## **Yingang Feng**

List of Publications by Year in descending order

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119 papers	2,465 citations	27 h-index	276875 41 g-index
125	125	125	3376
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Consolidated bio-saccharification: Leading lignocellulose bioconversion into the real world. Biotechnology Advances, 2020, 40, 107535.	11.7	102
2	Structural Insight into Poplar Glutaredoxin C1 with a Bridging Ironâ^Sulfur Cluster at the Active Siteâ€,‡. Biochemistry, 2006, 45, 7998-8008.	2.5	94
3	Structural and Biochemical Characterization Reveals LysGH15 as an Unprecedented "EF-Hand-Like― Calcium-Binding Phage Lysin. PLoS Pathogens, 2014, 10, e1004109.	4.7	85
4	Metabolic profiles of Nannochloropsis oceanica IMET1 under nitrogen-deficiency stress. Bioresource Technology, 2013, 130, 731-738.	9.6	84
5	Biochemical and structural characterization of Cren7, a novel chromatin protein conserved among Crenarchaea. Nucleic Acids Research, 2008, 36, 1129-1137.	14.5	82
6	Isolation and characterization of Aurantiochytrium species: high docosahexaenoic acid (DHA) production by the newly isolated microalga, Aurantiochytrium sp. SD116. Journal of Oleo Science, 2013, 62, 143-151.	1.4	73
7	Overexpression of glucose-6-phosphate dehydrogenase enhanced the polyunsaturated fatty acid composition of Aurantiochytrium sp. SD116. Algal Research, 2016, 19, 138-145.	4.6	67
8	Targeted gene engineering in Clostridium cellulolyticum H10 without methylation. Journal of Microbiological Methods, 2012, 89, 201-208.	1.6	59
9	Transcriptome and gene expression analysis of DHA producer Aurantiochytrium under low temperature conditions. Scientific Reports, 2015, 5, 14446.	3.3	55
10	Different Impacts of Short-Chain Fatty Acids on Saturated and Polyunsaturated Fatty Acid Biosynthesis in Aurantiochytrium sp. SD116. Journal of Agricultural and Food Chemistry, 2013, 61, 9876-9881.	5.2	48
11	New insights into the structural basis of DNA recognition by HINa and HINb domains of IFI16. Journal of Molecular Cell Biology, 2016, 8, 51-61.	3.3	48
12	NMR-derived Topology of a GFP-photoprotein Energy Transfer Complex*. Journal of Biological Chemistry, 2010, 285, 40891-40900.	3.4	47
13	The contribution of cellulosomal scaffoldins to cellulose hydrolysis by Clostridium thermocellum analyzed by using thermotargetrons. Biotechnology for Biofuels, 2014, 7, 80.	6.2	46
14	Solution structure and mapping of a very weak calcium-binding site of human translationally controlled tumor protein by NMR. Archives of Biochemistry and Biophysics, 2007, 467, 48-57.	3.0	42
15	Molecular Basis of Wnt Activation via the DIX Domain Protein Ccd1. Journal of Biological Chemistry, 2011, 286, 8597-8608.	3.4	39
16	Efficient whole-cell-catalyzing cellulose saccharification using engineered Clostridium thermocellum. Biotechnology for Biofuels, 2017, 10, 124.	6.2	39
17	Simultaneous accumulation of neutral lipids and biomass in Nannochloropsis oceanica IMET1 under high light intensity and nitrogen replete conditions. Algal Research, 2015, 11, 55-62.	4.6	37
18	H-Bonding Networks Dictate the Molecular Mechanism of H <sub>2</sub> O <sub>2</sub> Activation by P450. ACS Catalysis, 2021, 11, 8774-8785.	11.2	37

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19	Deactivation of Mclâ€1 by Dualâ€Function Smallâ€Molecule Inhibitors Targeting the Bclâ€2 Homology 3 Domain and Facilitating Mclâ€1 Ubiquitination. Angewandte Chemie - International Edition, 2016, 55, 14250-14256.	13.8	35
