

# Ki-Hyun Nam

## List of Publications by Year in descending order

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Version: 2024-02-01

105  
papers

2,960  
citations

236612

25  
h-index

189595

50  
g-index

112  
all docs

112  
docs citations

112  
times ranked

3441  
citing authors

#	ARTICLE	IF	CITATIONS
1	Glucose Isomerase: Functions, Structures, and Applications. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 428.	1.3	21
2	Biochemical and Structural Analysis of a Glucose-Tolerant $\beta$ -Glucosidase from the Hemicellulose-Degrading <i>Thermoanaerobacterium saccharolyticum</i> . <i>Molecules</i> , 2022, 27, 290.	1.7	13
3	Processing of Multicrystal Diffraction Patterns in Macromolecular Crystallography Using Serial Crystallography Programs. <i>Crystals</i> , 2022, 12, 103.	1.0	5
4	Serial X-ray Crystallography. <i>Crystals</i> , 2022, 12, 99.	1.0	6
5	Beef tallow injection matrix for serial crystallography. <i>Scientific Reports</i> , 2022, 12, 694.	1.6	18
6	Hit and Indexing Rate in Serial Crystallography: Incomparable Statistics. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 858815.	1.6	3
7	Crystal structure of the domain-swapped dimeric maltodextrin-binding protein MalE from <i>Salmonella enterica</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 613-622.	1.1	2
8	Crystal Structure of Human Lysozyme Complexed with N-Acetyl- $\beta$ -D-glucosamine. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 4363.	1.3	4
9	Metal-Induced Fluorescence Quenching of Photoconvertible Fluorescent Protein DendFP. <i>Molecules</i> , 2022, 27, 2922.	1.7	8
10	Molecular Dynamics From Macromolecule to Small Molecules. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5676.	1.8	1
11	Preliminary XFEL data from spontaneously grown endo-1,4- $\beta$ -xylanase crystals from <i>Hypocrea virens</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2022, 78, 226-231.	0.4	7
12	Allosteric control of type I-A CRISPR-Cas3 complexes and establishment as effective nucleic acid detection and human genome editing tools. <i>Molecular Cell</i> , 2022, 82, 2754-2768.e5.	4.5	23
13	Combination of an inject-and-transfer system for serial femtosecond crystallography. <i>Journal of Applied Crystallography</i> , 2022, 55, 813-822.	1.9	12
14	Structural analysis of metal chelation of the metalloproteinase thermolysin by 1,10-phenanthroline. <i>Journal of Inorganic Biochemistry</i> , 2021, 215, 111319.	1.5	8
15	Spectroscopic Analysis of Fe Ion-Induced Fluorescence Quenching of the Green Fluorescent Protein ZsGreen. <i>Journal of Fluorescence</i> , 2021, 31, 307-314.	1.3	10
16	Structural Flexibility of Peripheral Loops and Extended C-terminal Domain of Short Length Substrate Binding Protein from <i>Rhodothermus marinus</i> . <i>Protein Journal</i> , 2021, 40, 184-191.	0.7	3
17	Molecular Dynamics From Small Molecules to Macromolecules. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3761.	1.8	17
18	Crystal structure of the metal-free state of glucose isomerase reveals its minimal open configuration for metal binding. <i>Biochemical and Biophysical Research Communications</i> , 2021, 547, 69-74.	1.0	7

