

Huidong Shi

List of Publications by Year in descending order

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137
papers

8,410
citations

50276

46
h-index

48315

88
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143
all docs

143
docs citations

143
times ranked

14319
citing authors

#	ARTICLE	IF	CITATIONS
1	Restoring FAS Expression via Lipid-Encapsulated FAS DNA Nanoparticle Delivery Is Sufficient to Suppress Colon Tumor Growth In Vivo. <i>Cancers</i> , 2022, 14, 361.	3.7	8
2	G6PD functions as a metabolic checkpoint to regulate granzyme B expression in tumor-specific cytotoxic T lymphocytes. , 2022, 10, e003543.		10
3	Novel lowâ€avidity glypicanâ€3 specific CARTs resist exhaustion and mediate durable antitumor effects against HCC. <i>Hepatology</i> , 2022, 76, 330-344.	7.3	11
4	H3K9me3 represses G6PD expression to suppress the pentose phosphate pathway and ROS production to promote human mesothelioma growth. <i>Oncogene</i> , 2022, , .	5.9	10
5	Integrative analysis of multiple types of genomic data using an accelerated failure time frailty model. <i>Computational Statistics</i> , 2021, 36, 1499-1532.	1.5	0
6	Dnmt3b Deficiency in Myf5+-Brown Fat Precursor Cells Promotes Obesity in Female Mice. <i>Biomolecules</i> , 2021, 11, 1087.	4.0	8
7	WDR5-H3K4me3 epigenetic axis regulates OPN expression to compensate PD-L1 function to promote pancreatic cancer immune escape. , 2021, 9, e002624.		36
8	Adipose tissue-derived neurotrophic factor 3 regulates sympathetic innervation and thermogenesis in adipose tissue. <i>Nature Communications</i> , 2021, 12, 5362.	12.8	27
9	Inhibition of the BTK-IDO-mTOR axis promotes differentiation of monocyte-lineage dendritic cells and enhances anti-tumor T cell immunity. <i>Immunity</i> , 2021, 54, 2354-2371.e8.	14.3	34
10	Brown Fat Dnmt3b Deficiency Ameliorates Obesity in Female Mice. <i>Life</i> , 2021, 11, 1325.	2.4	2
11	Epigenetic interaction between UTX and DNMT1 regulates diet-induced myogenic remodeling in brown fat. <i>Nature Communications</i> , 2021, 12, 6838.	12.8	11
12	NRF2 mediates β -globin gene regulation through epigenetic modifications in a β -YAC transgenic mouse model. <i>Experimental Biology and Medicine</i> , 2020, 245, 1308-1318.	2.4	5
13	Persistent STAT5 activation reprograms the epigenetic landscape in CD4 ⁺ T cells to drive polyfunctionality and antitumor immunity. <i>Science Immunology</i> , 2020, 5, .	11.9	40
14	Autocrine IL6-Mediated Activation of the STAT3â€DNMT Axis Silences the TNFÎ±â€RIP1 Necroptosis Pathway to Sustain Survival and Accumulation of Myeloid-Derived Suppressor Cells. <i>Cancer Research</i> , 2020, 80, 3145-3156.	0.9	47
15	CD73 on cancer-associated fibroblasts enhanced by the A2B-mediated feedforward circuit enforces an immune checkpoint. <i>Nature Communications</i> , 2020, 11, 515.	12.8	117
16	The Monocytes That Repopulate in Mice After Cyclophosphamide Treatment Acquire a Neutrophil Precursor Gene Signature and Immunosuppressive Activity. <i>Frontiers in Immunology</i> , 2020, 11, 594540.	4.8	6
17	Detection of Differentially Methylated Regions Using Bayes Factor for Ordinal Group Responses. <i>Genes</i> , 2019, 10, 721.	2.4	2
18	Computational Methods for Detection of Differentially Methylated Regions Using Kernel Distance and Scan Statistics. <i>Genes</i> , 2019, 10, 298.	2.4	1

