Balazs Gyorffy

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

247	13,742 citations	55	112
papers		h-index	g-index
283	17,874 ext. citations	6.4	7.34
ext. papers		avg, IF	L-index

#	Paper	IF	Citations
247	Gene Expression Profiling in Early Breast Cancer-Patient Stratification Based on Molecular and Tumor Microenvironment Features <i>Biomedicines</i> , 2022 , 10,	4.8	3
246	The cell cycle-related genes RHAMM, AURKA, TPX2, PLK1, and PLK4 are associated with the poor prognosis of breast cancer patients <i>Journal of Cellular Biochemistry</i> , 2022 ,	4.7	3
245	Identification of a Tumor Cell Associated Type I IFN Resistance Gene Expression Signature of Human Melanoma, the Components of Which Have a Predictive Potential for Immunotherapy <i>International Journal of Molecular Sciences</i> , 2022 , 23,	6.3	2
244	DNA methylation-based diagnostic, prognostic, and predictive biomarkers in colorectal cancer <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2022 , 188722	11.2	1
243	RIP140 inhibits glycolysis-dependent proliferation of breast cancer cells by regulating GLUT3 expression through transcriptional crosstalk between hypoxia induced factor and p53 <i>Cellular and Molecular Life Sciences</i> , 2022 , 79, 270	10.3	O
242	Transcriptomic Mapping of Non-Small Cell Lung Cancer p.G12C Mutated Tumors: Identification of Surfaceome Targets and Immunologic Correlates <i>Frontiers in Immunology</i> , 2021 , 12, 786069	8.4	1
241	Transcriptomic Correlates of Immunologic Activation in Head and Neck and Cervical Cancer. <i>Frontiers in Oncology</i> , 2021 , 11, 714550	5.3	1
240	Oncogene-mediated metabolic gene signature predicts breast cancer outcome. <i>Npj Breast Cancer</i> , 2021 , 7, 141	7.8	2
239	Induction of APOBEC3B expression by chemotherapy drugs is mediated by DNA-PK-directed activation of NF- B . <i>Oncogene</i> , 2021 , 40, 1077-1090	9.2	9
238	Pancancer survival analysis of cancer hallmark genes. Scientific Reports, 2021, 11, 6047	4.9	243
237	TNMplot.com: A Web Tool for the Comparison of Gene Expression in Normal, Tumor and Metastatic Tissues. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	99
236	Prognostic impact of the glypican family of heparan sulfate proteoglycans on the survival of breast cancer patients. <i>Journal of Cancer Research and Clinical Oncology</i> , 2021 , 147, 1937-1955	4.9	2
235	Mini-Factor H Modulates Complement-Dependent IL-6 and IL-10 Release in an Immune Cell Culture (PBMC) Model: Potential Benefits Against Cytokine Storm. <i>Frontiers in Immunology</i> , 2021 , 12, 642860	8.4	6
234	A bioinformatic analysis of the inhibin-betaglycan-endoglin/CD105 network reveals prognostic value in multiple solid tumors. <i>PLoS ONE</i> , 2021 , 16, e0249558	3.7	3
233	HGK promotes metastatic dissemination in prostate cancer. Scientific Reports, 2021, 11, 12287	4.9	3
232	The prognostic significance of FOXC2 gene expression in cancer: A comprehensive analysis of RNA-seq data from the cancer genome atlas. <i>Cancer Genetics</i> , 2021 , 254-255, 58-64	2.3	1
231	MultipleTesting.com: A tool for life science researchers for multiple hypothesis testing correction. <i>PLoS ONE</i> , 2021 , 16, e0245824	3.7	13

(2021-2021)

230	RNA sequencing of long-term label-retaining colon cancer stem cells identifies novel regulators of quiescence. <i>IScience</i> , 2021 , 24, 102618	6.1	2	
229	Clinical Correlations of Polycomb Repressive Complex 2 in Different Tumor Types. <i>Cancers</i> , 2021 , 13,	6.6	3	
228	Complement-mediated hypersensitivity reactions to an amphotericin B-containing lipid complex (Abelcet) in pediatric patients and anesthetized rats: Benefits of slow infusion. <i>Nanomedicine: Nanotechnology, Biology, and Medicine</i> , 2021 , 34, 102366	6	2	
227	Down-regulation of A20 promotes immune escape of lung adenocarcinomas. <i>Science Translational Medicine</i> , 2021 , 13,	17.5	3	
226	BRD4 regulates key transcription factors that drive epithelial-mesenchymal transition in castration-resistant prostate cancer. <i>Prostate Cancer and Prostatic Diseases</i> , 2021 , 24, 268-277	6.2	10	
225	Different mutations in SARS-CoV-2 associate with severe and mild outcome. <i>International Journal of Antimicrobial Agents</i> , 2021 , 57, 106272	14.3	59	
224	muTarget: A platform linking gene expression changes and mutation status in solid tumors. <i>International Journal of Cancer</i> , 2021 , 148, 502-511	7·5	21	
223	Prognostic significance of hedgehog signaling network-related gene expression in breast cancer patients. <i>Journal of Cellular Biochemistry</i> , 2021 , 122, 577-597	4.7	4	
222	In silico transcriptomic mapping of integrins and immune activation in Basal-like and HER2+ breast cancer. <i>Cellular Oncology (Dordrecht)</i> , 2021 , 44, 569-580	7.2	5	
221	Survival analysis across the entire transcriptome identifies biomarkers with the highest prognostic power in breast cancer. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 4101-4109	6.8	97	
220	Multi-omics approaches in cancer research with applications in tumor subtyping, prognosis, and diagnosis. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 949-960	6.8	27	
219	Mapping of Genomic Vulnerabilities in the Post-Translational Ubiquitination, SUMOylation and Neddylation Machinery in Breast Cancer. <i>Cancers</i> , 2021 , 13,	6.6	5	
218	Gene expression-based biomarkers designating glioblastomas resistant to multiple treatment strategies. <i>Carcinogenesis</i> , 2021 , 42, 804-813	4.6	3	
217	Web-Based Survival Analysis Tool Tailored for Medical Research (KMplot): Development and Implementation. <i>Journal of Medical Internet Research</i> , 2021 , 23, e27633	7.6	88	
216	Exploring the Significance of the Exon 4-Skipping Isoform of the ZNF217 Oncogene in Breast Cancer. <i>Frontiers in Oncology</i> , 2021 , 11, 647269	5.3	0	
215	Survival analysis in breast cancer using proteomic data from four independent datasets. <i>Scientific Reports</i> , 2021 , 11, 16787	4.9	7	
214	Genomic Mapping of Splicing-Related Genes Identify Amplifications in , and in Luminal Breast Cancers. <i>Cancers</i> , 2021 , 13,	6.6	1	
213	COVIDOUTCOME-estimating COVID severity based on mutation signatures in the SARS-CoV-2 genome. <i>Database: the Journal of Biological Databases and Curation</i> , 2021 , 2021,	5	5	

