

Nam-Chul Ha

List of Publications by Year in descending order

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95
papers

1,731
citations

361413
20
h-index

345221
36
g-index

100
all docs

100
docs citations

100
times ranked

2206
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural details of the OxyR peroxide-sensing mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6443-6448.	7.1	122
2	Crystal Structure of the Periplasmic Component of a Tripartite Macrolide-Specific Efflux Pump. Journal of Molecular Biology, 2009, 387, 1286-1297.	4.2	111
3	Calcium-Dependent Catalytic Activity of a Novel Phytase from <i>Bacillus amyloliquefaciens</i> DS11. Biochemistry, 2001, 40, 9669-9676.	2.5	87
4	Morin attenuates tau hyperphosphorylation by inhibiting GSK3 β . Neurobiology of Disease, 2011, 44, 223-230.	4.4	87
5	Structural basis for lamin assembly at the molecular level. Nature Communications, 2019, 10, 3757.	12.8	73
6	Structure of the Tripartite Multidrug Efflux Pump AcrAB-TolC Suggests an Alternative Assembly Mode. Molecules and Cells, 2015, 38, 180-186.	2.6	67
7	KDM2B is a histone H3K79 demethylase and induces transcriptional repression via sirtuin β -mediated chromatin silencing. FASEB Journal, 2018, 32, 5737-5750.	0.5	67
8	Funnel-like Hexameric Assembly of the Periplasmic Adapter Protein in the Tripartite Multidrug Efflux Pump in Gram-negative Bacteria. Journal of Biological Chemistry, 2011, 286, 17910-17920.	3.4	58
9	Epigallocatechin Gallate Inhibits the Uridylate-Specific Endoribonuclease Nsp15 and Efficiently Neutralizes the SARS-CoV-2 Strain. Journal of Agricultural and Food Chemistry, 2021, 69, 5948-5954.	5.2	54
10	Functional Implications of an Intermeshing Cogwheel-like Interaction between TolC and MacA in the Action of Macrolide-specific Efflux Pump MacAB-TolC. Journal of Biological Chemistry, 2011, 286, 13541-13549.	3.4	49
11	Crystal Structure of a Soluble Fragment of the Membrane Fusion Protein HlyD in a Type I Secretion System of Gram-Negative Bacteria. Structure, 2016, 24, 477-485.	3.3	49
12	Pseudoatomic Structure of the Tripartite Multidrug Efflux Pump AcrAB-TolC Reveals the Intermeshing Cogwheel-like Interaction between AcrA and TolC. Structure, 2016, 24, 272-276.	3.3	49
13	Gold nanoparticle-DNA aptamer composites as a universal carrier for in vivo delivery of biologically functional proteins. Journal of Controlled Release, 2014, 196, 287-294.	9.9	48
14	Crystal Structure of the Periplasmic Region of MacB, a Noncanonic ABC Transporter ^{<sup>} </sup>. Biochemistry, 2009, 48, 5218-5225.	2.5	44
15	Structural basis for the recognition of lysozyme by MliC, a periplasmic lysozyme inhibitor in Gram-negative bacteria. Biochemical and Biophysical Research Communications, 2009, 378, 244-248.	2.1	43
16	Inhibiting DX2-p14/ARF Interaction Exerts Antitumor Effects in Lung Cancer and Delays Tumor Progression. Cancer Research, 2016, 76, 4791-4804.	0.9	28
17	Structural basis for the transglycosylase activity of a GH57-type glycogen branching enzyme from <i>Pyrococcus horikoshii</i> . Biochemical and Biophysical Research Communications, 2017, 484, 850-856.	2.1	28
18	LysPBC2, a Novel Endolysin Harboring a <i>Bacillus cereus</i> Spore Binding Domain. Applied and Environmental Microbiology, 2019, 85, .	3.1	27

