Zhifu Sun

List of Publications by Year
in descending order

135 papers	8,329 citations	46984 47 h-index	53190 85 g-index
138 all docs	138 docs citations	138 times ranked	17454 citing authors

#	ARTICLE	IF	CITATIONS
1	Characterization of human plasma-derived exosomal RNAs by deep sequencing. BMC Genomics, 2013, 14, 319.	1.2	860
2	CrossMap: a versatile tool for coordinate conversion between genome assemblies. Bioinformatics, 2014, 30, 1006-1007.	1.8	553
3	Exosomal miR-1290 and miR-375 as Prognostic Markers in Castration-resistant Prostate Cancer. European Urology, 2015, 67, 33-41.	0.9	533
4	A Gene Expression Signature Predicts Survival of Patients with Stage I Non-Small Cell Lung Cancer. PLoS Medicine, 2006, 3, e467.	3.9	272
5	Role of imbalance between neutrophil elastase and Î±1-antitrypsin in cancer development and progression. Lancet Oncology, The, 2004, 5, 182-190.	5.1	227
6	Genetic variants and risk of lung cancer in never smokers: a genome-wide association study. Lancet Oncology, The, 2010, 11, 321-330.	5.1	218
7	Longitudinal Multi-omics Reveals Subset-Specific Mechanisms Underlying Irritable Bowel Syndrome. Cell, 2020, 182, 1460-1473.e17.	13.5	217
8	Chronic Caloric Restriction Preserves Mitochondrial Function in Senescence without Increasing Mitochondrial Biogenesis. Cell Metabolism, 2012, 16, 777-788.	7.2	183
9	Distinct epigenetic landscapes underlie the pathobiology of pancreatic cancer subtypes. Nature Communications, 2018, 9, 1978.	5.8	177
10	LncRNA <i>MALAT1</i> enhances oncogenic activities of EZH2 in castration-resistant prostate cancer. Oncotarget, 2015, 6, 41045-41055.	0.8	154
11	Alpha1-Antitrypsin Deficiency Carriers, Tobacco Smoke, Chronic Obstructive Pulmonary Disease, and Lung Cancer Risk. Archives of Internal Medicine, 2008, 168, 1097.	4.3	139
12	CAP-miRSeq: a comprehensive analysis pipeline for microRNA sequencing data. BMC Genomics, 2014, 15, 423.	1.2	138
13	Histologic grade is an independent prognostic factor for survival in nonâ€"small cell lung cancer: An analysis of 5018 hospital- and 712 population-based cases. Journal of Thoracic and Cardiovascular Surgery, 2006, 131, 1014-1020.	0.4	128
14	Integrated Analysis of Gene Expression, CpG Island Methylation, and Gene Copy Number in Breast Cancer Cells by Deep Sequencing. PLoS ONE, 2011, 6, e17490.	1.1	128
15	Role of the Glutathione Metabolic Pathway in Lung Cancer Treatment and Prognosis: A Review. Journal of Clinical Oncology, 2006, 24, 1761-1769.	0.8	119
16	Global Methylation Profiling for Risk Prediction of Prostate Cancer. Clinical Cancer Research, 2012, 18, 2882-2895.	3.2	118
17	Batch effect correction for genome-wide methylation data with Illumina Infinium platform. BMC Medical Genomics, 2011, 4, 84.	0.7	108
18	New DNA Methylation Markers for Pancreatic Cancer: Discovery, Tissue Validation, and Pilot Testing in Pancreatic Juice. Clinical Cancer Research, 2015, 21, 4473-4481.	3.2	108

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19	Increased miR-708 Expression in NSCLC and Its Association with Poor Survival in Lung Adenocarcinoma from Never Smokers. Clinical Cancer Research, 2012, 18, 3658-3667.	3.2	105
20	Folate Receptor-α (FOLR1) Expression and Function in Triple Negative Tumors. PLoS ONE, 2015, 10, e0122209.	1.1	103
21	Base resolution methylome profiling: considerations in platform selection, data preprocessing and analysis. Epigenomics, 2015, 7, 813-828.	1.0	97
22	Molecular profiling reveals immunogenic cues in anaplastic large cell lymphomas with DUSP22 rearrangements. Blood, 2018, 132, 1386-1398.	0.6	97