212	TGF-II potentiates VIVI Titell adoptive immunotherapy of cancer Cell Reports Medicine, 2021, 2, 100473	18	4
211	Characterization of Stem-like Circulating Tumor Cells in Pancreatic Cancer. <i>Diagnostics</i> , 2020 , 10,	3.8	3
210	Research funding: past performance is a stronger predictor of future scientific output than reviewer scores. <i>Journal of Informetrics</i> , 2020 , 14, 101050	3.1	13
209	Long-Term Exposure of Early-Transformed Human Mammary Cells to Low Doses of Benzo[a]pyrene and/or Bisphenol A Enhances Their Cancerous Phenotype via an AhR/GPR30 Interplay. <i>Frontiers in Oncology</i> , 2020 , 10, 712	5.3	3
208	Is there a golden age in publication activity? In analysis of age-related scholarly performance across all scientific disciplines. <i>Scientometrics</i> , 2020 , 124, 1081-1097	3	6
207	Identification of a stemness-related gene panel associated with BET inhibition in triple negative breast cancer. <i>Cellular Oncology (Dordrecht)</i> , 2020 , 43, 431-444	7.2	5
206	RNA-binding protein NONO contributes to cancer cell growth and confers drug resistance as a theranostic target in TNBC. <i>Theranostics</i> , 2020 , 10, 7974-7992	12.1	18
205	Targeting RICTOR Sensitizes SMAD4-Negative Colon Cancer to Irinotecan. <i>Molecular Cancer Research</i> , 2020 , 18, 414-423	6.6	6
204	Molecular stratifications, biomarker candidates and new therapeutic options in current medulloblastoma treatment approaches. <i>Cancer and Metastasis Reviews</i> , 2020 , 39, 211-233	9.6	19
203	Predictive biomarkers of platinum and taxane resistance using the transcriptomic data of 1816 ovarian cancer patients. <i>Gynecologic Oncology</i> , 2020 , 156, 654-661	4.9	18
202	miRNA Expression Signatures of Therapy Response in Squamous Cell Carcinomas. <i>Cancers</i> , 2020 , 13,	6.6	3
201	SETD3 acts as a prognostic marker in breast cancer patients and modulates the viability and invasion of breast cancer cells. <i>Scientific Reports</i> , 2020 , 10, 2262	4.9	20
200	FOXM1 functions collaboratively with PLAU to promote gastric cancer progression. <i>Journal of Cancer</i> , 2020 , 11, 788-794	4.5	16
199	The orphan nuclear receptor estrogen-related receptor beta (ERRI) in triple-negative breast cancer. Breast Cancer Research and Treatment, 2020, 179, 585-604	4.4	3
198	Histotype-specific analysis of acid ceramidase expression in ovarian cancer. <i>Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin</i> , 2020 , 476, 855-862	5.1	2
197	A novel mesenchymal-associated transcriptomic signature for risk-stratification and therapeutic response prediction in colorectal cancer. <i>International Journal of Cancer</i> , 2020 , 147, 3250-3261	7.5	4
196	Currently favored sampling practices for tumor sequencing can produce optimal results in the clinical setting. <i>Scientific Reports</i> , 2020 , 10, 14403	4.9	5
195	Genomic Mapping Identifies Mutations in RYR2 and AHNAK as Associated with Favorable Outcome in Basal-Like Breast Tumors Expressing PD1/PD-L1. <i>Cancers</i> , 2020 , 12,	6.6	11

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194	Association of Sperm-Associated Antigen 5 and Treatment Response in Patients With Estrogen Receptor-Positive Breast Cancer. <i>JAMA Network Open</i> , 2020 , 3, e209486	10.4	2
193	Evidence for Enhanced Exosome Production in Aromatase Inhibitor-Resistant Breast Cancer Cells. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	16
192	GAS2L1 Is a Potential Biomarker of Circulating Tumor Cells in Pancreatic Cancer. Cancers, 2020, 12,	6.6	2
191	The FOXC2 Transcription Factor Promotes Melanoma Outgrowth and Regulates Expression of Genes Associated With Drug Resistance and Interferon Responsiveness. <i>Cancer Genomics and Proteomics</i> , 2019 , 16, 491-503	3.3	7
190	Evidence for the Oocyte Mosaicism Selection model on the origin of Patau syndrome (trisomy 13). <i>Acta Obstetricia Et Gynecologica Scandinavica</i> , 2019 , 98, 1558-1564	3.8	1
189	Independent validation of induced overexpression efficiency across 242 experiments shows a success rate of 39. <i>Scientific Reports</i> , 2019 , 9, 343	4.9	2
188	Principles of tumorigenesis and emerging molecular drivers of SHH-activated medulloblastomas. <i>Annals of Clinical and Translational Neurology</i> , 2019 , 6, 990-1005	5.3	7
187	Gene Expression Indicates Altered Immune Modulation and Signaling Pathway Activation in Ovarian Cancer Patients Resistant to Topotecan. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	8
186	BRD4 Regulates Metastatic Potential of Castration-Resistant Prostate Cancer through AHNAK. <i>Molecular Cancer Research</i> , 2019 , 17, 1627-1638	6.6	20
185	SREBP1 drives Keratin-80-dependent cytoskeletal changes and invasive behavior in endocrine-resistant ERIbreast cancer. <i>Nature Communications</i> , 2019 , 10, 2115	17.4	27
184	ROCplot.org: Validating predictive biomarkers of chemotherapy/hormonal therapy/anti-HER2 therapy using transcriptomic data of 3,104 breast cancer patients. <i>International Journal of Cancer</i> , 2019 , 145, 3140-3151	7.5	64
183	Genetic mutational status of genes regulating epigenetics: Role of the histone methyltransferase KMT2D in triple negative breast tumors. <i>PLoS ONE</i> , 2019 , 14, e0209134	3.7	8
182	Molecular markers and potential therapeutic targets in non-WNT/non-SHH (group 3 and group 4) medulloblastomas. <i>Journal of Hematology and Oncology</i> , 2019 , 12, 29	22.4	19
181	Mapping Bromodomains in breast cancer and association with clinical outcome. <i>Scientific Reports</i> , 2019 , 9, 5734	4.9	5
180	Genomic Signatures of Immune Activation Predict Outcome in Advanced Stages of Ovarian Cancer and Basal-Like Breast Tumors. <i>Frontiers in Oncology</i> , 2019 , 9, 1486	5.3	15
179	Identifying Cancers Impacted by CDK8/19. <i>Cells</i> , 2019 , 8,	7.9	17
178	JAK-STAT inhibition impairs K-RAS-driven lung adenocarcinoma progression. <i>International Journal of Cancer</i> , 2019 , 145, 3376-3388	7·5	34
177	Elevated HOX gene expression in acute myeloid leukemia is associated with NPM1 mutations and poor survival. <i>Journal of Advanced Research</i> , 2019 , 20, 105-116	13	18

