

# Hideya Kawaji

## List of Publications by Citations

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140  
papers

14,979  
citations

47  
h-index

122  
g-index

154  
ext. papers

18,972  
ext. citations

11.7  
avg, IF

5.3  
L-index

#	Paper	IF	Citations
140	An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , <b>2014</b> , 507, 455-461	50.4	1595
139	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. <i>Nature</i> , <b>2002</b> , 420, 563-73	50.4	1350
138	A promoter-level mammalian expression atlas. <i>Nature</i> , <b>2014</b> , 507, 462-70	50.4	1301
137	Genome-wide analysis of mammalian promoter architecture and evolution. <i>Nature Genetics</i> , <b>2006</b> , 38, 626-35	36.3	1021
136	The Systems Biology Graphical Notation. <i>Nature Biotechnology</i> , <b>2009</b> , 27, 735-41	44.5	651
135	An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , <b>2017</b> , 543, 199-204	50.4	581
134	Functional annotation of a full-length mouse cDNA collection. <i>Nature</i> , <b>2001</b> , 409, 685-90	50.4	560
133	An atlas of combinatorial transcriptional regulation in mouse and man. <i>Cell</i> , <b>2010</b> , 140, 744-52	56.2	555
132	Cap analysis gene expression for high-throughput analysis of transcriptional starting point and identification of promoter usage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2003</b> , 100, 15776-81	11.5	554
131	The BioMart community portal: an innovative alternative to large, centralized data repositories. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, W589-98	20.1	468
130	Gateways to the FANTOM5 promoter level mammalian expression atlas. <i>Genome Biology</i> , <b>2015</b> , 16, 22	18.3	443
129	A draft network of ligand-receptor-mediated multicellular signalling in human. <i>Nature Communications</i> , <b>2015</b> , 6, 7866	17.4	393
128	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. <i>Science</i> , <b>2015</b> , 347, 1010-4	33.3	384
127	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , <b>2009</b> , 41, 553-62	36.3	356
126	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 872-878	44.5	282
125	ChIP-Atlas: a data-mining suite powered by full integration of public ChIP-seq data. <i>EMBO Reports</i> , <b>2018</b> , 19,	6.5	238
124	Hierarchical folding and reorganization of chromosomes are linked to transcriptional changes in cellular differentiation. <i>Molecular Systems Biology</i> , <b>2015</b> , 11, 852	12.2	229

123	Hidden layers of human small RNAs. <i>BMC Genomics</i> , <b>2008</b> , 9, 157	4.5	226
122	Conservation and divergence in Toll-like receptor 4-regulated gene expression in primary human versus mouse macrophages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, E944-53	11.5	212
121	Effects of cytosine methylation on transcription factor binding sites. <i>BMC Genomics</i> , <b>2014</b> , 15, 119	4.5	156
120	Unamplified cap analysis of gene expression on a single-molecule sequencer. <i>Genome Research</i> , <b>2011</b> , 21, 1150-9	9.7	143
119	Redefinition of the human mast cell transcriptome by deep-CAGE sequencing. <i>Blood</i> , <b>2014</b> , 123, e58-67	2.2	126
118	Interactive visualization and analysis of large-scale sequencing datasets using ZENBU. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 217-9	44.5	124
117	Cross-mapping and the identification of editing sites in mature microRNAs in high-throughput sequencing libraries. <i>Genome Research</i> , <b>2010</b> , 20, 257-64	9.7	105
116	Transcription and enhancer profiling in human monocyte subsets. <i>Blood</i> , <b>2014</b> , 123, e90-9	2.2	101
115	CD157 Marks Tissue-Resident Endothelial Stem Cells with Homeostatic and Regenerative Properties. <i>Cell Stem Cell</i> , <b>2018</b> , 22, 384-397.e6	18	92
114	Novel small noncoding RNAs in mouse spermatozoa, zygotes and early embryos. <i>PLoS ONE</i> , <b>2012</b> , 7, e44542	5.7	89
113	FANTOM5 CAGE profiles of human and mouse samples. <i>Scientific Data</i> , <b>2017</b> , 4, 170112	8.2	88
112	Differential roles of epigenetic changes and Foxp3 expression in regulatory T cell-specific transcriptional regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 5289-94	11.5	85
111	Update of the FANTOM web resource: high resolution transcriptome of diverse cell types in mammals. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D737-D743	20.1	80
110	Update of the FANTOM web resource: expansion to provide additional transcriptome atlases. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D752-D758	20.1	80
109	Mouse proteome analysis. <i>Genome Research</i> , <b>2003</b> , 13, 1335-44	9.7	75
108	Exploration of small RNAs. <i>PLoS Genetics</i> , <b>2008</b> , 4, e22	6	71
107	CAGE Basic/Analysis Databases: the CAGE resource for comprehensive promoter analysis. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D632-6	20.1	69
106	Comparison of CAGE and RNA-seq transcriptome profiling using clonally amplified and single-molecule next-generation sequencing. <i>Genome Research</i> , <b>2014</b> , 24, 708-17	9.7	66

