

Fei-Ling Lim

List of Publications by Year in descending order

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17
papers

872
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566801

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887659

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times ranked

1575
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptomic analysis of <i>Sorghum bicolor</i> responding to combined heat and drought stress. <i>BMC Genomics</i> , 2014, 15, 456.	1.2	188
2	Linking Molecular and Population Stress Responses in <i>Daphnia magna</i> exposed to cadmium. <i>Environmental Science & Technology</i> , 2008, 42, 2181-2188.	4.6	94
3	Microarray analysis identifies matrix metalloproteinases (MMPs) as key genes whose expression is up-regulated in human adipocytes by macrophage-conditioned medium. <i>Pflugers Archiv European Journal of Physiology</i> , 2009, 458, 1103-1114.	1.3	94
4	Hybridization array technology coupled with chemostat culture: Tools to interrogate gene expression in <i>Saccharomyces cerevisiae</i> . <i>Methods</i> , 2002, 26, 281-290.	1.9	79
5	A microarray analysis of the hypoxia-induced modulation of gene expression in human adipocytes. <i>Archives of Physiology and Biochemistry</i> , 2012, 118, 112-120.	1.0	64
6	Gene Ontology Mapping as an Unbiased Method for Identifying Molecular Pathways and Processes Affected by Toxicant Exposure: Application to Acute Effects Caused by the Rodent Non-Genotoxic Carcinogen Diethylhexylphthalate. <i>Toxicological Sciences</i> , 2005, 86, 453-469.	1.4	62
7	Phenotypic Anchoring of Gene Expression Changes during Estrogen-Induced Uterine Growth. <i>Environmental Health Perspectives</i> , 2004, 112, 1589-1606.	2.8	54
8	Muscle unloading-induced metabolic remodeling is associated with acute alterations in PPAR α and UCP-3 expression. <i>Physiological Genomics</i> , 2008, 34, 149-161.	1.0	42
9	Molecular determinants of the cell-cycle regulated Mcm1p-Fkh2p transcription factor complex. <i>Nucleic Acids Research</i> , 2003, 31, 2279-2288.	6.5	33
10	Mcm1p-Induced DNA Bending Regulates the Formation of Ternary Transcription Factor Complexes. <i>Molecular and Cellular Biology</i> , 2003, 23, 450-461.	1.1	32
11	Induction of iron homeostasis genes during estrogen-induced uterine growth and differentiation. <i>Molecular and Cellular Endocrinology</i> , 2006, 253, 22-29.	1.6	29
12	Whole-genome microarray analysis identifies up-regulation of Nr4a nuclear receptors in muscle and liver from diet-restricted rats. <i>Mechanisms of Ageing and Development</i> , 2009, 130, 240-247.	2.2	28
13	Stimulation of inflammatory gene expression in human preadipocytes by macrophage-conditioned medium: Upregulation of IL-6 production by macrophage-derived IL-1 β . <i>Molecular and Cellular Endocrinology</i> , 2012, 349, 239-247.	1.6	28
14	Identification of early molecular pathways affected by paraquat in rat lung. <i>Toxicology</i> , 2006, 225, 157-172.	2.0	22
15	Microarray-based identification of age-dependent differences in gene expression of human dermal fibroblasts. <i>Mechanisms of Ageing and Development</i> , 2012, 133, 498-507.	2.2	16
16	From musk to body odor: Decoding olfaction through genetic variation. <i>PLoS Genetics</i> , 2022, 18, e1009564.	1.5	5
17	Lower polyunsaturated fatty acid levels and FADS2 expression in adult compared to neonatal keratinocytes are associated with FADS2 promotor hypermethylation. <i>Biochemical and Biophysical Research Communications</i> , 2022, 601, 9-15.	1.0	2