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19	Discovery and Validation of a Novel Neutrophil Activation Marker Associated with Obesity. Scientific Reports, 2019, 9, 3433.	3.3	19
20	The co-chaperone UNC45A is essential for the expression of mitotic kinase NEK7 and tumorigenesis. Journal of Biological Chemistry, 2019, 294, 5246-5260.	3.4	27
21	THZ1 suppresses human non-small-cell lung cancer cells in vitro through interference with cancer metabolism. Acta Pharmacologica Sinica, 2019, 40, 814-822.	6.1	31
22	Recruitment of monocytes and epigenetic silencing of intratumoral CYP7B1 primarily contribute to the accumulation of 27-hydroxycholesterol in breast cancer. American Journal of Cancer Research, 2019, 9, 2194-2208.	1.4	9
23	FKBP12.6 protects heart from AngII-induced hypertrophy through inhibiting Ca ²⁺ /calmodulin-mediated signalling pathways in vivo and in vitro. Journal of Cellular and Molecular Medicine, 2018, 22, 3638-3651.	3.6	13
24	Activation of p53 in Immature Myeloid Precursor Cells Controls Differentiation into Ly6c+CD103+ Monocytic Antigen-Presenting Cells in Tumors. Immunity, 2018, 48, 91-106.e6.	14.3	95
25	Complete genome sequence and analysis of the industrial Saccharomyces cerevisiae strain N85 used in Chinese rice wine production. DNA Research, 2018, 25, 297-306.	3.4	8
26	A similar effect of P16 hydroxymethylation and true-methylation on the prediction of malignant transformation of oral epithelial dysplasia: observation from a prospective study. BMC Cancer, 2018, 18, 918.	2.6	6
27	Genome wide DNA differential methylation regions in colorectal cancer patients in relation to blood related family members, obese and non-obese controls - a preliminary report. Oncotarget, 2018, 9, 25557-25571.	1.8	3
28	Haemophagocytic lymphohistiocytosis occurred during induction chemotherapy in an acute monocytic leukemia patient with FLT3-ITD and DNMT3A mutations. BMC Cancer, 2018, 18, 604.	2.6	2
29	CD38 Deficiency Promotes Inflammatory Response through Activating Sirt1/NF- κ B-Mediated Inhibition of TLR2 Expression in Macrophages. Mediators of Inflammation, 2018, 2018, 1-13.	3.0	18
30	An epigenome-wide study of obesity in African American youth and young adults: novel findings, replication in neutrophils, and relationship with gene expression. Clinical Epigenetics, 2018, 10, 3.	4.1	33
31	Indoximod Combined with Standard Induction Chemotherapy Is Well Tolerated and Induces a High Rate of Complete Remission with MRD-Negativity in Patients with Newly Diagnosed AML: Results from a Phase I Trial. Blood, 2018, 132, 332-332.	1.4	7
32	ALPL, A Novel Marker Of Neutrophil Activation In Response To Obesity. FASEB Journal, 2018, 32, lb477.	0.5	0
33	Transcriptome Sequencing Reveals Alternative Splicing Patterns and an Increased Sensitivity to Spliceosome Inhibition Associated MYD88 L265P Mutation in Chronic Lymphocytic Leukemia. Blood, 2018, 132, 5535-5535.	1.4	0
34	CAME: identification of chromatin accessibility from nucleosome occupancy and methylome sequencing. Bioinformatics, 2017, 33, 1139-1146.	4.1	4
35	Promoter Methylation Modulates Indoleamine 2,3-Dioxygenase 1 Induction by Activated T Cells in Human Breast Cancers. Cancer Immunology Research, 2017, 5, 330-344.	3.4	28
36	Hypermethylated LTR retrotransposon exhibits enhancer activity. Epigenetics, 2017, 12, 226-237.	2.7	14