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19	Structural basis for HOCl recognition and regulation mechanisms of HypT, a hypochlorite-specific transcriptional regulator. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 3740-3745.	7.1	26
20	Progerinin, an optimized progerin-lamin A binding inhibitor, ameliorates premature senescence phenotypes of Hutchinson-Gilford progeria syndrome. Communications Biology, 2021, 4, 5.	4.4	23
21	p53 induces senescence through Lamin A/C stabilization-mediated nuclear deformation. Cell Death and Disease, 2019, 10, 107.	6.3	22
22	Crystal Structure of the Regulatory Domain of AphB from <i>Vibrio vulnificus</i> , a Virulence Gene Regulator. Molecules and Cells, 2017, 40, 299-306.	2.6	21
23	Small-molecule inhibitor of HlyU attenuates virulence of <i>Vibrio</i> species. Scientific Reports, 2019, 9, 4346.	3.3	19
24	Crystal structure of GSK3 β in complex with the flavonoid, morin. Biochemical and Biophysical Research Communications, 2018, 504, 519-524.	2.1	18
25	Structure and function of the hypochlorous acid-induced flavoprotein RclA from <i>Escherichia coli</i> . Journal of Biological Chemistry, 2020, 295, 3202-3212.	3.4	18
26	Interaction Mediated by the Putative Tip Regions of MdsA and MdsC in the Formation of a <i>Salmonella</i> -Specific Tripartite Efflux Pump. PLoS ONE, 2014, 9, e100881.	2.5	17
27	Structure-based protein engineering of bacterial β -xylosidase to increase the production yield of xylobiose from xylose. Biochemical and Biophysical Research Communications, 2018, 501, 703-710.	2.1	17
28	The Crystal Structure of the YknZ Extracellular Domain of ABC Transporter YknWXYZ from <i>Bacillus amyloliquefaciens</i> . PLoS ONE, 2016, 11, e0155846.	2.5	17
29	Structural Basis for the Inhibition of Human Lysozyme by Plc from <i>Brucella abortus</i> . Biochemistry, 2013, 52, 9385-9393.	2.5	16
30	Plant growth-promoting activity of beta-propeller protein YxaL secreted from <i>Bacillus velezensis</i> strain GH1-13. PLoS ONE, 2019, 14, e0207968.	2.5	16
31	MdsABC-Mediated Pathway for Pathogenicity in <i>Salmonella enterica</i> Serovar Typhimurium. Infection and Immunity, 2015, 83, 4266-4276.	2.2	15
32	The hydrogen peroxide hypersensitivity of OxyR2 in <i>Vibrio vulnificus</i> depends on conformational constraints. Journal of Biological Chemistry, 2017, 292, 7223-7232.	3.4	14
33	Identification of Amino Acid Residues in the Catalytic Domain of RNase E Essential for Survival of <i>Escherichia coli</i> : Functional Analysis of DNase I Subdomain. Genetics, 2008, 179, 1871-1879.	2.9	13
34	Development of Akt-activated GSK3 β inhibitory peptide. Biochemical and Biophysical Research Communications, 2013, 434, 735-739.	2.1	12
35	Periplasmic disulfide isomerase DsbC is involved in the reduction of copper binding protein CueP from <i>Salmonella enterica</i> serovar Typhimurium. Biochemical and Biophysical Research Communications, 2014, 446, 971-976.	2.1	12
36	Molecular architecture of the bacterial tripartite multidrug efflux pump focusing on the adaptor bridging model. Journal of Microbiology, 2015, 53, 355-364.	2.8	12

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37	Tetrahydrobiopterin enhances mitochondrial biogenesis and cardiac contractility via stimulation of PGC1 α signaling. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2019, 1865, 165524.	3.8	12
38	Anti-cancer effect of novel PAK1 inhibitor via induction of PUMA-mediated cell death and p21-mediated cell cycle arrest. <i>Oncotarget</i> , 2017, 8, 23690-23701.	1.8	12
39	OxyR2 Functions as a Three-state Redox Switch to Tightly Regulate Production of Prx2, a Peroxiredoxin of <i>Vibrio vulnificus</i> . <i>Journal of Biological Chemistry</i> , 2016, 291, 16038-16047.	3.4	11
40	Crystal Structure of Bacterial Cystathionine β -Lyase in The Cysteine Biosynthesis Pathway of <i>Staphylococcus aureus</i> . <i>Crystals</i> , 2019, 9, 656.	2.2	11
41	Stoichiometry and mechanistic implications of the MacAB-TolC tripartite efflux pump. <i>Biochemical and Biophysical Research Communications</i> , 2017, 494, 668-673.	2.1	10
42	Crystal structure of peroxiredoxin 3 from <i>Vibrio vulnificus</i> and its implications for scavenging peroxides and nitric oxide. <i>IUCr</i> , 2018, 5, 82-92.	2.2	10
43	BH4 activates CaMKK2 and rescues the cardiomyopathic phenotype in rodent models of diabetes. <i>Life Science Alliance</i> , 2020, 3, e201900619.	2.8	10
44	Separation of Coiled-Coil Structures in Lamin A/C Is Required for the Elongation of the Filament. <i>Cells</i> , 2021, 10, 55.	4.1	10
45	A pGpG-specific phosphodiesterase regulates cyclic di-GMP signaling in <i>Vibrio cholerae</i> . <i>Journal of Biological Chemistry</i> , 2022, 298, 101626.	3.4	10
46	Upregulation of RNase E activity by mutation of a site that uncompetitively interferes with RNA binding. <i>RNA Biology</i> , 2011, 8, 1022-1034.	3.1	9
47	Transcriptomic Identification and Biochemical Characterization of HmpA, a Nitric Oxide Dioxygenase, Essential for Pathogenesis of <i>Vibrio vulnificus</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2208.	3.5	9
48	Acetylation of UHRF1 Regulates Hemi-methylated DNA Binding and Maintenance of Genome-wide DNA Methylation. <i>Cell Reports</i> , 2020, 32, 107958.	6.4	9
49	Substrate-dependent effects of quaternary structure on RNase E activity. <i>Genes and Development</i> , 2021, 35, 286-299.	5.9	9
50	A Novel Tetrameric Assembly Configuration in VV2_1132, a LysR-Type Transcriptional Regulator in. <i>Molecules and Cells</i> , 2018, 41, 301-310.	2.6	9
51	RraAS2 requires both scaffold domains of RNase ES for high-affinity binding and inhibitory action on the ribonucleolytic activity. <i>Journal of Microbiology</i> , 2016, 54, 660-666.	2.8	8
52	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.	2.1	8
53	Recent paradigm shift in the assembly of bacterial tripartite efflux pumps and the type I secretion system. <i>Journal of Microbiology</i> , 2019, 57, 185-194.	2.8	8
54	The coordinated action of RNase III and RNase G controls enolase expression in response to oxygen availability in <i>Escherichia coli</i> . <i>Scientific Reports</i> , 2019, 9, 17257.	3.3	8

