

Krishna R Kalari

List of Publications by Year in descending order

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Version: 2024-02-01

116
papers

6,545
citations

94433

37
h-index

74163

75
g-index

134
all docs

134
docs citations

134
times ranked

12408
citing authors

#	ARTICLE	IF	CITATIONS
1	Anastrozole Regulates Fatty Acid Synthase in Breast Cancer. <i>Molecular Cancer Therapeutics</i> , 2022, 21, 206-216.	4.1	4
2	Estrogen receptor beta repurposes EZH2 to suppress oncogenic NF κ B/p65 signaling in triple negative breast cancer. <i>Npj Breast Cancer</i> , 2022, 8, 20.	5.2	9
3	Biomarkers for Predicting Abiraterone Treatment Outcome and Selecting Alternative Therapies in Castration-Resistant Prostate Cancer. <i>Clinical Pharmacology and Therapeutics</i> , 2022, 111, 1296-1306.	4.7	6
4	Implementation of preemptive DNA sequence-based pharmacogenomics testing across a large academic medical center: The Mayo-Baylor RIGHT 10K Study. <i>Genetics in Medicine</i> , 2022, 24, 1062-1072.	2.4	28
5	Toward Individualized Prediction of Response to Methotrexate in Early Rheumatoid Arthritis: A Pharmacogenomics-Driven Machine Learning Approach. <i>Arthritis Care and Research</i> , 2022, 74, 879-888.	3.4	15
6	A clinical calculator to predict disease outcomes in women with triple-negative breast cancer. <i>Breast Cancer Research and Treatment</i> , 2021, 185, 557-566.	2.5	19
7	SLCO1B1: Application and Limitations of Deep Mutational Scanning for Genomic Missense Variant Function. <i>Drug Metabolism and Disposition</i> , 2021, 49, 395-404.	3.3	17
8	Patient-Derived Xenograft Engraftment and Breast Cancer Outcomes in a Prospective Neoadjuvant Study (BEAUTY). <i>Clinical Cancer Research</i> , 2021, 27, 4696-4699.	7.0	7
9	Interaction Between SNP Genotype and Efficacy of Anastrozole and Exemestane in Early-stage Breast Cancer. <i>Clinical Pharmacology and Therapeutics</i> , 2021, 110, 1038-1049.	4.7	5
10	Establishment and characterization of immortalized human breast cancer cell lines from breast cancer patient-derived xenografts (PDX). <i>Npj Breast Cancer</i> , 2021, 7, 79.	5.2	5
11	Characteristics and Spatially Defined Immune (micro)landscapes of Early-stage PD-L1-positive Triple-negative Breast Cancer. <i>Clinical Cancer Research</i> , 2021, 27, 5628-5637.	7.0	32
12	FOXA1 overexpression suppresses interferon signaling and immune response in cancer. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	48
13	Multi-Omics Analyses Show Disease, Diet, and Transcriptome Interactions With the Virome. <i>Gastroenterology</i> , 2021, 161, 1194-1207.e8.	1.3	28
14	COVID-19 Transmission, Current Treatment, and Future Therapeutic Strategies. <i>Molecular Pharmaceutics</i> , 2021, 18, 754-771.	4.6	193
15	CDC25B partners with PP2A to induce AMPK activation and tumor suppression in triple negative breast cancer. <i>NAR Cancer</i> , 2021, 2, zcaa039.	3.1	13
16	Single-nucleotide polymorphism biomarkers of adjuvant anastrozole-induced estrogen suppression in early breast cancer. <i>Pharmacogenetics and Genomics</i> , 2021, 31, 1-9.	1.5	0
17	Alternating EM algorithm for a bilinear model in isoform quantification from RNA-seq data. <i>Bioinformatics</i> , 2020, 36, 805-812.	4.1	8
18	Longitudinal Multi-omics Reveals Subset-Specific Mechanisms Underlying Irritable Bowel Syndrome. <i>Cell</i> , 2020, 182, 1460-1473.e17.	28.9	217

