Kyongbum Lee

List of Publications by Year
in descending order

78 papers	4,914 citations	126858 33 h-index	95218 68 g-index
81 all docs	81 docs citations	81 times ranked	8131 citing authors

#	Article	IF	Citations
1	Vascularization Strategies for Tissue Engineering. Tissue Engineering - Part B: Reviews, 2009, 15, 353-370.	2.5	765
2	Gut Microbiota-Derived Tryptophan Metabolites Modulate Inflammatory Response in Hepatocytes and Macrophages. Cell Reports, 2018, 23, 1099-1111.	2.9	406
3	Microbiome-Derived Tryptophan Metabolites and Their Aryl Hydrocarbon Receptor-Dependent Agonist and Antagonist Activities. Molecular Pharmacology, 2014, 85, 777-788.	1.0	254
4	Quantitative metabolic imaging using endogenous fluorescence to detect stem cell differentiation. Scientific Reports, 2013, 3, 3432.	1.6	215
5	Adipose Tissue Engineering for Soft Tissue Regeneration. Tissue Engineering - Part B: Reviews, 2010, 16, 413-426.	2.5	212
6	An algorithm for modularity analysis of directed and weighted biological networks based on edge-betweenness centrality. Bioinformatics, 2006, 22, 3106-3108.	1.8	203
7	Prediction and quantification of bioactive microbiota metabolites in the mouse gut. Nature Communications, 2014, 5, 5492.	5.8	195
8	Dynamic model of CHO cell metabolism. Metabolic Engineering, 2011, 13, 108-124.	3.6	163
9	Relationships between degradability of silk scaffolds and osteogenesis. Biomaterials, 2010, 31, 6162-6172.	5.7	146
10	Pathways and functions of gut microbiota metabolism impacting host physiology. Current Opinion in Biotechnology, 2015, 36, 137-145.	3.3	140
11	Endogenous Two-Photon Fluorescence Imaging Elucidates Metabolic Changes Related to Enhanced Glycolysis and Glutamine Consumption in Precancerous Epithelial Tissues. Cancer Research, 2014, 74, 3067-3075.	0.4	129
12	An Aryl Hydrocarbon Receptor-Mediated Amplification Loop That Enforces Cell Migration in ER^{â^'}/PR^{â^'}/Her2^{â^'}Human Breast Cancer Cells. Molecular Pharmacology, 2016, 90, 674-688.	1.0	124
13	Novel In Vivo -Degradable Cellulose-Chitin Copolymer from Metabolically Engineered Gluconacetobacter xylinus. Applied and Environmental Microbiology, 2010, 76, 6257-6265.	1.4	100
14	Parabacteroides distasonis attenuates tollâ€like receptor 4 signaling and Akt activation and blocks colon tumor formation in highâ€fat dietâ€fed azoxymethaneâ€treated mice. International Journal of Cancer, 2018, 143, 1797-1805.	2.3	85
15	Metabolic Flux Analysis of Postburn Hepatic Hypermetabolism. Metabolic Engineering, 2000, 2, 312-327.	3.6	79
16	Interactions between gut microbiota and non-alcoholic liver disease: The role of microbiota-derived metabolites. Pharmacological Research, 2019, 141, 521-529.	3.1	78
17	Characterization of metabolic changes associated with the functional development of 3D engineered tissues by non-invasive, dynamic measurement of individual cell redox ratios. Biomaterials, 2012, 33, 5341-5348.	5.7	77
18	Metabolic flux analysis of cultured hepatocytes exposed to plasma. Biotechnology and Bioengineering, 2003, 81, 33-49.	1.7	75

