Cancer Patients. Frontiers in Pharmacology, 2018, 9, 158.	3.5	21
90	Targeting DNA methylation for treating triple-negative breast cancer. Pharmacogenomics, 2019, 20, 1151-1157.	1.3	21

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91	Human 3Î²-hydroxysteroid dehydrogenase types 1 and 2: Gene sequence variation and functional genomics. Journal of Steroid Biochemistry and Molecular Biology, 2007, 107, 88-99.	2.5	20
92	Multi-omics driven predictions of response to acute phase combination antidepressant therapy: a machine learning approach with cross-trial replication. Translational Psychiatry, 2021, 11, 513.	4.8	20
93	Principled multi-omic analysis reveals gene regulatory mechanisms of phenotype variation. Genome Research, 2018, 28, 1207-1216.	5.5	19
94	Metformin pharmacogenomics: a genome-wide association study to identify genetic and epigenetic biomarkers involved in metformin anticancer response using human lymphoblastoid cell lines. Human Molecular Genetics, 2016, 25, ddw301.	2.9	18
95	Sirolimus Therapy Is Associated with Elevation in Circulating PCSK9 Levels in Cardiac Transplant Patients. Journal of Cardiovascular Translational Research, 2017, 10, 9-15.	2.4	18
96	Breast cancer chemoprevention pharmacogenomics: Deep sequencing and functional genomics of the ZNF423 and CTSO genes. Npj Breast Cancer, 2017, 3, 30.	5.2	18
97	TCL1A Single-Nucleotide Polymorphisms and Estrogen-Mediated Toll-Like Receptor-MYD88â€“Dependent Nuclear Factor-Î¹B Activation: Single-Nucleotide Polymorphismâ€“ and Selective Estrogen Receptor Modulatorâ€“Dependent Modification of Inflammation and Immune Response. Molecular Pharmacology, 2017, 92, 175-184.	2.3	18
98	SLCO1B1 polymorphisms and plasma estrone conjugates in postmenopausal women with ER+Âbreast cancer: genome-wide association studies of the estrone pathway. Breast Cancer Research and Treatment, 2017, 164, 189-199.	2.5	17
99	The novel function of tumor protein D54 in regulating pyruvate dehydrogenase and metformin cytotoxicity in breast cancer. Cancer & Metabolism, 2019, 7, 1.	5.0	17
100	Pharmacogenomic Next-Generation DNA Sequencing: Lessons from the Identification and Functional Characterization of Variants of Unknown Significance inCYP2C9andCYP2C19. Drug Metabolism and Disposition, 2019, 47, 425-435.	3.3	17
101	ERICH3: vesicular association and antidepressant treatment response. Molecular Psychiatry, 2021, 26, 2415-2428.	7.9	17
102	Plasma cell-free DNA-based predictors of response to abiraterone acetate/prednisone and prognostic factors in metastatic castration-resistant prostate cancer. Prostate Cancer and Prostatic Diseases, 2020, 23, 705-713.	3.9	17
103	Anastrozole has an Association between Degree of Estrogen Suppression and Outcomes in Early Breast Cancer and is a Ligand for Estrogen Receptor Î±. Clinical Cancer Research, 2020, 26, 2986-2996.	7.0	17
104	SLCO1B1: Application and Limitations of Deep Mutational Scanning for Genomic Missense Variant Function. Drug Metabolism and Disposition, 2021, 49, 395-404.	3.3	17
105	Considerations for automated machine learning in clinical metabolic profiling: Altered homocysteine plasma concentration associated with metformin exposure. , 2018, , .		16
106	Pharmacokinetic-Pharmacodynamic interaction associated with venlafaxine-XR remission in patients with major depressive disorder with history of citalopram / escitalopram treatment failure. Journal of Affective Disorders, 2019, 246, 62-68.	4.1	16