23	A novel bioinformatics pipeline for identification and characterization of fusion transcripts in breast cancer and normal cell lines. Nucleic Acids Research, 2011, 39, e100-e100.	6.5	94
24	Non-Overlapping and Non–Cell-Type–Specific Gene Expression Signatures Predict Lung Cancer Survival. Journal of Clinical Oncology, 2008, 26, 877-883.	0.8	92
25	Genetic Variation Predicting Cisplatin Cytotoxicity Associated with Overall Survival in Lung Cancer Patients Receiving Platinum-Based Chemotherapy. Clinical Cancer Research, 2011, 17, 5801-5811.	3.2	87
26	Genetic predisposition to lung cancer: comprehensive literature integration, meta-analysis, and multiple evidence assessment of candidate-gene association studies. Scientific Reports, 2017, 7, 8371.	1.6	87
27	MACE: model based analysis of ChIP-exo. Nucleic Acids Research, 2014, 42, e156-e156.	6.5	84
28	MicroRNA expression in ACTH-producing pituitary tumors: up-regulation of microRNA-122 and -493 in pituitary carcinomas. Endocrine, 2010, 38, 67-75.	1.1	83
29	Fine Mapping of Chromosome 6q23-25 Region in Familial Lung Cancer Families Reveals *RGS17* as a Likely Candidate Gene. Clinical Cancer Research, 2009, 15, 2666-2674.	3.2	80
30	Prognostic factors for limited-stage small cell lung cancer: A study of 284 patients. Lung Cancer, 2010, 67, 221-226.	0.9	80
31	α1 -Antitrypsin and Neutrophil Elastase Imbalance and Lung Cancer Risk. Chest, 2005, 128, 445-452.	0.4	77
32	The Role of Desmoglein-3 in the Diagnosis of Squamous Cell Carcinoma of the Lung. American Journal of Pathology, 2009, 174, 1629-1637.	1.9	76
33	Pharmacologic reversion of epigenetic silencing of the PRKD1promoter blocks breast tumor cell invasion and metastasis. Breast Cancer Research, 2013, 15, R66.	2.2	74
34	Contraction of T cell richness in lung cancer brain metastases. Scientific Reports, 2018, 8, 2171.	1.6	74
35	DNA methylation profiling: comparison of genome-wide sequencing methods and the Infinium Human Methylation 450 Bead Chip. Epigenomics, 2015, 7, 1287-1302.	1.0	66
36	Use of FFPE-derived DNA in next generation sequencing: DNA extraction methods. PLoS ONE, 2019, 14, e0211400.	1.1	62

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37	TREAT: a bioinformatics tool for variant annotations and visualizations in targeted and exome sequencing data. Bioinformatics, 2012, 28, 277-278.	1.8	59
38	Long noncoding and circular RNAs in lung cancer: advances and perspectives. Epigenomics, 2016, 8, 1275-1287.	1.0	59
39	The Role of the Histone Methyltransferase Enhancer of Zeste Homolog 2 (EZH2) in the Pathobiological Mechanisms Underlying Inflammatory Bowel Disease (IBD). Journal of Biological Chemistry, 2017, 292, 706-722.	1.6	59
40	Estrogen receptor-beta sensitizes breast cancer cells to the anti-estrogenic actions of endoxifen. Breast Cancer Research, 2011, 13, R27.	2.2	58
41	The Cistrome and Gene Signature of Androgen Receptor Splice Variants in Castration Resistant Prostate Cancer Cells. Journal of Urology, 2015, 193, 690-698.	0.2	57
42	Sulfatase 1 and sulfatase 2 in hepatocellular carcinoma: Associated signaling pathways, tumor phenotypes, and survival. Genes Chromosomes and Cancer, 2011, 50, 122-135.	1.5	55
43	Concordance of Changes in Metabolic Pathways Based on Plasma Metabolomics and Skeletal Muscle Transcriptomics in Type 1 Diabetes. Diabetes, 2012, 61, 1004-1016.	0.3	55
44	Aberrant signature methylome by DNMT1 hot spot mutation in hereditary sensory and autonomic neuropathy 1E. Epigenetics, 2014, 9, 1184-1193.	1.3	55
45	HiChIP: a high-throughput pipeline for integrative analysis of ChIP-Seq data. BMC Bioinformatics, 2014, 15, 280.	1.2	55