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19	Frequency of MicroRNA Response Elements Identifies Pathologically Relevant Signaling Pathways in Triple-Negative Breast Cancer. <i>IScience</i> , 2020, 23, 101249.	4.1	5
20	Antitumor activity of Z-endoxifen in aromatase inhibitor-sensitive and aromatase inhibitor-resistant estrogen receptor-positive breast cancer. <i>Breast Cancer Research</i> , 2020, 22, 51.	5.0	11
21	Patient-specific multi-omics models and the application in personalized combination therapy. <i>Future Oncology</i> , 2020, 16, 1737-1750.	2.4	10
22	Concordance between predicted HLA type using next generation sequencing data generated for non-HLA purposes and clinical HLA type. <i>Human Immunology</i> , 2020, 81, 423-429.	2.4	4
23	Folate receptor alpha expression associates with improved disease-free survival in triple negative breast cancer patients. <i>Npj Breast Cancer</i> , 2020, 6, 4.	5.2	49
24	Knowledge-guided analysis of "omics" data using the KnowEnG cloud platform. <i>PLoS Biology</i> , 2020, 18, e3000583.	5.6	34
25	<i>CYP2C9</i> and <i>CYP2C19</i> : Deep Mutational Scanning and Functional Characterization of Genomic Missense Variants. <i>Clinical and Translational Science</i> , 2020, 13, 727-742.	3.1	33
26	Anastrozole has an Association between Degree of Estrogen Suppression and Outcomes in Early Breast Cancer and is a Ligand for Estrogen Receptor I±. <i>Clinical Cancer Research</i> , 2020, 26, 2986-2996.	7.0	17
27	A Transcriptionally Definable Subgroup of Triple-Negative Breast and Ovarian Cancer Samples Shows Sensitivity to HSP90 Inhibition. <i>Clinical Cancer Research</i> , 2020, 26, 159-170.	7.0	2
28	Pharmacogenomics of aromatase inhibitors in postmenopausal breast cancer and additional mechanisms of anastrozole action. <i>JCI Insight</i> , 2020, 5, .	5.0	16
29	Stochastic changes in gene expression promote chaotic dysregulation of homeostasis in clonal breast tumors. <i>Communications Biology</i> , 2019, 2, 206.	4.4	2
30	Gene Expression and Missplicing in the Corneal Endothelium of Patients With a TCF4 Trinucleotide Repeat Expansion Without Fuchs' Endothelial Corneal Dystrophy. , 2019, 60, 3636.		17
31	Comparison of 99mTc-Sestamibi Molecular Breast Imaging and Breast MRI in Patients With Invasive Breast Cancer Receiving Neoadjuvant Chemotherapy. <i>American Journal of Roentgenology</i> , 2019, 213, 932-943.	2.2	15
32	Cell-level somatic mutation detection from single-cell RNA sequencing. <i>Bioinformatics</i> , 2019, 35, 4679-4687.	4.1	34
33	The lncRNA MIR2052HG regulates ER± levels and aromatase inhibitor resistance through LMTK3 by recruiting EGR1. <i>Breast Cancer Research</i> , 2019, 21, 47.	5.0	36
34	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. <i>Pharmacogenetics and Genomics</i> , 2019, 29, 183-191.	1.5	0
35	Anastrozole Aromatase Inhibitor Plasma Drug Concentration Genome-Wide Association Study: Functional Epistatic Interaction Between <i>SLC38A7</i> and <i>ALPPL2</i> . <i>Clinical Pharmacology and Therapeutics</i> , 2019, 106, 219-227.	4.7	10
36	Isoform-level gene expression patterns in single-cell RNA-sequencing data. <i>Bioinformatics</i> , 2018, 34, 2392-2400.	4.1	15