176	Expression of MHC class I, HLA-A and HLA-B identifies immune-activated breast tumors with favorable outcome. <i>OncoImmunology</i> , 2019 , 8, e1629780	7.2	12
175	Prognostic value of DLGAP5 in colorectal cancer. <i>International Journal of Colorectal Disease</i> , 2019 , 34, 1455-1465	3	17
174	Uncovering Potential Therapeutic Targets in Colorectal Cancer by Deciphering Mutational Status and Expression of Druggable Oncogenes. <i>Cancers</i> , 2019 , 11,	6.6	8
173	Serum PlGF and EGF are independent prognostic markers in non-metastatic colorectal cancer. <i>Scientific Reports</i> , 2019 , 9, 10921	4.9	2
172	Low level of exosomal long non-coding RNA is a prognostic biomarker in colorectal cancer. <i>RNA Biology</i> , 2019 , 16, 1339-1345	4.8	40
171	The prognostic association of SPAG5 gene expression in breast cancer patients with systematic therapy. <i>BMC Cancer</i> , 2019 , 19, 1046	4.8	7
170	Phosphodiesterase 5 (PDE5) Is Highly Expressed in Cancer-Associated Fibroblasts and Enhances Breast Tumor Progression. <i>Cancers</i> , 2019 , 11,	6.6	15
169	Comprehensive Outline of Whole Exome Sequencing Data Analysis Tools Available in Clinical Oncology. <i>Cancers</i> , 2019 , 11,	6.6	9
168	FAK activity sustains intrinsic and acquired ovarian cancer resistance to platinum chemotherapy. <i>ELife</i> , 2019 , 8,	8.9	41
167	A Transcriptomic Immunologic Signature Predicts Favorable Outcome in Neoadjuvant Chemotherapy Treated Triple Negative Breast Tumors. <i>Frontiers in Immunology</i> , 2019 , 10, 2802	8.4	13
166	Differential impact of classical and non-canonical NF- B pathway-related gene expression on the survival of breast cancer patients. <i>Journal of Cancer</i> , 2019 , 10, 5191-5211	4.5	11
165	Challenging the heterogeneity of disease presentation in malignant melanoma-impact on patient treatment. <i>Cell Biology and Toxicology</i> , 2019 , 35, 1-14	7.4	13
164	A snapshot of 3649 Web-based services published between 1994 and 2017 shows a decrease in availability after 2 years. <i>Briefings in Bioinformatics</i> , 2019 , 20, 1004-1010	13.4	6
163	Mutations Defining Patient Cohorts With Elevated PD-L1 Expression in Gastric Cancer. <i>Frontiers in Pharmacology</i> , 2018 , 9, 1522	5.6	18
162	Evaluating mRNA Expression Levels as a Predictor of Response to Endocrine Therapy in ER+ Breast Cancer. <i>Frontiers in Pharmacology</i> , 2018 , 9, 1581	5.6	7
161	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	12.9	28
160	An integrative bioinformatics approach reveals coding and non-coding gene variants associated with gene expression profiles and outcome in breast cancer molecular subtypes. <i>British Journal of Cancer</i> , 2018 , 118, 1107-1114	8.7	17
159	Integrated molecular analysis of Tamoxifen-resistant invasive lobular breast cancer cells identifies MAPK and GRM/mGluR signaling as therapeutic vulnerabilities. <i>Molecular and Cellular Endocrinology</i> , 2018 , 471, 105-117	4.4	12