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37	Long non-coding RNAs transcribed by ERV-9 LTR retrotransposon act in cis to modulate long-range LTR enhancer function. <i>Nucleic Acids Research</i> , 2017, 45, gkx055.	14.5	32
38	The MLL1-H3K4me3 Axis-Mediated PD-L1 Expression and Pancreatic Cancer Immune Evasion. <i>Journal of the National Cancer Institute</i> , 2017, 109, djw283.	6.3	182
39	A novel immunohistochemical score to predict early mortality in acute myeloid leukemia patients based on indoleamine 2,3 dioxygenase expression. <i>Scientific Reports</i> , 2017, 7, 12892.	3.3	31
40	DNA methylation protects against cisplatin-induced kidney injury by regulating specific genes, including interferon regulatory factor 8. <i>Kidney International</i> , 2017, 92, 1194-1205.	5.2	43
41	Mediator complex components are frequent targets for genetic alterations in various types of human cancer. <i>Journal of Genetics and Genomics</i> , 2017, 44, 587-591.	3.9	0
42	Computational Methods and Correlation of Exon-skipping Events with Splicing, Transcription, and Epigenetic Factors. <i>Methods in Molecular Biology</i> , 2017, 1513, 163-170.	0.9	12
43	The expression of <i>RUNDC3B</i> is associated with promoter methylation in lymphoid malignancies. <i>Hematological Oncology</i> , 2017, 35, 25-33.	1.7	11
44	Unlocking the epigenetic code of T cell exhaustion. <i>Translational Cancer Research</i> , 2017, 6, S384-S387.	1.0	12
45	Combined Inhibition of DNMT and HDAC Blocks the Tumorigenicity of Cancer Stem-like Cells and Attenuates Mammary Tumor Growth. <i>Cancer Research</i> , 2016, 76, 3224-3235.	0.9	122
46	Hypomethylation coordinates antagonistically with hypermethylation in cancer development: a case study of leukemia. <i>Human Genomics</i> , 2016, 10, 18.	2.9	40
47	Predicting DNA Methylation State of CpG Dinucleotide Using Genome Topological Features and Deep Networks. <i>Scientific Reports</i> , 2016, 6, 19598.	3.3	75
48	Roles of Distal and Genic Methylation in the Development of Prostate Tumorigenesis Revealed by Genome-wide DNA Methylation Analysis. <i>Scientific Reports</i> , 2016, 6, 22051.	3.3	19
49	Differential methylation tests of regulatory regions. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2016, 15, 237-251.	0.6	5
50	Epigenetic regulation of macrophage polarization and inflammation by DNA methylation in obesity. <i>JCI Insight</i> , 2016, 1, e87748.	5.0	138
51	DNA Hypomethylation within B-Cell Enhancers and Super Enhancers Reveal a Dependency on Immune and Metabolic Mechanisms in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2016, 128, 1049-1049.	1.4	5
52	Phenotypic alteration of CD8+ T cells in chronic lymphocytic leukemia is associated with epigenetic reprogramming. <i>Oncotarget</i> , 2016, 7, 40558-40570.	1.8	30
53	New approaches to identify cancer heterogeneity in DNA methylation studies using the lepage test and multinomial logistic regression. , 2015, , .		1
54	Targeting HSF1 disrupts HSP90 chaperone function in chronic lymphocytic leukemia. <i>Oncotarget</i> , 2015, 6, 31767-31779.	1.8	28

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55	A survey of computational methods in transcriptome-wide alternative splicing analysis. <i>Biomolecular Concepts</i> , 2015, 6, 59-66.	2.2	18
56	Identification of Global DNA Methylation Signatures in Glioblastoma-Derived Cancer Stem Cells. <i>Journal of Genetics and Genomics</i> , 2015, 42, 355-371.	3.9	47
57	DNMT1 is essential for mammary and cancer stem cell maintenance and tumorigenesis. <i>Nature Communications</i> , 2015, 6, 6910.	12.8	204
58	Sequencing the Cancer Methylome. <i>Methods in Molecular Biology</i> , 2015, 1238, 627-651.	0.9	15
59	Heat Shock Factor 1 Promotes NF-Kb and B-Cell Signaling in a Preclinical Model of Chronic Lymphocytic Leukemia. <i>Blood</i> , 2015, 126, 5297-5297.	1.4	1
60	RPPA-based protein profiling reveals eIF4G overexpression and 4E-BP1 serine 65 phosphorylation as molecular events that correspond with a pro-survival phenotype in chronic lymphocytic leukemia. <i>Oncotarget</i> , 2015, 6, 14632-14645.	1.8	19
61	Inhibiting DNA Methylation by 5-Aza-2- β -deoxycytidine Ameliorates Atherosclerosis Through Suppressing Macrophage Inflammation. <i>Endocrinology</i> , 2014, 155, 4925-4938.	2.8	138
62	SHOX2 Is a Direct miR-375 Target and a Novel Epithelial-to-Mesenchymal Transition Inducer in Breast Cancer Cells. <i>Neoplasia</i> , 2014, 16, 279-290.e5.	5.3	72
63	Activation of Gpr109a, Receptor for Niacin and the Commensal Metabolite Butyrate, Suppresses Colonic Inflammation and Carcinogenesis. <i>Immunity</i> , 2014, 40, 128-139.	14.3	1,654
64	Large-Scale Characterization of DNA Methylation Changes in Human Gastric Carcinomas with and without Metastasis. <i>Clinical Cancer Research</i> , 2014, 20, 4598-4612.	7.0	73
65	Genome-Wide DNA Methylation Analysis Identifies Aberrant Epigenetic Changes in CD8+ T Cells from Chronic Lymphocytic Leukemia Patients. <i>Blood</i> , 2014, 124, 3552-3552.	1.4	0
66	A systematic evaluation of miRNA:mRNA interactions involved in the migration and invasion of breast cancer cells. <i>Journal of Translational Medicine</i> , 2013, 11, 57.	4.4	117
67	A Genome-Wide Methylation Study of Severe Vitamin D Deficiency in African American Adolescents. <i>Journal of Pediatrics</i> , 2013, 162, 1004-1009.e1.	1.8	87
68	HOXC9 directly regulates distinct sets of genes to coordinate diverse cellular processes during neuronal differentiation. <i>BMC Genomics</i> , 2013, 14, 830.	2.8	24
69	Analyzing the cancer methylome through targeted bisulfite sequencing. <i>Cancer Letters</i> , 2013, 340, 171-178.	7.2	75
70	An Inherently Bifunctional Subset of Foxp3+ T Helper Cells Is Controlled by the Transcription Factor Eos. <i>Immunity</i> , 2013, 38, 998-1012.	14.3	159
71	Aberrant Epigenetic Gene Regulation in Lymphoid Malignancies. <i>Seminars in Hematology</i> , 2013, 50, 38-47.	3.4	17
72	A genome-wide methylation study on obesity. <i>Epigenetics</i> , 2013, 8, 522-533.	2.7	174

