

# Sung Joon Kim

## List of Publications by Year in descending order

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45  
papers

1,590  
citations

279701

23  
h-index

315616

38  
g-index

48  
all docs

48  
docs citations

48  
times ranked

1387  
citing authors

#	ARTICLE	IF	CITATIONS
1	Peptidoglycan architecture of Gram-positive bacteria by solid-state NMR. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015, 1848, 350-362.	1.4	137
2	Oritavancin Exhibits Dual Mode of Action to Inhibit Cell-Wall Biosynthesis in <i>Staphylococcus aureus</i> . <i>Journal of Molecular Biology</i> , 2008, 377, 281-293.	2.0	129
3	Structures of <i>Staphylococcus aureus</i> Cell-Wall Complexes with Vancomycin, Eremomycin, and Chloroeremomycin Derivatives by $^{13}\text{C}\{^{19}\text{F}\}$ and $^{15}\text{N}\{^{19}\text{F}\}$ Rotational-Echo Double Resonance. <i>Biochemistry</i> , 2006, 45, 5235-5250.	1.2	85
4	Rotational-Echo Double Resonance Characterization of Vancomycin Binding Sites in <i>Staphylococcus aureus</i> . <i>Biochemistry</i> , 2002, 41, 6967-6977.	1.2	80
5	Secondary Structure and Lipid Contact of a Peptide Antibiotic in Phospholipid Bilayers by REDOR. <i>Biophysical Journal</i> , 2004, 87, 662-674.	0.2	74
6	Vancomycin and Oritavancin Have Different Modes of Action in <i>Enterococcus faecium</i> . <i>Journal of Molecular Biology</i> , 2009, 392, 1178-1191.	2.0	74
7	Rotational-Echo Double Resonance Characterization of the Effects of Vancomycin on Cell Wall Synthesis in <i>Staphylococcus aureus</i> . <i>Biochemistry</i> , 2002, 41, 13053-13058.	1.2	72
8	Vancomycin Derivative with Damaged $\text{D-Ala-D-Ala}$ Binding Cleft Binds to Cross-linked Peptidoglycan in the Cell Wall of <i>Staphylococcus aureus</i> . <i>Biochemistry</i> , 2008, 47, 3822-3831.	1.2	68
9	Insights into Key Interactions between Vancomycin and Bacterial Cell Wall Structures. <i>ACS Omega</i> , 2018, 3, 37-45.	1.6	56
10	<i>Staphylococcus aureus</i> Peptidoglycan Tertiary Structure from Carbon-13 Spin Diffusion. <i>Journal of the American Chemical Society</i> , 2009, 131, 7023-7030.	6.6	53
11	Cross-Link Formation and Peptidoglycan Lattice Assembly in the FemA Mutant of <i>Staphylococcus aureus</i> . <i>Biochemistry</i> , 2014, 53, 1420-1427.	1.2	46
12	L,D-Transpeptidase Specific Probe Reveals Spatial Activity of Peptidoglycan Cross-Linking. <i>ACS Chemical Biology</i> , 2019, 14, 2185-2196.	1.6	45
13	<i>Staphylococcus aureus</i> Peptidoglycan Stem Packing by Rotational-Echo Double Resonance NMR Spectroscopy. <i>Biochemistry</i> , 2013, 52, 3651-3659.	1.2	44
14	A Proteolytic Complex Targets Multiple Cell Wall Hydrolases in <i>Pseudomonas aeruginosa</i> . <i>MBio</i> , 2018, 9, .	1.8	40
15	The Isotridecanyl Side Chain of Plusbacin-A <sub>3</sub> Is Essential for the Transglycosylase Inhibition of Peptidoglycan Biosynthesis. <i>Biochemistry</i> , 2013, 52, 1973-1979.	1.2	38
16	Locations of the Hydrophobic Side Chains of Lipoglycopeptides Bound to the Peptidoglycan of <i>Staphylococcus aureus</i> . <i>Biochemistry</i> , 2013, 52, 3405-3414.	1.2	37
17	Characterization of Peptidoglycan in <i>Fem</i> -Deletion Mutants of Methicillin-Resistant <i>Staphylococcus aureus</i> by Solid-State NMR. <i>Biochemistry</i> , 2009, 48, 3100-3108.	1.2	33
18	Characterization of the Peptidoglycan of Vancomycin-Susceptible <i>Enterococcus faecium</i> . <i>Biochemistry</i> , 2008, 47, 8378-8385.	1.2	32

