

# Hyun Seok Kim

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9335426/publications.pdf>

Version: 2024-02-01

30  
papers

1,129  
citations

566801

15  
h-index

454577

30  
g-index

31  
all docs

31  
docs citations

31  
times ranked

2578  
citing authors

#	ARTICLE	IF	CITATIONS
1	XPO1-dependent nuclear export is a druggable vulnerability in KRAS-mutant lung cancer. <i>Nature</i> , 2016, 538, 114-117.	13.7	162
2	Systematic Identification of Molecular Subtype-Selective Vulnerabilities in Non-Small-Cell Lung Cancer. <i>Cell</i> , 2013, 155, 552-566.	13.5	151
3	Metabolic Diversity in Human Non-Small Cell Lung Cancer Cells. <i>Molecular Cell</i> , 2019, 76, 838-851.e5.	4.5	119
4	Chemistry-First Approach for Nomination of Personalized Treatment in Lung Cancer. <i>Cell</i> , 2018, 173, 864-878.e29.	13.5	102
5	Selective Cytotoxicity of the NAMPT Inhibitor FK866 Toward Gastric Cancer Cells With Markers of the Epithelial-Mesenchymal Transition, Due to Loss of NAPRT. <i>Gastroenterology</i> , 2018, 155, 799-814.e13.	0.6	83
6	Using Functional Signature Ontology (FUSION) to Identify Mechanisms of Action for Natural Products. <i>Science Signaling</i> , 2013, 6, ra90.	1.6	66
7	Cross-species oncogenic signatures of breast cancer in canine mammary tumors. <i>Nature Communications</i> , 2020, 11, 3616.	5.8	58
8	Mode of action and pharmacogenomic biomarkers for exceptional responders to didemnin B. <i>Nature Chemical Biology</i> , 2015, 11, 401-408.	3.9	54
9	Integrated pharmaco-proteogenomics defines two subgroups in isocitrate dehydrogenase wild-type glioblastoma with prognostic and therapeutic opportunities. <i>Nature Communications</i> , 2020, 11, 3288.	5.8	44
10	Regulation of La/SSB-dependent viral gene expression by pre-tRNA 3' trailer-derived tRNA fragments. <i>Nucleic Acids Research</i> , 2019, 47, 9888-9901.	6.5	41
11	AMPK Promotes Aberrant PGC1 $\beta$ Expression To Support Human Colon Tumor Cell Survival. <i>Molecular and Cellular Biology</i> , 2015, 35, 3866-3879.	1.1	33
12	Cancer-Specific Production of N-Acetylaspartate via NAT8L Overexpression in Non-Small Cell Lung Cancer and Its Potential as a Circulating Biomarker. <i>Cancer Prevention Research</i> , 2016, 9, 43-52.	0.7	33
13	A Noncomplementation Screen for Quantitative Trait Alleles in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 753-760.	0.8	21
14	Computational detection and suppression of sequence-specific off-target phenotypes from whole genome RNAi screens. <i>Nucleic Acids Research</i> , 2014, 42, 8214-8222.	6.5	20
15	Meta-Analysis of Large-Scale Toxicogenomic Data Finds Neuronal Regeneration Related Protein and Cathepsin D to Be Novel Biomarkers of Drug-Induced Toxicity. <i>PLoS ONE</i> , 2015, 10, e0136698.	1.1	16
16	Pharmacogenomic Analysis Reveals CCNA2 as a Predictive Biomarker of Sensitivity to Polo-Like Kinase I Inhibitor in Gastric Cancer. <i>Cancers</i> , 2020, 12, 1418.	1.7	15
17	Snail acetylation by autophagy-derived acetyl-coenzyme A promotes invasion and metastasis of KRAS-mutated lung cancer cells. <i>Cancer Communications</i> , 2022, 42, 716-749.	3.7	15
18	Cancer Cell Line Panels Empower Genomics-Based Discovery of Precision Cancer Medicine. <i>Yonsei Medical Journal</i> , 2015, 56, 1186.	0.9	14

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19	A Functional Signature Ontology (FUSION) screen detects an AMPK inhibitor with selective toxicity toward human colon tumor cells. <i>Scientific Reports</i> , 2018, 8, 3770.	1.6	14
20	Multi-layered proteogenomic analysis unravels cancer metastasis directed by MMP-2 and focal adhesion kinase signaling. <i>Scientific Reports</i> , 2021, 11, 17130.	1.6	14
21	Computational discovery of pathway-level genetic vulnerabilities in non-small-cell lung cancer. <i>Bioinformatics</i> , 2016, 32, 1373-1379.	1.8	11
22	A genome-scale screen reveals context-dependent ovarian cancer sensitivity to miRNA overexpression. <i>Molecular Systems Biology</i> , 2015, 11, 842.	3.2	10
23	A Genome-wide Functional Signature Ontology Map and Applications to Natural Product Mechanism of Action Discovery. <i>Cell Chemical Biology</i> , 2019, 26, 1380-1392.e6.	2.5	8
24	siMacro: A Fast and Easy Data Processing Tool for Cell-Based Genomewide siRNA Screens. <i>Genomics and Informatics</i> , 2013, 11, 55.	0.4	7
25	Somatic mutation driven codon transition bias in human cancer. <i>Scientific Reports</i> , 2017, 7, 14204.	1.6	5
26	Identification of Pharmacologically Tractable Protein Complexes in Cancer Using the R-Based Network Clustering and Visualization Program MCODER. <i>BioMed Research International</i> , 2017, 2017, 1-8.	0.9	4
27	Gold(I)-Catalyzed Intramolecular Hydrothiophenylation of <i>N</i> -Thiophen-3-yl Alkynylamides for Accessing Thieno[3,2- <i>b</i> ]pyridine-5(4 <i>H</i> )-ones: Development of F-Actin Specific Fluorescent Probes. <i>Journal of Organic Chemistry</i> , 2022, 87, 4936-4950.	1.7	4
28	High-throughput identification of protein functional similarities using a gene-expression-based siRNA screen. <i>Scientific Data</i> , 2020, 7, 27.	2.4	2
29	Emerging power of proteomics for delineation of intrinsic tumor subtypes and resistance mechanisms to anti-cancer therapies. <i>Expert Review of Proteomics</i> , 2016, 13, 929-939.	1.3	1
30	Establishment of reference standards for multifaceted mosaic variant analysis. <i>Scientific Data</i> , 2022, 9, 35.	2.4	1