20	3-Thiomorpholin-8-oxo-8H-acenaphtho [1,2-b] pyrrole-9-carbonitrile (S1) derivatives as pan-Bcl-2-inhibitors of Bcl-2, Bcl-xL and Mcl-1. Bioorganic and Medicinal Chemistry, 2013, 21, 11-20.	3.0	32
21	An RNA-Binding Complex Involved in Ribosome Biogenesis Contains a Protein with Homology to tRNA CCA-Adding Enzyme. PLoS Biology, 2013, 11, e1001669.	5.6	32
22	Binding of Reduced Nicotinamide Adenine Dinucleotide Phosphate Destabilizes the Ironâ-'Sulfur Clusters of Human MitoNEET. Biochemistry, 2010, 49, 9604-9612.	2.5	31
23	Structural Insight into Recognition of Methylated Histone Tails by Retinoblastoma-binding Protein 1. Journal of Biological Chemistry, 2012, 287, 8531-8540.	3.4	31
24	Glutathione regulates the transfer of iron-sulfur cluster from monothiol and dithiol glutaredoxins to apo ferredoxin. Protein and Cell, 2012, 3, 714-721.	11.0	31
25	Determination of the native features of the exoglucanase Cel48S from Clostridium thermocellum. Biotechnology for Biofuels, 2018, 11, 6.	6.2	30
26	Structural Insight into the Stabilizing Effect of O-Glycosylation. Biochemistry, 2017, 56, 2897-2906.	2.5	29
27	Native-like Partially Folded Conformations and Folding Process Revealed in the N-terminal Large Fragments of Staphylococcal Nuclease: A Study by NMR Spectroscopy. Journal of Molecular Biology, 2003, 330, 821-837.	4.2	28
28	Structural insights into the N-terminal GIY–YIG endonuclease activity of <i>Arabidopsis</i> glutaredoxin AtGRXS16 in chloroplasts. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 9565-9570.	7.1	28
29	Structural basis of X chromosome DNA recognition by the MSL2 CXC domain during <i>Drosophila</i> dosage compensation. Genes and Development, 2014, 28, 2652-2662.	5.9	28
30	Novel soluble myeloid cell leukemia sequence 1 (Mcl-1) inhibitor (E,E)-2-(benzylaminocarbonyl)-3-styrylacrylonitrile (4g) developed using a fragment-based approach. European Journal of Medicinal Chemistry, 2013, 59, 141-149.	5.5	27
31	Mechanism of the Rpn13-induced activation of Uch37. Protein and Cell, 2014, 5, 616-630.	11.0	27
32	Integration of bacterial expansin-like proteins into cellulosome promotes the cellulose degradation. Applied Microbiology and Biotechnology, 2016, 100, 2203-2212.	3.6	27
33	Artificial creation of Chlorella pyrenoidosa mutants for economic sustainable food production. Bioresource Technology, 2018, 268, 340-345.	9.6	27
34	Construction of consolidated bio-saccharification biocatalyst and process optimization for highly efficient lignocellulose solubilization. Biotechnology for Biofuels, 2019, 12, 35.	6.2	27
35	Coordinated $\hat{i}^2$ -glucosidase activity with the cellulosome is effective for enhanced lignocellulose saccharification. Bioresource Technology, 2021, 337, 125441.	9.6	26
36	An Anthraquinone Scaffold for Putative, Two-Face Bim BH3 α-Helix Mimic. Journal of Medicinal Chemistry, 2012, 55, 10735-10741.	6.4	25

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37	Evolutionarily Conserved Binding of Translationally Controlled Tumor Protein to Eukaryotic Elongation Factor 1B. Journal of Biological Chemistry, 2015, 290, 8694-8710.	3.4	25
38	Anti-apoptosis Proteins Mcl-1 and Bcl-xL Have Different p53-Binding Profiles. Biochemistry, 2013, 52, 6324-6334.	2.5	24
39	Regulation of biomass degradation by alternative $\ddot{l}f$ factors in cellulolytic clostridia. Scientific Reports, 2018, 8, 11036.	3.3	24
40	Two Conformations of Archaeal Ssh10b. Journal of Biological Chemistry, 2003, 278, 51015-51022.	3.4	23
41	High Production of Squalene Using a Newly Isolated Yeast-like Strain <i>Pseudozyma</i> sp. SD301. Journal of Agricultural and Food Chemistry, 2015, 63, 8445-8451.	5.2	23