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19	Room-Temperature Structure of Xylitol-Bound Glucose Isomerase by Serial Crystallography: Xylitol Binding in the M1 Site Induces Release of Metal Bound in the M2 Site. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3892.	1.8	17
20	Polyimide mesh-based sample holder with irregular crystal mounting holes for fixed-target serial crystallography. <i>Scientific Reports</i> , 2021, 11, 13115.	1.6	17
21	Approach of Serial Crystallography II. <i>Crystals</i> , 2021, 11, 655.	1.0	1
22	Crystal structure of human brain-type fatty acid-binding protein FABP7 complexed with palmitic acid. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 954-965.	1.1	10
23	Stable sample delivery in a viscous medium via a polyimide-based single-channel microfluidic chip for serial crystallography. <i>Journal of Applied Crystallography</i> , 2021, 54, 1081-1087.	1.9	13
24	Mechanism for Cas4-assisted directional spacer acquisition in CRISPR-Cas. <i>Nature</i> , 2021, 598, 515-520.	13.7	29
25	Functional and structural analysis of catabolite control protein C that responds to citrate. <i>Scientific Reports</i> , 2021, 11, 20285.	1.6	3
26	Stable sample delivery in viscous media via a capillary for serial crystallography. <i>Journal of Applied Crystallography</i> , 2020, 53, 45-50.	1.9	33
27	Approach of Serial Crystallography. <i>Crystals</i> , 2020, 10, 854.	1.0	9
28	Viscous-medium-based crystal support in a sample holder for fixed-target serial femtosecond crystallography. <i>Journal of Applied Crystallography</i> , 2020, 53, 1051-1059.	1.9	22
29	Lard Injection Matrix for Serial Crystallography. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5977.	1.8	25
30	Fixed-Target Serial Synchrotron Crystallography Using Nylon Mesh and Enclosed Film-Based Sample Holder. <i>Crystals</i> , 2020, 10, 803.	1.0	24
31	Polysaccharide-Based Injection Matrix for Serial Crystallography. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3332.	1.8	25
32	Spectroscopic and Structural Analysis of Cu <sup>2+</sup> -Induced Fluorescence Quenching of ZsYellow. <i>Biosensors</i> , 2020, 10, 29.	2.3	7
33	Shortening injection matrix for serial crystallography. <i>Scientific Reports</i> , 2020, 10, 107.	1.6	28
34	Application of a high-throughput microcrystal delivery system to serial femtosecond crystallography. <i>Journal of Applied Crystallography</i> , 2020, 53, 477-485.	1.9	25
35	Crystal Structure of <i>Aeromonas hydrophila</i> Cytoplasmic 5'-Methylthioadenosine-Adenosylhomocysteine Nucleosidase. <i>Biochemistry</i> , 2019, 58, 3136-3143.	1.2	0
36	Triglycine-Based Approach for Identifying the Substrate Recognition Site of an Enzyme. <i>Crystals</i> , 2019, 9, 444.	1.0	2

