Ki-Hyun Nam

List of Publications by Year in descending order

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KI-HVIIN NAM

#	Article	IF	CITATIONS
1	Glucose Isomerase: Functions, Structures, and Applications. Applied Sciences (Switzerland), 2022, 12, 428.	2.5	21
2	Biochemical and Structural Analysis of a Glucose-Tolerant β-Glucosidase from the Hemicellulose-Degrading Thermoanaerobacterium saccharolyticum. Molecules, 2022, 27, 290.	3.8	13
3	Processing of Multicrystal Diffraction Patterns in Macromolecular Crystallography Using Serial Crystallography Programs. Crystals, 2022, 12, 103.	2.2	5
4	Serial X-ray Crystallography. Crystals, 2022, 12, 99.	2.2	6
5	Beef tallow injection matrix for serial crystallography. Scientific Reports, 2022, 12, 694.	3.3	18
6	Hit and Indexing Rate in Serial Crystallography: Incomparable Statistics. Frontiers in Molecular Biosciences, 2022, 9, 858815.	3.5	3
7	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
8	Crystal Structure of Human Lysozyme Complexed with N-Acetyl-α-d-glucosamine. Applied Sciences (Switzerland), 2022, 12, 4363.	2.5	4
9	Metal-Induced Fluorescence Quenching of Photoconvertible Fluorescent Protein DendFP. Molecules, 2022, 27, 2922.	3.8	8
10	Molecular Dynamics—From Macromolecule to Small Molecules. International Journal of Molecular Sciences, 2022, 23, 5676.	4.1	1
11	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
12	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
13	Combination of an inject-and-transfer system for serial femtosecond crystallography. Journal of Applied Crystallography, 2022, 55, 813-822.	4.5	12
14	Structural analysis of metal chelation of the metalloproteinase thermolysin by 1,10-phenanthroline. Journal of Inorganic Biochemistry, 2021, 215, 111319.	3.5	8
15	Spectroscopic Analysis of Fe Ion-Induced Fluorescence Quenching of the Green Fluorescent Protein ZsGreen. Journal of Fluorescence, 2021, 31, 307-314.	2.5	10
16	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
17	Molecular Dynamics—From Small Molecules to Macromolecules. International Journal of Molecular Sciences, 2021, 22, 3761	4.1	17
18	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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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. International Journal of Molecular Sciences, 2021, 22, 3892.	4.1	17
20	Polyimide mesh-based sample holder with irregular crystal mounting holes for fixed-target serial crystallography. Scientific Reports, 2021, 11, 13115.	3.3	17
21	Approach of Serial Crystallography II. Crystals, 2021, 11, 655.	2.2	1
22	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
23	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
24	Mechanism for Cas4-assisted directional spacer acquisition in CRISPR–Cas. Nature, 2021, 598, 515-520.	27.8	29
25	Functional and structural analysis of catabolite control protein C that responds to citrate. Scientific Reports, 2021, 11, 20285.	3.3	3
26	Stable sample delivery in viscous media via a capillary for serial crystallography. Journal of Applied Crystallography, 2020, 53, 45-50.	4.5	33
27	Approach of Serial Crystallography. Crystals, 2020, 10, 854.	2.2	9
28	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
29	Lard Injection Matrix for Serial Crystallography. International Journal of Molecular Sciences, 2020, 21, 5977.	4.1	25
30	Fixed-Target Serial Synchrotron Crystallography Using Nylon Mesh and Enclosed Film-Based Sample Holder. Crystals, 2020, 10, 803.	2.2	24
31	Polysaccharide-Based Injection Matrix for Serial Crystallography. International Journal of Molecular Sciences, 2020, 21, 3332.	4.1	25
32	Spectroscopic and Structural Analysis of Cu2+-Induced Fluorescence Quenching of ZsYellow. Biosensors, 2020, 10, 29.	4.7	7
33	Shortening injection matrix for serial crystallography. Scientific Reports, 2020, 10, 107.	3.3	28
34	Application of a high-throughput microcrystal delivery system to serial femtosecond crystallography. Journal of Applied Crystallography, 2020, 53, 477-485.	4.5	25
35	Crystal Structure of <i>Aeromonas hydrophila</i> Cytoplasmic 5′-Methylthioadenosine/ <i>S</i> -Adenosylhomocysteine Nucleosidase. Biochemistry, 2019, 58, 3136-3143.	2.5	0
36	Triglycine-Based Approach for Identifying the Substrate Recognition Site of an Enzyme. Crystals, 2019, 9, 444.	2.2	2

