

Gangning Liang

List of Publications by Year in descending order

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Version: 2024-02-01

124
papers

18,245
citations

22153

59
h-index

22166

113
g-index

125
all docs

125
docs citations

125
times ranked

23356
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenetics in human disease and prospects for epigenetic therapy. <i>Nature</i> , 2004, 429, 457-463.	27.8	2,833
2	Specific activation of microRNA-127 with downregulation of the proto-oncogene BCL6 by chromatin-modifying drugs in human cancer cells. <i>Cancer Cell</i> , 2006, 9, 435-443.	16.8	1,253
3	DNA-Demethylating Agents Target Colorectal Cancer Cells by Inducing Viral Mimicry by Endogenous Transcripts. <i>Cell</i> , 2015, 162, 961-973.	28.9	1,075
4	Gene Body Methylation Can Alter Gene Expression and Is a Therapeutic Target in Cancer. <i>Cancer Cell</i> , 2014, 26, 577-590.	16.8	959
5	The human DNA methyltransferases (DNMTs) 1, 3a and 3b: coordinate mRNA expression in normal tissues and overexpression in tumors. <i>Nucleic Acids Research</i> , 1999, 27, 2291-2298.	14.5	765
6	Rethinking how DNA methylation patterns are maintained. <i>Nature Reviews Genetics</i> , 2009, 10, 805-811.	16.3	693
7	DZNep is a global histone methylation inhibitor that reactivates developmental genes not silenced by DNA methylation. <i>Molecular Cancer Therapeutics</i> , 2009, 8, 1579-1588.	4.1	518
8	Cooperativity between DNA Methyltransferases in the Maintenance Methylation of Repetitive Elements. <i>Molecular and Cellular Biology</i> , 2002, 22, 480-491.	2.3	508
9	Distinct localization of histone H3 acetylation and H3-K4 methylation to the transcription start sites in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7357-7362.	7.1	435
10	The Putative Tumor Suppressor microRNA-101 Modulates the Cancer Epigenome by Repressing the Polycomb Group Protein EZH2. <i>Cancer Research</i> , 2009, 69, 2623-2629.	0.9	381
11	Genome-wide mapping of nucleosome positioning and DNA methylation within individual DNA molecules. <i>Genome Research</i> , 2012, 22, 2497-2506.	5.5	381
12	Frequent switching of Polycomb repressive marks and DNA hypermethylation in the PC3 prostate cancer cell line. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 12979-12984.	7.1	325
13	Histone H3-lysine 9 methylation is associated with aberrant gene silencing in cancer cells and is rapidly reversed by 5-aza-2'-deoxycytidine. <i>Cancer Research</i> , 2002, 62, 6456-61.	0.9	310
14	Preferential response of cancer cells to zebularine. <i>Cancer Cell</i> , 2004, 6, 151-158.	16.8	282
15	Hypomethylation of a LINE-1 Promoter Activates an Alternate Transcript of the MET Oncogene in Bladders with Cancer. <i>PLoS Genetics</i> , 2010, 6, e1000917.	3.5	252
16	DNA Methylation Screening Identifies Driver Epigenetic Events of Cancer Cell Survival. <i>Cancer Cell</i> , 2012, 21, 655-667.	16.8	240
17	Epigenetic therapy upregulates the tumor suppressor microRNA-126 and its host gene EGFL7 in human cancer cells. <i>Biochemical and Biophysical Research Communications</i> , 2009, 379, 726-731.	2.1	214
18	Continuous Zebularine Treatment Effectively Sustains Demethylation in Human Bladder Cancer Cells. <i>Molecular and Cellular Biology</i> , 2004, 24, 1270-1278.	2.3	205