42	Response mechanism of the docosahexaenoic acid producer Aurantiochytrium under cold stress. Algal Research, 2017, 25, 191-199.	4.6	22
43	Expression of Vitreoscilla hemoglobin enhances production of arachidonic acid and lipids in Mortierella alpina. BMC Biotechnology, 2017, 17, 68.	3.3	22
44	Revisiting the NMR solution structure of the Cel48S type-I dockerin module from Clostridium thermocellum reveals a cohesin-primed conformation. Journal of Structural Biology, 2014, 188, 188-193.	2.8	21
45	Retinoblastoma-binding Protein 1 Has an Interdigitated Double Tudor Domain with DNA Binding Activity. Journal of Biological Chemistry, 2014, 289, 4882-4895.	3.4	21
46	Improvement of ClosTron for successive gene disruption in Clostridium cellulolyticum using a pyrF-based screening system. Applied Microbiology and Biotechnology, 2014, 98, 313-323.	3.6	21
47	Bcl-2/MDM2 Dual Inhibitors Based on Universal Pyramid-Like α-Helical Mimetics. Journal of Medicinal Chemistry, 2016, 59, 3152-3162.	6.4	21
48	Protein-protein complexation in bioluminescence. Protein and Cell, 2011, 2, 957-972.	11.0	20
49	Efficiency and Stability Enhancement of Cis-epoxysuccinic Acid Hydrolase by Fusion with a Carbohydrate Binding Module and Immobilization onto Cellulose. Applied Biochemistry and Biotechnology, 2012, 168, 708-717.	2.9	20
50	Solution Structure of MSL2 CXC Domain Reveals an Unusual Zn3Cys9 Cluster and Similarity to Pre-SET Domains of Histone Lysine Methyltransferases. PLoS ONE, 2012, 7, e45437.	2.5	20
51	The chaperone Hsp70 is a BH3 receptor activated by the pro-apoptotic Bim to stabilize anti-apoptotic clients. Journal of Biological Chemistry, 2020, 295, 12900-12909.	3.4	20
52	Bacillaenes: Decomposition Trigger Point and Biofilm Enhancement in <i>Bacillus</i> . ACS Omega, 2021, 6, 1093-1098.	3.5	20
53	Selective oxidation of aliphatic C–H bonds in alkylphenols by a chemomimetic biocatalytic system. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E5129-E5137.	7.1	19
54	Changes in peptidomes and Fischer ratios of corn-derived oligopeptides depending on enzyme hydrolysis approaches. Food Chemistry, 2019, 297, 124931.	8.2	19

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55	Alternative $ f $ anti- $ f $ factors represent a unique form of bacterial $ f $ anti- $ f $ complex. Nucleic Acids Research, 2019, 47, 5988-5997.	14.5	19
56	Crystal structure of the crenarchaeal conserved chromatin protein Cren7 and doubleâ€stranded DNA complex. Protein Science, 2010, 19, 1253-1257.	7.6	18
57	Type All lantibiotic bovicin HJ50 with a rare disulfide bond: structure, structure–activity relationships and mode of action. Biochemical Journal, 2014, 461, 497-508.	3.7	17
58	Structural insights into the substrate specificity of a glycoside hydrolase family 5 lichenase from <i>Caldicellulosiruptor</i> sp. F32. Biochemical Journal, 2017, 474, 3373-3389.	3.7	17
59	The spatial proximity effect of beta-glucosidase and cellulosomes on cellulose degradation. Enzyme and Microbial Technology, 2018, 115, 52-61.	3.2	17
60	Enantiomeric Tartaric Acid Production Using cis-Epoxysuccinate Hydrolase: History and Perspectives. Molecules, 2019, 24, 903.	3.8	17
61	Metabolic Adaption of Ethanol-Tolerant Clostridium thermocellum. PLoS ONE, 2013, 8, e70631.	2.5	17
62	Discovery and mechanism of a pH-dependent dual-binding-site switch in the interaction of a pair of protein modules. Science Advances, 2020, 6, .	10.3	16
63	The N-terminal 26-residue fragment of human programmed cell death 5 protein can form a stable α-helix having unique electrostatic potential character. Biochemical Journal, 2005, 392, 47-54.	3.7	15