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15	8 Enhancer mapping uncovers phenotypic heterogeneity and evolution in patients with luminal breast cancer. <i>Nature Medicine</i> , 2018 , 24, 1469-1480	50.5	64	
15	Validation of miRNA prognostic power in hepatocellular carcinoma using expression data of independent datasets. <i>Scientific Reports</i> , 2018 , 8, 9227	4.9	787	
15	6 Afatinib restrains K-RAS-driven lung tumorigenesis. Science Translational Medicine, 2018 , 10,	17.5	70	
15	Dynamin impacts homology-directed repair and breast cancer response to chemotherapy. <i>Journal of Clinical Investigation</i> , 2018 , 128, 5307-5321	15.9	12	
15.	Alterations in SCAI Expression during Cell Plasticity, Fibrosis and Cancer. <i>Pathology and Oncology Research</i> , 2018 , 24, 641-651	2.6	5	
15	linc00673 (ERRLR01) is a prognostic indicator of overall survival in breast cancer. <i>Transcription</i> , 2018 , 9, 17-29	4.8	20	
15	Determining consistent prognostic biomarkers of overall survival and vascular invasion in hepatocellular carcinoma. <i>Royal Society Open Science</i> , 2018 , 5, 181006	3.3	197	
15	Exploratory Analysis of Single-Gene Predictive Biomarkers in HERA DASL Cohort Reveals That C8A mRNA Expression Is Prognostic of Outcome and Predictive of Benefit of Trastuzumab. <i>JCO Precision Oncology</i> , 2018 , 2,	3.6	2	
15	Induction of cell cycle arrest and inflammatory genes by combined treatment with epigenetic, differentiating, and chemotherapeutic agents in triple-negative breast cancer. <i>Breast Cancer Research</i> , 2018 , 20, 145	8.3	11	
14	Evaluation of transcriptionally regulated genes identifies NCOR1 in hormone receptor negative breast tumors and lung adenocarcinomas as a potential tumor suppressor gene. <i>PLoS ONE</i> , 2018 , 13, e0207776	3.7	4	
14	Demographic shift disproportionately increases cancer burden in an aging nation: current and expected incidence and mortality in Hungary up to 2030. <i>Clinical Epidemiology</i> , 2018 , 10, 1093-1108	5.9	16	
14	Integrated analysis of the immunological and genetic status in and across cancer types: impact of mutational signatures beyond tumor mutational burden. <i>OncoImmunology</i> , 2018 , 7, e1526613	7.2	40	
14	6 Transcriptome evolution from breast epithelial cells to basal-like tumors. <i>Oncotarget</i> , 2018 , 9, 453-463	3.3	9	
14	Epigenetic modulation of FOXM1-gene interacting network by BET inhibitors in breast cancer. 5 Breast Cancer Research and Treatment, 2018 , 172, 725-732	4.4	7	
14	Factors influencing the scientific performance of Momentum grant holders: an evaluation of the first 117 research groups. <i>Scientometrics</i> , 2018 , 117, 409-426	3	8	
14	Activation of Farnesoid X Receptor impairs the tumor-promoting function of breast cancer-associated fibroblasts. <i>Cancer Letters</i> , 2018 , 437, 89-99	9.9	16	
14	MLL-fusion-driven leukemia requires SETD2 to safeguard genomic integrity. <i>Nature</i> Communications, 2018 , 9, 1983	17.4	31	
14	HUWE1 is a critical colonic tumour suppressor gene that prevents MYC signalling, DNA damage accumulation and tumour initiation. <i>EMBO Molecular Medicine</i> , 2017 , 9, 181-197	12	46	

140	Benzyl Isothiocyanate potentiates p53 signaling and antitumor effects against breast cancer through activation of p53-LKB1 and p73-LKB1 axes. <i>Scientific Reports</i> , 2017 , 7, 40070	4.9	23
139	The critical role of the ZNF217 oncogene in promoting breast cancer metastasis to the bone. <i>Journal of Pathology</i> , 2017 , 242, 73-89	9.4	28
138	ZEB1-induced tumourigenesis requires senescence inhibition via activation of DKK1/mutant p53/Mdm2/CtBP and repression of macroH2A1. <i>Gut</i> , 2017 , 66, 666-682	19.2	21
137	Comparison of 5 Ki-67 antibodies regarding reproducibility and capacity to predict prognosis in breast cancer: does the antibody matter?. <i>Human Pathology</i> , 2017 , 65, 31-40	3.7	14
136	Immune Gene Expression Is Associated with Genomic Aberrations in Breast Cancer. <i>Cancer Research</i> , 2017 , 77, 3317-3324	10.1	80
135	Effect of extended oral contraception use on the prevalence of fetal trisomy 21 in women aged at least 35 years. <i>International Journal of Gynecology and Obstetrics</i> , 2017 , 138, 261-266	4	2
134	Tumor-associated macrophages (TAMs) depend on ZEB1 for their cancer-promoting roles. <i>EMBO Journal</i> , 2017 , 36, 3336-3355	13	69
133	Quantitative proteomics identifies STEAP4 as a critical regulator of mitochondrial dysfunction linking inflammation and colon cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E9608-E9617	11.5	45
132	Inhibition of CDK8 mediator kinase suppresses estrogen dependent transcription and the growth of estrogen receptor positive breast cancer. <i>Oncotarget</i> , 2017 , 8, 12558-12575	3.3	70
131	Infiltrating T Cells Increase IDO1 Expression in Glioblastoma and Contribute to Decreased Patient Survival. <i>Clinical Cancer Research</i> , 2017 , 23, 6650-6660	12.9	104
131		12.9	104
	Survival. Clinical Cancer Research, 2017, 23, 6650-6660 Cell Dispersal Influences Tumor Heterogeneity and Introduces a Bias in NGS Data Interpretation.		6
130	Survival. Clinical Cancer Research, 2017, 23, 6650-6660 Cell Dispersal Influences Tumor Heterogeneity and Introduces a Bias in NGS Data Interpretation. Scientific Reports, 2017, 7, 7358 ADIPOQ/adiponectin induces cytotoxic autophagy in breast cancer cells through	4.9	6
130 129	Survival. Clinical Cancer Research, 2017, 23, 6650-6660 Cell Dispersal Influences Tumor Heterogeneity and Introduces a Bias in NGS Data Interpretation. Scientific Reports, 2017, 7, 7358 ADIPOQ/adiponectin induces cytotoxic autophagy in breast cancer cells through STK11/LKB1-mediated activation of the AMPK-ULK1 axis. Autophagy, 2017, 13, 1386-1403 KRAS driven expression signature has prognostic power superior to mutation status in non-small	4.9	6 86
130 129 128	Cell Dispersal Influences Tumor Heterogeneity and Introduces a Bias in NGS Data Interpretation. <i>Scientific Reports</i> , 2017 , 7, 7358 ADIPOQ/adiponectin induces cytotoxic autophagy in breast cancer cells through STK11/LKB1-mediated activation of the AMPK-ULK1 axis. <i>Autophagy</i> , 2017 , 13, 1386-1403 KRAS driven expression signature has prognostic power superior to mutation status in non-small cell lung cancer. <i>International Journal of Cancer</i> , 2017 , 140, 930-937 Cancer heterogeneity determined by functional proteomics. <i>Seminars in Cell and Developmental</i>	4·9 10.2 7·5	6 86 18
130 129 128	Cell Dispersal Influences Tumor Heterogeneity and Introduces a Bias in NGS Data Interpretation. <i>Scientific Reports</i> , 2017 , 7, 7358 ADIPOQ/adiponectin induces cytotoxic autophagy in breast cancer cells through STK11/LKB1-mediated activation of the AMPK-ULK1 axis. <i>Autophagy</i> , 2017 , 13, 1386-1403 KRAS driven expression signature has prognostic power superior to mutation status in non-small cell lung cancer. <i>International Journal of Cancer</i> , 2017 , 140, 930-937 Cancer heterogeneity determined by functional proteomics. <i>Seminars in Cell and Developmental Biology</i> , 2017 , 64, 132-142 Activation of tumor suppressor LKB1 by honokiol abrogates cancer stem-like phenotype in breast	4.9 10.2 7.5	6 86 18
130 129 128 127	Cell Dispersal Influences Tumor Heterogeneity and Introduces a Bias in NGS Data Interpretation. <i>Scientific Reports</i> , 2017 , 7, 7358 ADIPOQ/adiponectin induces cytotoxic autophagy in breast cancer cells through STK11/LKB1-mediated activation of the AMPK-ULK1 axis. <i>Autophagy</i> , 2017 , 13, 1386-1403 KRAS driven expression signature has prognostic power superior to mutation status in non-small cell lung cancer. <i>International Journal of Cancer</i> , 2017 , 140, 930-937 Cancer heterogeneity determined by functional proteomics. <i>Seminars in Cell and Developmental Biology</i> , 2017 , 64, 132-142 Activation of tumor suppressor LKB1 by honokiol abrogates cancer stem-like phenotype in breast cancer via inhibition of oncogenic Stat3. <i>Oncogene</i> , 2017 , 36, 5709-5721	4·9 10.2 7·5 7·5	6 86 18 10 61