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73	Presence of an Early Lineage Stem Cell Phenotype in Meningioma-Initiating Cells. , 2013, , 211-218.		0
74	MBD3 Localizes at Promoters, Gene Bodies and Enhancers of Active Genes. PLoS Genetics, 2013, 9, e1004028.	3.5	97
75	A Method to Detect Differentially Methylated Loci With Next-Generation Sequencing. Genetic Epidemiology, 2013, 37, 377-382.	1.3	14
76	A Genome-Wide Methylation Study on Essential Hypertension in Young African American Males. PLoS ONE, 2013, 8, e53938.	2.5	57
77	Butyrate suppresses colonic inflammation through HDAC1-dependent Fas upregulation and Fas-mediated apoptosis of T cells. American Journal of Physiology - Renal Physiology, 2012, 302, G1405-G1415.	3.4	218
78	Genome-wide DNA methylation analysis reveals novel epigenetic changes in chronic lymphocytic leukemia. Epigenetics, 2012, 7, 567-578.	2.7	85
79	DNA Hypomethylation Leads to Aberrant Expression of PD-1 in Chronic Lymphocytic Leukemia. Blood, 2012, 120, 3504-3504.	1.4	1
80	A genome-wide methylation study of vitamin D deficiency in African American adolescents. FASEB Journal, 2012, 26, 116.7.	0.5	0
81	Genome-Wide DNA Methylation Landscape Defines IGHV Mutated and Unmutated B Cell Chronic Lymphocytic Leukemias. Blood, 2012, 120, 526-526.	1.4	0
82	A software package for next-gen bisulfite sequencing data analysis. , 2011, , .		0
83	Metabolomic Profiling Reveals Potential Markers and Bioprocesses Altered in Bladder Cancer Progression. Cancer Research, 2011, 71, 7376-7386.	0.9	166
84	Isolation and characterization of a population of stem-like progenitor cells from an atypical meningioma. Experimental and Molecular Pathology, 2011, 90, 179-188.	2.1	45
85	Loss of Methyl-CpG-Binding Domain Protein 2 Enhances Endothelial Angiogenesis and Protects Mice Against Hind-Limb Ischemic Injury. Circulation, 2011, 123, 2964-2974.	1.6	104
86	Targeted bisulfite sequencing by solution hybrid selection and massively parallel sequencing. Nucleic Acids Research, 2011, 39, e127-e127.	14.5	61
87	Next Generation Sequencing: Advances in Characterizing the Methylome. Genes, 2010, 1, 143-165.	2.4	4
88	Obesity related methylation changes in DNA of peripheral blood leukocytes. BMC Medicine, 2010, 8, 87.	5.5	187
89	Label-free DNA methylation analysis using opto-fluidic ring resonators. Biosensors and Bioelectronics, 2010, 26, 1016-1020.	10.1	50
90	Developmental cues and persistent neurogenic potential within an in vitro neural niche. BMC Developmental Biology, 2010, 10, 5.	2.1	21

