

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 | Structure of the plant growth-promoting factor YxaL from the rhizobacterium <i>Bacillus velezensis</i> and its application to protein engineering. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 104-112. | 2.3 | 0 |
| 2 | 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 |
| 3 | 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 |
| 4 | 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 |
| 5 | 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 |
| 6 | NADH-dependent butanol dehydrogenase from <i>Fusobacterium nucleatum</i> : purification, crystallization, and X-ray crystallographic analysis. <i>Biodesign</i> , 2022, 10, 29-33. | 0.4 | 1 |
| 7 | 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 |
| 8 | 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 |
| 9 | Progerinin, an optimized progerin-lamin A binding inhibitor, ameliorates premature senescence phenotypes of Hutchinson-Gilford progeria syndrome. <i>Communications Biology</i> , 2021, 4, 5. | 4.4 | 23 |
| 10 | Substrate-dependent effects of quaternary structure on RNase E activity. <i>Genes and Development</i> , 2021, 35, 286-299. | 5.9 | 9 |
| 11 | 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 |
| 12 | 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 |
| 13 | 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 |
| 14 | Crystal structure of the nuclease and capping domain of SbcD from <i>Staphylococcus aureus</i> . <i>Journal of Microbiology</i> , 2021, 59, 584-589. | 2.8 | 0 |
| 15 | Human WRN is an intrinsic inhibitor of progerin, abnormal splicing product of lamin A. <i>Scientific Reports</i> , 2021, 11, 9122. | 3.3 | 4 |
| 16 | Epigallocatechin Gallate Inhibits the Uridylate-Specific Endoribonuclease Nsp15 and Efficiently Neutralizes the SARS-CoV-2 Strain. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 5948-5954. | 5.2 | 54 |
| 17 | Purification and preliminary X-ray analysis of YbeY from <i>Staphylococcus aureus</i> . <i>Biodesign</i> , 2021, 9, 41-45. | 0.4 | 0 |
| 18 | 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 |

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|----|--|------|-----------|
| 19 | Separation of Coiled-Coil Structures in Lamin A/C Is Required for the Elongation of the Filament. Cells, 2021, 10, 55. | 4.1 | 10 |
| 20 | Novel chemical inhibitor against SOD1 misfolding and aggregation protects neuron-loss and ameliorates disease symptoms in ALS mouse model. Communications Biology, 2021, 4, 1397. | 4.4 | 8 |
| 21 | High-resolution structures of annexin A5 in a two-dimensional array. Journal of Structural Biology, 2020, 209, 107401. | 2.8 | 6 |
| 22 | Acetylation of UHRF1 Regulates Hemi-methylated DNA Binding and Maintenance of Genome-wide DNA Methylation. Cell Reports, 2020, 32, 107958. | 6.4 | 9 |
| 23 | Structure and function of the hypochlorous acid-induced flavoprotein RclA from Escherichia coli. Journal of Biological Chemistry, 2020, 295, 3202-3212. | 3.4 | 18 |
| 24 | BH4 activates CaMKK2 and rescues the cardiomyopathic phenotype in rodent models of diabetes. Life Science Alliance, 2020, 3, e201900619. | 2.8 | 10 |
| 25 | Purification, crystallization, and preliminary analysis of the lysozyme-like enzyme SagA from Brucella abortus. Biodesign, 2020, 8, 64-67. | 0.4 | 1 |
| 26 | Real-Time Measurement of the Liquid Amount in Cryo-Electron Microscopy Grids Using Laser Diffraction of Regular 2-D Holes of the Grids. Molecules and Cells, 2020, 43, 298-303. | 2.6 | 2 |
| 27 | Cleavage-Dependent Activation of ATP-Dependent Protease HslUV from. Molecules and Cells, 2020, 43, 694-704. | 2.6 | 3 |
| 28 | Tetrahydrobiopterin enhances mitochondrial biogenesis and cardiac contractility via stimulation of PGC1 α signaling. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2019, 1865, 165524. | 3.8 | 12 |
| 29 | Structural basis for lamin assembly at the molecular level. Nature Communications, 2019, 10, 3757. | 12.8 | 73 |
| 30 | Crystal Structure of Aeromonas hydrophila Cytoplasmic 5'-Methylthioadenosine-S-Adenosylhomocysteine Nucleosidase. Biochemistry, 2019, 58, 3136-3143. | 2.5 | 0 |
| 31 | Structural insight into the carboxylesterase BioH from Klebsiella pneumoniae. Biochemical and Biophysical Research Communications, 2019, 520, 538-543. | 2.1 | 5 |
| 32 | Crystal structure of the Siderophore-interacting protein SIP from Aeromonas hydrophila. Biochemical and Biophysical Research Communications, 2019, 519, 23-28. | 2.1 | 2 |
| 33 | 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 |
| 34 | Structural and functional analyses of the lipase CinB from Enterobacter asburiae. Biochemical and Biophysical Research Communications, 2019, 519, 274-279. | 2.1 | 4 |
| 35 | Biochemical and structural analysis of the Klebsiella pneumoniae cytidine deaminase CDA. Biochemical and Biophysical Research Communications, 2019, 519, 280-286. | 2.1 | 5 |
| 36 | Transcriptomic Identification and Biochemical Characterization of HmpA, a Nitric Oxide Dioxygenase, Essential for Pathogenesis of Vibrio vulnificus. Frontiers in Microbiology, 2019, 10, 2208. | 3.5 | 9 |