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19	Delivery of 5-Aza-2â€²-Deoxycytidine to Cells Using Oligodeoxynucleotides. <i>Cancer Research</i> , 2007, 67, 6400-6408.	0.9	204
20	Comparison of biological effects of non-nucleoside DNA methylation inhibitors versus 5-aza-2â€²-deoxycytidine. <i>Molecular Cancer Therapeutics</i> , 2005, 4, 1515-1520.	4.1	203
21	Detection of Methylated Apoptosis-Associated Genes in Urine Sediments of Bladder Cancer Patients. <i>Clinical Cancer Research</i> , 2004, 10, 7457-7465.	7.0	202
22	Role of Nucleosomal Occupancy in the Epigenetic Silencing of the MLH1 CpG Island. <i>Cancer Cell</i> , 2007, 12, 432-444.	16.8	189
23	Identification of DNMT1 (DNA methyltransferase 1) hypomorphs in somatic knockouts suggests an essential role for DNMT1 in cell survival. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 14080-14085.	7.1	186
24	Selective Anchoring of DNA Methyltransferases 3A and 3B to Nucleosomes Containing Methylated DNA. <i>Molecular and Cellular Biology</i> , 2009, 29, 5366-5376.	2.3	179
25	DNA methylation directly silences genes with non-CpG island promoters and establishes a nucleosome occupied promoter. <i>Human Molecular Genetics</i> , 2011, 20, 4299-4310.	2.9	172
26	Vitamin C increases viral mimicry induced by 5-aza-2â€²-deoxycytidine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10238-10244.	7.1	171
27	Hypomethylation and hypermethylation of DNA in Wilms tumors. <i>Oncogene</i> , 2002, 21, 6694-6702.	5.9	165
28	Polycomb-Repressed Genes Have Permissive Enhancers that Initiate Reprogramming. <i>Cell</i> , 2011, 147, 1283-1294.	28.9	161
29	Analysis of gene induction in human fibroblasts and bladder cancer cells exposed to the methylation inhibitor 5-aza-2'-deoxycytidine. <i>Cancer Research</i> , 2002, 62, 961-6.	0.9	158
30	Role of the DNA Methyltransferase Variant DNMT3b3 in DNA Methylation. <i>Molecular Cancer Research</i> , 2004, 2, 62-72.	3.4	151
31	Unique DNA Methylation Patterns Distinguish Noninvasive and Invasive Urothelial Cancers and Establish an Epigenetic Field Defect in Premalignant Tissue. <i>Cancer Research</i> , 2010, 70, 8169-8178.	0.9	148
32	H2A.Z Maintenance during Mitosis Reveals Nucleosome Shifting on Mitotically Silenced Genes. <i>Molecular Cell</i> , 2010, 39, 901-911.	9.7	136
33	Susceptibility of Nonpromoter CpG Islands to De Novo Methylation in Normal and Neoplastic Cells. <i>Journal of the National Cancer Institute</i> , 2001, 93, 1465-1472.	6.3	134
34	Changes in DNA methylation of tandem DNA repeats are different from interspersed repeats in cancer. <i>International Journal of Cancer</i> , 2009, 125, 723-729.	5.1	134
35	The Roles of Human DNA Methyltransferases and Their Isoforms in Shaping the Epigenome. <i>Genes</i> , 2019, 10, 172.	2.4	134
36	DNA methylation analysis by digital bisulfite genomic sequencing and digital MethyLight. <i>Nucleic Acids Research</i> , 2008, 36, 4689-4698.	14.5	133