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91	Future Directions in Research on the Epigenetics of Aging. , 2010, , 433-446.		0
92	Genome-Wide DNA Methylation Maps in Follicular Lymphoma Cells Determined by Methylation-Enriched Bisulfite Sequencing. PLoS ONE, 2010, 5, e13020.	2.5	35
93	The Epigenetics of Age-Related Cancers. , 2010, , 285-313.		0
94	Molecular detection of B-cell neoplasms by specific DNA methylation biomarkers. International Journal of Clinical and Experimental Pathology, 2010, 3, 265-79.	0.5	7
95	Label-free analysis of DNA methylation using optofluidic ring resonators. , 2009, 2009, 2760-2.		0
96	Soy Isoflavones Have an Antiestrogenic Effect and Alter Mammary Promoter Hypermethylation in Healthy Premenopausal Women. Nutrition and Cancer, 2009, 61, 238-244.	2.0	126
97	Large-scale analysis of DNA methylation in chronic lymphocytic leukemia. Epigenomics, 2009, 1, 39-61.	2.1	57
98	DNA hypermethylation accompanied by transcriptional repression in follicular lymphoma. Genes Chromosomes and Cancer, 2009, 48, 828-841.	2.8	59
99	Label-free DNA methylation analysis using the optofluidic ring resonator sensor. Proceedings of SPIE, 2009, , .	0.8	0
100	Relational Analysis of CpG Islands Methylation and Gene Expression in Human Lymphomas Using Possibilistic C-Means Clustering and Modified Cluster Fuzzy Density. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, , .	3.0	0
101	Combined epigenetic therapy with the histone methyltransferase EZH2 inhibitor 3-deazaneplanocin A and the histone deacetylase inhibitor panobinostat against human AML cells. Blood, 2009, 114, 2733-2743.	1.4	336
102	Stem Cells as Vectors to Deliver HSV/tk Gene Therapy for Malignant Gliomas. Current Stem Cell Research and Therapy, 2009, 4, 44-49.	1.3	43
103	Label-free quantitative DNA detection using the liquid core optical ring resonator. Biosensors and Bioelectronics, 2008, 23, 1003-1009.	10.1	145
104	PRIMEGENS-v2: genome-wide primer design for analyzing DNA methylation patterns of CpG islands. Bioinformatics, 2008, 24, 1837-1842.	4.1	19
105	A Sensitive Molecular Method for Detection of Disseminating Hematopoietic Tumor Cells by Using Specific Epigenetic DNA Methylation Biomarkers. Blood, 2008, 112, 4850-4850.	1.4	0
106	Label-free DNA detection using liquid core optical ring resonators. Proceedings of SPIE, 2007, , .	0.8	1
107	CpG islands: their potential as biomarkers for cancer. Expert Review of Molecular Diagnostics, 2007, 7, 519-531.	3.1	55
108	Discovery of novel epigenetic markers in non-Hodgkin's lymphoma. Carcinogenesis, 2007, 28, 60-70.	2.8	83