46	A genetic cell context-dependent role for ZEB1 in lung cancer. Nature Communications, 2016, 7, 12231.	5.8	54
47	Pathways Impacted by Genomic Alterations in Pulmonary Carcinoid Tumors. Clinical Cancer Research, 2018, 24, 1691-1704.	3.2	53
48	Changes in cardiac gene expression after pigâ€toâ€primate orthotopic xenotransplantation. Xenotransplantation, 2011, 18, 14-27.	1.6	50
49	SAAP-RRBS: streamlined analysis and annotation pipeline for reduced representation bisulfite sequencing. Bioinformatics, 2012, 28, 2180-2181.	1.8	49
50	Conserved recurrent gene mutations correlate with pathway deregulation and clinical outcomes of lung adenocarcinoma in never-smokers. BMC Medical Genomics, 2014, 7, 32.	0.7	49
51	Gene expression, methylation and neuropathology correlations at progressive supranuclear palsy risk loci. Acta Neuropathologica, 2016, 132, 197-211.	3.9	49
52	Marked Up-Regulation of ACE2 in Hearts of Patients With Obstructive Hypertrophic Cardiomyopathy: Implications for SARS-CoV-2â€"Mediated COVID-19. Mayo Clinic Proceedings, 2020, 95, 1354-1368.	1.4	49
53	Gene Expression, Single Nucleotide Variant and Fusion Transcript Discovery in Archival Material from Breast Tumors. PLoS ONE, 2013, 8, e81925.	1.1	49
54	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. Frontiers in Oncology, 2012, 2, 12.	1.3	46

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55	Spectrum of EGFR aberrations and potential clinical implications: insights from integrative panâ€cancer analysis. Cancer Communications, 2020, 40, 43-59.	3.7	45
56	Indel detection from RNA-seq data: tool evaluation and strategies for accurate detection of actionable mutations. Briefings in Bioinformatics, 2017, 18, bbw069.	3.2	44
57	Common Oncogene Mutations and Novel SND1-BRAF Transcript Fusion in Lung Adenocarcinoma from Never Smokers. Scientific Reports, 2015, 5, 9755.	1.6	43
58	Glutathione Pathway Genetic Polymorphisms and Lung Cancer Survival After Platinum-Based Chemotherapy. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 811-821.	1.1	42
59	Cystic fibrosis transmembrane conductance regulator gene mutation and lung cancer risk. Lung Cancer, 2010, 70, 14-21.	0.9	42
60	Multiple-level validation identifies <i>PARK2</i> in the development of lung cancer and chronic obstructive pulmonary disease. Oncotarget, 2016, 7, 44211-44223.	0.8	42
61	Gene Expression Profiling on Lung Cancer Outcome Prediction: Present Clinical Value and Future Premise. Cancer Epidemiology Biomarkers and Prevention, 2006, 15, 2063-2068.	1.1	41
62	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. BMC Cancer, 2012, 12, 422.	1.1	40
63	Identification of a Clinically Relevant Androgen-Dependent Gene Signature in Prostate Cancer. Cancer Research, 2011, 71, 1978-1988.	0.4	38
64	Endoxifenâ€™s Molecular Mechanisms of Action Are Concentration Dependent and Different than That of Other Anti-Estrogens. PLoS ONE, 2013, 8, e54613.	1.1	38
65	Genes Associated with Recurrence of Hepatocellular Carcinoma: Integrated Analysis by Gene Expression and Methylation Profiling. Journal of Korean Medical Science, 2011, 26, 1428.	1.1	37
66	Custom Gene Capture and Next-Generation Sequencing to Resolve Discordant ALK Status by FISHÂand IHC in Lung Adenocarcinoma. Journal of Thoracic Oncology, 2016, 11, 1891-1900.	0.5	37
67	Network-based approach identified cell cycle genes as predictor of overall survival in lung adenocarcinoma patients. Lung Cancer, 2013, 80, 91-98.	0.9	36
68	Predict drug sensitivity of cancer cells with pathway activity inference. BMC Medical Genomics, 2019, 12, 15.	0.7	36