107	Inhibition of ATM Induces Hypersensitivity to Proton Irradiation by Upregulating Toxic End Joining. Cancer Research, 2021, 81, 3333-3346.	0.9	16
108	Quantitative Analysis of Tyrosine Phosphorylation from FFPE Tissues Reveals Patient-Specific Signaling Networks. Cancer Research, 2021, 81, 3930-3941.	0.9	16

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109	TCF7L2 lncRNA: a link between bipolar disorder and body mass index through glucocorticoid signaling. Molecular Psychiatry, 2021, 26, 7454-7464.	7.9	16
110	Isoform-level gene expression patterns in single-cell RNA-sequencing data. Bioinformatics, 2018, 34, 2392-2400.	4.1	15
111	Comparison of99mTc-Sestamibi Molecular Breast Imaging and Breast MRI in Patients With Invasive Breast Cancer Receiving Neoadjuvant Chemotherapy. American Journal of Roentgenology, 2019, 213, 932-943.	2.2	15
112	Model-based unsupervised learning informs metformin-induced cell-migration inhibition through an AMPK-independent mechanism in breast cancer. Oncotarget, 2017, 8, 27199-27215.	1.8	15
113	Toward Individualized Prediction of Response to Methotrexate in Early Rheumatoid Arthritis: A <scp>Pharmacogenomicsâ€Driven</scp> Machine Learning Approach. Arthritis Care and Research, 2022, 74, 879-888.	3.4	15
114	Metformin Pharmacogenomics: Biomarkers to Mechanisms. Diabetes, 2014, 63, 2609-2610.	0.6	14
115	HGT-ID: an efficient and sensitive workflow to detect human-viral insertion sites using next-generation sequencing data. BMC Bioinformatics, 2018, 19, 271.	2.6	14
116	Prediction of short-term antidepressant response using probabilistic graphical models with replication across multiple drugs and treatment settings. Neuropsychopharmacology, 2021, 46, 1272-1282.	5.4	14
117	Single Nucleotide Polymorphisms at a Distance from Aryl Hydrocarbon Receptor (AHR) Binding Sites Influence AHR Ligandâ€“Dependent Gene Expression. Drug Metabolism and Disposition, 2019, 47, 983-994.	3.3	13
118	CDC25B partners with PP2A to induce AMPK activation and tumor suppression in triple negative breast cancer. NAR Cancer, 2021, 2, zcaa039.	3.1	13
119	Targeted Genotyping in Clinical Pharmacogenomics. Journal of Molecular Diagnostics, 2022, 24, 253-261.	2.8	13
120	Single Nucleotide Polymorphisms (SNPs) Distant from Xenobiotic Response Elements Can Modulate Aryl Hydrocarbon Receptor Function: SNP-Dependent CYP1A1 Induction. Drug Metabolism and Disposition, 2018, 46, 1372-1381.	3.3	11
121	Dual Roles for the TSPYL Family in Mediating Serotonin Transport and the Metabolism of Selective Serotonin Reuptake Inhibitors in Patients with Major Depressive Disorder. Clinical Pharmacology and Therapeutics, 2020, 107, 662-670.	4.7	11
122	Spontaneous murine tumors in the development of patient-derived xenografts: a potential pitfall. Oncotarget, 2019, 10, 3924-3930.	1.8	11
123	Genetic predictors of chemotherapy-related amenorrhea inÂwomen with breast cancer. Fertility and Sterility, 2019, 112, 731-739.e1.	1.0	10
124	Anastrozole Aromatase Inhibitor Plasma Drug Concentration Genomeâ€Wide Association Study: Functional Epistatic Interaction Between <scp>SLC</scp>38A7 and <scp>ALPPL</scp>2. Clinical Pharmacology and Therapeutics, 2019, 106, 219-227.	4.7	10
125	Patient-specific multi-omics models and the application in personalized combination therapy. Future Oncology, 2020, 16, 1737-1750.	2.4	10
126	Luminal androgen receptor breast cancer subtype and investigation of the microenvironment and neoadjuvant chemotherapy response. NAR Cancer, 2022, 4, .	3.1	10