105	The FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation. <i>Genome Biology</i> , <b>2009</b> , 10, R40	18.3	65
104	Analysis of the human monocyte-derived macrophage transcriptome and response to lipopolysaccharide provides new insights into genetic aetiology of inflammatory bowel disease. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006641	6	64
103	Dynamic usage of transcription start sites within core promoters. <i>Genome Biology</i> , <b>2006</b> , 7, R118	18.3	64
102	Next-generation sequencing-based small RNA profiling of cerebrospinal fluid exosomes. <i>Neuroscience Letters</i> , <b>2017</b> , 636, 48-57	3.3	63
101	Alternate transcription of the Toll-like receptor signaling cascade. <i>Genome Biology</i> , <b>2006</b> , 7, R10	18.3	63
100	Complementing tissue characterization by integrating transcriptome profiling from the Human Protein Atlas and from the FANTOM5 consortium. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, 6787-98	20.1	61
99	Enhanced Identification of Transcriptional Enhancers Provides Mechanistic Insights into Diseases. <i>Trends in Genetics</i> , <b>2016</b> , 32, 76-88	8.5	59
98	Analysis of the DNA methylome and transcriptome in granulopoiesis reveals timed changes and dynamic enhancer methylation. <i>Blood</i> , <b>2014</b> , 123, e79-89	2.2	59
97	The enhancer and promoter landscape of human regulatory and conventional T-cell subpopulations. <i>Blood</i> , <b>2014</b> , 123, e68-78	2.2	58
96	Transcriptome Analysis of Recurrently Deregulated Genes across Multiple Cancers Identifies New Pan-Cancer Biomarkers. <i>Cancer Research</i> , <b>2016</b> , 76, 216-26	10.1	56
95	FANTOM4 EdgeExpressDB: an integrated database of promoters, genes, microRNAs, expression dynamics and regulatory interactions. <i>Genome Biology</i> , <b>2009</b> , 10, R39	18.3	56
94	Pseudo-messenger RNA: phantoms of the transcriptome. <i>PLoS Genetics</i> , <b>2006</b> , 2, e23	6	51
93	Update of the FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D856-60	20.1	45
92	FANTOM5 transcriptome catalog of cellular states based on Semantic MediaWiki. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2016</b> , 2016,	5	44
91	Transcriptional landscape of Mycobacterium tuberculosis infection in macrophages. <i>Scientific Reports</i> , <b>2018</b> , 8, 6758	4.9	41
90	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , <b>2020</b> , 30, 1060-1072	9.7	41
89	Redefining the transcriptional regulatory dynamics of classically and alternatively activated macrophages by deepCAGE transcriptomics. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, 6969-82	20.1	38
88	Nuclear pore complex protein mediated nuclear localization of dicer protein in human cells. <i>PLoS ONE</i> , <b>2011</b> , 6, e23385	3.7	37