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122	Mitotic read-out genes confer poor outcome in luminal A breast cancer tumors. <i>Oncotarget</i> , 2017 , 8, 21733-21740	3.3	13	
121	PDGFRA, HSD17B4 and HMGB2 are potential therapeutic targets in polycystic ovarian syndrome and breast cancer. <i>Oncotarget</i> , 2017 , 8, 69520-69526	3.3	8	
120	DUSP4 is associated with increased resistance against anti-HER2 therapy in breast cancer. <i>Oncotarget</i> , 2017 , 8, 77207-77218	3.3	20	
119	Propagation on Molecular Interaction Networks: Prediction of Effective Drug Combinations and Biomarkers in Cancer Treatment. <i>Current Pharmaceutical Design</i> , 2017 , 23, 5-28	3.3	1	
118	Iron Uptake via DMT1 Integrates Cell Cycle with JAK-STAT3 Signaling to Promote Colorectal Tumorigenesis. <i>Cell Metabolism</i> , 2016 , 24, 447-461	24.6	108	
117	AXL-associated tumor inflammation as a poor prognostic signature in chemotherapy-treated triple-negative breast cancer patients. <i>Npj Breast Cancer</i> , 2016 , 2, 16033	7.8	29	
116	miRpower: a web-tool to validate survival-associated miRNAs utilizing expression data from 2178 breast cancer patients. <i>Breast Cancer Research and Treatment</i> , 2016 , 160, 439-446	4.4	507	
115	Guidelines for the selection of functional assays to evaluate the hallmarks of cancer. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2016 , 1866, 300-319	11.2	60	
114	Colon cancer subtypes: concordance, effect on survival and selection of the most representative preclinical models. <i>Scientific Reports</i> , 2016 , 6, 37169	4.9	20	
113	Transcription Factor ZBP-89 Drives a Feedforward Loop of Ecatenin Expression in Colorectal Cancer. <i>Cancer Research</i> , 2016 , 76, 6877-6887	10.1	15	
112	HOXC10 Expression Supports the Development of Chemotherapy Resistance by Fine Tuning DNA Repair in Breast Cancer Cells. <i>Cancer Research</i> , 2016 , 76, 4443-56	10.1	41	
111	Expression of CDK7, Cyclin H, and MAT1 Is Elevated in Breast Cancer and Is Prognostic in Estrogen Receptor-Positive Breast Cancer. <i>Clinical Cancer Research</i> , 2016 , 22, 5929-5938	12.9	47	
110	Expression and Function of Phosphodiesterase Type 5 in Human Breast Cancer Cell Lines and Tissues: Implications for Targeted Therapy. <i>Clinical Cancer Research</i> , 2016 , 22, 2271-82	12.9	39	
109	BRCA Mutation-Related and Claudin-Low Breast Cancer: Blood Relatives or Stepsisters. <i>Pathobiology</i> , 2016 , 83, 1-12	3.6	5	
108	miR-34a Silences c-SRC to Attenuate Tumor Growth in Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2016 , 76, 927-39	10.1	103	
107	Predictors of Chemosensitivity in Triple Negative Breast Cancer: An Integrated Genomic Analysis. <i>PLoS Medicine</i> , 2016 , 13, e1002193	11.6	48	
106	TP53 mutation hits energy metabolism and increases glycolysis in breast cancer. <i>Oncotarget</i> , 2016 , 7, 67183-67195	3.3	34	
105	LDB1 overexpression is a negative prognostic factor in colorectal cancer. <i>Oncotarget</i> , 2016 , 7, 84258-84	2379	7	

