

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	Whole-proteome tree of life suggests a deep burst of organism diversity. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 3678-3686.	7.1	14
2	Reply to Li et al.: Organism tree of life: Gene phylogeny vs. whole-proteome phylogeny. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 31582-31582.	7.1	0
3	Benchmarking of alignment-free sequence comparison methods. Genome Biology, 2019, 20, 144.	8.8	147
4	Prediction of inherited genomic susceptibility to 20 common cancer types by a supervised machine-learning method. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 1322-1327.	7.1	24
5	A genome Tree of Life for the Fungi kingdom. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 9391-9396.	7.1	116
6	Empirical prediction of genomic susceptibilities for multiple cancer classes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 1921-1926.	7.1	6
7	Whole-proteome phylogeny of prokaryotes by feature frequency profiles: An alignment-free method with optimal feature resolution. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 133-138.	7.1	138
8	Alignment-free genome comparison with feature frequency profiles (FFP) and optimal resolutions. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 2677-2682.	7.1	360
9	Whole-genome phylogeny of mammals: Evolutionary information in genic and nongenic regions. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 17077-17082.	7.1	64
10	Structural Genomics of Minimal Organisms: Pipeline and Results. Methods in Molecular Biology, 2008, 426, 475-496.	0.9	3
11	High-throughput Detergent Exchange Screening Method for Membrane Protein Crystallization. FASEB Journal, 2008, 22, 280-280.	0.5	0
12	Structural Genomics of Minimal Organisms and Protein Fold Space. Journal of Structural and Functional Genomics, 2005, 6, 63-70.	1.2	29
13	Structure-based functional inference in structural genomics. Journal of Structural and Functional Genomics, 2003, 4, 129-135.	1.2	60
14	Dynamic and clustering model of bacterial chemotaxis receptors: Structural basis for signaling and high sensitivity. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 11611-11615.	7.1	141
15	Comparison of nitrophenylethyl and hydroxyphenacyl caging groups. Biopolymers, 2001, 62, 147-149.	2.4	17
16	Structure-based identification of a novel NTPase from Methanococcus jannaschii. Nature Structural Biology, 1999, 6, 691-696.	9.7	128
17	Symposia lectures. Journal of Biosciences, 1999, 24, 5-31.	1.1	0
18	Recognition of a protein fold in the context of the SCOP classification. Proteins: Structure, Function and Bioinformatics, 1999, 35, 401-407.	2.6	218

#	ARTICLE	IF	CITATIONS
19	Two indices can approximate four hundred and two amino acid properties. , 1999, , .		3
20	Crystal structure of the Î ² -glycosidase from the hyperthermophile Thermosphaera aggregans : insights into its activity and thermostability. FEBS Letters, 1999, 445, 375-383.	2.8	71
21	Recognition of a protein fold in the context of the SCOP classification. Proteins: Structure, Function and Bioinformatics, 1999, 35, 401-407.	2.6	70
22	THE EFFECT OF DYNAMIC RECEPTOR CLUSTERING ON THE SENSITIVITY OF BIOCHEMICAL SIGNALING. , 1999, , .		0
23	Inhibition of Cyclin-Dependent Kinases by Purine Analogues. Crystal Structure of Human cdk2 Complexed with Roscovitine. FEBS Journal, 1997, 243, 518-526.	0.2	590
24	Random sequence analysis of genomic DNA of a hyperthermophile: Aquifex pyrophilus. Extremophiles, 1997, 1, 125-134.	2.3	11
25	High-Resolution Crystal Structures of Human Cyclin-Dependent Kinase 2 with and without ATP:â€‰ Bound Waters and Natural Ligand as Guides for Inhibitor Design. Journal of Medicinal Chemistry, 1996, 39, 4540-4546.	6.4	192
26	Three-dimensional structure of human cyclin H, a positive regulator of the CDK-activating kinase. Nature Structural and Molecular Biology, 1996, 3, 849-855.	8.2	69
27	Multiple modes of ligand recognition: Crystal structures of cyclin-dependent protein kinase 2 in complex with ATP and two inhibitors, olomoucine and isopentenyladenine. Proteins: Structure, Function and Bioinformatics, 1995, 22, 378-391.	2.6	258
28	â€‰Frozenâ€‰dynamic dimer model for transmembrane signaling in bacterial chemotaxis receptors. Protein Science, 1994, 3, 159-165.	7.6	50
29	Prediction of protein folding class from amino acid composition. Proteins: Structure, Function and Bioinformatics, 1993, 16, 79-91.	2.6	66
30	Crystal structure of human annexin I at 2.5 Å... resolution. Protein Science, 1993, 2, 448-458.	7.6	163
31	Crystal structure of cyclin-dependent kinase 2. Nature, 1993, 363, 595-602.	27.8	979
32	Physical organization of lipids in the cell wall of Mycobacterium chelonae. Molecular Microbiology, 1993, 8, 1025-1030.	2.5	185
33	1H resonance assignments, secondary structure and general topology of single-chain monellin in solution as determined by1H 2D-NMR. Journal of Biomolecular NMR, 1992, 2, 557-572.	2.8	15
34	Sweet Proteins. ACS Symposium Series, 1991, , 28-40.	0.5	17
35	Crystal structure of an RNA double helix incorporating a track of non-Watsonâ€‰Crick base pairs. Nature, 1991, 353, 579-581.	27.8	339
36	Structural differences between a ras oncogene protein and the normal protein. Nature, 1989, 337, 90-93.	27.8	136

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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	Crystal structure of the intensely sweet protein monellin. <i>Nature</i> , 1987, 328, 739-742.	27.8	126
39	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
40	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
41	Determinations of atomic partial charges for nucleic acid constituents from x-ray diffraction data. I. 2'-Deoxycytidine-5'-monophosphate. <i>Biopolymers</i> , 1985, 24, 327-357.	2.4	42
42	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
43	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
44	Correlation between chemical modification and surface accessibility in yeast phenylalanine transfer RNA. <i>Biopolymers</i> , 1983, 22, 1145-1166.	2.4	42