69	Gemcitabine metabolic pathway genetic polymorphisms and response in patients with non-small cell lung cancer. Pharmacogenetics and Genomics, 2012, 22, 105-116.	0.7	33
70	Discovery, Validation, and Application of Novel Methylated DNA Markers for Detection of Esophageal Cancer in Plasma. Clinical Cancer Research, 2019, 25, 7396-7404.	3.2	33
71	Can gene expression profiling predict survival for patients with squamous cell carcinoma of the lung?. Molecular Cancer, 2004, 3, 35.	7.9	31
72	Cell Proliferation and Epidermal Growth Factor Signaling in Non-small Cell Lung Adenocarcinoma Cell Lines Are Dependent on Rin1. Journal of Biological Chemistry, 2009, 284, 26331-26339.	1.6	31

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73	Genome-wide methylation profiling demonstrates hypermethylation in maternal leukocyte DNA in preeclamptic compared to normotensive pregnancies. Hypertension in Pregnancy, 2013, 32, 257-269.	0.5	31
74	Impact of sample acquisition and linear amplification on gene expression profiling of lung adenocarcinoma: laser capture micro-dissection cell-sampling versus bulk tissue-sampling. BMC Medical Genomics, 2009, 2, 13.	0.7	29
75	UClncR: Ultrafast and comprehensive long non-coding RNA detection from RNA-seq. Scientific Reports, 2017, 7, 14196.	1.6	29
76	CpGFilter: model-based CpG probe filtering with replicates for epigenome-wide association studies. Bioinformatics, 2016, 32, 469-471.	1.8	27
77	Genetic Variants Associated with the Risk of Chronic Obstructive Pulmonary Disease with and without Lung Cancer. Cancer Prevention Research, 2012, 5, 365-373.	0.7	26
78	Genetic Variations in Multiple Drug Action Pathways and Survival in Advanced Stage Non€"Small Cell Lung Cancer Treated with Chemotherapy. Clinical Cancer Research, 2011, 17, 3830-3840.	3.2	25
79	A novel ferroptosis phenotype€related clinical€molecular prognostic signature for hepatocellular carcinoma. Journal of Cellular and Molecular Medicine, 2021, 25, 6618-6633.	1.6	24
80	Epigenetic silencing of WNT5A in Epstein-Barr virus-associated gastric carcinoma. Archives of Virology, 2013, 158, 123-132.	0.9	23
81	Genome-Wide Epigenetic Studies in Human Disease: A Primer on -Omic Technologies. American Journal of Epidemiology, 2016, 183, kwv187.	1.6	23
82	Nomogram prediction of overall survival for patients with non-small-cell lung cancer incorporating pretreatment peripheral blood markers€. European Journal of Cardio-thoracic Surgery, 2018, 53, 1214-1222.	0.6	23
83	Normal early pregnancy. Epigenetics, 2012, 7, 729-734.	1.3	22
84	Preeclampsia/Eclampsia candidate genes show altered methylation in maternal leukocytes of preeclamptic women at the time of delivery. Hypertension in Pregnancy, 2016, 35, 394-404.	0.5	22
85	ChIP-seq in studying epigenetic mechanisms of disease and promoting precision medicine: progresses and future directions. Epigenomics, 2016, 8, 1239-1258.	1.0	22
86	Statistical method evaluation for differentially methylated CpGs in base resolution next-generation DNA sequencing data. Briefings in Bioinformatics, 2016, 19, bbw133.	3.2	21
87	Evaluation of Glutathione Metabolic Genes on Outcomes in Advanced Non-small Cell Lung Cancer Patients after Initial Treatment with Platinum-Based Chemotherapy: An NCCTG-97-24-51 Based Study. Journal of Thoracic Oncology, 2009, 4, 479-485.	0.5	20
88	Impact of Library Preparation on Downstream Analysis and Interpretation of RNA-Seq Data: Comparison between Illumina PolyA and NuGEN Ovation Protocol. PLoS ONE, 2013, 8, e71745.	1.1	19