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37	Structural insight into the carboxylesterase BioH from <i>Klebsiella pneumoniae</i> . <i>Biochemical and Biophysical Research Communications</i> , 2019, 520, 538-543.	1.0	5
38	Sample delivery using viscous media, a syringe and a syringe pump for serial crystallography. <i>Journal of Synchrotron Radiation</i> , 2019, 26, 1815-1819.	1.0	29
39	Crystal structure of the Siderophore-interacting protein SIP from <i>Aeromonas hydrophila</i> . <i>Biochemical and Biophysical Research Communications</i> , 2019, 519, 23-28.	1.0	2
40	Structural insight of the 5-(Hydroxyethyl)-methylthiazole kinase ThiM involving vitamin B1 biosynthetic pathway from the <i>Klebsiella pneumoniae</i> . <i>Biochemical and Biophysical Research Communications</i> , 2019, 518, 513-518.	1.0	3
41	Structural and functional analyses of the lipase CinB from <i>Enterobacter asburiae</i> . <i>Biochemical and Biophysical Research Communications</i> , 2019, 519, 274-279.	1.0	4
42	Biochemical and structural analysis of the <i>Klebsiella pneumoniae</i> cytidine deaminase CDA. <i>Biochemical and Biophysical Research Communications</i> , 2019, 519, 280-286.	1.0	5
43	Apparent power-law behavior of water's isothermal compressibility and correlation length upon supercooling. <i>Physical Chemistry Chemical Physics</i> , 2019, 21, 26-31.	1.3	28
44	Nylon mesh-based sample holder for fixed-target serial femtosecond crystallography. <i>Scientific Reports</i> , 2019, 9, 6971.	1.6	51
45	Polyacrylamide injection matrix for serial femtosecond crystallography. <i>Scientific Reports</i> , 2019, 9, 2525.	1.6	37
46	Sample Delivery Media for Serial Crystallography. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1094.	1.8	49
47	Enzymatic synthesis of l-fucose from l-fuculose using a fucose isomerase from <i>Raoultella</i> sp. and the biochemical and structural analyses of the enzyme. <i>Biotechnology for Biofuels</i> , 2019, 12, 282.	6.2	13
48	Spectral and structural analysis of a red fluorescent protein from <i>Acropora digitifera</i> . <i>Protein Science</i> , 2019, 28, 375-381.	3.1	9
49	Crystal structure of a substrate-binding protein from <i>Rhodothermus marinus</i> reveals a single $\beta$ -domain. <i>Biochemical and Biophysical Research Communications</i> , 2018, 497, 368-373.	1.0	8
50	Focusing X-ray free-electron laser pulses using Kirkpatrick-Baez mirrors at the NCI hutch of the PAL-XFEL. <i>Journal of Synchrotron Radiation</i> , 2018, 25, 289-292.	1.0	44
51	Structural and Biochemical Analysis of the Citrate-Responsive Mechanism of the Regulatory Domain of Catabolite Control Protein E from <i>Staphylococcus aureus</i> . <i>Biochemistry</i> , 2018, 57, 6054-6060.	1.2	5
52	Spectral and structural analysis of large Stokes shift fluorescent protein dKeima570. <i>Journal of Microbiology</i> , 2018, 56, 822-827.	1.3	4
53	Response to Comment on "Maxima in the thermodynamic response and correlation functions of deeply supercooled water". <i>Science</i> , 2018, 360, .	6.0	25
54	Spectroscopic Analysis of the Cu <sup>2+</sup> -Induced Fluorescence Quenching of Fluorescent Proteins AmCyan and mOrange2. <i>Molecular Biotechnology</i> , 2018, 60, 485-491.	1.3	9

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55	Crystal structure of <i>E. coli</i> ZinT with one zinc-binding mode and complexed with citrate. <i>Biochemical and Biophysical Research Communications</i> , 2018, 500, 139-144.	1.0	8
56	Multifarious injection chamber for molecular structure study (MICOSS) system: development and application for serial femtosecond crystallography at Pohang Accelerator Laboratory X-ray Free-Electron Laser. <i>Journal of Synchrotron Radiation</i> , 2018, 25, 323-328.	1.0	14
57	Crystal structure of the nicotinamidase/pyrazinamidase PncA from <i>Bacillus subtilis</i> . <i>Biochemical and Biophysical Research Communications</i> , 2018, 503, 2906-2911.	1.0	4
58	Structural analysis of substrate recognition by glucose isomerase in Mn <sup>2+</sup> binding mode at M2 site in <i>S. rubiginosus</i> . <i>Biochemical and Biophysical Research Communications</i> , 2018, 503, 770-775.	1.0	18
59	Spacer acquisition mechanism in type II-A CRISPR system. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2018, 74, a444-a444.	0.0	2
60	Hard X-ray free-electron laser with femtosecond-scale timing jitter. <i>Nature Photonics</i> , 2017, 11, 708-713.	15.6	389
61	Crystal structure of glucose isomerase in complex with xylitol inhibitor in one metal binding mode. <i>Biochemical and Biophysical Research Communications</i> , 2017, 493, 666-670.	1.0	13
62	Disruption of the hydrogen bonding network determines the pH-induced non-fluorescent state of the fluorescent protein ZsYellow by protonation of Glu221. <i>Biochemical and Biophysical Research Communications</i> , 2017, 493, 562-567.	1.0	10
63	How type II CRISPR-Cas establish immunity through Cas1-Cas2-mediated spacer integration. <i>Nature</i> , 2017, 550, 137-141.	13.7	111
64	Maxima in the thermodynamic response and correlation functions of deeply supercooled water. <i>Science</i> , 2017, 358, 1589-1593.	6.0	270
65	Construction and Commissioning of PAL-XFEL Facility. <i>Applied Sciences (Switzerland)</i> , 2017, 7, 479.	1.3	108
66	Current status of the CXI beamline at the PAL-XFEL. <i>Journal of the Korean Physical Society</i> , 2016, 69, 1089-1093.	0.3	26
67	Crystal structures of Dronpa complexed with quenchable metal ions provide insight into metal biosensor development. <i>FEBS Letters</i> , 2016, 590, 2982-2990.	1.3	12
68	Crystal structure of <i>Thermoplasma acidophilum</i> XerA recombinase shows large C-shape clamp conformation and cis-cleavage mode for nucleophilic tyrosine. <i>FEBS Letters</i> , 2016, 590, 848-856.	1.3	6
69	Design of a hard X-ray beamline and end-station for pump and probe experiments at Pohang Accelerator Laboratory X-ray Free Electron Laser facility. <i>Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment</i> , 2016, 810, 74-79.	0.7	19
70	Optimization of synergism of a recombinant auxiliary activity 9 from <i>Chaetomium globosum</i> with cellulase in cellulose hydrolysis. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 8537-8547.	1.7	54
71	Characterizing Metal-Dependent Nucleases of CRISPR-Cas Prokaryotic Adaptive Immunity Systems. <i>Methods in Molecular Biology</i> , 2015, 1311, 265-276.	0.4	0
72	Construction status of CXI beamline at PAL-XFEL. <i>Proceedings of SPIE</i> , 2015, , .	0.8	1

