Ki-Hyun Nam

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Hard X-ray free-electron laser with femtosecond-scale timing jitter. Nature Photonics, 2017, 11, 708-713.	31.4	389
2	Maxima in the thermodynamic response and correlation functions of deeply supercooled water. Science, 2017, 358, 1589-1593.	12.6	270
3	Cas5d Protein Processes Pre-crRNA and Assembles into a Cascade-like Interference Complex in Subtype I-C/Dvulg CRISPR-Cas System. Structure, 2012, 20, 1574-1584.	3.3	192
4	Structures of CRISPR Cas3 offer mechanistic insights into Cascade-activated DNA unwinding and degradation. Nature Structural and Molecular Biology, 2014, 21, 771-777.	8.2	167
5	Envelope stress is a trigger of CRISPR RNA-mediated DNA silencing in Escherichia coli. Molecular Microbiology, 2011, 79, 584-599.	2.5	112
6	How type II CRISPR–Cas establish immunity through Cas1–Cas2-mediated spacer integration. Nature, 2017, 550, 137-141.	27.8	111
7	Construction and Commissioning of PAL-XFEL Facility. Applied Sciences (Switzerland), 2017, 7, 479.	2.5	108
8	Double-stranded Endonuclease Activity in Bacillus halodurans Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)-associated Cas2 Protein. Journal of Biological Chemistry, 2012, 287, 35943-35952.	3.4	78
9	Structural studies of human brainâ€type creatine kinase complexed with the ADP–Mg ²⁺ –NO ^{3â^'} –creatine transitionâ€state analogue complex. FEBS Letters, 2008, 582, 3959-3965.	2.8	68
10	Optimization of synergism of a recombinant auxiliary activity 9 from Chaetomium globosum with cellulase in cellulose hydrolysis. Applied Microbiology and Biotechnology, 2015, 99, 8537-8547.	3.6	54
11	Nylon mesh-based sample holder for fixed-target serial femtosecond crystallography. Scientific Reports, 2019, 9, 6971.	3.3	51
12	Crystal Structure of Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)-associated Csn2 Protein Revealed Ca2+-dependent Double-stranded DNA Binding Activity*. Journal of Biological Chemistry, 2011, 286, 30759-30768.	3.4	49
13	Sample Delivery Media for Serial Crystallography. International Journal of Molecular Sciences, 2019, 20, 1094.	4.1	49
14	Crystal Structure of the Periplasmic Region of MacB, a Noncanonic ABC Transporter [,] . Biochemistry, 2009, 48, 5218-5225.	2.5	44
15	Focusing X-ray free-electron laser pulses using Kirkpatrick–Baez mirrors at the NCI hutch of theÂPAL-XFEL. Journal of Synchrotron Radiation, 2018, 25, 289-292.	2.4	44
16	Binding characteristics of a bacterial expansin (BsEXLX1) for various types of pretreated lignocellulose. Applied Microbiology and Biotechnology, 2013, 97, 5381-5388.	3.6	39
17	Polyacrylamide injection matrix for serial femtosecond crystallography. Scientific Reports, 2019, 9, 2525.	3.3	37
18	Structural insights into the substrate recognition properties of Î ² -glucosidase. Biochemical and Biophysical Research Communications, 2010, 391, 1131-1135.	2.1	36

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19	Structural and functional analysis of a novel EstE5 belonging to the subfamily of hormone-sensitive lipase. Biochemical and Biophysical Research Communications, 2009, 379, 553-556.	2.1	35
20	A Mutation of the RNA Polymerase β′ Subunit (<i>rpoC</i>) Confers Cephalosporin Resistance in Bacillus subtilis. Antimicrobial Agents and Chemotherapy, 2013, 57, 56-65.	3.2	33
21	Stable sample delivery in viscous media via a capillary for serial crystallography. Journal of Applied Crystallography, 2020, 53, 45-50.	4.5	33
22	Sample delivery using viscous media, a syringe andÂaÂsyringe pump for serial crystallography. Journal of Synchrotron Radiation, 2019, 26, 1815-1819.	2.4	29
23	Mechanism for Cas4-assisted directional spacer acquisition in CRISPR–Cas. Nature, 2021, 598, 515-520.	27.8	29
24	Structural insights into the alanine racemase from Enterococcus faecalis. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2009, 1794, 1030-1040.	2.3	28
25	Apparent power-law behavior of water's isothermal compressibility and correlation length upon supercooling. Physical Chemistry Chemical Physics, 2019, 21, 26-31.	2.8	28
26	Shortening injection matrix for serial crystallography. Scientific Reports, 2020, 10, 107.	3.3	28
27	Structural characterization of the photoswitchable fluorescent protein Dronpa-C62S. Biochemical and Biophysical Research Communications, 2007, 354, 962-967.	2.1	26
