Sunjae Lee

List of Publications by Year
in descending order

42 papers	6,936 citations	331670 21 h-index	302126 39 g-index
50 all docs	50 docs citations	50 times ranked	14380 citing authors

#	Article	IF	Citations
1	Rifaximin-α reduces gut-derived inflammation and mucin degradation in cirrhosis and encephalopathy: RIFSYS randomised controlled trial. Journal of Hepatology, 2022, 76, 332-342.	3.7	79
2	A Genome-Wide Screen Reveals That Endocytic Genes Are Important for Pma1p Asymmetry during Cell Division in Saccharomyces cerevisiae. International Journal of Molecular Sciences, 2022, 23, 2364.	4.1	2
3	SRSF6 Regulates the Alternative Splicing of the Apoptotic Fas Gene by Targeting a Novel RNA Sequence. Cancers, 2022, 14, 1990.	3.7	6
4	Mitoribosomal defects aggravate liver cancer via aberrant glycolytic flux and T cell exhaustion. , 2022, 10, e004337.		12
5	Genome-scale metabolic modelling of the human gut microbiome reveals changes in the glyoxylate and dicarboxylate metabolism in metabolic disorders. IScience, 2022, 25, 104513.	4.1	15
6	Acute kidney injury leading to CKD is associated with a persistence of metabolic dysfunction and hypertriglyceridemia. IScience, 2021, 24, 102046.	4.1	22
7	A Systems Biology Approach to Investigating the Interaction between Serotonin Synthesis by Tryptophan Hydroxylase and the Metabolic Homeostasis. International Journal of Molecular Sciences, 2021, 22, 2452.	4.1	12
8	Systematic analysis of gut microbiome reveals the role of bacterial folate and homocysteine metabolism in Parkinson's disease. Cell Reports, 2021, 34, 108807.	6.4	77
9	NSrp70 is a lymphocyte-essential splicing factor that controls thymocyte development. Nucleic Acids Research, 2021, 49, 5760-5778.	14.5	5
10	Aberrant activation of the CD45-Wnt signaling axis promotes stemness and therapy resistance in colorectal cancer cells. Theranostics, 2021, 11, 8755-8770.	10.0	19
11	Precise Characterization of Genetic Interactions in Cancer via Molecular Network Refining Processes. International Journal of Molecular Sciences, 2021, 22, 11114.	4.1	1
12	Compositional and functional differences of the mucosal microbiota along the intestine of healthy individuals. Scientific Reports, 2020, 10, 14977.	3.3	78
13	Integration of molecular profiles in a longitudinal wellness profiling cohort. Nature Communications, 2020, 11, 4487.	12.8	66
14	MEMOTE for standardized genome-scale metabolic model testing. Nature Biotechnology, 2020, 38, 272-276.	17.5	314
15	Abundance and diversity of resistomes differ between healthy human oral cavities and gut. Nature Communications, 2020, 11, 693.	12.8	49
16	Systems Biology: A Multi-Omics Integration Approach to Metabolism and the Microbiome. Endocrinology and Metabolism, 2020, 35, 507-514.	3.0	7
17	The Intestine Harbors Functionally Distinct Homeostatic Tissue-Resident and Inflammatory Th17 Cells. Immunity, 2019, 51, 77-89.e6.	14.3	220
18	Simplified Intestinal Microbiota to Study Microbe-Diet-Host Interactions in a Mouse Model. Cell Reports, 2019, 26, 3772-3783.e6.	6.4	61

#	ARTICLE	IF	CITATIONS
19	Mature Human White Adipocytes Cultured under Membranes Maintain Identity, Function, and Can Transdifferentiate into Brown-like Adipocytes. Cell Reports, 2019, 27, 213-225.e5.	6.4	83
20	Characterization of heterogeneous redox responses in hepatocellular carcinoma patients using network analysis. EBioMedicine, 2019, 40, 471-487.	6.1	38
21	Pyruvate kinase L/R is a regulator of lipid metabolism and mitochondrial function. Metabolic Engineering, 2019, 52, 263-272.	7.0	37
22	An Integrated Understanding of the Rapid Metabolic Benefits of a Carbohydrate-Restricted Diet on Hepatic Steatosis in Humans. Cell Metabolism, 2018, 27, 559-571.e5.	16.2	321
23	Integrative Personal Omics Profiles during Periods of Weight Gain and Loss. Cell Systems, 2018, 6, 157-170.e8.	6.2	183
24	TCSBN: a database of tissue and cancer specific biological networks. Nucleic Acids Research, 2018, 46, D595-D600.	14.5	55
25	ESS: A Tool for Genome-Scale Quantification of Essentiality Score for Reaction/Genes in Constraint-Based Modeling. Frontiers in Physiology, 2018, 9, 1355.	2.8	8
26	A subcellular map of the human proteome. Science, 2017, 356, .	12.6	2,079
27	Network analyses identify liver€specific targets for treating liver diseases. Molecular Systems Biology, 2017, 13, 938.	7.2	112
28	Improving the economics of NASH/NAFLD treatment through the use of systems biology. Drug Discovery Today, 2017, 22, 1532-1538.	6.4	28
29	A pathology atlas of the human cancer transcriptome. Science, 2017, 357, .	12.6	2,570
30	Investigating the Combinatory Effects of Biological Networks on Gene Co-expression. Frontiers in Physiology, 2016, 7, 160.	2.8	7
31	Dysregulated signaling hubs of liver lipid metabolism reveal hepatocellular carcinoma pathogenesis. Nucleic Acids Research, 2016, 44, 5529-5539.	14.5	35
32	Integrated Network Analysis Reveals an Association between Plasma Mannose Levels and Insulin Resistance. Cell Metabolism, 2016, 24, 172-184.	16.2	133
33	Predicting unintended effects of drugs based on off-target tissue effects. Biochemical and Biophysical Research Communications, 2016, 469, 399-404.	2.1	18
34	Anomalies in Network Bridges Involved in Bile Acid Metabolism Predict Outcomes of Colorectal Cancer Patients. PLoS ONE, 2014, 9, e107925.	2.5	4
35	Rule-based multi-scale simulation for drug effect pathway analysis. BMC Medical Informatics and Decision Making, 2013, 13, S4.	3.0	15
36	Systematic approach for analyzing drug combination by using target-enzyme distance. Interdisciplinary Bio Central, 2013, 5, 1-7.	0.1	0

#	Article	IF	Citations
37	Rule-based whole body modeling for analyzing multi-compound effects. , 2012, , .		2
38	Prioritization of SNPs for Genome-Wide Association Studies Using an Interaction Model of Genetic Variation, Gene Expression, and Trait Variation. Molecules and Cells, 2012, 33, 351-362.	2.6	2
39	Synthetic inter-species cooperation of host and virus for targeted genetic evolution. Journal of Biotechnology, 2011, 153, 35-41.	3.8	5
40	Mathematical modeling of translation initiation for the estimation of its efficiency to computationally design mRNA sequences with desired expression levels in prokaryotes. BMC Systems Biology, 2010, 4, 71.	3.0	82
41	bZIPDB : A database of regulatory information for human bZIP transcription factors. BMC Genomics, 2007, 8, 136.	2.8	13
42	Network Analysis Reveals Heterogeneous Response of Redox Metabolism in Hepatocellular Carcinoma Patients. SSRN Electronic Journal, 0, , .	0.4	0