87	Ceruloplasmin is a novel adipokine which is overexpressed in adipose tissue of obese subjects and in obesity-associated cancer cells. <i>PLoS ONE</i> , <b>2014</b> , 9, e80274	3.7	36
86	The FANTOM5 collection, a data series underpinning mammalian transcriptome atlases in diverse cell types. <i>Scientific Data</i> , <b>2017</b> , 4, 170113	8.2	35
85	Hotspots of De Novo Point Mutations in Induced Pluripotent Stem Cells. <i>Cell Reports</i> , <b>2017</b> , 21, 308-315	10.6	33
84	NET-CAGE characterizes the dynamics and topology of human transcribed cis-regulatory elements. <i>Nature Genetics</i> , <b>2019</b> , 51, 1369-1379	36.3	33
83	The frequent evolutionary birth and death of functional promoters in mouse and human. <i>Genome Research</i> , <b>2015</b> , 25, 1546-57	9.7	33
82	Graph-based clustering for finding distant relationships in a large set of protein sequences. <i>Bioinformatics</i> , <b>2004</b> , 20, 243-52	7.2	31
81	Novel biomarkers that assist in accurate discrimination of squamous cell carcinoma from adenocarcinoma of the lung. <i>BMC Cancer</i> , <b>2016</b> , 16, 760	4.8	30
80	FANTOM5 CAGE profiles of human and mouse reprocessed for GRCh38 and GRCm38 genome assemblies. <i>Scientific Data</i> , <b>2017</b> , 4, 170107	8.2	29
79	Reduction of non-insert sequence reads by dimer eliminator LNA oligonucleotide for small RNA deep sequencing. <i>BioTechniques</i> , <b>2010</b> , 49, 751-5	2.5	27
78	Integration of genetics and miRNA-target gene network identified disease biology implicated in tissue specificity. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, 11898-11909	20.1	26
77	Transcriptional profiling of the human fibrillin/LTBP gene family, key regulators of mesenchymal cell functions. <i>Molecular Genetics and Metabolism</i> , <b>2014</b> , 112, 73-83	3.7	25
76	DeepCAGE Transcriptomics Reveal an Important Role of the Transcription Factor MAFB in the Lymphatic Endothelium. <i>Cell Reports</i> , <b>2015</b> , 13, 1493-1504	10.6	25
75	Promoter-level expression clustering identifies time development of transcriptional regulatory cascades initiated by ErbB receptors in breast cancer cells. <i>Scientific Reports</i> , <b>2015</b> , 5, 11999	4.9	24
74	A transient disruption of fibroblastic transcriptional regulatory network facilitates trans-differentiation. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 8905-13	20.1	23
73	Systematic analysis of transcription start sites in avian development. <i>PLoS Biology</i> , <b>2017</b> , 15, e2002887	9.7	22
72	The 3rd DBCLS BioHackathon: improving life science data integration with Semantic Web technologies. <i>Journal of Biomedical Semantics</i> , <b>2013</b> , 4, 6	2.2	22
71	Construction of representative transcript and protein sets of human, mouse, and rat as a platform for their transcriptome and proteome analysis. <i>Genomics</i> , <b>2004</b> , 84, 913-21	4.3	22
70	Functional annotation of the vlinc class of non-coding RNAs using systems biology approach. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, 3233-52	20.1	21

69	refTSS: A Reference Data Set for Human and Mouse Transcription Start Sites. <i>Journal of Molecular Biology</i> , <b>2019</b> , 431, 2407-2422	6.5	20
68	Integrative CAGE and DNA Methylation Profiling Identify Epigenetically Regulated Genes in NSCLC. <i>Molecular Cancer Research</i> , <b>2017</b> , 15, 1354-1365	6.6	20
67	High-throughput transcription profiling identifies putative epigenetic regulators of hematopoiesis. <i>Blood</i> , <b>2014</b> , 123, e46-57	2.2	19
66	Transcriptional Dynamics During Human Adipogenesis and Its Link to Adipose Morphology and Distribution. <i>Diabetes</i> , <b>2017</b> , 66, 218-230	0.9	19
65	Discovery of molecular markers to discriminate corneal endothelial cells in the human body. <i>PLoS ONE</i> , <b>2015</b> , 10, e0117581	3.7	19
64	FANTOM enters 20th year: expansion of transcriptomic atlases and functional annotation of non-coding RNAs. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D892-D898	20.1	19
63	Automated workflow for preparation of cDNA for cap analysis of gene expression on a single molecule sequencer. <i>PLoS ONE</i> , <b>2012</b> , 7, e30809	3.7	18
62	The RIKEN integrated database of mammals. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D861-70	20.1	18
61	Technical Advance: Transcription factor, promoter, and enhancer utilization in human myeloid cells. <i>Journal of Leukocyte Biology</i> , <b>2015</b> , 97, 985-995	6.5	17
60	Correlation of EGFR or KRAS mutation status with 18F-FDG uptake on PET-CT scan in lung adenocarcinoma. <i>PLoS ONE</i> , <b>2017</b> , 12, e0175622	3.7	16
59	YY1 binding association with sex-biased transcription revealed through X-linked transcript levels and allelic binding analyses. <i>Scientific Reports</i> , <b>2016</b> , 6, 37324	4.9	16
58	Exploration of novel motifs derived from mouse cDNA sequences. <i>Genome Research</i> , <b>2002</b> , 12, 367-78	9.7	16
57	Transcriptional dynamics reveal critical roles for non-coding RNAs in the immediate-early response. <i>PLoS Computational Biology</i> , <b>2015</b> , 11, e1004217	5	15
56	Identification of chromatin marks at TERRA promoter and encoding region. <i>Biochemical and Biophysical Research Communications</i> , <b>2015</b> , 467, 1052-7	3.4	15
55	Chromatin states reveal functional associations for globally defined transcription start sites in four human cell lines. <i>BMC Genomics</i> , <b>2014</b> , 15, 120	4.5	15
54	Antisense Transcription in Loci Associated to Hereditary Neurodegenerative Diseases. <i>Molecular Neurobiology</i> , <b>2019</b> , 56, 5392-5415	6.2	15
53	Specific mesothelial signature marks the heterogeneity of mesenchymal stem cells from high-grade serous ovarian cancer. <i>Stem Cells</i> , <b>2014</b> , 32, 2998-3011	5.8	14
52	Transcriptome analysis of periodontitis-associated fibroblasts by CAGE sequencing identified DLX5 and RUNX2 long variant as novel regulators involved in periodontitis. <i>Scientific Reports</i> , <b>2016</b> , 6, 33666	4.9	14