28	Development of Bimolecular Fluorescence Complementation Using Dronpa for Visualization of Protein–Protein Interactions in Cells. Molecular Imaging and Biology, 2010, 12, 468-478.	2.6	26
29	Current status of the CXI beamline at the PAL-XFEL. Journal of the Korean Physical Society, 2016, 69, 1089-1093.	0.7	26
30	Structural and functional analysis of a novel hormoneâ€sensitive lipase from a metagenome library. Proteins: Structure, Function and Bioinformatics, 2009, 74, 1036-1040.	2.6	25
31	The crystal structure of an HSL-homolog EstE5 complex with PMSF reveals a unique configuration that inhibits the nucleophile Ser144 in catalytic triads. Biochemical and Biophysical Research Communications, 2009, 389, 247-250.	2.1	25
32	Response to Comment on "Maxima in the thermodynamic response and correlation functions of deeply supercooled water― Science, 2018, 360, .	12.6	25
33	Lard Injection Matrix for Serial Crystallography. International Journal of Molecular Sciences, 2020, 21, 5977.	4.1	25
34	Polysaccharide-Based Injection Matrix for Serial Crystallography. International Journal of Molecular Sciences, 2020, 21, 3332.	4.1	25
35	Application of a high-throughput microcrystal delivery system to serial femtosecond crystallography. Journal of Applied Crystallography, 2020, 53, 477-485.	4.5	25
36	Fixed-Target Serial Synchrotron Crystallography Using Nylon Mesh and Enclosed Film-Based Sample Holder. Crystals, 2020, 10, 803.	2.2	24

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37	Crystal structure of CelM2, a bifunctional glucanase–xylanase protein from a metagenome library. Biochemical and Biophysical Research Communications, 2009, 383, 183-186.	2.1	23
38	Allosteric control of type I-A CRISPR-Cas3 complexes and establishment as effective nucleic acid detection and human genome editing tools. Molecular Cell, 2022, 82, 2754-2768.e5.	9.7	23
39	Viscous-medium-based crystal support in a sample holder for fixed-target serial femtosecond crystallography. Journal of Applied Crystallography, 2020, 53, 1051-1059.	4.5	22
40	Glucose Isomerase: Functions, Structures, and Applications. Applied Sciences (Switzerland), 2022, 12, 428.	2.5	21
41	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. Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment, 2016, 810–74-79	1.6	19
42	Crystal structure of engineered βâ€glucosidase from a soil metagenome. Proteins: Structure, Function and Bioinformatics, 2008, 73, 788-793.	2.6	18
43	Structural analysis of substrate recognition by glucose isomerase in Mn2+ binding mode at M2 site in S.Ârubiginosus. Biochemical and Biophysical Research Communications, 2018, 503, 770-775.	2.1	18
44	Beef tallow injection matrix for serial crystallography. Scientific Reports, 2022, 12, 694.	3.3	18
45	Nucleic acid binding surface and dimer interface revealed by CRISPRâ€∎ssociated CasB protein structures. FEBS Letters, 2012, 586, 3956-3961.	2.8	17
46	Molecular Dynamics—From Small Molecules to Macromolecules. International Journal of Molecular Sciences, 2021, 22, 3761.	4.1	17
47	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. International Journal of Molecular Sciences, 2021, 22, 3892.	4.1	17
48	Polyimide mesh-based sample holder with irregular crystal mounting holes for fixed-target serial crystallography. Scientific Reports, 2021, 11, 13115.	3.3	17
49	Structural and Mutational Analysis of tRNA Intron-Splicing Endonuclease from <i>Thermoplasma acidophilum</i> DSM 1728: Catalytic Mechanism of tRNA Intron-Splicing Endonucleases. Journal of Bacteriology, 2007, 189, 8339-8346.	2.2	14
50	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. Journal of Synchrotron Radiation, 2018, 25, 323-328.	2.4	14
51	Crystal structure of glucose isomerase in complex with xylitol inhibitor in one metal binding mode. Biochemical and Biophysical Research Communications, 2017, 493, 666-670.	2.1	13
52	Enzymatic synthesis of l-fucose from l-fuculose using a fucose isomerase from Raoultella sp. and the biochemical and structural analyses of the enzyme. Biotechnology for Biofuels, 2019, 12, 282.	6.2	13
53	Stable sample delivery in a viscous medium via a polyimide-based single-channel microfluidic chip for serial crystallography. Journal of Applied Crystallography, 2021, 54, 1081-1087.	4.5	13
54	Biochemical and Structural Analysis of a Glucose-Tolerant Î ² -Glucosidase from the Hemicellulose-Degrading Thermoanaerobacterium saccharolyticum. Molecules, 2022, 27, 290.	3.8	13

