

Ning Gao

List of Publications by Year in descending order

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Version: 2024-02-01

88
papers

7,402
citations

76326

40
h-index

64796

79
g-index

97
all docs

97
docs citations

97
times ranked

13026
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterization of Photorhabdus Virulence Cassette as a causative agent in the emerging pathogen Photorhabdus asymbiotica. Science China Life Sciences, 2022, 65, 618-630.	4.9	12
2	Structural insights into the membrane microdomain organization by SPFH family proteins. Cell Research, 2022, 32, 176-189.	12.0	24
3	Cryo-EM structure of <i>Mycobacterium tuberculosis</i> 50S ribosomal subunit bound with clarithromycin reveals dynamic and specific interactions with macrolides. Emerging Microbes and Infections, 2022, 11, 293-305.	6.5	5
4	Engineering and functional analysis of yeast with a monotypic 40S ribosome subunit. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	9
5	Structural insights into how GlcNAc-1-phosphotransferase directs lysosomal protein transport. Journal of Biological Chemistry, 2022, 298, 101702.	3.4	3
6	Structural Insight into the MCM double hexamer activation by Dbf4-Cdc7 kinase. Nature Communications, 2022, 13, 1396.	12.8	15
7	N-terminal signal peptides facilitate the engineering of PVC complex as a potent protein delivery system. Science Advances, 2022, 8, eabm2343.	10.3	16
8	Ribosomal protein eL39 is important for maturation of the nascent polypeptide exit tunnel and proper protein folding during translation. Nucleic Acids Research, 2022, 50, 6453-6473.	14.5	8
9	Structural remodeling of ribosome associated Hsp40-Hsp70 chaperones during co-translational folding. Nature Communications, 2022, 13, .	12.8	17
10	Disome-seq reveals widespread ribosome collisions that promote cotranslational protein folding. Genome Biology, 2021, 22, 16.	8.8	63
11	Structural insights into TSC complex assembly and GAP activity on Rheb. Nature Communications, 2021, 12, 339.	12.8	44
12	Cryo-EM structures of human GMPPA-GMPPB complex reveal how cells maintain GDP-mannose homeostasis. Nature Structural and Molecular Biology, 2021, 28, 1-12.	8.2	26
13	Transcription shapes DNA replication initiation to preserve genome integrity. Genome Biology, 2021, 22, 176.	8.8	20
14	VHUT-cryo-FIB, a method to fabricate frozen hydrated lamellae from tissue specimens for in situ cryo-electron tomography. Journal of Structural Biology, 2021, 213, 107763.	2.8	15
15	Structural insight into the mechanism of energy transfer in cyanobacterial phycobilisomes. Nature Communications, 2021, 12, 5497.	12.8	59
16	Structure, function and pharmacology of human itch receptor complexes. Nature, 2021, 600, 164-169.	27.8	67
17	Structural snapshots of human pre-60S ribosomal particles before and after nuclear export. Nature Communications, 2020, 11, 3542.	12.8	44
18	Structural insight into the assembly and conformational activation of human origin recognition complex. Cell Discovery, 2020, 6, 88.	6.7	3

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19	Coupling of 5S RNP rotation with maturation of functional centers during large ribosomal subunit assembly. <i>Nature Communications</i> , 2020, 11, 3751.	12.8	24
20	Structural insights into assembly of the ribosomal nascent polypeptide exit tunnel. <i>Nature Communications</i> , 2020, 11, 5111.	12.8	21
21	Structurally Resolved SARS-CoV-2 Antibody Shows High Efficacy in Severely Infected Hamsters and Provides a Potent Cocktail Pairing Strategy. <i>Cell</i> , 2020, 183, 1013-1023.e13.	28.9	227
22	Potent Neutralizing Antibodies against SARS-CoV-2 Identified by High-Throughput Single-Cell Sequencing of Convalescent Patients's B Cells. <i>Cell</i> , 2020, 182, 73-84.e16.	28.9	1,139
23	Structural insights into secretory immunoglobulin A and its interaction with a pneumococcal adhesin. <i>Cell Research</i> , 2020, 30, 602-609.	12.0	35
24	Cooperative transport mechanism of human monocarboxylate transporter 2. <i>Nature Communications</i> , 2020, 11, 2429.	12.8	33
25	Loss of a single methylation in 23S rRNA delays 50S assembly at multiple late stages and impairs translation initiation and elongation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 15609-15619.	7.1	27
26	Cryo-EM structures of human pannexin 1 channel. <i>Cell Research</i> , 2020, 30, 449-451.	12.0	41
27	Structural insights into immunoglobulin M. <i>Science</i> , 2020, 367, 1014-1017.	12.6	88
28	Structure of the substrate-engaged SecA-SecY protein translocation machine. <i>Nature Communications</i> , 2019, 10, 2872.	12.8	55
29	Structural and functional insights into the tetrameric photosystem I from heterocyst-forming cyanobacteria. <i>Nature Plants</i> , 2019, 5, 1087-1097.	9.3	57
30	Structure of the RSC complex bound to the nucleosome. <i>Science</i> , 2019, 366, 838-843.	12.6	92
31	Structural basis of assembly of the human T cell receptor's CD3 complex. <i>Nature</i> , 2019, 573, 546-552.	27.8	218
32	Noc4L-Mediated Ribosome Biogenesis Controls Activation of Regulatory and Conventional T Cells. <i>Cell Reports</i> , 2019, 27, 1205-1220.e4.	6.4	15
33	Cryo-EM Structure and Assembly of an Extracellular Contractile Injection System. <i>Cell</i> , 2019, 177, 370-383.e15.	28.9	68
34	Structures of the ISWI's nucleosome complex reveal a conserved mechanism of chromatin remodeling. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 258-266.	8.2	75
35	An anti-CRISPR protein disables type V Cas12a by acetylation. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 308-314.	8.2	104
36	Ligand-triggered allosteric ADP release primes a plant NLR complex. <i>Science</i> , 2019, 364, .	12.6	334