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73	Structures of CRISPR Cas3 offer mechanistic insights into Cascade-activated DNA unwinding and degradation. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 771-777.	3.6	167
74	A SAXS Study of the CRISPR Associated Gene (Cas) Csn2 in the Presence and Absence of Calcium Ions. <i>Biophysical Journal</i> , 2013, 104, 252a-253a.	0.2	0
75	Binding characteristics of a bacterial expansin (BsEXLX1) for various types of pretreated lignocellulose. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 5381-5388.	1.7	39
76	A Mutation of the RNA Polymerase $\sigma$ Subunit ( <i>rpoC</i> ) Confers Cephalosporin Resistance in <i>Bacillus subtilis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 56-65.	1.4	33
77	Nucleic acid binding surface and dimer interface revealed by CRISPR-associated CasB protein structures. <i>FEBS Letters</i> , 2012, 586, 3956-3961.	1.3	17
78	Double-stranded Endonuclease Activity in <i>Bacillus halodurans</i> Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)-associated Cas2 Protein. <i>Journal of Biological Chemistry</i> , 2012, 287, 35943-35952.	1.6	78
79	Cas5d Protein Processes Pre-crRNA and Assembles into a Cascade-like Interference Complex in Subtype I-C/D/vulg CRISPR-Cas System. <i>Structure</i> , 2012, 20, 1574-1584.	1.6	192
80	Envelope stress is a trigger of CRISPR RNA-mediated DNA silencing in <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2011, 79, 584-599.	1.2	112
81	Crystal Structure of Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)-associated Csn2 Protein Revealed Ca <sup>2+</sup> -dependent Double-stranded DNA Binding Activity*. <i>Journal of Biological Chemistry</i> , 2011, 286, 30759-30768.	1.6	49
82	Development of Bimolecular Fluorescence Complementation Using Dronpa for Visualization of Protein-Protein Interactions in Cells. <i>Molecular Imaging and Biology</i> , 2010, 12, 468-478.	1.3	26
83	Crystal structure of bacterioferritin from <i>Rhodobacter sphaeroides</i> . <i>Biochemical and Biophysical Research Communications</i> , 2010, 391, 990-994.	1.0	7
84	Structural insights into the substrate recognition properties of $\beta$ -glucosidase. <i>Biochemical and Biophysical Research Communications</i> , 2010, 391, 1131-1135.	1.0	36
85	Structural characterization of the bifunctional glucanase-xylanase CelM2 reveals the metal effect and substrate-binding moiety. <i>Biochemical and Biophysical Research Communications</i> , 2010, 391, 1726-1730.	1.0	9
86	Biochemical and Structural Analysis of Hormone-sensitive Lipase Homolog EstE7: Insight into the Stabilized Dimerization of HSL-Homolog Proteins. <i>Bulletin of the Korean Chemical Society</i> , 2010, 31, 2627-2632.	1.0	4
87	Insight into the antibacterial drug design and architectural mechanism of peptide recognition from the <i>E. faecium</i> peptide deformylase structure. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 261-265.	1.5	3
88	Structural and functional analysis of a novel hormone-sensitive lipase from a metagenome library. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 1036-1040.	1.5	25
89	Cloning, purification and preliminary X-ray crystallographic analysis of a hypothetical protein, MJ0754, from <i>Methanococcus jannaschii</i> DSM 2661. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 1065-1067.	0.7	1
90	Structural insights into the alanine racemase from <i>Enterococcus faecalis</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009, 1794, 1030-1040.	1.1	28