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55	Structural insights of the MenD from Escherichia coli reveal ThDP affinity. Biochemical and Biophysical Research Communications, 2009, 380, 797-801.	2.1	12
56	Crystal structures of Dronpa complexed with quenchable metal ions provide insight into metal biosensor development. FEBS Letters, 2016, 590, 2982-2990.	2.8	12
57	Combination of an inject-and-transfer system for serial femtosecond crystallography. Journal of Applied Crystallography, 2022, 55, 813-822.	4.5	12
58	Disruption of the hydrogen bonding network determines the pH-induced non-fluorescent state of the fluorescent protein ZsYellow by protonation of Glu221. Biochemical and Biophysical Research Communications, 2017, 493, 562-567.	2.1	10
59	Spectroscopic Analysis of Fe Ion-Induced Fluorescence Quenching of the Green Fluorescent Protein ZsGreen. Journal of Fluorescence, 2021, 31, 307-314.	2.5	10
60	Crystal structure of human brain-type fatty acid-binding protein FABP7 complexed with palmitic acid. Acta Crystallographica Section D: Structural Biology, 2021, 77, 954-965.	2.3	10
61	Structural characterization of the bifunctional glucanase–xylanase CelM2 reveals the metal effect and substrate-binding moiety. Biochemical and Biophysical Research Communications, 2010, 391, 1726-1730.	2.1	9
62	Spectroscopic Analysis of the Cu2+-Induced Fluorescence Quenching of Fluorescent Proteins AmCyan and mOrange2. Molecular Biotechnology, 2018, 60, 485-491.	2.4	9
63	Spectral and structural analysis of a red fluorescent protein from Acropora digitifera. Protein Science, 2019, 28, 375-381.	7.6	9
64	Approach of Serial Crystallography. Crystals, 2020, 10, 854.	2.2	9
65	Crystal structure of a substrate-binding protein from Rhodothermus marinus reveals a single α/β-domain. Biochemical and Biophysical Research Communications, 2018, 497, 368-373.	2.1	8
66	Crystal structure of E.Âcoli ZinT with one zinc-binding mode and complexed with citrate. Biochemical and Biophysical Research Communications, 2018, 500, 139-144.	2.1	8
67	Structural analysis of metal chelation of the metalloproteinase thermolysin by 1,10-phenanthroline. Journal of Inorganic Biochemistry, 2021, 215, 111319.	3.5	8
68	Metal-Induced Fluorescence Quenching of Photoconvertible Fluorescent Protein DendFP. Molecules, 2022, 27, 2922.	3.8	8
69	Crystal structure of the tRNA-specific adenosine deaminase from Streptococcus pyogenes. Proteins: Structure, Function and Bioinformatics, 2007, 68, 1016-1019.	2.6	7
70	Crystal structure of bacterioferritin from Rhodobacter sphaeroides. Biochemical and Biophysical Research Communications, 2010, 391, 990-994.	2.1	7
71	Spectroscopic and Structural Analysis of Cu2+-Induced Fluorescence Quenching of ZsYellow. Biosensors, 2020, 10, 29.	4.7	7
72	Crystal structure of the metal-free state of glucose isomerase reveals its minimal open configuration for metal binding. Biochemical and Biophysical Research Communications, 2021, 547, 69-74.	2.1	7

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73	Preliminary XFEL data from spontaneously grown endo-1,4-β-xylanase crystals from <i>Hypocrea virens</i> . Acta Crystallographica Section F, Structural Biology Communications, 2022, 78, 226-231.	0.8	7
74	Crystal structure of <i>Thermoplasma acidophilum</i> XerA recombinase shows large Câ€shape clamp conformation and <i>cis</i> â€cleavage mode for nucleophilic tyrosine. FEBS Letters, 2016, 590, 848-856.	2.8	6
75	Serial X-ray Crystallography. Crystals, 2022, 12, 99.	2.2	6
76	Structural and Biochemical Analysis of the Citrate-Responsive Mechanism of the Regulatory Domain of Catabolite Control Protein E from <i>Staphylococcus aureus</i> . Biochemistry, 2018, 57, 6054-6060.	2.5	5
77	Structural insight into the carboxylesterase BioH from Klebsiella pneumoniae. Biochemical and Biophysical Research Communications, 2019, 520, 538-543.	2.1	5
78	Biochemical and structural analysis of the Klebsiella pneumoniae cytidine deaminase CDA. Biochemical and Biophysical Research Communications, 2019, 519, 280-286.	2.1	5
79	Processing of Multicrystal Diffraction Patterns in Macromolecular Crystallography Using Serial Crystallography Programs. Crystals, 2022, 12, 103.	2.2	5