51	Transcriptome Analysis Uncovers a Growth-Promoting Activity of Orosomucoid-1 on Hepatocytes. <i>EBioMedicine</i> , <b>2017</b> , 24, 257-266	8.8	13
50	The evolution of human cells in terms of protein innovation. <i>Molecular Biology and Evolution</i> , <b>2014</b> , 31, 1364-74	8.3	13
49	CDK1 dependent phosphorylation of hTERT contributes to cancer progression. <i>Nature Communications</i> , <b>2020</b> , 11, 1557	17.4	12
48	Comparative transcriptomics of primary cells in vertebrates. <i>Genome Research</i> , <b>2020</b> , 30, 951-961	9.7	12
47	On-the-fly selection of cell-specific enhancers, genes, miRNAs and proteins across the human body using SlideBase. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2016</b> , 2016,	5	12
46	CAGED-oPOSSUM: motif enrichment analysis from CAGE-derived TSSs. <i>Bioinformatics</i> , <b>2016</b> , 32, 2858-60	7.2	11
45	Mapping Mammalian Cell-type-specific Transcriptional Regulatory Networks Using KD-CAGE and CHIP-seq Data in the TC-YIK Cell Line. <i>Frontiers in Genetics</i> , <b>2015</b> , 6, 331	4.5	11
44	DeepCAGE transcriptomics identify HOXD10 as a transcription factor regulating lymphatic endothelial responses to VEGF-C. <i>Journal of Cell Science</i> , <b>2016</b> , 129, 2573-85	5.3	11
43	Linking FANTOM5 CAGE peaks to annotations with CAGEScan. <i>Scientific Data</i> , <b>2017</b> , 4, 170147	8.2	10
42	Nuclear AGO1 Regulates Gene Expression by Affecting Chromatin Architecture in Human Cells. <i>Cell Systems</i> , <b>2019</b> , 9, 446-458.e6	10.6	10
41	RNA sequencing analysis revealed the induction of CCL3 expression in human intracranial aneurysms. <i>Scientific Reports</i> , <b>2019</b> , 9, 10387	4.9	9
40	Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease. <i>PLoS Computational Biology</i> , <b>2018</b> , 14, e1005934	5	8
39	CAGE-defined promoter regions of the genes implicated in Rett Syndrome. <i>BMC Genomics</i> , <b>2014</b> , 15, 1177	4.5	7
38	Promoter-level transcriptome in primary lesions of endometrial cancer identified biomarkers associated with lymph node metastasis. <i>Scientific Reports</i> , <b>2017</b> , 7, 14160	4.9	7
37	Integrative analysis of transcription factor occupancy at enhancers and disease risk loci in noncoding genomic regions		7
36	Cap Analysis of Gene Expression (CAGE): A Quantitative and Genome-Wide Assay of Transcription Start Sites. <i>Methods in Molecular Biology</i> , <b>2020</b> , 2120, 277-301	1.4	7
35	High-resolution promoter map of human limbal epithelial cells cultured with keratinocyte growth factor and rho kinase inhibitor. <i>Scientific Reports</i> , <b>2017</b> , 7, 2845	4.9	6
34	Genome annotation. <i>Methods in Molecular Biology</i> , <b>2008</b> , 452, 125-39	1.4	6