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37	Examination of <i>IGF2</i> and <i>H19</i> Loss of Imprinting in Bladder Cancer. <i>Cancer Research</i> , 2007, 67, 10753-10758.	0.9	127
38	OCT4 establishes and maintains nucleosome-depleted regions that provide additional layers of epigenetic regulation of its target genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 14497-14502.	7.1	117
39	Mechanisms of Disease: genetic and epigenetic alterations that drive bladder cancer. <i>Nature Reviews Urology</i> , 2005, 2, 502-510.	1.4	110
40	Prognostic relevance of methylation markers in patients with non-muscle invasive bladder carcinoma. <i>European Journal of Cancer</i> , 2005, 41, 2769-2778.	2.8	109
41	DNMT3B isoforms without catalytic activity stimulate gene body methylation as accessory proteins in somatic cells. <i>Nature Communications</i> , 2016, 7, 11453.	12.8	109
42	DNA methylation enables transposable element-driven genome expansion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 19359-19366.	7.1	109
43	miR-30d, miR-181a and miR-199a-5p cooperatively suppress the endoplasmic reticulum chaperone and signaling regulator GRP78 in cancer. <i>Oncogene</i> , 2013, 32, 4694-4701.	5.9	108
44	Bivalent Regions of Cytosine Methylation and H3K27 Acetylation Suggest an Active Role for DNA Methylation at Enhancers. <i>Molecular Cell</i> , 2016, 62, 422-431.	9.7	106
45	Nucleosomes Containing Methylated DNA Stabilize DNA Methyltransferases 3A/3B and Ensure Faithful Epigenetic Inheritance. <i>PLoS Genetics</i> , 2011, 7, e1001286.	3.5	103
46	DNA Methylation Differences Associated with Tumor Tissues Identified by Genome Scanning Analysis. <i>Genomics</i> , 1998, 53, 260-268.	2.9	100
47	DNA methylation aberrancies as a guide for surveillance and treatment of human cancers. <i>Epigenetics</i> , 2017, 12, 416-432.	2.7	98
48	Allelic methylation levels of the noncoding VTRNA2-1 located on chromosome 5q31.1 predict outcome in AML. <i>Blood</i> , 2012, 119, 206-216.	1.4	97
49	The endothelin receptor B (EDNRB) promoter displays heterogeneous, site specific methylation patterns in normal and tumor cells. <i>Human Molecular Genetics</i> , 2001, 10, 903-910.	2.9	87
50	Dual Inhibition of DNA and Histone Methyltransferases Increases Viral Mimicry in Ovarian Cancer Cells. <i>Cancer Research</i> , 2018, 78, 5754-5766.	0.9	83
51	Switching roles for DNA and histone methylation depend on evolutionary ages of human endogenous retroviruses. <i>Genome Research</i> , 2018, 28, 1147-1157.	5.5	82
52	Functional DNA demethylation is accompanied by chromatin accessibility. <i>Nucleic Acids Research</i> , 2013, 41, 3973-3985.	14.5	77
53	A Panel of Three Markers Hyper- and Hypomethylated in Urine Sediments Accurately Predicts Bladder Cancer Recurrence. <i>Clinical Cancer Research</i> , 2014, 20, 1978-1989.	7.0	77
54	The Role of DNA Methylation in Cancer. <i>Advances in Experimental Medicine and Biology</i> , 2016, 945, 151-172.	1.6	76