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109	Ultradeep Bisulfite Sequencing Analysis of DNA Methylation Patterns in Multiple Gene Promoters by 454 Sequencing. <i>Cancer Research</i> , 2007, 67, 8511-8518.	0.9	252
110	Large-Scale CpG Methylation Analysis Identifies Novel Candidate Genes and Reveals Methylation Hotspots in Acute Lymphoblastic Leukemia. <i>Cancer Research</i> , 2007, 67, 2617-2625.	0.9	134
111	Relational Analysis of CpG Islands Methylation and Gene Expression in Human Lymphomas Using Possibilistic C-Means Clustering and Modified Cluster Fuzzy Density. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2007, 4, 176-189.	3.0	5
112	Differential DNA methylation patterns of small B-cell lymphoma subclasses with different clinical behavior. <i>Leukemia</i> , 2006, 20, 1855-1862.	7.2	74
113	Promoter DNA methylation of CD10 in lymphoid malignancies. <i>Leukemia</i> , 2006, 20, 1910-1912.	7.2	10
114	Differential DNA Methylation of Gene Promoters in Small B-Cell Lymphomas. <i>American Journal of Clinical Pathology</i> , 2005, 124, 430-439.	0.7	30
115	Epigenetic Hypothesis Tests for Methylation and Acetylation in a Triple Microarray System. <i>Journal of Computational Biology</i> , 2005, 12, 370-390.	1.6	21
116	Differential DNA Methylation of Gene Promoters in Small B-Cell Lymphomas. <i>American Journal of Clinical Pathology</i> , 2005, 124, 430-439.	0.7	14
117	Detection of Minimal Residual Disease in Precursor B Lymphoblastic Leukemia (B-ALL) Patients by a Novel Epigenetic DNA Methylation Biomarker.. <i>Blood</i> , 2005, 106, 4524-4524.	1.4	0
118	Dual Therapeutic Utility of Proteasome Modulating Agents for Pharmacogene Therapy of the Cystic Fibrosis Airway. <i>Molecular Therapy</i> , 2004, 10, 990-1002.	8.2	46
119	Oligonucleotide-based microarray for DNA methylation analysis: Principles and applications. <i>Journal of Cellular Biochemistry</i> , 2003, 88, 138-143.	2.6	119
120	Methylation Target Array for Rapid Analysis of CpG Island Hypermethylation in Multiple Tissue Genomes. <i>American Journal of Pathology</i> , 2003, 163, 37-45.	3.8	92
121	Triple analysis of the cancer epigenome: an integrated microarray system for assessing gene expression, DNA methylation, and histone acetylation. <i>Cancer Research</i> , 2003, 63, 2164-71.	0.9	109
122	The androgen receptor gene is preferentially hypermethylated in follicular non-Hodgkin's lymphomas. <i>Clinical Cancer Research</i> , 2003, 9, 4034-42.	7.0	29
123	Double RNA interference of DNMT3b and DNMT1 enhances DNA demethylation and gene reactivation. <i>Cancer Research</i> , 2003, 63, 6110-5.	0.9	109
124	Differential distribution of DNA methylation within the RASSF1A CpG island in breast cancer. <i>Cancer Research</i> , 2003, 63, 6178-86.	0.9	88
125	Methylation-Specific Oligonucleotide Microarray: A New Potential for High-Throughput Methylation Analysis. <i>Genome Research</i> , 2002, 12, 158-164.	5.5	247
126	Applications of CpG Island Microarrays for High-Throughput Analysis of DNA Methylation. <i>Journal of Nutrition</i> , 2002, 132, 2430S-2434S.	2.9	73

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127	Expressed CpG island sequence tag microarray for dual screening of DNA hypermethylation and gene silencing in cancer cells. <i>Cancer Research</i> , 2002, 62, 3214-20.	0.9	61
128	Methylation microarray analysis of late-stage ovarian carcinomas distinguishes progression-free survival in patients and identifies candidate epigenetic markers. <i>Clinical Cancer Research</i> , 2002, 8, 2246-52.	7.0	156
129	Display of green fluorescent protein on <i>Escherichia coli</i> cell surface. <i>Enzyme and Microbial Technology</i> , 2001, 28, 25-34.	3.2	68
130	Temperature-induced expression of <i>phb</i> genes in <i>Escherichia coli</i> and the effect of temperature patterns on the production of poly-3-hydroxybutyrate. <i>Journal of Bioscience and Bioengineering</i> , 2001, 91, 21-26.	2.2	7
131	Effect of modifying metabolic network on poly-3-hydroxybutyrate biosynthesis in recombinant <i>Escherichia coli</i> . <i>Journal of Bioscience and Bioengineering</i> , 1999, 87, 666-677.	2.2	42
132	Dynamics and modeling on fermentative production of poly ($\hat{1}^2$ -hydroxybutyric acid) from sugars via lactate by a mixed culture of <i>Lactobacillus delbrueckii</i> and <i>Alcaligenes eutrophus</i> . <i>Journal of Biotechnology</i> , 1999, 67, 113-134.	3.8	55
133	Fermentation Characteristics in Conversion of Organic Acids Obtained by Oxidation of Low-Rank Coals to Poly(.BETA.-hydroxybutyrate) Using <i>A. eutrophus</i> Cells with Some Analysis on Metabolic Flux Distribution.. <i>Kagaku Kogaku Ronbunshu</i> , 1999, 25, 226-232.	0.3	0
134	On-line metabolic pathway analysis based on metabolic signal flow diagram. , 1998, 58, 139-148.		14
135	A Metabolic Model for On-Line Estimation of Poly- $\hat{1}^2$ -Hydroxybutyrate (PHB) Production. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 1998, 31, 343-348.	0.4	0
136	An integrated metabolic pathway analysis based on metabolic signal flow diagram and cellular energetics for <i>Saccharomyces cerevisiae</i> . <i>Journal of Bioscience and Bioengineering</i> , 1997, 83, 275-280.	0.9	6
137	Metabolic flux analysis for biosynthesis of poly($\hat{1}^2$ -hydroxybutyric acid) in <i>Alcaligenes eutrophus</i> from various carbon sources. <i>Journal of Bioscience and Bioengineering</i> , 1997, 84, 579-587.	0.9	98