64	Human programmed cell death 5 protein has a helical-core and two dissociated structural regions. Biochemical and Biophysical Research Communications, 2004, 318, 391-396.	2.1	14
65	Obtaining High-Purity Docosahexaenoic Acid Oil in Thraustochytrid <i>Aurantiochytrium </i> through a Combined Metabolic Engineering Strategy. Journal of Agricultural and Food Chemistry, 2021, 69, 10215-10222.	5.2	13
66	A Stabilizing $\hat{l}\pm\hat{l}^2$ -Hydrophobic Core Greatly Contributes to Hyperthermostability of Archaeal [P62A]Ssh10b. Biochemistry, 2008, 47, 11212-11221.	2.5	12
67	Solution Structure of Synbindin Atypical PDZ Domain and Interaction with Syndecan-2. Protein and Peptide Letters, 2009, 16, 189-195.	0.9	12
68	Heavy ion mutagenesis combined with triclosan screening provides a new strategy for improving the arachidonic acid yield in Mortierella alpina. BMC Biotechnology, 2018, 18, 23.	3.3	12
69	PBN11-8, a Cytotoxic Polypeptide Purified from Marine Bacillus, Suppresses Invasion and Migration of Human Hepatocellular Carcinoma Cells by Targeting Focal Adhesion Kinase Pathways. Polymers, 2018, 10, 1043.	4.5	11
70	Inducing effects of cellulosic hydrolysate components of lignocellulose on cellulosome synthesis in <i>Clostridium thermocellum</i> . Microbial Biotechnology, 2018, 11, 905-916.	4.2	11
71	Folding Stability and Cooperativity of the Three Forms of 1–110 Residues Fragment of Staphylococcal Nuclease. Biophysical Journal, 2007, 92, 2090-2107.	0.5	10
72	NMR Studies of the Interaction between Human Programmed Cell Death 5 and Human p53. Biochemistry, 2012, 51, 2684-2693.	2.5	10

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73	Twoâ€Face, Twoâ€Turn αâ€Helix Mimetics Based on a Crossâ€Acridine Scaffold: Analogues of the Bim BH3 Domain. ChemBioChem, 2014, 15, 1280-1285.	2.6	10
74	Structural insight into a GH1 $\hat{l}^2$ -glucosidase from the oleaginous microalga, Nannochloropsis oceanica. International Journal of Biological Macromolecules, 2021, 170, 196-206.	7.5	10
75	Searching for folding initiation sites of staphylococcal nuclease: A study of N-terminal short fragments. Biopolymers, 2004, 75, 229-241.	2.4	9
76	Structure–function correlation of human programmed cell death 5 protein. Archives of Biochemistry and Biophysics, 2009, 486, 141-149.	3.0	9
77	The Archaeal Sac10b Protein Family: Conserved Proteins with Divergent Functions. Current Protein and Peptide Science, 2012, 13, 258-266.	1.4	9
78	Separation and Quantification of Water-Soluble Cellular Metabolites in <i>Clostridium thermocellum</i> using Liquid Chromatography-Isotope Dilution Tandem Mass Spectrometry. Analytical Letters, 2013, 46, 2767-2786.	1.8	9
79	Phytohormones as stimulators to improve arachidonic acid biosynthesis in Mortierella alpina. Enzyme and Microbial Technology, 2019, 131, 109381.	3.2	9
80	Importance of the C-Terminal Loop L137â^'S141 for the Folding and Folding Stability of Staphylococcal Nuclease <sup>,</sup> . Biochemistry, 2010, 49, 4318-4326.	2.5	8
81	High Yield Recombinant Expression, Characterization and Homology Modeling of Two Types of Cis-epoxysuccinic Acid Hydrolases. Protein Journal, 2012, 31, 432-438.	1.6	8
82	Resonance assignments of cohesin and dockerin domains from Clostridium acetobutylicum ATCC824. Biomolecular NMR Assignments, 2013, 7, 73-76.	0.8	8
83	An Effective Strategy for Identification of Highly Unstable Bacillaenes. Journal of Natural Products, 2019, 82, 3340-3346.	3.0	8