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55	Role of the DNA methyltransferase variant DNMT3b3 in DNA methylation. <i>Molecular Cancer Research</i> , 2004, 2, 62-72.	3.4	74
56	Epigenetic Alterations and MicroRNA Misexpression in Cancer and Autoimmune Diseases: a Critical Review. <i>Clinical Reviews in Allergy and Immunology</i> , 2014, 47, 128-135.	6.5	71
57	PAX6 methylation and ectopic expression in human tumor cells. <i>International Journal of Cancer</i> , 2000, 87, 179-185.	5.1	69
58	Methylation-sensitive single-nucleotide primer extension (Ms-SNuPE) for quantitative measurement of DNA methylation. <i>Nature Protocols</i> , 2007, 2, 1931-1936.	12.0	69
59	Identification of DNA methylation differences during tumorigenesis by methylation-sensitive arbitrarily primed polymerase chain reaction. <i>Methods</i> , 2002, 27, 150-155.	3.8	62
60	Locus-Wide Chromatin Remodeling and Enhanced Androgen Receptor-Mediated Transcription in Recurrent Prostate Tumor Cells. <i>Molecular and Cellular Biology</i> , 2006, 26, 7331-7341.	2.3	62
61	Dual inhibition of DNMTs and EZH2 can overcome both intrinsic and acquired resistance of myeloma cells to IMiDs in a cereblon-independent manner. <i>Molecular Oncology</i> , 2018, 12, 180-195.	4.6	62
62	Structure of nucleosome-bound DNA methyltransferases DNMT3A and DNMT3B. <i>Nature</i> , 2020, 586, 151-155.	27.8	61
63	Equitoxic Doses of 5-Azacytidine and 5-Aza-2-Deoxycytidine Induce Diverse Immediate and Overlapping Heritable Changes in the Transcriptome. <i>PLoS ONE</i> , 2010, 5, e12994.	2.5	57
64	RUNX3 Methylation Reveals that Bladder Tumors Are Older in Patients with a History of Smoking. <i>Cancer Research</i> , 2008, 68, 6208-6214.	0.9	55
65	Gene Reactivation by 5-Aza-2-Deoxycytidine-Induced Demethylation Requires SRCAP-Mediated H2A.Z Insertion to Establish Nucleosome Depleted Regions. <i>PLoS Genetics</i> , 2012, 8, e1002604.	3.5	52
66	Identification and characterization of alternatively spliced variants of DNA methyltransferase 3a in mammalian cells. <i>Gene</i> , 2002, 298, 91-99.	2.2	51
67	Genetic and Epigenetic Alterations in Bladder Cancer. <i>International Neurourology Journal</i> , 2016, 20, S84-94.	1.2	49
68	Integrative Epigenetic Analysis Reveals Therapeutic Targets to the DNA Methyltransferase Inhibitor Guadecitabine (SGI-110) in Hepatocellular Carcinoma. <i>Hepatology</i> , 2018, 68, 1412-1428.	7.3	48
69	Linker histone H1.2 establishes chromatin compaction and gene silencing through recognition of H3K27me3. <i>Scientific Reports</i> , 2015, 5, 16714.	3.3	44
70	A phase 1 study of azacitidine combined with chemotherapy in childhood leukemia: a report from the TACL consortium. <i>Blood</i> , 2018, 131, 1145-1148.	1.4	44
71	SNF5 Is an Essential Executor of Epigenetic Regulation during Differentiation. <i>PLoS Genetics</i> , 2013, 9, e1003459.	3.5	43
72	Identifying aggressive prostate cancer foci using a DNA methylation classifier. <i>Genome Biology</i> , 2017, 18, 3.	8.8	43

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73	Down-regulation of ARID1A is sufficient to initiate neoplastic transformation along with epigenetic reprogramming in non-tumorigenic endometriotic cells. <i>Cancer Letters</i> , 2017, 401, 11-19.	7.2	42
74	Rewiring of cisplatin-resistant bladder cancer cells through epigenetic regulation of genes involved in amino acid metabolism. <i>Theranostics</i> , 2018, 8, 4520-4534.	10.0	40
75	Epigenetic reprogramming as a key contributor to melanocyte malignant transformation. <i>Epigenetics</i> , 2011, 6, 450-464.	2.7	39
76	Diagnostic markers of urothelial cancer based on DNA methylation analysis. <i>BMC Cancer</i> , 2013, 13, 275.	2.6	39
77	The tumor suppressor microRNA-101 becomes an epigenetic player by targeting the Polycomb group protein EZH2 in cancer. <i>Cell Cycle</i> , 2009, 8, 2313-2314.	2.6	35
78	Heterogeneous patterns of DNA methylation-based field effects in histologically normal prostate tissue from cancer patients. <i>Scientific Reports</i> , 2017, 7, 40636.	3.3	35
79	Synergistic Re-Activation of Epigenetically Silenced Genes by Combinatorial Inhibition of DNMTs and LSD1 in Cancer Cells. <i>PLoS ONE</i> , 2013, 8, e75136.	2.5	33
80	CT prediction of the Fuhrman grade of clear cell renal cell carcinoma (RCC): towards the development of computer-assisted diagnostic method. <i>Abdominal Imaging</i> , 2015, 40, 3168-3174.	2.0	33
81	Mother-child transmission of epigenetic information by tunable polymorphic imprinting. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11970-E11977.	7.1	33
82	Activation of a Subset of Evolutionarily Young Transposable Elements and Innate Immunity Are Linked to Clinical Responses to 5-Azacytidine. <i>Cancer Research</i> , 2020, 80, 2441-2450.	0.9	33
83	Reaction of N-(2-Chloroethyl)-N-nitrosoureas with DNA: Effect of Buffers on DNA Adduction, Cross-Linking, and Cytotoxicity. <i>Chemical Research in Toxicology</i> , 1996, 9, 208-214.	3.3	32
84	Role of Electrostatics in the Sequence-Selective Reaction of Charged Alkylating Agents with DNA. <i>Journal of the American Chemical Society</i> , 1995, 117, 10135-10136.	13.7	31
85	Nucleosome Positioning and NDR Structure at RNA Polymerase III Promoters. <i>Scientific Reports</i> , 2017, 7, 41947.	3.3	29
86	Identification of DNA Methylation-independent Epigenetic Events Underlying Clear Cell Renal Cell Carcinoma. <i>Cancer Research</i> , 2016, 76, 1954-1964.	0.9	28
87	Tissue Inhibitor of Metalloproteinase 1 Expression Associated with Gene Demethylation Confers Anoikis Resistance in Early Phases of Melanocyte Malignant Transformation. <i>Translational Oncology</i> , 2009, 2, 329-340.	3.7	26
88	Data integration by multi-tuning parameter elastic net regression. <i>BMC Bioinformatics</i> , 2018, 19, 369.	2.6	26
89	Regioselective Effect of Zwitterionic DNA Substitutions on DNA Alkylation: Evidence for a Strong Side Chain Orientational Preference. <i>Biochemistry</i> , 1997, 36, 6024-6032.	2.5	25
90	Epigenetic Alterations in Bladder Cancer and Their Potential Clinical Implications. <i>Advances in Urology</i> , 2012, 2012, 1-11.	1.3	24