104	Leptin as a mediator of tumor-stromal interactions promotes breast cancer stem cell activity. Oncotarget, 2016 , 7, 1262-75	3.3	58
103	HIF-3¶ promotes colorectal tumor cell growth by activation of JAK-STAT3 signaling. <i>Oncotarget</i> , 2016 , 7, 11567-79	3.3	17
102	Potential options for managing LOX+ ER- breast cancer patients. <i>Oncotarget</i> , 2016 , 7, 32893-901	3.3	8
101	Cross-validation of survival associated biomarkers in gastric cancer using transcriptomic data of 1,065 patients. <i>Oncotarget</i> , 2016 , 7, 49322-49333	3.3	643
100	Systematic Analysis of AU-Rich Element Expression in Cancer Reveals Common Functional Clusters Regulated by Key RNA-Binding Proteins. <i>Cancer Research</i> , 2016 , 76, 4068-80	10.1	50
99	Validation of RNAi Silencing Efficiency Using Gene Array Data shows 18.5% Failure Rate across 429 Independent Experiments. <i>Molecular Therapy - Nucleic Acids</i> , 2016 , 5, e366	10.7	8
98	Deciphering and Targeting Oncogenic Mutations and Pathways in Breast Cancer. <i>Oncologist</i> , 2016 , 21, 1063-78	5.7	35
97	Aberrant DNA methylation impacts gene expression and prognosis in breast cancer subtypes. <i>International Journal of Cancer</i> , 2016 , 138, 87-97	7.5	79
96	Multigene prognostic tests in breast cancer: past, present, future. <i>Breast Cancer Research</i> , 2015 , 17, 11	8.3	173
95	Shp2 signaling suppresses senescence in PyMT-induced mammary gland cancer in mice. <i>EMBO Journal</i> , 2015 , 34, 1493-508	13	24
94	HOXB7 Is an ERICofactor in the Activation of HER2 and Multiple ER Target Genes Leading to Endocrine Resistance. <i>Cancer Discovery</i> , 2015 , 5, 944-59	24.4	56
93	Synaptic mitochondria: a brain mitochondria cluster with a specific proteome. <i>Journal of Proteomics</i> , 2015 , 120, 142-57	3.9	40
92	Type I IFN induces protein ISGylation to enhance cytokine expression and augments colonic inflammation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 14313-8	11.5	30
91	A genome-wide approach to link genotype to clinical outcome by utilizing next generation sequencing and gene chip data of 6,697 breast cancer patients. <i>Genome Medicine</i> , 2015 , 7, 104	14.4	49
90	Classical pathology and mutational load of breast cancer - integration of two worlds. <i>Journal of Pathology: Clinical Research</i> , 2015 , 1, 225-38	5.3	57
89	Tumor-selective proteotoxicity of verteporfin inhibits colon cancer progression independently of YAP1. <i>Science Signaling</i> , 2015 , 8, ra98	8.8	114
88	APOBEC3B-Mediated Cytidine Deamination Is Required for Estrogen Receptor Action in Breast Cancer. <i>Cell Reports</i> , 2015 , 13, 108-121	10.6	64
87	Signal Transduction Pathways of TNAP: Molecular Network Analyses. <i>Sub-Cellular Biochemistry</i> , 2015 , 76, 185-205	5.5	2

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86	Differential epigenetic reprogramming in response to specific endocrine therapies promotes cholesterol biosynthesis and cellular invasion. <i>Nature Communications</i> , 2015 , 6, 10044	17.4	81
85	Acid ceramidase is associated with an improved prognosis in both DCIS and invasive breast cancer. <i>Molecular Oncology</i> , 2015 , 9, 58-67	7.9	25
84	Glutamate enrichment as new diagnostic opportunity in breast cancer. <i>International Journal of Cancer</i> , 2015 , 136, 1619-28	7.5	76
83	Dynamic classification using case-specific training cohorts outperforms static gene expression signatures in breast cancer. <i>International Journal of Cancer</i> , 2015 , 136, 2091-8	7.5	8
82	Association of PDCD1 and CTLA-4 Gene Expression with Clinicopathological Factors and Survival in Non-Small-Cell Lung Cancer: Results from a Large and Pooled Microarray Database. <i>Journal of Thoracic Oncology</i> , 2015 , 10, 1020-6	8.9	29
81	A Comprehensive Outline of Trastuzumab Resistance Biomarkers in HER2 Overexpressing Breast Cancer. <i>Current Cancer Drug Targets</i> , 2015 , 15, 665-83	2.8	31
80	A Network-Based Target Overlap Score for Characterizing Drug Combinations: High Correlation with Cancer Clinical Trial Results. <i>PLoS ONE</i> , 2015 , 10, e0129267	3.7	9
79	Proteomic identification of prognostic tumour biomarkers, using chemotherapy-induced cancer-associated fibroblasts. <i>Aging</i> , 2015 , 7, 816-38	5.6	25
78	Effects of RAL signal transduction in KRAS- and BRAF-mutated cells and prognostic potential of the RAL signature in colorectal cancer. <i>Oncotarget</i> , 2015 , 6, 13334-46	3.3	17
77	Disruption of STAT3 signalling promotes KRAS-induced lung tumorigenesis. <i>Nature Communications</i> , 2015 , 6, 6285	17.4	95
76	BCL9/9L-Etatenin Signaling is Associated With Poor Outcome in Colorectal Cancer. <i>EBioMedicine</i> , 2015 , 2, 1932-43	8.8	41
75	The pioneer factor PBX1 is a novel driver of metastatic progression in EREpositive breast cancer. <i>Oncotarget</i> , 2015 , 6, 21878-91	3.3	28
74	Expression of CDK8 and CDK8-interacting Genes as Potential Biomarkers in Breast Cancer. <i>Current Cancer Drug Targets</i> , 2015 , 15, 739-49	2.8	50
73	Combined analysis of gene expression, DNA copy number, and mutation profiling data to display biological process anomalies in individual breast cancers. <i>Breast Cancer Research and Treatment</i> , 2014 , 144, 561-8	4.4	3
72	Brain protein expression changes in WAG/Rij rats, a genetic rat model of absence epilepsy after peripheral lipopolysaccharide treatment. <i>Brain, Behavior, and Immunity</i> , 2014 , 35, 86-95	16.6	18
71	A functional interplay between ZNF217 and estrogen receptor alpha exists in luminal breast cancers. <i>Molecular Oncology</i> , 2014 , 8, 1441-57	7.9	24
70	Correlations of differentially expressed gap junction connexins Cx26, Cx30, Cx32, Cx43 and Cx46 with breast cancer progression and prognosis. <i>PLoS ONE</i> , 2014 , 9, e112541	3.7	58
69	MEK1 is associated with carboplatin resistance and is a prognostic biomarker in epithelial ovarian cancer. <i>BMC Cancer</i> , 2014 , 14, 837	4.8	41