89	Systematic Evaluation of Genetic Variants in Three Biological Pathways on Patient Survival in Low-Stage Non-small Cell Lung Cancer. Journal of Thoracic Oncology, 2011, 6, 1488-1495.	0.5	18
90	An Integrated Model of the Transcriptome of HER2-Positive Breast Cancer. PLoS ONE, 2013, 8, e79298.	1.1	18

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91	Deregulation of Long Intergenic Non-coding RNAs in CD4+ T Cells of Lamina Propria in Crohn's Disease Through Transcriptome Profiling. Journal of Crohn's and Colitis, 2020, 14, 96-109.	0.6	18
92	Effects of the 5 alpha-reductase inhibitor dutasteride on gene expression in prostate cancer xenografts. Prostate, 2009, 69, 1730-1743.	1.2	17
93	Increased BCAR1 Predicts Poor Outcomes of Non-small Cell Lung Cancer in Multiple-Center Patients. Annals of Surgical Oncology, 2013, 20, 701-708.	0.7	15
94	Clinical biomarkers of pulmonary carcinoid tumors in never smokers via profiling miRNA and target mRNA. Cell and Bioscience, 2014, 4, 35.	2.1	15
95	Sequence analysis of the Epstein-Barr virus (EBV) BRLF1 gene in nasopharyngeal and gastric carcinomas. Virology Journal, 2010, 7, 341.	1.4	14
96	DNA methylation and RNA expression profiles in lung adenocarcinomas of never-smokers. Cancer Genetics, 2015, 208, 253-260.	0.2	14
97	Apatinib Reverses Paclitaxel-resistant Lung Cancer Cells (A549) Through Blocking the Function of ABCB1 Transporter. Anticancer Research, 2019, 39, 5461-5471.	0.5	14
98	Chromosome X genomic and epigenomic aberrations and clinical implications in breast cancer by base resolution profiling. Epigenomics, 2015, 7, 1099-1110.	1.0	12
99	Germline Copy Number Variation and Ovarian Cancer Survival. Frontiers in Genetics, 2012, 3, 142.	1.1	11
100	Sequence analysis of Epstein-Barr virus EBNA-2 gene coding amino acid 148-487 in nasopharyngeal and gastric carcinomas. Virology Journal, 2012, 9, 49.	1.4	11
101	Inactivation ofLLC1 gene in nonsmall cell lung cancer. International Journal of Cancer, 2007, 120, 2353-2358.	2.3	10
102	Transcriptome Profiling of Acquired Gefitinib Resistant Lung Cancer Cells Reveals Dramatically Changed Transcription Programs and New Treatment Targets. Frontiers in Oncology, 2020, 10, 1424.	1.3	10
103	RNF20 and RNF40 regulate vitamin D receptor-dependent signaling in inflammatory bowel disease. Cell Death and Differentiation, 2021, 28, 3161-3175.	5.0	10
104	BMI1 maintains the Treg epigenomic landscape to prevent inflammatory bowel disease. Journal of Clinical Investigation, 2021, 131, .	3.9	10
105	DNA methylation patterns in human iPSC-derived sensory neuronal differentiation. Epigenetics, 2019, 14, 927-937.	1.3	9
106	Estrogen receptor beta repurposes EZH2 to suppress oncogenic NFκB/p65 signaling in triple negative breast cancer. Npj Breast Cancer, 2022, 8, 20.	2.3	9
107	Characterization of Epstein-Barr virus gp350/220 gene variants in virus isolates from gastric carcinoma and nasopharyngeal carcinoma. Archives of Virology, 2012, 157, 207-216.	0.9	8
108	Adipose tissue DNA methylome changes in development of new-onset diabetes after kidney transplantation. Epigenomics, 2017, 9, 1423-1435.	1.0	8

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109	Comprehensive Profiling of lincRNAs in Lung Adenocarcinoma of Never Smokers Reveals Their Roles in Cancer Development and Prognosis. Genes, 2017, 8, 321.	1.0	8
110	Comprehensive Genomic Profiling of a Rare Thyroid Follicular Dendritic Cell Sarcoma. Rare Tumors, 2017, 9, 50-53.	0.3	8
111	Sequence Variation Analysis of Epstein-Barr Virus Nuclear Antigen 1 Gene in the Virus Associated Lymphomas of Northern China. PLoS ONE, 2015, 10, e0140529.	1.1	8