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91	Quantitative Contour Analysis as an Image-based Discriminator Between Benign and Malignant Renal Tumors. <i>Urology</i> , 2018, 114, 121-127.	1.0	23
92	Immunogenic cell death pathway polymorphisms for predicting oxaliplatin efficacy in metastatic colorectal cancer. , 2020, 8, e001714.		23
93	Novel endothelin B receptor transcripts with the potential of generating a new receptor. <i>Gene</i> , 1999, 228, 43-49.	2.2	20
94	Lysine methyltransferase G9a is not required for DNMT3A/3B anchoring to methylated nucleosomes and maintenance of DNA methylation in somatic cells. <i>Epigenetics and Chromatin</i> , 2012, 5, 3.	3.9	20
95	Hypermethylation of the VTRNA1-3 Promoter is Associated with Poor Outcome in Lower Risk Myelodysplastic Syndrome Patients. <i>Genes</i> , 2015, 6, 977-990.	2.4	19
96	DNA methylator and mismatch repair phenotypes are not mutually exclusive in colorectal cancer cell lines. <i>Oncogene</i> , 2000, 19, 943-952.	5.9	17
97	Improving needle biopsy accuracy in small renal mass using tumor-specific DNA methylation markers. <i>Oncotarget</i> , 2017, 8, 5439-5448.	1.8	17
98	Reprogramming of the human intestinal epigenome by surgical tissue transposition. <i>Genome Research</i> , 2014, 24, 545-553.	5.5	16
99	Isoform switching and exon skipping induced by the DNA methylation inhibitor 5-Aza-2â€²-deoxycytidine. <i>Scientific Reports</i> , 2016, 6, 24545.	3.3	15
100	Clinical evaluation of Bladder CARE, a new epigenetic test for bladder cancer detection in urine samples. <i>Clinical Epigenetics</i> , 2021, 13, 84.	4.1	15
101	Epigenetic landscape change analysis during human EMT sheds light on a key EMT mediator TRIM29. <i>Oncotarget</i> , 2017, 8, 98322-98335.	1.8	13
102	Characterizing DNA methylation signatures and their potential functional roles in Merkel cell carcinoma. <i>Genome Medicine</i> , 2021, 13, 130.	8.2	12
103	Telomerase Variants in Patients with Cirrhosis Awaiting Liver Transplantation. <i>Hepatology</i> , 2019, 69, 2652-2663.	7.3	10
104	Epigenetic plasticity potentiates a rapid cyclical shift to and from an aggressive cancer phenotype. <i>International Journal of Cancer</i> , 2020, 146, 3065-3076.	5.1	10
105	Creating a flexible multiple microRNA expression vector by linking precursor microRNAs. <i>Biochemical and Biophysical Research Communications</i> , 2011, 411, 276-280.	2.1	9
106	epiG: statistical inference and profiling of DNA methylation from whole-genome bisulfite sequencing data. <i>Genome Biology</i> , 2017, 18, 38.	8.8	6
107	Albumin levels predict prognosis in advanced renal cell carcinoma treated with tyrosine kinase inhibitors: a systematic review and meta-analysis. <i>Urologic Oncology: Seminars and Original Investigations</i> , 2022, 40, 12.e13-12.e22.	1.6	6
108	A Novel DNA Methylation Signature as an Independent Prognostic Factor in Muscle-Invasive Bladder Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 614927.	2.8	5