68	Predicting the chance of relapse after tamoxifen treatment in breast cancer. <i>Biomarkers in Medicine</i> , 2014 , 8, 77-9	2.3	1
67	TP53 mutation-correlated genes predict the risk of tumor relapse and identify MPS1 as a potential therapeutic kinase in TP53-mutated breast cancers. <i>Molecular Oncology</i> , 2014 , 8, 508-19	7.9	49
66	Biomarkers for systemic therapy in ovarian cancer. Current Cancer Drug Targets, 2014, 14, 259-73	2.8	6
65	Inhibition of MEK1 increases carboplatin sensitivity in ovarian cancer <i>Journal of Clinical Oncology</i> , 2014 , 32, 5557-5557	2.2	
64	Application of a dynamic retraining for each patient using case-specific training cohorts to predict survival in breast cancer patients <i>Journal of Clinical Oncology</i> , 2014 , 32, 1065-1065	2.2	
63	A meta-analysis of gene expression-based biomarkers predicting outcome after tamoxifen treatment in breast cancer. <i>Breast Cancer Research and Treatment</i> , 2013 , 140, 219-32	4.4	140
62	Combined Wnt/Ecatenin, Met, and CXCL12/CXCR4 signals characterize basal breast cancer and predict disease outcome. <i>Cell Reports</i> , 2013 , 5, 1214-27	10.6	57
61	Predicting effective drug combinations via network propagation 2013,		1
60	New network topology approaches reveal differential correlation patterns in breast cancer. <i>BMC Systems Biology</i> , 2013 , 7, 78	3.5	29
59	Lower risk for Down syndrome associated with longer oral contraceptive use: a case-control study of women of advanced maternal age presenting for prenatal diagnosis. <i>Contraception</i> , 2013 , 87, 455-8	2.5	7
58	Elevated BUBR1 expression is associated with poor survival in early breast cancer patients: 15-year follow-up analysis. <i>Journal of Histochemistry and Cytochemistry</i> , 2013 , 61, 330-9	3.4	24
57	Genome-wide reprogramming of the chromatin landscape underlies endocrine therapy resistance in breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, E1490-9	11.5	120
56	Improving Pathological Assessment of Breast Cancer by Employing Array-Based Transcriptome Analysis. <i>Microarrays (Basel, Switzerland)</i> , 2013 , 2, 228-42		20
55	Identifying resistance mechanisms against five tyrosine kinase inhibitors targeting the ERBB/RAS pathway in 45 cancer cell lines. <i>PLoS ONE</i> , 2013 , 8, e59503	3.7	16
54	Current composite-feature classification methods do not outperform simple single-genes classifiers in breast cancer prognosis. <i>Frontiers in Genetics</i> , 2013 , 4, 289	4.5	30
53	The CIN4 chromosomal instability qPCR classifier defines tumor aneuploidy and stratifies outcome in grade 2 breast cancer. <i>PLoS ONE</i> , 2013 , 8, e56707	3.7	23
52	Online survival analysis software to assess the prognostic value of biomarkers using transcriptomic data in non-small-cell lung cancer. <i>PLoS ONE</i> , 2013 , 8, e82241	3.7	1161
51	Meta-analysis of 59 gene expression based biomarker candidates predicting survival after tamoxifen treatment in breast cancer <i>Journal of Clinical Oncology</i> , 2013 , 31, e11564-e11564	2.2	

(2010-2012)

50	Cyclin-dependent kinase 8 mediates chemotherapy-induced tumor-promoting paracrine activities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 13799-804	11.5	108
49	Remodeling of central metabolism in invasive breast cancer compared to normal breast tissue - a GC-TOFMS based metabolomics study. <i>BMC Genomics</i> , 2012 , 13, 334	4.5	102
48	Cutoff Finder: a comprehensive and straightforward Web application enabling rapid biomarker cutoff optimization. <i>PLoS ONE</i> , 2012 , 7, e51862	3.7	749
47	Meta-analysis of gene expression profiles associated with histological classification and survival in 829 ovarian cancer samples. <i>International Journal of Cancer</i> , 2012 , 131, 95-105	7.5	33
46	ABCC2 (MRP2, cMOAT) localized in the nuclear envelope of breast carcinoma cells correlates with poor clinical outcome. <i>Pathology and Oncology Research</i> , 2012 , 18, 331-42	2.6	36
45	RecurrenceOnline: an online analysis tool to determine breast cancer recurrence and hormone receptor status using microarray data. <i>Breast Cancer Research and Treatment</i> , 2012 , 132, 1025-34	4.4	76
44	Enhanced immunoreactivity of TIMP-2 in the stromal compartment of tumor as a marker of favorable prognosis in ovarian cancer patients. <i>Journal of Histochemistry and Cytochemistry</i> , 2012 , 60, 491-501	3.4	15
43	Implementing an online tool for genome-wide validation of survival-associated biomarkers in ovarian-cancer using microarray data from 1287 patients. <i>Endocrine-Related Cancer</i> , 2012 , 19, 197-208	5.7	550
42	A comprehensive overview of targeted therapy in metastatic renal cell carcinoma. <i>Current Cancer Drug Targets</i> , 2012 , 12, 857-72	2.8	42
41	Parallel evolution under chemotherapy pressure in 29 breast cancer cell lines results in dissimilar mechanisms of resistance. <i>PLoS ONE</i> , 2012 , 7, e30804	3.7	40
40	Could tivozanib be a new potent pan-VEGF inhibitor in RCC therapy?. <i>Translational Andrology and Urology</i> , 2012 , 1, 192-3	2.3	
39	Identification of a claudin-4 and E-cadherin score to predict prognosis in breast cancer. <i>Cancer Science</i> , 2011 , 102, 2248-54	6.9	42
38	Jetset: selecting the optimal microarray probe set to represent a gene. <i>BMC Bioinformatics</i> , 2011 , 12, 474	3.6	189
37	Loss of estrogen receptor beta expression correlates with shorter overall survival and lack of clinical response to chemotherapy in ovarian cancer patients. <i>Anticancer Research</i> , 2011 , 31, 711-8	2.3	31
36	Expression of classical NF-kappaB pathway effectors in human ovarian carcinoma. <i>Histopathology</i> , 2010 , 56, 727-39	7.3	30
35	PSMB7 is associated with anthracycline resistance and is a prognostic biomarker in breast cancer. <i>British Journal of Cancer</i> , 2010 , 102, 361-8	8.7	30
34	Biomarkers downstream of RAS: a search for robust transcriptional targets. <i>Current Cancer Drug Targets</i> , 2010 , 10, 858-68	2.8	21
33	Predictive biomarker discovery through the parallel integration of clinical trial and functional genomics datasets. <i>Genome Medicine</i> , 2010 , 2, 53	14.4	36

