

# Sung-Hou Kim

## List of Publications by Year in descending order

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44  
papers

5,015  
citations

201674

27  
h-index

302126

39  
g-index

51  
all docs

51  
docs citations

51  
times ranked

4457  
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal structure of cyclin-dependent kinase 2. <i>Nature</i> , 1993, 363, 595-602.	27.8	979
2	Inhibition of Cyclin-Dependent Kinases by Purine Analogues. Crystal Structure of Human cdk2 Complexed with Roscovitine. <i>FEBS Journal</i> , 1997, 243, 518-526.	0.2	590
3	Alignment-free genome comparison with feature frequency profiles (FFP) and optimal resolutions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 2677-2682.	7.1	360
4	Crystal structure of an RNA double helix incorporating a track of non-Watson-Crick base pairs. <i>Nature</i> , 1991, 353, 579-581.	27.8	339
5	Multiple modes of ligand recognition: Crystal structures of cyclin-dependent protein kinase 2 in complex with ATP and two inhibitors, olomoucine and isopentenyladenine. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 22, 378-391.	2.6	258
6	Recognition of a protein fold in the context of the SCOP classification. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 35, 401-407.	2.6	218
7	High-Resolution Crystal Structures of Human Cyclin-Dependent Kinase 2 with and without ATP: Bound Waters and Natural Ligand as Guides for Inhibitor Design. <i>Journal of Medicinal Chemistry</i> , 1996, 39, 4540-4546.	6.4	192
8	Physical organization of lipids in the cell wall of <i>Mycobacterium chelonae</i> . <i>Molecular Microbiology</i> , 1993, 8, 1025-1030.	2.5	185
9	Crystal structure of human annexin I at 2.5 Å... resolution. <i>Protein Science</i> , 1993, 2, 448-458.	7.6	163
10	Benchmarking of alignment-free sequence comparison methods. <i>Genome Biology</i> , 2019, 20, 144.	8.8	147
11	Dynamic and clustering model of bacterial chemotaxis receptors: Structural basis for signaling and high sensitivity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 11611-11615.	7.1	141
12	Whole-proteome phylogeny of prokaryotes by feature frequency profiles: An alignment-free method with optimal feature resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 133-138.	7.1	138
13	Structural differences between a ras oncogene protein and the normal protein. <i>Nature</i> , 1989, 337, 90-93.	27.8	136
14	Structure-based identification of a novel NTPase from <i>Methanococcus jannaschii</i> . <i>Nature Structural Biology</i> , 1999, 6, 691-696.	9.7	128
15	Crystal structure of the intensely sweet protein monellin. <i>Nature</i> , 1987, 328, 739-742.	27.8	126
16	A genome Tree of Life for the Fungi kingdom. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 9391-9396.	7.1	116
17	Crystal structure of the Î <sup>2</sup> -glycosidase from the hyperthermophile <i>Thermosphaera aggregans</i> : insights into its activity and thermostability. <i>FEBS Letters</i> , 1999, 445, 375-383.	2.8	71
18	Recognition of a protein fold in the context of the SCOP classification. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 35, 401-407.	2.6	70

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19	Three-dimensional structure of human cyclin H, a positive regulator of the CDK-activating kinase. <i>Nature Structural and Molecular Biology</i> , 1996, 3, 849-855.	8.2	69
20	Prediction of protein folding class from amino acid composition. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 16, 79-91.	2.6	66
21	Whole-genome phylogeny of mammals: Evolutionary information in genic and nongenic regions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 17077-17082.	7.1	64
22	Structure-based functional inference in structural genomics. <i>Journal of Structural and Functional Genomics</i> , 2003, 4, 129-135.	1.2	60
23	â€œFrozenâ€-dynamic dimer model for transmembrane signaling in bacterial chemotaxis receptors. <i>Protein Science</i> , 1994, 3, 159-165.	7.6	50
24	Conformational Studies of Nucleic Acids II. The Conformational Energetics of Commonly Occurring Nucleosides. <i>Journal of Biomolecular Structure and Dynamics</i> , 1985, 3, 99-125.	3.5	44
25	Correlation between chemical modification and surface accessibility in yeast phenylalanine transfer RNA. <i>Biopolymers</i> , 1983, 22, 1145-1166.	2.4	42
26	Determinations of atomic partial charges for nucleic acid constituents from x-ray diffraction data. I. 2â€²-Deoxycytidine-5â€²-monophosphate. <i>Biopolymers</i> , 1985, 24, 327-357.	2.4	42
27	Structural Genomics of Minimal Organisms and Protein Fold Space. <i>Journal of Structural and Functional Genomics</i> , 2005, 6, 63-70.	1.2	29
28	Conformational Studies of Nucleic Acids I. A Rapid and Direct Method for Generating Furanose Coordinates from the Pseudorotation Angle. <i>Journal of Biomolecular Structure and Dynamics</i> , 1985, 3, 85-98.	3.5	25
29	Prediction of inherited genomic susceptibility to 20 common cancer types by a supervised machine-learning method. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1322-1327.	7.1	24
30	Conformational Studies of Nucleic Acids: III. Empirical Multiple Correlation Functions for Nucleic Acid Torsion Angles. <i>Journal of Biomolecular Structure and Dynamics</i> , 1986, 4, 49-67.	3.5	21
31	Conformational Studies of Nucleic Acids: IV. The Conformational Energetics of Oligonucleotides: d(ApApApA) and ApApApA. <i>Journal of Biomolecular Structure and Dynamics</i> , 1986, 4, 69-98.	3.5	17
32	Sweet Proteins. <i>ACS Symposium Series</i> , 1991, , 28-40.	0.5	17
33	Comparison of nitrophenylethyl and hydroxyphenacyl caging groups. <i>Biopolymers</i> , 2001, 62, 147-149.	2.4	17
34	<sup>1</sup> H resonance assignments, secondary structure and general topology of single-chain monellin in solution as determined by <sup>1</sup> H 2D-NMR. <i>Journal of Biomolecular NMR</i> , 1992, 2, 557-572.	2.8	15
35	Whole-proteome tree of life suggests a deep burst of organism diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 3678-3686.	7.1	14
36	Random sequence analysis of genomic DNA of a hyperthermophile: <i>Aquifex pyrophilus</i> . <i>Extremophiles</i> , 1997, 1, 125-134.	2.3	11

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37	Conformational studies of nucleic acids. V. Sequence specificities in the conformational energetics of oligonucleotides: The homo-tetramers. <i>Biopolymers</i> , 1988, 27, 59-77.	2.4	8
38	Empirical prediction of genomic susceptibilities for multiple cancer classes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 1921-1926.	7.1	6
39	Two indices can approximate four hundred and two amino acid properties. , 1999, , .		3
40	Structural Genomics of Minimal Organisms: Pipeline and Results. <i>Methods in Molecular Biology</i> , 2008, 426, 475-496.	0.9	3
41	Symposia lectures. <i>Journal of Biosciences</i> , 1999, 24, 5-31.	1.1	0
42	High-throughput Detergent Exchange Screening Method for Membrane Protein Crystallization. <i>FASEB Journal</i> , 2008, 22, 280-280.	0.5	0
43	THE EFFECT OF DYNAMIC RECEPTOR CLUSTERING ON THE SENSITIVITY OF BIOCHEMICAL SIGNALING. , 1999, , .		0
44	Reply to Li et al.: Organism tree of life: Gene phylogeny vs. whole-proteome phylogeny. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31582-31582.	7.1	0