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19	Intrahepatic amino acid and glucose metabolism in a ?-galactosamineâ€“induced rat liver failure model. Hepatology, 2001, 34, 360-371.	3.6	66
20	Rational identification of diet-derived postbiotics for improving intestinal microbiota function. Current Opinion in Biotechnology, 2014, 26, 85-90.	3.3	65
21	Identification of neutrophil gelatinase-associated lipocalin (NGAL) as a discriminatory marker of the hepatocyte-secreted protein response to IL-1Î²: a proteomic analysis. Biotechnology and Bioengineering, 2005, 91, 502-515.	1.7	60
22	Profiling of dynamic changes in hypermetabolic livers. Biotechnology and Bioengineering, 2003, 83, 400-415.	1.7	58
23	Metabolic flux analysis of hepatocyte function in hormone- and amino acid-supplemented plasma. Metabolic Engineering, 2003, 5, 1-15.	3.6	57
24	Phagocytosis and remodeling of collagen matrices. Experimental Cell Research, 2007, 313, 1045-1055.	1.2	55
25	Monoethylhexyl Phthalate Elicits an Inflammatory Response in Adipocytes Characterized by Alterations in Lipid and Cytokine Pathways. Environmental Health Perspectives, 2017, 125, 615-622.	2.8	47
26	Adipogenesis of adipose-derived stem cells may be regulated via the cytoskeleton at physiological oxygen levels in vitro. Stem Cell Research and Therapy, 2013, 4, 79.	2.4	45
27	Effects of forced uncoupling protein 1 expression in 3T3-L1 cells on mitochondrial function and lipid metabolism. Journal of Lipid Research, 2007, 48, 826-836.	2.0	44
28	Metabolic Flux Analysis: A Powerful Tool for Monitoring Tissue Function. Tissue Engineering, 1999, 5, 347-368.	4.9	42
29	Identification of distributed metabolic objectives in the hypermetabolic liver by flux and energy balance analysis. Metabolic Engineering, 2006, 8, 30-45.	3.6	41
30	Environmental Chemical Diethylhexyl Phthalate Alters Intestinal Microbiota Community Structure and Metabolite Profile in Mice. MSystems, 2019, 4, .	1.7	41
31	Biologically Consistent Annotation of Metabolomics Data. Analytical Chemistry, 2017, 89, 13097-13104.	3.2	39
32	Enhanced Proliferation of Human Umbilical Vein Endothelial Cells and Differentiation of 3T3-L1 Adipocytes in Coculture. Tissue Engineering - Part A, 2009, 15, 1053-1061.	1.6	38
33	N-acetylglucosamine 6-Phosphate Deacetylase (nagA) Is Required for N-acetyl Glucosamine Assimilation in Gluconacetobacter xylinus. PLoS ONE, 2011, 6, e18099.	1.1	37
34	Hypoxia and Amino Acid Supplementation Synergistically Promote the Osteogenesis of Human Mesenchymal Stem Cells on Silk Protein Scaffolds. Tissue Engineering - Part A, 2010, 16, 3623-3634.	1.6	35
35	Probabilistic pathway construction. Metabolic Engineering, 2011, 13, 435-444.	3.6	34
36	Dynamic model for CHO cell engineering. Journal of Biotechnology, 2012, 158, 24-33.	1.9	34

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37	Flux profile and modularity analysis of time-dependent metabolic changes of de novo adipocyte formation. American Journal of Physiology - Endocrinology and Metabolism, 2007, 292, E1637-E1646.	1.8	33
38	Utilizing elementary mode analysis, pathway thermodynamics, and a genetic algorithm for metabolic flux determination and optimal metabolic network design. BMC Systems Biology, 2010, 4, 49.	3.0	33
39	Systems biology of adipose tissue metabolism: regulation of growth, signaling and inflammation. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2013, 5, 425-447.	6.6	32
40	Impact of perturbed pyruvate metabolism on adipocyte triglyceride accumulation. Metabolic Engineering, 2009, 11, 382-390.	3.6	31
41	Engineering Selectively Targeting Antimicrobial Peptides. Annual Review of Biomedical Engineering, 2021, 23, 339-357.	5.7	31
42	Metabolic Flux Analysis of Mitochondrial Uncoupling in 3T3-L1 Adipocytes. PLoS ONE, 2009, 4, e7000.	1.1	30
43	Ridinilazole, a narrow spectrum antibiotic for treatment of Clostridioides difficile infection, enhances preservation of microbiota-dependent bile acids. American Journal of Physiology - Renal Physiology, 2020, 319, G227-G237.	1.6	29
44	PROXIMAL: a method for Prediction of Xenobiotic Metabolism. BMC Systems Biology, 2015, 9, 94.	3.0	28
45	Isoflavones as Ah Receptor Agonists in Colon-Derived Cell Lines: Structureâ€“Activity Relationships. Chemical Research in Toxicology, 2019, 32, 2353-2364.	1.7	25
46	Adipocyte Induction of Preadipocyte Differentiation in a Gradient Chamber. Tissue Engineering - Part C: Methods, 2012, 18, 958-967.	1.1	24
47	Modular decomposition of metabolic reaction networks based on flux analysis and pathway projection. Bioinformatics, 2007, 23, 2433-2440.	1.8	22
48	Effect of diet and intestinal AhR expression on fecal microbiome and metabolomic profiles. Microbial Cell Factories, 2020, 19, 219.	1.9	22
49	Towards high resolution analysis of metabolic flux in cells and tissues. Current Opinion in Biotechnology, 2013, 24, 933-939.	3.3	21
50	Identification of Biochemical Network Modules Based on Shortest Retroactive Distances. PLoS Computational Biology, 2011, 7, e1002262.	1.5	17
51	Engineering E. coli for triglyceride accumulation through native and heterologous metabolic reactions. Applied Microbiology and Biotechnology, 2013, 97, 2753-2759.	1.7	17
52	Induction of a hypermetabolic state in cultured hepatocytes by glucagon and H2O2. Metabolic Engineering, 2003, 5, 221-229.	3.6	16
53	Extracellular matrix remodelingâ€”Methods to quantify cellâ€“matrix interactions. Biomaterials, 2007, 28, 151-161.	5.7	16
54	Computational analysis of phenotypic space in heterologous polyketide biosynthesisâ€”Applications to Escherichia coli, Bacillus subtilis, and Saccharomyces cerevisiae. Journal of Theoretical Biology, 2010, 262, 197-207.	0.8	16