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91	Structural and functional analysis of a novel EstE5 belonging to the subfamily of hormone-sensitive lipase. <i>Biochemical and Biophysical Research Communications</i> , 2009, 379, 553-556.	1.0	35
92	Structural insights of the MenD from <i>Escherichia coli</i> reveal ThDP affinity. <i>Biochemical and Biophysical Research Communications</i> , 2009, 380, 797-801.	1.0	12
93	Crystal structure of an EFPDF complex with Met-Ala-Ser based on crystallographic packing. <i>Biochemical and Biophysical Research Communications</i> , 2009, 381, 630-633.	1.0	4
94	Crystal structure of CelM2, a bifunctional glucanase-xylanase protein from a metagenome library. <i>Biochemical and Biophysical Research Communications</i> , 2009, 383, 183-186.	1.0	23
95	The crystal structure of an HSL-homolog EstE5 complex with PMSF reveals a unique configuration that inhibits the nucleophile Ser144 in catalytic triads. <i>Biochemical and Biophysical Research Communications</i> , 2009, 389, 247-250.	1.0	25
96	Crystal Structure of the Periplasmic Region of MacB, a Noncanonic ABC Transporter. <i>Biochemistry</i> , 2009, 48, 5218-5225.	1.2	44
97	Crystallization and preliminary X-ray crystallographic analysis of the probable tRNA-modification GTPase (TrmE) from <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 1166-1168.	0.7	0
98	Crystal structure of engineered $\beta$ -glucosidase from a soil metagenome. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 788-793.	1.5	18
99	Structural studies of human brain-type creatine kinase complexed with the ADP-Mg <sup>2+</sup> -NO <sup>3-</sup> -creatine transition-state analogue complex. <i>FEBS Letters</i> , 2008, 582, 3959-3965.	1.3	68
100	Crystallization and preliminary X-ray diffraction analysis of 5,10- methylenetetrahydrofolate dehydrogenase/cyclohydrolase from <i>Thermoplasma acidophilum</i> DSM 1728. <i>Journal of Microbiology and Biotechnology</i> , 2008, 18, 283-6.	0.9	2
101	Structural and Mutational Analysis of tRNA Intron-Splicing Endonuclease from <i>Thermoplasma acidophilum</i> DSM 1728: Catalytic Mechanism of tRNA Intron-Splicing Endonucleases. <i>Journal of Bacteriology</i> , 2007, 189, 8339-8346.	1.0	14
102	Structural characterization of the photoswitchable fluorescent protein Dronpa-C62S. <i>Biochemical and Biophysical Research Communications</i> , 2007, 354, 962-967.	1.0	26
103	Crystal structure of the tRNA-specific adenosine deaminase from <i>Streptococcus pyogenes</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 1016-1019.	1.5	7
104	Expression, Purification, and Preliminary X-Ray Crystallographic Analysis of the Complex of G $\beta$ 3-RGS5 from Human with GDP/Mg <sup>2+</sup> /AlF <sub>4</sub> <sup>-</sup> . <i>Protein and Peptide Letters</i> , 2006, 13, 945-949.	0.4	0
105	Crystallization and preliminary X-ray crystallographic analysis of the tRNA-specific adenosine deaminase from <i>Streptococcus pyogenes</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 375-377.	0.7	1