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37	Discovery of a Glucocorticoid Receptor (GR) Activity Signature Using Selective GR Antagonism in ER-Negative Breast Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 3433-3446.	7.0	49
38	Beta-defensin 1, aryl hydrocarbon receptor and plasma kynurenine in major depressive disorder: metabolomics-informed genomics. <i>Translational Psychiatry</i> , 2018, 8, 10.	4.8	59
39	Differential Effects of Alzheimer's Disease A β 40 and 42 on Endocytosis and Intraneuronal Trafficking. <i>Neuroscience</i> , 2018, 373, 159-168.	2.3	12
40	Impact of histopathology, tumor-infiltrating lymphocytes, and adjuvant chemotherapy on prognosis of triple-negative breast cancer. <i>Breast Cancer Research and Treatment</i> , 2018, 167, 89-99.	2.5	74
41	Vitamin D Levels, Vitamin D Receptor Polymorphisms, and Inflammatory Cytokines in Aromatase Inhibitor-Induced Arthralgias: An Analysis of CCTG MA.27. <i>Clinical Breast Cancer</i> , 2018, 18, 78-87.	2.4	13
42	PANOPLY: Omics-Guided Drug Prioritization Method Tailored to an Individual Patient. <i>JCO Clinical Cancer Informatics</i> , 2018, 2, 1-11.	2.1	8
43	Your brain scan may be a reflection of your genes. <i>Brain</i> , 2018, 141, 2539-2541.	7.6	0
44	DNA methyltransferase expression in triple-negative breast cancer predicts sensitivity to decitabine. <i>Journal of Clinical Investigation</i> , 2018, 128, 2376-2388.	8.2	134
45	ATR Inhibition Is a Promising Radiosensitizing Strategy for Triple-Negative Breast Cancer. <i>Molecular Cancer Therapeutics</i> , 2018, 17, 2462-2472.	4.1	59
46	Machine Learning Helps Identify New Drug Mechanisms in Triple-Negative Breast Cancer. <i>IEEE Transactions on Nanobioscience</i> , 2018, 17, 251-259.	3.3	8
47	Pathway-Based Analysis of Genome-Wide Association Data Identified SNPs in HMMR as Biomarker for Chemotherapy- Induced Neutropenia in Breast Cancer Patients. <i>Frontiers in Pharmacology</i> , 2018, 9, 158.	3.5	21
48	HGT-ID: an efficient and sensitive workflow to detect human-viral insertion sites using next-generation sequencing data. <i>BMC Bioinformatics</i> , 2018, 19, 271.	2.6	14
49	Gene expression in the corneal endothelium of Fuchs endothelial corneal dystrophy patients with and without expansion of a trinucleotide repeat in TCF4. <i>PLoS ONE</i> , 2018, 13, e0200005.	2.5	20
50	Single Nucleotide Polymorphisms (SNPs) Distant from Xenobiotic Response Elements Can Modulate Aryl Hydrocarbon Receptor Function: SNP-Dependent CYP1A1 Induction. <i>Drug Metabolism and Disposition</i> , 2018, 46, 1372-1381.	3.3	11
51	SLCO1B1 polymorphisms and plasma estrone conjugates in postmenopausal women with ER+ breast cancer: genome-wide association studies of the estrone pathway. <i>Breast Cancer Research and Treatment</i> , 2017, 164, 189-199.	2.5	17
52	Tumor Sequencing and Patient-Derived Xenografts in the Neoadjuvant Treatment of Breast Cancer. <i>Journal of the National Cancer Institute</i> , 2017, 109, .	6.3	61
53	Breast cancer chemoprevention pharmacogenomics: Deep sequencing and functional genomics of the ZNF423 and CTSO genes. <i>Npj Breast Cancer</i> , 2017, 3, 30.	5.2	18
54	Single-Nucleotide Polymorphisms and Estrogen-Mediated Toll-Like Receptor-MYD88-Dependent Nuclear Factor- κ B Activation: Single-Nucleotide Polymorphism and Selective Estrogen Receptor Modulator-Dependent Modification of Inflammation and Immune Response. <i>Molecular Pharmacology</i> , 2017, 92, 175-184.	2.3	18