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127	A network-based phenotype mapping approach to identify genes that modulate drug response phenotypes. Scientific Reports, 2016, 6, 37003.	3.3	9
128	TCL1A, a Novel Transcription Factor and a Coregulator of Nuclear Factor ÎºB p65: Single Nucleotide Polymorphism and Estrogen Dependence. Journal of Pharmacology and Experimental Therapeutics, 2018, 365, 700-710.	2.5	9
129	Pharmacogenomics in Practice. Clinical Pharmacology and Therapeutics, 2019, 106, 936-938.	4.7	9
130	Integration of machine learning and pharmacogenomic biomarkers for predicting response to antidepressant treatment: can computational intelligence be used to augment clinical assessments?. Pharmacogenomics, 2019, 20, 983-988.	1.3	9
131	Alternating EM algorithm for a bilinear model in isoform quantification from RNA-seq data. Bioinformatics, 2020, 36, 805-812.	4.1	8
132	A Prospective Correlation of Tissue Histopathology With Nucleic Acid Yield in Metastatic Castration-Resistant Prostate Cancer Biopsy Specimens. Mayo Clinic Proceedings Innovations, Quality & Outcomes, 2019, 3, 14-22.	2.4	8
133	NDUFA4L2 promotes trastuzumab resistance in HER2-positive breast cancer. Therapeutic Advances in Medical Oncology, 2021, 13, 175883592110278.	3.2	8
134	Data-driven longitudinal modeling and prediction of symptom dynamics in major depressive disorder: Integrating factor graphs and learning methods. , 2017, , .		7
135	Pharmacogenomic Discovery to Function and Mechanism: Breast Cancer as a Case Study. Clinical Pharmacology and Therapeutics, 2018, 103, 243-252.	4.7	7
136	Patient-Derived Xenograft Engraftment and Breast Cancer Outcomes in a Prospective Neoadjuvant Study (BEAUTY). Clinical Cancer Research, 2021, 27, 4696-4699.	7.0	7
137	Multi-Omics Characterization of Early- and Adult-Onset Major Depressive Disorder. Journal of Personalized Medicine, 2022, 12, 412.	2.5	7
138	4-Hydroxytamoxifen enhances sensitivity of estrogen receptor Î±-positive breast cancer to docetaxel in an estrogen and ZNF423 SNP-dependent fashion. Breast Cancer Research and Treatment, 2019, 175, 567-578.	2.5	6
139	Comparing outcomes and costs among warfarin-sensitive patients versus warfarin-insensitive patients using The Right Drug, Right Dose, Right Time: Using genomic data to individualize treatment (RIGHT) 10K warfarin cohort. PLoS ONE, 2020, 15, e0233316.	2.5	6
140	Next-Generation Sequencing of CYP2C19 in Stent Thrombosis: Implications for Clopidogrel Pharmacogenomics. Cardiovascular Drugs and Therapy, 2021, 35, 549-559.	2.6	6
141	A genome-wide association study in human lymphoblastoid cells supports safety of mitochondrial complex I inhibitor. Mitochondrion, 2021, 58, 83-94.	3.4	6
142	Clinical validation of genetic variants associated with in vitro chemotherapy-related lymphoblastoid cell toxicity. Oncotarget, 2017, 8, 78133-78143.	1.8	6
143	Biomarkers for Predicting Abiraterone Treatment Outcome and Selecting Alternative Therapies in Castrationâ€Resistant Prostate Cancer. Clinical Pharmacology and Therapeutics, 2022, 111, 1296-1306.	4.7	6
144	Bora Downregulation Results in Radioresistance by Promoting Repair of Double Strand Breaks. PLoS ONE, 2015, 10, e0119208.	2.5	5

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145	Identification of genetic variants or genes that are associated with Homoharringtonine (HHT) response through a genome-wide association study in human lymphoblastoid cell lines (LCLs). Frontiers in Genetics, 2015, 5, 465.	2.3	5