32	An online survival analysis tool to rapidly assess the effect of 22,277 genes on breast cancer prognosis using microarray data of 1,809 patients. <i>Breast Cancer Research and Treatment</i> , 2010 , 123, 725-31	4.4	1940
31	Gene signature of the metastatic potential of cutaneous melanoma: too much for too little?. <i>Clinical and Experimental Metastasis</i> , 2010 , 27, 371-87	4.7	62
30	Systematic evaluation of the miRNA-ome and its downstream effects on mRNA expression identifies gastric cancer progression. <i>Journal of Pathology</i> , 2010 , 222, 310-9	9.4	107
29	Evaluation of microarray preprocessing algorithms based on concordance with RT-PCR in clinical samples. <i>PLoS ONE</i> , 2009 , 4, e5645	3.7	67
28	Meta-analysis of gene expression profiles related to relapse-free survival in 1,079 breast cancer patients. <i>Breast Cancer Research and Treatment</i> , 2009 , 118, 433-41	4.4	68
27	A prognostic gene expression index in ovarian cancer - validation across different independent data sets. <i>Journal of Pathology</i> , 2009 , 218, 273-80	9.4	80
26	Inflammation, adenoma and cancer: objective classification of colon biopsy specimens with gene expression signature. <i>Disease Markers</i> , 2008 , 25, 1-16	3.2	76
25	Acquired cisplatin resistance in the head-neck cancer cell line Cal27 is associated with decreased DKK1 expression and can partially be reversed by overexpression of DKK1. <i>International Journal of Cancer</i> , 2008 , 123, 2013-9	7.5	63
24	Helicobacter pylori and antrum erosion-specific gene expression patterns: the discriminative role of CXCL13 and VCAM1 transcripts. <i>Helicobacter</i> , 2008 , 13, 112-26	4.9	37
23	A Web-based data warehouse on gene expression in human malignant melanoma. <i>Journal of Investigative Dermatology</i> , 2007 , 127, 394-9	4.3	36
22	Functional transcriptomics: an experimental basis for understanding the systems biology for cancer cells. <i>Advances in Enzyme Regulation</i> , 2007 , 47, 41-62		
21	Highly expressed genes are associated with inverse antisense transcription in mouse. <i>Journal of Genetics</i> , 2007 , 86, 103-9	1.2	7
20	Identification of consensus genes and key regulatory elements in 5-fluorouracil resistance in gastric and colon cancer. <i>Oncology Research and Treatment</i> , 2007 , 30, 421-6	2.8	7
19	Resistance-associated signatures in breast cancer. <i>Recent Results in Cancer Research</i> , 2007 , 176, 37-50	1.5	
18	Gene expression profiling of 30 cancer cell lines predicts resistance towards 11 anticancer drugs at clinically achieved concentrations. <i>International Journal of Cancer</i> , 2006 , 118, 1699-712	7.5	120
17	Use of routinely collected amniotic fluid for whole-genome expression analysis of polygenic disorders. <i>Clinical Chemistry</i> , 2006 , 52, 2013-20	5.5	12
16	Computational analysis reveals 43% antisense transcription in 1182 transcripts in mouse muscle. <i>DNA Sequence</i> , 2006 , 17, 422-30		3
15	Single-nucleotide polymorphisms of VEGF gene are associated with risk of congenital valvuloseptal heart defects. <i>American Heart Journal</i> , 2006 , 151, 878-81	4.9	28

LIST OF PUBLICATIONS

14	Analysis of gene expression profiles in melanoma cells with acquired resistance against antineoplastic drugs. <i>Melanoma Research</i> , 2006 , 16, 147-55	3.3	11	
13	Multivariate analysis of oestrogen receptor alpha, pS2, metallothionein and CD24 expression in invasive breast cancers. <i>British Journal of Cancer</i> , 2006 , 95, 339-46	8.7	42	
12	The PI3K inhibitor LY294002 blocks drug export from resistant colon carcinoma cells overexpressing MRP1. <i>Oncogene</i> , 2006 , 25, 1743-52	9.2	95	
11	Stromal myofibroblasts in breast cancer: relations between their occurrence, tumor grade and expression of some tumour markers. <i>Folia Histochemica Et Cytobiologica</i> , 2006 , 44, 111-6	1.4	30	
10	Prediction of doxorubicin sensitivity in breast tumors based on gene expression profiles of drug-resistant cell lines correlates with patient survival. <i>Oncogene</i> , 2005 , 24, 7542-51	9.2	62	
9	Application of Microarrays for the Prediction of Therapy Response in Breast Cancer. <i>Cancer Genomics and Proteomics</i> , 2005 , 2, 255-263	3.3		
8	Examination of Hardy-Weinberg equilibrium in papers of Kidney International: an underused tool. <i>Kidney International</i> , 2004 , 65, 1956-8	9.9	24	
7	Missed calculations and new conclusions: re-calculation of genotype distribution data published in Journal of Investigative Dermatology, 1998-2003. <i>Journal of Investigative Dermatology</i> , 2004 , 122, 644-	·6 ^{4·3}	13	
6	Re-calculated Hardy-Weinberg values in papers published in Atherosclerosis between 1995 and 2003. <i>Atherosclerosis</i> , 2004 , 173, 141-3	3.1	13	
5	Gender-specific association of vitamin D receptor polymorphism combinations with type 1 diabetes mellitus. <i>European Journal of Endocrinology</i> , 2002 , 147, 803-8	6.5	60	
4	Survival analysis in breast cancer using proteomic data from four independent datasets		1	
3	Genome-wide alterations of uracil distribution patterns in human DNA upon chemotherapeutic treatm	ents	1	
2	TNMplot.com: a web tool for the comparison of gene expression in normal, tumor and metastatic tissu	es	6	
1	SREBP1 drives KRT80-dependent cytoskeletal changes and invasive behavior in endocrine resistant ERIbreast cancer		1	