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55	Knowledge-guided gene prioritization reveals new insights into the mechanisms of chemoresistance. <i>Genome Biology</i> , 2017, 18, 153.	8.8	33
56	Establishing and characterizing patient-derived xenografts using pre-chemotherapy percutaneous biopsy and post-chemotherapy surgical samples from a prospective neoadjuvant breast cancer study. <i>Breast Cancer Research</i> , 2017, 19, 130.	5.0	53
57	Trinucleotide Repeat Expansion in the Transcription Factor 4 (<i>TCF4</i>) Gene Leads to Widespread mRNA Splicing Changes in Fuchs' Endothelial Corneal Dystrophy. , 2017, 58, 343.		59
58	A comprehensive analysis of breast cancer microbiota and host gene expression. <i>PLoS ONE</i> , 2017, 12, e0188873.	2.5	111
59	Model-based unsupervised learning informs metformin-induced cell-migration inhibition through an AMPK-independent mechanism in breast cancer. <i>Oncotarget</i> , 2017, 8, 27199-27215.	1.8	15
60	BBBomics-Human Blood Brain Barrier Transcriptomics Hub. <i>Frontiers in Neuroscience</i> , 2016, 10, 71.	2.8	31
61	Circular RNAs and their associations with breast cancer subtypes. <i>Oncotarget</i> , 2016, 7, 80967-80979.	1.8	140
62	Genetic Polymorphisms in the Long Noncoding RNA MIR2052HG Offer a Pharmacogenomic Basis for the Response of Breast Cancer Patients to Aromatase Inhibitor Therapy. <i>Cancer Research</i> , 2016, 76, 7012-7023.	0.9	47
63	Unsupervised single-cell analysis in triple-negative breast cancer: A case study. , 2016, , .		4
64	Determining the frequency of pathogenic germline variants from exome sequencing in patients with castrate-resistant prostate cancer. <i>BMJ Open</i> , 2016, 6, e010332.	1.9	32
65	Beta-Poisson model for single-cell RNA-seq data analyses. <i>Bioinformatics</i> , 2016, 32, 2128-2135.	4.1	151
66	Metformin pharmacogenomics: a genome-wide association study to identify genetic and epigenetic biomarkers involved in metformin anticancer response using human lymphoblastoid cell lines. <i>Human Molecular Genetics</i> , 2016, 25, ddw301.	2.9	18
67	Multiple sclerosis patients have a distinct gut microbiota compared to healthy controls. <i>Scientific Reports</i> , 2016, 6, 28484.	3.3	660
68	The Microbiome of Aseptically Collected Human Breast Tissue in Benign and Malignant Disease. <i>Scientific Reports</i> , 2016, 6, 30751.	3.3	299
69	Clonal expansion of antitumor T cells in breast cancer correlates with response to neoadjuvant chemotherapy. <i>International Journal of Oncology</i> , 2016, 49, 471-478.	3.3	32
70	Estrogen, SNP-Dependent Chemokine Expression and Selective Estrogen Receptor Modulator Regulation. <i>Molecular Endocrinology</i> , 2016, 30, 382-398.	3.7	27
71	TSPAN5, ERICH3 and selective serotonin reuptake inhibitors in major depressive disorder: pharmacometabolomics-informed pharmacogenomics. <i>Molecular Psychiatry</i> , 2016, 21, 1717-1725.	7.9	96
72	A cell cycle-dependent BRCA1-UHRF1 cascade regulates DNA double-strand break repair pathway choice. <i>Nature Communications</i> , 2016, 7, 10201.	12.8	95

