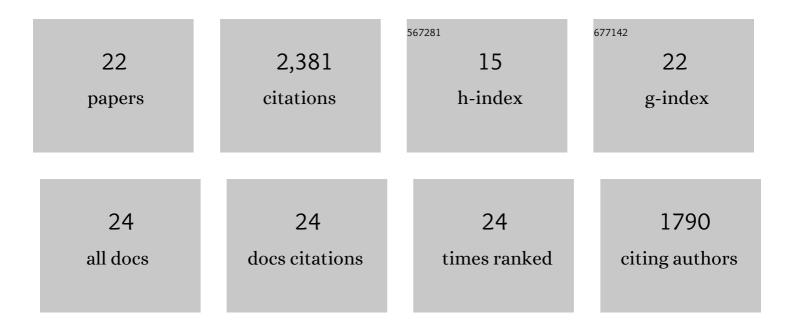
Seokhee Kim

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7567082/publications.pdf Version: 2024-02-01



SEOKHEE KIM

#	Article	IF	CITATIONS
1	Identification of a Multicomponent Complex Required for Outer Membrane Biogenesis in Escherichia coli. Cell, 2005, 121, 235-245.	28.9	656
2	New developments in RiPP discovery, enzymology and engineering. Natural Product Reports, 2021, 38, 130-239.	10.3	412
3	Structure and Function of an Essential Component of the Outer Membrane Protein Assembly Machine. Science, 2007, 317, 961-964.	12.6	327
4	YfiO stabilizes the YaeT complex and is essential for outer membrane protein assembly in Escherichia $\hat{a} \in f$ coli. Molecular Microbiology, 2006, 61, 151-164.	2.5	278
5	Reconstitution of Outer Membrane Protein Assembly from Purified Components. Science, 2010, 328, 890-892.	12.6	243
6	Covalent Linkage of Distinct Substrate Degrons Controls Assembly and Disassembly of DegP Proteolytic Cages. Cell, 2011, 145, 67-78.	28.9	81
7	Cage assembly of DegP protease is not required for substrate-dependent regulation of proteolytic activity or high-temperature cell survival. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 7263-7268.	7.1	51
8	Enzymatic Cross-Linking of Side Chains Generates a Modified Peptide with Four Hairpin-like Bicyclic Repeats. Biochemistry, 2017, 56, 4927-4930.	2.5	42
9	In vivo hypermutation and continuous evolution. Nature Reviews Methods Primers, 2022, 2, .	21.2	39
10	Genome Mining Reveals High Topological Diversity of ω-Ester-Containing Peptides and Divergent Evolution of ATP-Grasp Macrocyclases. Journal of the American Chemical Society, 2020, 142, 3013-3023.	13.7	37
11	Gene-specific mutagenesis enables rapid continuous evolution of enzymes <i>in vivo</i> . Nucleic Acids Research, 2021, 49, e32-e32.	14.5	37
12	A Conserved Activation Cluster Is Required for Allosteric Communication in HtrA-Family Proteases. Structure, 2015, 23, 517-526.	3.3	32
13	Distinct regulatory mechanisms balance DegP proteolysis to maintain cellular fitness during heat stress. Genes and Development, 2014, 28, 902-911.	5.9	29
14	A Topologically Distinct Modified Peptide with Multiple Bicyclic Core Motifs Expands the Diversity of Microviridin‣ike Peptides. ChemBioChem, 2019, 20, 1051-1059.	2.6	29
15	Introduction of Bifunctionality into the Multidomain Architecture of the ï‰-Ester-Containing Peptide Plesiocin. Biochemistry, 2020, 59, 285-289.	2.5	20
16	Over-activation of a nonessential bacterial protease DegP as an antibiotic strategy. Communications Biology, 2020, 3, 547.	4.4	20
17	Molecular mechanism underlying substrate recognition of the peptide macrocyclase PsnB. Nature Chemical Biology, 2021, 17, 1123-1131.	8.0	18
18	Bioinformatic Expansion of Borosins Uncovers Trans-Acting Peptide Backbone <i>N</i> -Methyltransferases in Bacteria. Biochemistry, 2022, 61, 183-194.	2.5	11

SEOKHEE KIM

#	Article	IF	CITATIONS
19	Development of a genome-targeting mutator for the adaptive evolution of microbial cells. Nucleic Acids Research, 2022, 50, e38-e38.	14.5	7
20	A Small Periplasmic Protein with a Hydrophobic C-Terminal Residue Enhances DegP Proteolysis as a Suicide Activator. Journal of Bacteriology, 2018, 200, .	2.2	6
21	Tripodal Lipoprotein Variants with C-Terminal Hydrophobic Residues Allosterically Modulate Activity of the DegP Protease. Journal of Molecular Biology, 2017, 429, 3090-3101.	4.2	5
22	Identification of Nucleophilic Probes for Protease-Mediated Transpeptidation. Molecules, 2018, 23, 2109.	3.8	1