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55	Beta-strand-mediated dimeric formation of the Ig-like domains of human lamin A/C and B1. <i>Biochemical and Biophysical Research Communications</i> , 2021, 550, 191-196.	2.1	8
56	Novel chemical inhibitor against SOD1 misfolding and aggregation protects neuron-loss and ameliorates disease symptoms in ALS mouse model. <i>Communications Biology</i> , 2021, 4, 1397.	4.4	8
57	Crystal Structure of DsbA from <i>Corynebacterium diphtheriae</i> and Its Functional Implications for CueP in Gram-Positive Bacteria. <i>Molecules and Cells</i> , 2015, 38, 715-722.	2.6	7
58	Crystal structures of the disulfide reductase DsbM from <i>Pseudomonas aeruginosa</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 1100-1109.	2.3	6
59	Crystal structure and functional implications of the tandem-type universal stress protein UspE from <i>Escherichia coli</i> . <i>BMC Structural Biology</i> , 2016, 16, 3.	2.3	6
60	Hexameric assembly of membrane fusion protein YknX of the sporulation delaying efflux pump from <i>Bacillus amyloliquefaciens</i> . <i>Biochemical and Biophysical Research Communications</i> , 2017, 493, 152-157.	2.1	6
61	Structural insights into the apo-structure of Cpf1 protein from <i>Francisella novicida</i> . <i>Biochemical and Biophysical Research Communications</i> , 2018, 498, 775-781.	2.1	6
62	High-resolution structures of annexin A5 in a two-dimensional array. <i>Journal of Structural Biology</i> , 2020, 209, 107401.	2.8	6
63	Crystal structures of YeiE from <i>Cronobacter sakazakii</i> and the role of sulfite tolerance in gram-negative bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2118002119.	7.1	6
64	Cyclin-dependent kinase 1 depolymerizes nuclear lamin filaments by disrupting the head-to-tail interaction of the lamin central rod domain. <i>Journal of Biological Chemistry</i> , 2022, 298, 102256.	3.4	6
65	Crystal structure of $\hat{2}$ -N-acetylglucosaminidase CbsA from <i>Thermotoga neapolitana</i> . <i>Biochemical and Biophysical Research Communications</i> , 2015, 464, 869-874.	2.1	5
66	Crystal structure of <i>Streptomyces coelicolor</i> RraAS2, an unusual member of the RNase E inhibitor RraA protein family. <i>Journal of Microbiology</i> , 2017, 55, 388-395.	2.8	5
67	Structural and Functional Analyses of Periplasmic 5'-Methylthioadenosine/ <i>S</i> -Adenosylhomocysteine Nucleosidase from <i>Aeromonas hydrophila</i> . <i>Biochemistry</i> , 2017, 56, 5347-5355.	2.5	5
68	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.	2.5	5
69	Structural insight into the carboxylesterase BioH from <i>Klebsiella pneumoniae</i> . <i>Biochemical and Biophysical Research Communications</i> , 2019, 520, 538-543.	2.1	5
70	Biochemical and structural analysis of the <i>Klebsiella pneumoniae</i> cytidine deaminase CDA. <i>Biochemical and Biophysical Research Communications</i> , 2019, 519, 280-286.	2.1	5
71	Functional implications of hexameric assembly of RraA proteins from <i>Vibrio vulnificus</i> . <i>PLoS ONE</i> , 2017, 12, e0190064.	2.5	5
72	Pharmacologic inhibition of AKT leads to cell death in relapsed multiple myeloma. <i>Cancer Letters</i> , 2018, 432, 205-215.	7.2	4