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109	FOXC1 Binds Enhancers and Promotes Cisplatin Resistance in Bladder Cancer. <i>Cancers</i> , 2022, 14, 1717.	3.7	5
110	Alterations in Deoxyribonucleic Acid (DNA) Methylation Patterns of Calca, Timp3, Mmp2, and Igf2r Are Associated With Chronic Cystitis in a Cyclophosphamide-induced Mouse Model. <i>Urology</i> , 2013, 82, 253.e9-253.e15.	1.0	4
111	Impact of polymorphisms within genes involved in regulating DNA methylation in patients with metastatic colorectal cancer enrolled in three independent, randomised, open-label clinical trials: a meta-analysis from TRIBE, MAVERICC and FIRE-3. <i>European Journal of Cancer</i> , 2019, 111, 138-147.	2.8	4
112	AMPK variant, a candidate of novel predictor for chemotherapy in metastatic colorectal cancer: A meta-analysis using TRIBE, MAVERICC and FIRE3. <i>International Journal of Cancer</i> , 2019, 145, 2082-2090.	5.1	4
113	The Human Epigenome. , 2012, , 5-20.		3
114	Epi Meets Genomics: Technologies for Finding and Reading the 5th Base. , 2005, , 39-64.		2
115	Epigenetics of Melanoma. , 2015, , 339-361.		1
116	PAX6 methylation and ectopic expression in human tumor cells. , 2000, 87, 179.		1
117	Outlining the limits of partial nephrectomy. <i>Translational Andrology and Urology</i> , 2015, 4, 294-300.	1.4	1
118	Genes regulated by DNA methylation are involved in distinct phenotypes during melanoma progression and are prognostic factors for patients. <i>Molecular Oncology</i> , 2022, 16, 1913-1930.	4.6	1
119	Unique Role for a DNA Methyltransferase Isoform in Lung Cancer. <i>EBioMedicine</i> , 2015, 2, 1272-1273.	6.1	0
120	Rethinking Demethylating Agents in Epigenetic Cancer Therapy. <i>Journal of Molecular Pharmaceutics & Organic Process Research</i> , 2016, 4, .	2.0	0
121	Epigenetic Silencing of a Novel Candidate Tumor Suppressor Predicts Poor Prognosis In High-Risk MDS and AML. <i>Blood</i> , 2010, 116, 3629-3629.	1.4	0
122	Allelic Methylation Levels of the Non-Coding RNA Gene VTRNA2-1 Located on Chromosome 5q31.1 Predict Outcome in AML. <i>Blood</i> , 2011, 118, 3450-3450.	1.4	0
123	Cereblon Is Downregulated By Promoter Nucleosome Occupancy in Acquired IMiD Resistance: The Potential of IMiD Resensitization By Epigenetic Therapy. <i>Blood</i> , 2016, 128, 3258-3258.	1.4	0
124	Abstract 3736: SETD2 aberrancy enhanced the synergetic anti-tumor effects of DNA hypomethylating agents and PARP inhibitors in aggressive clear cell renal cell carcinoma. <i>Cancer Research</i> , 2022, 82, 3736-3736.	0.9	0