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37	Chaperonin-GroEL as a Smart Hydrophobic Drug Delivery and Tumor Targeting Molecular Machine for Tumor Therapy. <i>Nano Letters</i> , 2018, 18, 921-928.	9.1	44
38	A binding-block ion selective mechanism revealed by a Na/K selective channel. <i>Protein and Cell</i> , 2018, 9, 629-639.	11.0	14
39	Structure of the origin recognition complex bound to DNA replication origin. <i>Nature</i> , 2018, 559, 217-222.	27.8	107
40	Cryo-EM structure of human mitochondrial trifunctional protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7039-7044.	7.1	42
41	The process of mRNA-tRNA translocation. <i>Journal of Hand Surgery Asian-Pacific Volume</i> , The, 2018, , 405-412.	0.4	0
42	Structural snapshot of cytoplasmic pre-60S ribosomal particles bound by Nmd3, Lsg1, Tif6 and Reh1. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 214-220.	8.2	94
43	Structure of a Pancreatic ATP-Sensitive Potassium Channel. <i>Cell</i> , 2017, 168, 101-110.e10.	28.9	221
44	Insights into remodeling events during eukaryotic large ribosomal subunit assembly provided by high resolution cryo-EM structures. <i>RNA Biology</i> , 2017, 14, 1306-1313.	3.1	13
45	Open-ringed structure of the Cdt1-Mcm2-7 complex as a precursor of the MCM double hexamer. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 300-308.	8.2	87
46	Mechanistic insights into the alternative translation termination by ArfA and RF2. <i>Nature</i> , 2017, 541, 550-553.	27.8	43
47	Alternate binding modes of anti-CRISPR viral suppressors AcrF1/2 to Csy surveillance complex revealed by cryo-EM structures. <i>Cell Research</i> , 2017, 27, 853-864.	12.0	64
48	Ribosome Profiling Reveals Genome-wide Cellular Translational Regulation upon Heat Stress in <i>Escherichia coli</i> . <i>Genomics, Proteomics and Bioinformatics</i> , 2017, 15, 324-330.	6.9	26
49	Cryo-EM structures of the mammalian endo-lysosomal TRPML1 channel elucidate the combined regulation mechanism. <i>Protein and Cell</i> , 2017, 8, 834-847.	11.0	39
50	Cryo-EM structure of <i>Mycobacterium smegmatis</i> ribosome reveals two unidentified ribosomal proteins close to the functional centers. <i>Protein and Cell</i> , 2017, 9, 384-388.	11.0	16
51	Unique Roles of the Non-identical MCM Subunits in DNA Replication Licensing. <i>Molecular Cell</i> , 2017, 67, 168-179.	9.7	51
52	Cryo-EM structures of the 80S ribosomes from human parasites <i>Trichomonas vaginalis</i> and <i>Toxoplasma gondii</i> . <i>Cell Research</i> , 2017, 27, 1275-1288.	12.0	23
53	Atomic modeling of the ITS2 ribosome assembly subcomplex from cryo-EM together with mass spectrometry-identified protein-protein crosslinks. <i>Protein Science</i> , 2017, 26, 103-112.	7.6	18
54	Trifunctional cross-linker for mapping protein-protein interaction networks and comparing protein conformational states. <i>ELife</i> , 2016, 5, .	6.0	105