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|----|--|-----|-----------|
| 37 | Plant growth-promoting activity of beta-propeller protein YxaL secreted from <i>Bacillus velezensis</i> strain GH1-13. <i>PLoS ONE</i> , 2019, 14, e0207968. | 2.5 | 16 |
| 38 | 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 |
| 39 | Small-molecule inhibitor of HlyU attenuates virulence of <i>Vibrio</i> species. <i>Scientific Reports</i> , 2019, 9, 4346. | 3.3 | 19 |
| 40 | p53 induces senescence through Lamin A/C stabilization-mediated nuclear deformation. <i>Cell Death and Disease</i> , 2019, 10, 107. | 6.3 | 22 |
| 41 | Structural basis for HOCl recognition and regulation mechanisms of HypT, a hypochlorite-specific transcriptional regulator. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 3740-3745. | 7.1 | 26 |
| 42 | Crystal Structure of Bacterial Cystathionine γ -Lyase in The Cysteine Biosynthesis Pathway of <i>Staphylococcus aureus</i> . <i>Crystals</i> , 2019, 9, 656. | 2.2 | 11 |
| 43 | 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 |
| 44 | LysPBC2, a Novel Endolysin Harboring a <i>Bacillus cereus</i> Spore Binding Domain. <i>Applied and Environmental Microbiology</i> , 2019, 85, . | 3.1 | 27 |
| 45 | Crystal Structure of SAV0927 and Its Functional Implications. <i>Journal of Microbiology and Biotechnology</i> , 2019, 29, 500-505. | 2.1 | 1 |
| 46 | Crystal Structure of LysB4, an Endolysin from ϕ -Targeting Bacteriophage B4. <i>Molecules and Cells</i> , 2019, 42, 79-86. | 2.6 | 4 |
| 47 | 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 |
| 48 | 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 |
| 49 | Crystal structure of GSK3 β in complex with the flavonoid, morin. <i>Biochemical and Biophysical Research Communications</i> , 2018, 504, 519-524. | 2.1 | 18 |
| 50 | Structure-based protein engineering of bacterial β -xylosidase to increase the production yield of xylobiose from xylose. <i>Biochemical and Biophysical Research Communications</i> , 2018, 501, 703-710. | 2.1 | 17 |
| 51 | Pharmacologic inhibition of AKT leads to cell death in relapsed multiple myeloma. <i>Cancer Letters</i> , 2018, 432, 205-215. | 7.2 | 4 |
| 52 | KDM2B is a histone H3K79 demethylase and induces transcriptional repression via α -tubulin-mediated chromatin silencing. <i>FASEB Journal</i> , 2018, 32, 5737-5750. | 0.5 | 67 |
| 53 | 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 |
| 54 | 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 |

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|----|--|-----|-----------|
| 55 | Crystal structure of peroxiredoxin 3 from <i>Vibrio vulnificus</i> and its implications for scavenging peroxides and nitric oxide. IUCr, 2018, 5, 82-92. | 2.2 | 10 |
| 56 | A Novel Tetrameric Assembly Configuration in VV2_1132, a LysR-Type Transcriptional Regulator in. Molecules and Cells, 2018, 41, 301-310. | 2.6 | 9 |
| 57 | 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 |
| 58 | 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 |
| 59 | Crystal structure of <i>Streptomyces coelicolor</i> RraAS2, an unusual member of the RNase E inhibitor RraA protein family. Journal of Microbiology, 2017, 55, 388-395. | 2.8 | 5 |
| 60 | Stoichiometry and mechanistic implications of the MacAB-TolC tripartite efflux pump. Biochemical and Biophysical Research Communications, 2017, 494, 668-673. | 2.1 | 10 |
| 61 | Hexameric assembly of membrane fusion protein YknX of the sporulation delaying efflux pump from <i>Bacillus amyloliquefaciens</i> . Biochemical and Biophysical Research Communications, 2017, 493, 152-157. | 2.1 | 6 |
| 62 | Structural and Functional Analyses of Periplasmic 5'-Methylthioadenosine-S-Adenosylhomocysteine Nucleosidase from <i>Aeromonas hydrophila</i> . Biochemistry, 2017, 56, 5347-5355. | 2.5 | 5 |
| 63 | Functional implications of hexameric assembly of RraA proteins from <i>Vibrio vulnificus</i> . PLoS ONE, 2017, 12, e0190064. | 2.5 | 5 |
| 64 | 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 |
| 65 | Anti-cancer effect of novel PAK1 inhibitor via induction of PUMA-mediated cell death and p21-mediated cell cycle arrest. Oncotarget, 2017, 8, 23690-23701. | 1.8 | 12 |
| 66 | 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 |
| 67 | RraAS2 requires both scaffold domains of RNase ES for high-affinity binding and inhibitory action on the ribonucleolytic activity. Journal of Microbiology, 2016, 54, 660-666. | 2.8 | 8 |
| 68 | Crystal structures of the disulfide reductase DsbM from <i>Pseudomonas aeruginosa</i> . Acta Crystallographica Section D: Structural Biology, 2016, 72, 1100-1109. | 2.3 | 6 |
| 69 | OxyR2 Functions as a Three-state Redox Switch to Tightly Regulate Production of Prx2, a Peroxiredoxin of <i>Vibrio vulnificus</i> . Journal of Biological Chemistry, 2016, 291, 16038-16047. | 3.4 | 11 |
| 70 | Crystal structure and functional implications of the tandem-type universal stress protein UspE from <i>Escherichia coli</i> . BMC Structural Biology, 2016, 16, 3. | 2.3 | 6 |
| 71 | Inhibiting DX2-p14/ARF Interaction Exerts Antitumor Effects in Lung Cancer and Delays Tumor Progression. Cancer Research, 2016, 76, 4791-4804. | 0.9 | 28 |
| 72 | 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 |