80	Crystal structure of an EfPDF complex with Met-Ala-Ser based on crystallographic packing. Biochemical and Biophysical Research Communications, 2009, 381, 630-633.	2.1	4
81	Spectral and structural analysis of large Stokes shift fluorescent protein dKeima570. Journal of Microbiology, 2018, 56, 822-827.	2.8	4
82	Crystal structure of the nicotinamidase/pyrazinamidase PncA from Bacillus subtilis. Biochemical and Biophysical Research Communications, 2018, 503, 2906-2911.	2.1	4
83	Structural and functional analyses of the lipase CinB from Enterobacter asburiae. Biochemical and Biophysical Research Communications, 2019, 519, 274-279.	2.1	4
84	Biochemical and Structural Analysis of Hormone-sensitive Lipase Homolog EstE7: Insight into the Stabilized Dimerization of HSL-Homolog Proteins. Bulletin of the Korean Chemical Society, 2010, 31, 2627-2632.	1.9	4
85	Crystal Structure of Human Lysozyme Complexed with N-Acetyl-α-d-glucosamine. Applied Sciences (Switzerland), 2022, 12, 4363.	2.5	4
86	Insight into the antibacterial drug design and architectural mechanism of peptide recognition from the <i>E. faecium</i> peptide deformylase structure. Proteins: Structure, Function and Bioinformatics, 2009, 74, 261-265.	2.6	3
87	Structural insight of the 5-(Hydroxyethyl)-methylthiazole kinase ThiM involving vitamin B1 biosynthetic pathway from the Klebsiella pneumoniae. Biochemical and Biophysical Research Communications, 2019, 518, 513-518.	2.1	3
88	Structural Flexibility of Peripheral Loops and Extended C-terminal Domain of Short Length Substrate Binding Protein from Rhodothermus marinus. Protein Journal, 2021, 40, 184-191.	1.6	3
89	Functional and structural analysis of catabolite control protein C that responds to citrate. Scientific Reports, 2021, 11, 20285.	3.3	3
90	Hit and Indexing Rate in Serial Crystallography: Incomparable Statistics. Frontiers in Molecular Biosciences, 2022, 9, 858815.	3.5	3

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91	Triglycine-Based Approach for Identifying the Substrate Recognition Site of an Enzyme. Crystals, 2019, 9, 444.	2.2	2
92	Crystal structure of the Siderophore-interacting protein SIP from Aeromonas hydrophila. Biochemical and Biophysical Research Communications, 2019, 519, 23-28.	2.1	2
93	Spacer acquisition mechanism in type II-A CRISPR system. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, a444-a444.	0.1	2
94	Crystallization and preliminary X-ray diffraction analysis of 5,10- methylenetetrahydrofolate dehydrogenase/cyclohydrolase from Thermoplasma acidophilum DSM 1728. Journal of Microbiology and Biotechnology, 2008, 18, 283-6.	2.1	2
95	Crystal structure of the domain-swapped dimeric maltodextrin-binding protein MalE from <i>Salmonella enterica</i> . Acta Crystallographica Section D: Structural Biology, 2022, 78, 613-622.	2.3	2
96	Crystallization and preliminary X-ray crystallographic analysis of the tRNA-specific adenosine deaminase fromStreptococcus pyogenes. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 375-377.	0.7	1
97	Cloning, purification and preliminary X-ray crystallographic analysis of a hypothetical protein, MJ0754, fromMethanococcus jannaschiiDSM 2661. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1065-1067.	0.7	1
98	Construction status of CXI beamline at PAL-XFEL. Proceedings of SPIE, 2015, , .	0.8	1
99	Approach of Serial Crystallography II. Crystals, 2021, 11, 655.	2.2	1
100	Molecular Dynamics—From Macromolecule to Small Molecules. International Journal of Molecular Sciences, 2022, 23, 5676.	4.1	1
101	Expression, Purification, and Preliminary X-Ray Crystallographic Analysis of the Complex of Gαi3-RGS5 from Human with GDP/Mg2+/AlF4 Protein and Peptide Letters, 2006, 13, 945-949.	0.9	0
102	Crystallization and preliminary X-ray crystallographic analysis of the probable tRNA-modification GTPase (TrmE) fromStaphylococcus aureus. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 1166-1168.	0.7	0
103	A SAXS Study of the CRISPR Associated Gene (Cas) Csn2 in the Presence and Absence of Calcium Ions. Biophysical Journal, 2013, 104, 252a-253a.	0.5	0
104	Characterizing Metal-Dependent Nucleases of CRISPR-Cas Prokaryotic Adaptive Immunity Systems. Methods in Molecular Biology, 2015, 1311, 265-276.	0.9	0
105	Crystal Structure of <i>Aeromonas hydrophila</i> Cytoplasmic 5′-Methylthioadenosine/ <i>S</i> -Adenosylhomocysteine Nucleosidase. Biochemistry, 2019, 58, 3136-3143.	2.5	0