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73	Interpreting functional effects of coding variants: challenges in proteome-scale prediction, annotation and assessment. <i>Briefings in Bioinformatics</i> , 2016, 17, 841-862.	6.5	23
74	Genomic Analysis Reveals That Immune Function Genes Are Strongly Linked to Clinical Outcome in the North Central Cancer Treatment Group N9831 Adjuvant Trastuzumab Trial. <i>Journal of Clinical Oncology</i> , 2015, 33, 701-708.	1.6	171
75	RNA Toxicity and Missplicing in the Common Eye Disease Fuchs Endothelial Corneal Dystrophy. <i>Journal of Biological Chemistry</i> , 2015, 290, 5979-5990.	3.4	104
76	Estrogens and their precursors in postmenopausal women with early breast cancer receiving anastrozole. <i>Steroids</i> , 2015, 99, 32-38.	1.8	38
77	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). <i>Frontiers in Genetics</i> , 2015, 5, 465.	2.3	5
78	Exome sequencing reveals frequent deleterious germline variants in cancer susceptibility genes in women with invasive breast cancer undergoing neoadjuvant chemotherapy. <i>Breast Cancer Research and Treatment</i> , 2015, 153, 435-443.	2.5	26
79	Loss of Heterozygosity at the CYP2D6 Locus in Breast Cancer: Implications for Germline Pharmacogenetic Studies. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	6.3	37
80	Folate Receptor-1 (FOLR1) Expression and Function in Triple Negative Tumors. <i>PLoS ONE</i> , 2015, 10, e0122209.	2.5	103
81	Transcriptome-Wide Analysis of UTRs in Non-Small Cell Lung Cancer Reveals Cancer-Related Genes with SNV-Induced Changes on RNA Secondary Structure and miRNA Target Sites. <i>PLoS ONE</i> , 2014, 9, e82699.	2.5	30
82	IM-TORNADO: A Tool for Comparison of 16S Reads from Paired-End Libraries. <i>PLoS ONE</i> , 2014, 9, e114804.	2.5	110
83	The eSNV-detect: a computational system to identify expressed single nucleotide variants from transcriptome sequencing data. <i>Nucleic Acids Research</i> , 2014, 42, e172-e172.	14.5	33
84	Discovery of genetic biomarkers contributing to variation in drug response of cytidine analogues using human lymphoblastoid cell lines. <i>BMC Genomics</i> , 2014, 15, 93.	2.8	30
85	MAP-RSeq: Mayo Analysis Pipeline for RNA sequencing. <i>BMC Bioinformatics</i> , 2014, 15, 224.	2.6	284
86	Inverse Association between Programmed Death Ligand 1 and Genes in the VEGF Pathway in Primary Clear Cell Renal Cell Carcinoma. <i>Cancer Immunology Research</i> , 2013, 1, 378-385.	3.4	37
87	An Integrated Model of the Transcriptome of HER2-Positive Breast Cancer. <i>PLoS ONE</i> , 2013, 8, e79298.	2.5	18
88	Impact of Library Preparation on Downstream Analysis and Interpretation of RNA-Seq Data: Comparison between Illumina PolyA and NuGEN Ovation Protocol. <i>PLoS ONE</i> , 2013, 8, e71745.	2.5	19
89	Gene Expression, Single Nucleotide Variant and Fusion Transcript Discovery in Archival Material from Breast Tumors. <i>PLoS ONE</i> , 2013, 8, e81925.	2.5	49
90	TREAT: a bioinformatics tool for variant annotations and visualizations in targeted and exome sequencing data. <i>Bioinformatics</i> , 2012, 28, 277-278.	4.1	59