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55	Using Metabolomics to Identify Cell Line-Independent Indicators of Growth Inhibition for Chinese Hamster Ovary Cell-Based Bioprocesses. Metabolites, 2020, 10, 199.	1.3	15
56	Dietary spinach reshapes the gut microbiome in an Apc-mutant genetic background: mechanistic insights from integrated multi-omics. Gut Microbes, 2021, 13, 1972756.	4.3	15
57	Biological Filtering and Substrate Promiscuity Prediction for Annotating Untargeted Metabolomics. Metabolites, 2020, 10, 160.	1.3	14
58	Identification of optimal classification functions for biological sample and state discrimination from metabolic profiling data. Bioinformatics, 2004, 20, 959-969.	1.8	12
59	Bioengineered models of Parkinsonâ€™s disease using patient-derived dopaminergic neurons exhibit distinct biological profiles in a 3D microenvironment. Cellular and Molecular Life Sciences, 2022, 79, 78.	2.4	12
60	Analysis of Transcription Factor Network Underlying 3T3-L1 Adipocyte Differentiation. PLoS ONE, 2014, 9, e100177.	1.1	11
61	Effect of uncoupling proteinâ€1 expression on 3T3â€L1 adipocyte gene expression. FEBS Letters, 2007, 581, 5865-5871.	1.3	10
62	Discovery of substrate cycles in large scale metabolic networks using hierarchical modularity. BMC Systems Biology, 2015, 9, 5.	3.0	10
63	Interactions between gut microbiota and non-alcoholic liver disease: The role of microbiota-derived metabolites. Pharmacological Research, 2019, 142, 314.	3.1	10
64	Tissue, cell and engineering. Current Opinion in Biotechnology, 2013, 24, 827-829.	3.3	9
65	Sequential Parameter Estimation for Mammalian Cell Model Based on In Silico Design of Experiments. Processes, 2018, 6, 100.	1.3	9
66	Emerging computational tools and models for studying gut microbiota composition and function. Current Opinion in Biotechnology, 2020, 66, 301-311.	3.3	9
67	A Metabolomics Approach to Increasing Chinese Hamster Ovary (CHO) Cell Productivity. Metabolites, 2021, 11, 823.	1.3	9
68	Probabilistic strain optimization under constraint uncertainty. BMC Systems Biology, 2013, 7, 29.	3.0	7
69	Automated Image Processing for Spatially Resolved Analysis of Lipid Droplets in Cultured 3T3-L1 Adipocytes. Tissue Engineering - Part C: Methods, 2015, 21, 605-613.	1.1	7
70	Biological engineering. Current Opinion in Chemical Engineering, 2013, 2, 1-2.	3.8	5
71	Untargeted proteomics reveals upregulation of stress response pathways during CHO-based monoclonal antibody manufacturing process leading to disulfide bond reduction. MAbs, 2021, 13, 1963094.	2.6	5
72	Metabolic Flux-Based Modularity using Shortest Retroactive distances. BMC Systems Biology, 2012, 6, 155.	3.0	4

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73	<italic>PreProPath</italic>: An Uncertainty-Aware Algorithm for Identifying Predictable Profitable Pathways in Biochemical Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 1405-1415.	1.9	4
74	Extracellular Matrix Remodeling and Mechanical Stresses as Modulators of Adipose Tissue Metabolism and Inflammation. Studies in Mechanobiology, Tissue Engineering and Biomaterials, 2013, , 105-122.	0.7	3
75	Effect of Norepinephrine on Gut Bacterial Community Structure and Function. FASEB Journal, 2019, 33, 724.4.	0.2	3
76	Metabolomics of Acute vs. Chronic Spinach Intake in an Apcâ€“Mutant Genetic Background: Linoleate and Butanoate Metabolites Targeting HDAC Activity and IFNâ€“Î³ Signaling. Cells, 2022, 11, 573.	1.8	3
77	Tendency Stoichiometric Modeling of Metabolic Pathways. Proceedings of the American Control Conference, 2007, , .	0.0	0
78	Editorial overview: Tissue, cell and pathway engineering. Current Opinion in Biotechnology, 2016, 40, iv-vi.	3.3	0