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19	Hydrophobic Side-Chain Length Determines Activity and Conformational Heterogeneity of a Vancomycin Derivative Bound to the Cell Wall of <i>Staphylococcus aureus</i> . <i>Biochemistry</i> , 2008, 47, 10155-10161.	1.2	31
20	Solid-state NMR reveals differential carbohydrate utilization in diapausing <i>Culex pipiens</i> . <i>Scientific Reports</i> , 2016, 6, 37350.	1.6	30
21	Oritavancin Binds to Isolated Protoplast Membranes but not Intact Protoplasts of <i>Staphylococcus aureus</i> . <i>Journal of Molecular Biology</i> , 2009, 391, 414-425.	2.0	26
22	An Amidase_3 domain-containing N-acetylmuramyl-L-alanine amidase is required for mycobacterial cell division. <i>Scientific Reports</i> , 2017, 7, 1140.	1.6	26
23	Dsi-RNA knockdown of genes regulated by Foxo reduces glycogen and lipid accumulations in diapausing <i>Culex pipiens</i> . <i>Scientific Reports</i> , 2020, 10, 17201.	1.6	26
24	Peptidoglycan Compositional Analysis of <i>Enterococcus faecalis</i> Biofilm by Stable Isotope Labeling by Amino Acids in a Bacterial Culture. <i>Biochemistry</i> , 2018, 57, 1274-1283.	1.2	25
25	The Contribution of Adjacent Subunits to the Active Sites of d-3-Phosphoglycerate Dehydrogenase. <i>Journal of Biological Chemistry</i> , 1999, 274, 5357-5361.	1.6	24
26	Characterization of the tertiary structure of the peptidoglycan of <i>Enterococcus faecalis</i> . <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2017, 1859, 2171-2180.	1.4	21
27	Solid-state NMR characterization of amphomycin effects on peptidoglycan and wall teichoic acid biosyntheses in <i>Staphylococcus aureus</i> . <i>Scientific Reports</i> , 2016, 6, 31757.	1.6	20
28	Peptidoglycan O-acetylation increases in response to vancomycin treatment in vancomycin-resistant <i>Enterococcus faecalis</i> . <i>Scientific Reports</i> , 2017, 7, 46500.	1.6	18
29	Dual Mode of Action for Plusbacin A <sub>3</sub> in <i>Staphylococcus aureus</i> . <i>Journal of Physical Chemistry B</i> , 2017, 121, 1499-1505.	1.2	17
30	Surface proteins and the formation of biofilms by <i>Staphylococcus aureus</i> . <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2018, 1860, 749-756.	1.4	16
31	Hidden Mode of Action of Glycopeptide Antibiotics: Inhibition of Wall Teichoic Acid Biosynthesis. <i>Journal of Physical Chemistry B</i> , 2017, 121, 3925-3932.	1.2	15
32	Uniformity of Glycyl Bridge Lengths in the Mature Cell Walls of Fem Mutants of Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>Journal of Bacteriology</i> , 2013, 195, 1421-1427.	1.0	14
33	Resuscitation-Promoting Factors Are Required for <i>Mycobacterium smegmatis</i> Biofilm Formation. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	14
34	Suppression of glycogen synthase expression reduces glycogen and lipid storage during mosquito overwintering diapause. <i>Journal of Insect Physiology</i> , 2020, 120, 103971.	0.9	14
35	REDOR constraints on the peptidoglycan lattice architecture of <i>Staphylococcus aureus</i> and its FemA mutant. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015, 1848, 363-368.	1.4	13
36	Inhibition of <i>Staphylococcus aureus</i> Cell Wall Biosynthesis by Desleucyl-Oritavancin: a Quantitative Peptidoglycan Composition Analysis by Mass Spectrometry. <i>Journal of Bacteriology</i> , 2017, 199, .	1.0	13

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37	Quantification of the $\alpha$ -Ala- $\beta$ -Lac-Terminated Peptidoglycan Structure in Vancomycin-Resistant <i>Enterococcus faecalis</i> Using a Combined Solid-State Nuclear Magnetic Resonance and Mass Spectrometry Analysis. <i>Biochemistry</i> , 2017, 56, 612-622.	1.2	13
38	Inhibition of <i>Bacillus anthracis</i> metallo- $\beta$ -lactamase by compounds with hydroxamic acid functionality. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2016, 31, 132-137.	2.5	12
39	Desleucyl-Oritavancin with a Damaged $\alpha$ -Ala- $\beta$ -Ala Binding Site Inhibits the Transpeptidation Step of Cell-Wall Biosynthesis in Whole Cells of <i>Staphylococcus aureus</i> . <i>Biochemistry</i> , 2017, 56, 1529-1535.	1.2	12
40	Molecular Dynamics Simulation of Atomic Interactions in the Vancomycin Binding Site. <i>ACS Omega</i> , 2021, 6, 775-785.	1.6	11
41	Hexaphenylbenzene and hexabenzocoronene-based porous polymers for the adsorption of volatile organic compounds. <i>RSC Advances</i> , 2016, 6, 65763-65769.	1.7	8
42	The Carboxyl Terminus of Eremomycin Facilitates Binding to the Non- $\alpha$ -Ala- $\beta$ -Ala Segment of the Peptidoglycan Pentapeptide Stem. <i>Biochemistry</i> , 2016, 55, 3383-3391.	1.2	8
43	Inhibition of $\alpha$ -Ala incorporation into wall teichoic acid in <i>Staphylococcus aureus</i> by desleucyl-oritavancin. <i>Chemical Communications</i> , 2017, 53, 5649-5652.	2.2	6
44	Peptidoglycan compositional analysis of <i>Mycobacterium smegmatis</i> using high-resolution LC-MS. <i>Scientific Reports</i> , 2022, 12, .	1.6	6
45	Molecular dynamics simulations of the secondary-binding site in disaccharide-modified glycopeptide antibiotics. <i>Scientific Reports</i> , 2022, 12, 7087.	1.6	2