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|----|--|-----|-----------|
| 73 | 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 |
| 74 | 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 |
| 75 | Structure of the Tripartite Multidrug Efflux Pump AcrAB-TolC Suggests an Alternative Assembly Mode. Molecules and Cells, 2015, 38, 180-186. | 2.6 | 67 |
| 76 | 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 |
| 77 | MdsABC-Mediated Pathway for Pathogenicity in <i>Salmonella enterica</i> Serovar Typhimurium. Infection and Immunity, 2015, 83, 4266-4276. | 2.2 | 15 |
| 78 | Structural and Mechanistic Insights into the <i>Pseudomonas fluorescens</i> 2-Nitrobenzoate 2-Nitroreductase NbaA. Applied and Environmental Microbiology, 2015, 81, 5266-5277. | 3.1 | 3 |
| 79 | Crystal structure of β -N-acetylglucosaminidase CbsA from <i>Thermotoga neapolitana</i> . Biochemical and Biophysical Research Communications, 2015, 464, 869-874. | 2.1 | 5 |
| 80 | Crystal Structure of DsbA from <i>Corynebacterium diphtheriae</i> and Its Functional Implications for CueP in Gram-Positive Bacteria. Molecules and Cells, 2015, 38, 715-722. | 2.6 | 7 |
| 81 | 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 |
| 82 | Structure of a DsbF homologue from <i>Corynebacterium diphtheriae</i> . Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1167-1172. | 0.8 | 3 |
| 83 | 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 |
| 84 | 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 |
| 85 | Development of Akt-activated GSK3 β inhibitory peptide. Biochemical and Biophysical Research Communications, 2013, 434, 735-739. | 2.1 | 12 |
| 86 | Structural Basis for the Inhibition of Human Lysozyme by Plc from <i>Brucella abortus</i> . Biochemistry, 2013, 52, 9385-9393. | 2.5 | 16 |
| 87 | Morin attenuates tau hyperphosphorylation by inhibiting GSK3 β . Neurobiology of Disease, 2011, 44, 223-230. | 4.4 | 87 |
| 88 | Upregulation of RNase E activity by mutation of a site that uncompetitively interferes with RNA binding. RNA Biology, 2011, 8, 1022-1034. | 3.1 | 9 |
| 89 | 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 |
| 90 | 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 |

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|----|--|-----|-----------|
| 91 | Structural basis for the recognition of lysozyme by MliC, a periplasmic lysozyme inhibitor in Gram-negative bacteria. <i>Biochemical and Biophysical Research Communications</i> , 2009, 378, 244-248. | 2.1 | 43 |
| 92 | Crystal Structure of the Periplasmic Component of a Tripartite Macrolide-Specific Efflux Pump. <i>Journal of Molecular Biology</i> , 2009, 387, 1286-1297. | 4.2 | 111 |
| 93 | Crystal Structure of the Periplasmic Region of MacB, a Noncanonic ABC Transporter ^{<sup></sup>} . <i>Biochemistry</i> , 2009, 48, 5218-5225. | 2.5 | 44 |
| 94 | 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. <i>Genetics</i> , 2008, 179, 1871-1879. | 2.9 | 13 |
| 95 | Calcium-Dependent Catalytic Activity of a Novel Phytase from <i>Bacillus amyloliquefaciens</i> DS11. <i>Biochemistry</i> , 2001, 40, 9669-9676. | 2.5 | 87 |