146	Interaction Between SNP Genotype and Efficacy of Anastrozole and Exemestane in Earlyâ€Stage Breast Cancer. Clinical Pharmacology and Therapeutics, 2021, 110, 1038-1049.	4.7	5
147	Establishment and characterization of immortalized human breast cancer cell lines from breast cancer patient-derived xenografts (PDX). Npj Breast Cancer, 2021, 7, 79.	5.2	5
148	Genetic Polymorphisms and Correlation with Treatment-Induced Cardiotoxicity and Prognosis in Patients with Breast Cancer. Clinical Cancer Research, 2022, 28, 1854-1862.	7.0	5
149	Germline genome-wide association studies in women receiving neoadjuvant chemotherapy with or without bevacizumab. Pharmacogenetics and Genomics, 2018, 28, 147-152.	1.5	4
150	Anastrozole Regulates Fatty Acid Synthase in Breast Cancer. Molecular Cancer Therapeutics, 2022, 21, 206-216.	4.1	4
151	Impact of Pharmacogenomic Information on Values of Care and Quality of Life Associated with Codeine and Tramadol-Related Adverse Drug Events. Mayo Clinic Proceedings Innovations, Quality & Outcomes, 2021, 5, 35-45.	2.4	3
152	Using EHR-Linked Biobank Data to Study Metformin Pharmacogenomics. Studies in Health Technology and Informatics, 2015, 210, 914-8.	0.3	3
153	Tumor protein <scp>D52</scp> (<scp>TPD52</scp>) affects cancer cell metabolism by negatively regulating <scp>AMPK</scp>. Cancer Medicine, 2023, 12, 488-499.	2.8	3
154	Identification of Two Genetic Loci Associated with Leukopenia after Chemotherapy in Patients with Breast Cancer. Clinical Cancer Research, 2022, 28, 3342-3355.	7.0	3
155	A Transcriptionally Definable Subgroup of Triple-Negative Breast and Ovarian Cancer Samples Shows Sensitivity to HSP90 Inhibition. Clinical Cancer Research, 2020, 26, 159-170.	7.0	2
156	Evidence for machine learning guided early prediction of acute outcomes in the treatment of depressed children and adolescents with antidepressants. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2022, 63, 1347-1358.	5.2	2
157	Functional genomics based on germline genome-wide association studies of endocrine therapy for breast cancer. Pharmacogenomics, 2020, 21, 615-625.	1.3	1
158	ZNF423 modulates the AMP-activated protein kinase pathway and metformin response in a single nucleotide polymorphisms, estrogen and selective estrogen receptor modulator dependent fashion. Pharmacogenetics and Genomics, 2021, 31, 155-164.	1.5	1
159	Deep sequencing across germline genome-wide association study signals relating to breast cancer events in women receiving aromatase inhibitors for adjuvant therapy of early breast cancer. Pharmacogenetics and Genomics, 2019, 29, 183-191.	1.5	0
160	Abstract 3012: Significant Genome Wide Association Identified Between the Glycine N-Methyltransferase Gene (GNMT) and Post-Methionine Load Test Homocysteine Levels in the Vitamin Intervention for Stroke Prevention (VISP) Cohort. Stroke, 2012, 43, .	2.0	0
161	SNPs Outside Response Elements Impact Aryl Hydrocarbon Receptor (AHR) Binding and Gene Regulation: Genomeâ€wide SNPâ€dependent Transcriptional Regulation. FASEB Journal, 2018, 32, 694.3.	0.5	0
162	ERICH3 Characterization: Function in Vesicular Trafficking and Antidepressant Treatment Response. FASEB Journal, 2019, 33, 680.1.	0.5	0

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163	Single-nucleotide polymorphism biomarkers of adjuvant anastrozole-induced estrogen suppression in early breast cancer. Pharmacogenetics and Genomics, 2021, 31, 1-9.	1.5	0