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55	The N-terminal extension of yeast ribosomal protein L8 is involved in two major remodeling events during late nuclear stages of 60S ribosomal subunit assembly. <i>Rna</i> , 2016, 22, 1386-1399.	3.5	18
56	Kinesin 1 Drives Autolysosome Tubulation. <i>Developmental Cell</i> , 2016, 37, 326-336.	7.0	129
57	Diverse roles of assembly factors revealed by structures of late nuclear pre-60S ribosomes. <i>Nature</i> , 2016, 534, 133-137.	27.8	193
58	The crystal structure of Cpf1 in complex with CRISPR RNA. <i>Nature</i> , 2016, 532, 522-526.	27.8	300
59	The architecture of the mammalian respirasome. <i>Nature</i> , 2016, 537, 639-643.	27.8	311
60	EF4 disengages the peptidyl-tRNA CCA end and facilitates back-translocation on the 70S ribosome. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 125-131.	8.2	21
61	Increasing the Depth of Mass-Spectrometry-Based Structural Analysis of Protein Complexes through the Use of Multiple Cross-Linkers. <i>Analytical Chemistry</i> , 2016, 88, 4461-4469.	6.5	40
62	Structural dynamics of the yeast Shwachman-Diamond syndrome protein (Sdo1) on the ribosome and its implication in the 60S subunit maturation. <i>Protein and Cell</i> , 2016, 7, 187-200.	11.0	8
63	Fine-Tuned H-Ferritin Nanocage with Multiple Gold Clusters as Near-Infrared Kidney Specific Targeting Nanoprobe. <i>Bioconjugate Chemistry</i> , 2015, 26, 193-196.	3.6	30
64	Structure of the eukaryotic MCM complex at 3.8 Å.... <i>Nature</i> , 2015, 524, 186-191.	27.8	207
65	CapZ regulates autophagosomal membrane shaping by promoting actin assembly inside the isolation membrane. <i>Nature Cell Biology</i> , 2015, 17, 1112-1123.	10.3	115
66	Architecture of the mammalian mechanosensitive Piezo1 channel. <i>Nature</i> , 2015, 527, 64-69.	27.8	363
67	New insights into the enzymatic role of EF-G in ribosome recycling. <i>Nucleic Acids Research</i> , 2015, 43, gkv995.	14.5	12
68	HflX is a ribosome-splitting factor rescuing stalled ribosomes under stress conditions. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 906-913.	8.2	88
69	Mechanisms of ribosome stalling by SecM at multiple elongation steps. <i>ELife</i> , 2015, 4, .	6.0	73
70	Structural insights into the function of a unique tandem GTPase EngA in bacterial ribosome assembly. <i>Nucleic Acids Research</i> , 2014, 42, 13430-13439.	14.5	38
71	Structural insights into the TRIM family of ubiquitin E3 ligases. <i>Cell Research</i> , 2014, 24, 762-765.	12.0	118
72	Structural and Functional Insights into the Mode of Action of a Universally Conserved Obg GTPase. <i>PLoS Biology</i> , 2014, 12, e1001866.	5.6	108

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73	Structural basis for interaction of a cotranslational chaperone with the eukaryotic ribosome. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 1042-1046.	8.2	61
74	XDist: an effective XML keyword search system with re-ranking model based on keyword distribution. <i>Science China Information Sciences</i> , 2014, 57, 1-17.	4.3	1
75	Structural insights into the assembly of the 30S ribosomal subunit in vivo: functional role of S5 and location of the 17S rRNA precursor sequence. <i>Protein and Cell</i> , 2014, 5, 394-407.	11.0	26
76	The Cryo-EM Structure of the Ribosome Bound to BipA. <i>Biophysical Journal</i> , 2014, 106, 492a.	0.5	0
77	LAF: a new XML encoding and indexing strategy for keyword-based XML search. <i>Concurrency Computation Practice and Experience</i> , 2013, 25, 1604-1621.	2.2	2
78	Dissecting the in vivo assembly of the 30S ribosomal subunit reveals the role of RimM and general features of the assembly process. <i>Nucleic Acids Research</i> , 2013, 41, 2609-2620.	14.5	72
79	Cryo-EM structures of the late-stage assembly intermediates of the bacterial 50S ribosomal subunit. <i>Nucleic Acids Research</i> , 2013, 41, 7073-7083.	14.5	56
80	Structural Dynamics of the Meca-ClpC Complex. <i>Journal of Biological Chemistry</i> , 2013, 288, 17597-17608.	3.4	28
81	Crystal structure and biochemical analyses reveal Beclin 1 as a novel membrane binding protein. <i>Cell Research</i> , 2012, 22, 473-489.	12.0	172
82	Toward a Cryo-Em Structure of the Ribosome Bound to BipA. <i>Biophysical Journal</i> , 2012, 102, 69a-70a.	0.5	0
83	Controlling Assembly of Paired Gold Clusters within Apoferritin Nanoreactor for in Vivo Kidney Targeting and Biomedical Imaging. <i>Journal of the American Chemical Society</i> , 2011, 133, 8617-8624.	13.7	258
84	Structural basis for the function of a small GTPase RsgA on the 30S ribosomal subunit maturation revealed by cryoelectron microscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13100-13105.	7.1	57
85	The process of mRNA-tRNA translocation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 19671-19678.	7.1	198
86	Specific Interaction between EF-G and RRF and Its Implication for GTP-Dependent Ribosome Splitting into Subunits. <i>Journal of Molecular Biology</i> , 2007, 374, 1345-1358.	4.2	49
87	A library of RNA bridges. , 2006, 2, 231-232.		9
88	Mechanism for the Disassembly of the Posttermination Complex Inferred from Cryo-EM Studies. <i>Molecular Cell</i> , 2005, 18, 663-674.	9.7	117