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37	Structural insight into the carboxylesterase BioH from Klebsiella pneumoniae. Biochemical and Biophysical Research Communications, 2019, 520, 538-543.	2.1	5
38	Sample delivery using viscous media, a syringe andÂaÂsyringe pump for serial crystallography. Journal of Synchrotron Radiation, 2019, 26, 1815-1819.	2.4	29
39	Crystal structure of the Siderophore-interacting protein SIP from Aeromonas hydrophila. Biochemical and Biophysical Research Communications, 2019, 519, 23-28.	2.1	2
40	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
41	Structural and functional analyses of the lipase CinB from Enterobacter asburiae. Biochemical and Biophysical Research Communications, 2019, 519, 274-279.	2.1	4
42	Biochemical and structural analysis of the Klebsiella pneumoniae cytidine deaminase CDA. Biochemical and Biophysical Research Communications, 2019, 519, 280-286.	2.1	5
43	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
44	Nylon mesh-based sample holder for fixed-target serial femtosecond crystallography. Scientific Reports, 2019, 9, 6971.	3.3	51
45	Polyacrylamide injection matrix for serial femtosecond crystallography. Scientific Reports, 2019, 9, 2525.	3.3	37
46	Sample Delivery Media for Serial Crystallography. International Journal of Molecular Sciences, 2019, 20, 1094.	4.1	49
47	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
48	Spectral and structural analysis of a red fluorescent protein from Acropora digitifera. Protein Science, 2019, 28, 375-381.	7.6	9
49	Crystal structure of a substrate-binding protein from Rhodothermus marinus reveals a single $\hat{I} \pm \hat{I}^2$ -domain. Biochemical and Biophysical Research Communications, 2018, 497, 368-373.	2.1	8
50	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
51	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
52	Spectral and structural analysis of large Stokes shift fluorescent protein dKeima570. Journal of Microbiology, 2018, 56, 822-827.	2.8	4
53	Response to Comment on "Maxima in the thermodynamic response and correlation functions of deeply supercooled water― Science, 2018, 360, .	12.6	25
54	Spectroscopic Analysis of the Cu2+-Induced Fluorescence Quenching of Fluorescent Proteins AmCyan and mOrange2. Molecular Biotechnology, 2018, 60, 485-491.	2.4	9

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55	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
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. Journal of Synchrotron Radiation, 2018, 25, 323-328.	2.4	14
57	Crystal structure of the nicotinamidase/pyrazinamidase PncA from Bacillus subtilis. Biochemical and Biophysical Research Communications, 2018, 503, 2906-2911.	2.1	4
58	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
59	Spacer acquisition mechanism in type II-A CRISPR system. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, a444-a444.	0.1	2
60	Hard X-ray free-electron laser with femtosecond-scale timing jitter. Nature Photonics, 2017, 11, 708-713.	31.4	389
61	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
62	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
63	How type II CRISPR–Cas establish immunity through Cas1–Cas2-mediated spacer integration. Nature, 2017, 550, 137-141.	27.8	111
64	Maxima in the thermodynamic response and correlation functions of deeply supercooled water. Science, 2017, 358, 1589-1593.	12.6	270
65	Construction and Commissioning of PAL-XFEL Facility. Applied Sciences (Switzerland), 2017, 7, 479.	2.5	108
66	Current status of the CXI beamline at the PAL-XFEL. Journal of the Korean Physical Society, 2016, 69, 1089-1093.	0.7	26
67	Crystal structures of Dronpa complexed with quenchable metal ions provide insight into metal biosensor development. FEBS Letters, 2016, 590, 2982-2990.	2.8	12
68	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
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. Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment, 2016, 810, 74-79.	1.6	19
70	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
71	Characterizing Metal-Dependent Nucleases of CRISPR-Cas Prokaryotic Adaptive Immunity Systems. Methods in Molecular Biology, 2015, 1311, 265-276.	0.9	0
72	Construction status of CXI beamline at PAL-XFEL. Proceedings of SPIE, 2015, , .	0.8	1

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73	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
74	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
75	Binding characteristics of a bacterial expansin (BsEXLX1) for various types of pretreated lignocellulose. Applied Microbiology and Biotechnology, 2013, 97, 5381-5388.	3.6	39
76	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
77	Nucleic acid binding surface and dimer interface revealed by CRISPRâ€associated CasB protein structures. FEBS Letters, 2012, 586, 3956-3961.	2.8	17
78	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
79	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
80	Envelope stress is a trigger of CRISPR RNA-mediated DNA silencing in Escherichia coli. Molecular Microbiology, 2011, 79, 584-599.	2.5	112
81	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
82	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
83	Crystal structure of bacterioferritin from Rhodobacter sphaeroides. Biochemical and Biophysical Research Communications, 2010, 391, 990-994.	2.1	7
84	Structural insights into the substrate recognition properties of β-glucosidase. Biochemical and Biophysical Research Communications, 2010, 391, 1131-1135.	2.1	36
85	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
86	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
87	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
88	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
89	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
90	Structural insights into the alanine racemase from Enterococcus faecalis. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2009, 1794, 1030-1040.	2.3	28

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91	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
92	Structural insights of the MenD from Escherichia coli reveal ThDP affinity. Biochemical and Biophysical Research Communications, 2009, 380, 797-801.	2.1	12
93	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
94	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
95	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
96	Crystal Structure of the Periplasmic Region of MacB, a Noncanonic ABC Transporter [,] . Biochemistry, 2009, 48, 5218-5225.	2.5	44
97	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
98	Crystal structure of engineered βâ€glucosidase from a soil metagenome. Proteins: Structure, Function and Bioinformatics, 2008, 73, 788-793.	2.6	18
99	Structural studies of human brainâ€ŧype creatine kinase complexed with the ADP–Mg ²⁺ –NO ^{3â°'} –creatine transitionâ€state analogue complex. FEBS Letters, 2008, 582, 3959-3965.	2.8	68
100	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
101	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
102	Structural characterization of the photoswitchable fluorescent protein Dronpa-C62S. Biochemical and Biophysical Research Communications, 2007, 354, 962-967.	2.1	26
103	Crystal structure of the tRNA-specific adenosine deaminase from Streptococcus pyogenes. Proteins: Structure, Function and Bioinformatics, 2007, 68, 1016-1019.	2.6	7
104	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
105	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