33	Functional Annotation of Human Long Non-Coding RNAs via Molecular Phenotyping		6
32	Promoter Usage and Dynamics in Vascular Smooth Muscle Cells Exposed to Fibroblast Growth Factor-2 or Interleukin-1 <i>Scientific Reports</i> , <b>2018</b> , 8, 13164	4.9	6
31	CAGEExploreR: an R package for the analysis and visualization of promoter dynamics across multiple experiments. <i>Bioinformatics</i> , <b>2014</b> , 30, 1183-1184	7.2	5
30	Restricted Presence of POU6F2 in Human Corneal Endothelial Cells Uncovered by Extension of the Promoter-level Expression Atlas. <i>EBioMedicine</i> , <b>2017</b> , 25, 175-186	8.8	5
29	CREB3L1 overexpression as a potential diagnostic marker of Philadelphia chromosome-negative myeloproliferative neoplasms. <i>Cancer Science</i> , <b>2021</b> , 112, 884-892	6.9	5
28	Monitoring transcription initiation activities in rat and dog. <i>Scientific Data</i> , <b>2017</b> , 4, 170173	8.2	4
27	APOBEC3B is preferentially expressed at the G2/M phase of cell cycle. <i>Biochemical and Biophysical Research Communications</i> , <b>2021</b> , 546, 178-184	3.4	4
26	Identification of novel cerebellar developmental transcriptional regulators with motif activity analysis. <i>BMC Genomics</i> , <b>2019</b> , 20, 718	4.5	3
25	CXCL4/PF4 is a predictive biomarker of cardiac differentiation potential of human induced pluripotent stem cells. <i>Scientific Reports</i> , <b>2019</b> , 9, 4638	4.9	3
24	A Transcriptional Switch Point During Hematopoietic Stem and Progenitor Cell Ontogeny. <i>Stem Cells and Development</i> , <b>2017</b> , 26, 314-327	4.4	3
23	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , <b>2010</b> , 141, 369	56.2	3
22	SDRF2GRAPH: a visualization tool of a spreadsheet-based description of experimental processes. <i>BMC Bioinformatics</i> , <b>2009</b> , 10, 133	3.6	3
21	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , <b>2021</b> , 12, 3297	17.4	3
20	Conserved temporal ordering of promoter activation implicates common mechanisms governing the immediate early response across cell types and stimuli. <i>Open Biology</i> , <b>2018</b> , 8,	7	3
19	Genome Annotation. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1525, 107-121	1.4	2
18	Transcription start site profiling of 15 anatomical regions of the Macaca mulatta central nervous system. <i>Scientific Data</i> , <b>2017</b> , 4, 170163	8.2	2
17	Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease		2
16	DUX4 regulates oocyte to embryo transition in human		2



15	Dysregulation of post-transcriptional modification by copy number variable microRNAs in schizophrenia with enhanced glycation stress. <i>Translational Psychiatry</i> , <b>2021</b> , 11, 331	8.6	2
14	Discovery of Transcription Factors Novel to Mouse Cerebellar Granule Cell Development Through Laser-Capture Microdissection. <i>Cerebellum</i> , <b>2018</b> , 17, 308-325	4.3	1
13	Application of Gene Expression Trajectories Initiated from ErbB Receptor Activation Highlights the Dynamics of Divergent Promoter Usage. <i>PLoS ONE</i> , <b>2015</b> , 10, e0144176	3.7	1
12	Capturing drug responses by quantitative promoter activity profiling. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , <b>2013</b> , 2, e77	4.5	1
11	Predicting cell-type-specific non-coding RNA transcription from genome sequence		1
10	CAGED-oPOSSUM: motif enrichment analysis from CAGE-derived TSSs		1
9	Chromosomal-scale de novo genome assemblies of Cynomolgus Macaque and Common Marmoset. <i>Scientific Data</i> , <b>2021</b> , 8, 159	8.2	1
8	is a multifunctional factor priming human embryonic genome activation.. <i>IScience</i> , <b>2022</b> , 25, 104137	6.1	1
7	Nanopore sequencing reveals TACC2 locus complexity and diversity of isoforms transcribed from an intronic promoter. <i>Scientific Reports</i> , <b>2021</b> , 11, 9355	4.9	0
6	Significance of HMGA2 expression as independent poor prognostic marker in perihilar and distal cholangiocarcinoma resected with curative intent. <i>European Journal of Surgical Oncology</i> , <b>2021</b> , 47, 394-400	3.6	0
5	Databases for CAGE Visualization and Analysis <b>2009</b> , 123-135		
4	CREB3L1 Overexpression Can Reliably Discriminate Ph-MPNs from Reactive Cases. <i>Blood</i> , <b>2020</b> , 136, 41-41	2.2	
3	Databases for CAGE Visualization and Analysis <b>2019</b> , 123-136		
2	BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services. <i>F1000Research</i> , 8, 1677	3.6	
1	Association between the EGFR or KRAS mutation status and the FDG-PET findings in surgically resected lung adenocarcinoma.. <i>Journal of Clinical Oncology</i> , <b>2015</b> , 33, 7535-7535	2.2	