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73	Crystal structure of the nicotinamidase/pyrazinamidase PncA from <i>Bacillus subtilis</i> . <i>Biochemical and Biophysical Research Communications</i> , 2018, 503, 2906-2911.	2.1	4
74	Structural and functional analyses of the lipase CinB from <i>Enterobacter asburiae</i> . <i>Biochemical and Biophysical Research Communications</i> , 2019, 519, 274-279.	2.1	4
75	Human WRN is an intrinsic inhibitor of progerin, abnormal splicing product of lamin A. <i>Scientific Reports</i> , 2021, 11, 9122.	3.3	4
76	Structure and Function of the Autolysin SagA in the Type IV Secretion System of <i>Brucella abortus</i> . <i>Molecules and Cells</i> , 2021, 44, 517-528.	2.6	4
77	Crystal Structure of LysB4, an Endolysin from -Targeting Bacteriophage B4. <i>Molecules and Cells</i> , 2019, 42, 79-86.	2.6	4
78	Structure of a DsbF homologue from <i>Corynebacterium diphtheriae</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1167-1172.	0.8	3
79	Structural and Mechanistic Insights into the <i>Pseudomonas fluorescens</i> 2-Nitrobenzoate 2-Nitroreductase NbaA. <i>Applied and Environmental Microbiology</i> , 2015, 81, 5266-5277.	3.1	3
80	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.	2.1	3
81	Design and evaluation of IKK-activated GSK3 β inhibitory peptide as an inflammation-responsive anti-colitic therapeutic. <i>Biomaterials Science</i> , 2021, 9, 6584-6596.	5.4	3
82	Cleavage-Dependent Activation of ATP-Dependent Protease HslUV from. <i>Molecules and Cells</i> , 2020, 43, 694-704.	2.6	3
83	Crystal structure of progeria mutant S143F lamin A/C reveals increased hydrophobicity driving nuclear deformation. <i>Communications Biology</i> , 2022, 5, 267.	4.4	3
84	Crystal structure of the Siderophore-interacting protein SIP from <i>Aeromonas hydrophila</i> . <i>Biochemical and Biophysical Research Communications</i> , 2019, 519, 23-28.	2.1	2
85	The flavonoid morin alleviates nuclear deformation in aged cells by disrupting progerin-lamin A/C binding. <i>Journal of Functional Foods</i> , 2021, 77, 104331.	3.4	2
86	Real-Time Measurement of the Liquid Amount in Cryo-Electron Microscopy Grids Using Laser Diffraction of Regular 2-D Holes of the Grids. <i>Molecules and Cells</i> , 2020, 43, 298-303.	2.6	2
87	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.	2.3	2
88	Purification, crystallization, and preliminary X-ray analysis of a putative N-terminal acetyltransferase encoded by a <i>Salmonella</i> -infecting bacteriophage. <i>Biodesign</i> , 2021, 9, 19-22.	0.4	1
89	Purification, crystallization, and preliminary analysis of the lysozyme-like enzyme SagA from <i>Brucella abortus</i> . <i>Biodesign</i> , 2020, 8, 64-67.	0.4	1
90	Crystal Structure of SAV0927 and Its Functional Implications. <i>Journal of Microbiology and Biotechnology</i> , 2019, 29, 500-505.	2.1	1

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91	NADH-dependent butanol dehydrogenase from <i>Fusobacterium nucleatum</i> : purification, crystallization, and X-ray crystallographic analysis. Biodesign, 2022, 10, 29-33.	0.4	1
92	Crystal Structure of <i>Aeromonas hydrophila</i> Cytoplasmic 5'-Methylthioadenosine/ <i>S</i> -Adenosylhomocysteine Nucleosidase. Biochemistry, 2019, 58, 3136-3143.	2.5	0
93	Crystal structure of the nuclease and capping domain of SbcD from <i>Staphylococcus aureus</i> . Journal of Microbiology, 2021, 59, 584-589.	2.8	0
94	Purification and preliminary X-ray analysis of YbeY from <i>Staphylococcus aureus</i> . Biodesign, 2021, 9, 41-45.	0.4	0
95	Structure of the plant growth-promoting factor YxaL from the rhizobacterium <i>Bacillus velezensis</i> and its application to protein engineering. Acta Crystallographica Section D: Structural Biology, 2022, 78, 104-112.	2.3	0