112	Sequence analysis of EBV immune evasion gene BNLF2a in EBV associated tumors and healthy individuals from nasopharyngeal carcinoma endemic and non‐endemic regions of China. Journal of Medical Virology, 2015, 87, 1946-1952.	2.5	7
113	High-throughput long noncoding RNA profiling for diagnostic and prognostic markers in cancer: opportunities and challenges. Epigenomics, 2015, 7, 1075-1078.	1.0	7
114	Association between ALS and retroviruses: evidence from bioinformatics analysis. BMC Bioinformatics, 2019, 20, 680.	1.2	7
115	Refining Prognosis in Non–Small-Cell Lung Cancer. New England Journal of Medicine, 2007, 356, 189-191.	13.9	6
116	Sequence analysis of EBV immediate-early gene BZLF1 and BRLF1 in lymphomas. Journal of Medical Virology, 2014, 86, 1788-1795.	2.5	5
117	Sequence variation of Epstein-Barr virus (EBV) BCRF1 in lymphomas in non-endemic areas of nasopharyngeal carcinoma. Archives of Virology, 2015, 160, 441-445.	0.9	5
118	X chromosome abnormal inactivation: a unique factor for women's diseases?. Epigenomics, 2016, 8, 447-450.	1.0	5
119	Indel sensitive and comprehensive variant/mutation detection from RNA sequencing data for precision medicine. BMC Medical Genomics, 2018, 11, 67.	0.7	5
120	Protein expression shift and potential diagnostic markers through proteomics profiling of tuberculous pleurisy biopsy tissues. International Journal of Infectious Diseases, 2020, 99, 245-252.	1.5	5
121	769 Novel Methylated DNA Markers Predict Site of Gastrointestinal Cancer. Gastroenterology, 2013, 144, S-84.	0.6	4
122	Androgen Mediation—and Antiandrogens Mitigation—of the Epidermal Growth Factor Receptor (EGFR) Inhibitor–Induced Rash: Results From a Pilot Randomized Trial and Small Translational Case Series. American Journal of Hospice and Palliative Medicine, 2019, 36, 519-525.	0.8	4
123	MCAM abnormal expression and clinical outcome associations are highly cancer dependent as revealed through pan-cancer analysis. Briefings in Bioinformatics, 2020, 21, 709-718.	3.2	4
124	Novel lincRNA Discovery and Tissue-Specific Gene Expression across 30 Normal Human Tissues. Genes, 2021, 12, 614.	1.0	4
125	Gene-expression profiling in lung cancer: still early days. Pharmacogenomics, 2007, 8, 129-132.	0.6	3
126	Model based user interface design for predicting lung cancer treatment outcomes. , 2011, 2011, 75-8.		3

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127	Targeted alignment and end repair elimination increase alignment and methylation measure accuracy for reduced representation bisulfite sequencing data. BMC Genomics, 2016, 17, 149.	1.2	3
128	Evaluation of circulating cell-free DNA in cholestatic liver disease using liver-specific methylation markers. BMC Gastroenterology, 2021, 21, 149.	0.8	3
129	Genome-wide methylation profiling reveals differentially methylated genes in blood DNA of small-cell lung cancer patients. Precision Clinical Medicine, 0, , .	1.3	3
130	Gene variations of Epstein-Barr virus nuclear antigen 3A in nasopharyngeal carcinomas, gastric carcinomas and healthy carriers in northern China. Archives of Virology, 2013, 158, 2041-2048.	0.9	2
131	DNA methylation profile of liver tissue in end-stage cholestatic liver disease. Epigenomics, 2022, 14, 481-497.	1.0	2
132	Epstein-Barr Virus EBNA-2 Polymorphic Patterns in Nasopharyngeal Carcinoma in Southern China. Intervirology, 2015, 58, 386-392.	1.2	1
133	Neutrophil Elastase. , 2011, , 2509-2512.		0
134	Neutrophil Elastase. , 2014, , 1-5.		0
135	Neutrophil Elastase. , 2017, , 3088-3091.		0