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91	Gemcitabine metabolic pathway genetic polymorphisms and response in patients with non-small cell lung cancer. <i>Pharmacogenetics and Genomics</i> , 2012, 22, 105-116.	1.5	33
92	Transcriptome Analysis of Garlic-Induced Hepatoprotection against Alcoholic Fatty Liver. <i>Journal of Agricultural and Food Chemistry</i> , 2012, 60, 11104-11119.	5.2	35
93	Genetic association with overall survival of taxane-treated lung cancer patients - a genome-wide association study in human lymphoblastoid cell lines followed by a clinical association study. <i>BMC Cancer</i> , 2012, 12, 422.	2.6	40
94	Deep Sequence Analysis of Non-Small Cell Lung Cancer: Integrated Analysis of Gene Expression, Alternative Splicing, and Single Nucleotide Variations in Lung Adenocarcinomas with and without Oncogenic KRAS Mutations. <i>Frontiers in Oncology</i> , 2012, 2, 12.	2.8	46
95	Detection of Redundant Fusion Transcripts as Biomarkers or Disease-Specific Therapeutic Targets in Breast Cancer. <i>Cancer Research</i> , 2012, 72, 1921-1928.	0.9	83
96	A novel bioinformatics pipeline for identification and characterization of fusion transcripts in breast cancer and normal cell lines. <i>Nucleic Acids Research</i> , 2011, 39, e100-e100.	14.5	94
97	Betaine-homocysteine methyltransferase: Human liver genotypeâ€“phenotype correlation. <i>Molecular Genetics and Metabolism</i> , 2011, 102, 126-133.	1.1	38
98	Protein kinase C δ expression and oncogenic signaling mechanisms in cancer. <i>Journal of Cellular Physiology</i> , 2011, 226, 879-887.	4.1	91
99	Acetaminophen-NAPQI Hepatotoxicity: A Cell Line Model System Genome-Wide Association Study. <i>Toxicological Sciences</i> , 2011, 120, 33-41.	3.1	61
100	Integrated Analysis of Gene Expression, CpG Island Methylation, and Gene Copy Number in Breast Cancer Cells by Deep Sequencing. <i>PLoS ONE</i> , 2011, 6, e17490.	2.5	128
101	Gemcitabine Cytotoxicity: Interaction of Efflux and Deamination. <i>Journal of Drug Metabolism & Toxicology</i> , 2011, 02, 1-10.	0.1	33
102	Copy number variation and cytidine analogue cytotoxicity: A genome-wide association approach. <i>BMC Genomics</i> , 2010, 11, 357.	2.8	19
103	Ecto-5 β -Nucleotidase and Thiopurine Cellular Circulation: Association with Cytotoxicity. <i>Drug Metabolism and Disposition</i> , 2010, 38, 2329-2338.	3.3	16
104	Radiation pharmacogenomics: A genome-wide association approach to identify radiation response biomarkers using human lymphoblastoid cell lines. <i>Genome Research</i> , 2010, 20, 1482-1492.	5.5	135
105	CD38 expression, function, and gene resequencing in a human lymphoblastoid cell line-based model system. <i>Leukemia and Lymphoma</i> , 2010, 51, 1315-1325.	1.3	15
106	Betaineâ€“homocysteine methyltransferase pharmacogenetics: human liver genotypeâ€“phenotype association study. <i>FASEB Journal</i> , 2010, 24, 756.2.	0.5	0
107	Human Glucocorticoid Receptor β Gene (<i>NR3C1</i>) Pharmacogenomics: Gene Resequencing and Functional Genomics. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2009, 94, 3072-3084.	3.6	32
108	FKBP51 Affects Cancer Cell Response to Chemotherapy by Negatively Regulating Akt. <i>Cancer Cell</i> , 2009, 16, 259-266.	16.8	643

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109	Human <i>S</i> adenosylhomocysteine hydrolase: common gene sequence variation and functional genomic characterization. <i>Journal of Neurochemistry</i> , 2009, 110, 1806-1817.	3.9	11
110	Cytosolic 5'-nucleotidase III (NT5C3): gene sequence variation and functional genomics. <i>Pharmacogenetics and Genomics</i> , 2009, 19, 567-576.	1.5	29
111	Gemcitabine and Arabinosylcytosin Pharmacogenomics: Genome-Wide Association and Drug Response Biomarkers. <i>PLoS ONE</i> , 2009, 4, e7765.	2.5	75
112	Proteasome β Subunit Pharmacogenomics: Gene Resequencing and Functional Genomics. <i>Clinical Cancer Research</i> , 2008, 14, 3503-3513.	7.0	35
113	A knowledge-based approach to predict intragenic deletions or duplications. <i>Bioinformatics</i> , 2008, 24, 1975-1979.	4.1	2
114	Gemcitabine and Cytosine Arabinoside Cytotoxicity: Association with Lymphoblastoid Cell Expression. <i>Cancer Research</i> , 2008, 68, 7050-7058.	0.9	155
115	First exons and introns—a survey of GC content and gene structure in the human genome. <i>In Silico Biology</i> , 2006, 6, 237-42.	0.9	37
116	India's Opportunities and Challenges in Establishing a Twin Registry: An Unexplored Human Resource for the World's Second-Most Populous Nation. <i>Twin Research and Human Genetics</i> , 0, , 1-9.	0.6	0