84	Structural basis for the DNA-binding activity of human ARID4B Tudor domain. Journal of Biological Chemistry, 2021, 296, 100506.	3.4	8
85	Dissolved xylan inhibits cellulosome-based saccharification by binding to the key cellulosomal component of Clostridium thermocellum. International Journal of Biological Macromolecules, 2022, 207, 784-790.	7.5	8
86	Letter to the Editor: 1H, 15N, and 13C resonance assignments of reduced glutaredoxin C1 from Populus tremula x tremuloides. Journal of Biomolecular NMR, 2005, 31, 263-264.	2.8	7
87	Resonance assignments of a cellulosomal double-dockerin from Clostridium thermocellum. Biomolecular NMR Assignments, 2019, 13, 97-101.	0.8	7
88	Structural Basis of Specificity for Carboxyl-Terminated Acyl Donors in a Bacterial Acyltransferase. Journal of the American Chemical Society, 2020, 142, 16031-16038.	13.7	7
89	Mapping the putative binding site for uPA protein in Esophageal Cancer-Related Gene 2 by heteronuclear NMR method. Archives of Biochemistry and Biophysics, 2008, 479, 153-157.	3.0	6
90	Structural insight into the catalytic mechanism of a <i>cis</i> enantiomerically pure <scp>d</scp> (â°')-tartaric acid. Chemical Communications, 2018, 54, 8482-8485.	4.1	6

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91	Compatible topologies and parameters for NMR structure determination of carbohydrates by simulated annealing. PLoS ONE, 2017, 12, e0189700.	2.5	6
92	Solution structure and calcium binding of protein SSO6904 from the hyperthermophilic archaeon <i>Sulfolobus solfataricus </i> In Proteins: Structure, Function and Bioinformatics, 2010, 78, 474-479.	2.6	5
93	NMR structure note: human esophageal cancer-related gene 2. Journal of Biomolecular NMR, 2012, 53, 65-70.	2.8	5
94	The C-terminal region of human eukaryotic elongation factor 1BÎ. Journal of Biomolecular NMR, 2016, 64, 181-187.	2.8	5
95	Cloning, expression and purification of DNA-binding protein Mvo10b from Methanococcus voltae. Protein Expression and Purification, 2009, 64, 162-166.	1.3	4
96	Favorable contribution of the C-terminal residue K97 to the stability of a hyperthermophilic archaeal [P62A]Ssh10b. Archives of Biochemistry and Biophysics, 2009, 481, 52-58.	3.0	4
97	Firmicutes-enriched IS1447 represents a group of IS3-family insertion sequences exhibiting unique + 1 transcriptional slippage. Biotechnology for Biofuels, 2018, 11, 300.	6.2	4
98	Targeting the Allosteric Pathway That Interconnects the Core-Functional Scaffold and the Distal Phosphorylation Sites for Specific Dephosphorylation of Bcl-2. Journal of Medicinal Chemistry, 2020, 63, 13733-13744.	6.4	4
99	Structural Insights into Transcription Initiation from De Novo RNA Synthesis to Transitioning into Elongation. IScience, 2020, 23, 101445.	4.1	4
100	Structural Insight into Chromatin Recognition by Multiple Domains of the Tumor Suppressor RBBP1. Journal of Molecular Biology, 2021, 433, 167224.	4.2	4
101	Resonance assignments of the periplasmic domain of a cellulose-sensing trans-membrane anti-sigma factor from Clostridium thermocellum. Biomolecular NMR Assignments, 2015, 9, 321-324.	0.8	3
102	1H, 15N, and 13C resonance assignments and secondary structure of the Ssh10b from hyperthermophilic archaeon Sulfolobus shibatae. Journal of Biomolecular NMR, 2002, 22, 385-386.	2.8	2
103	Folding of the C-Terminal Fragment V111-D143 of Staphylococcal Nuclease in Aqueous Solution. Protein and Peptide Letters, 2007, 14, 747-755.	0.9	2
104	Resonance assignments of a putative PilT N-terminus domain protein SSO1118 from hyperthermophilic archaeon Sulfolobus solfataricus P2. Biomolecular NMR Assignments, 2011, 5, 161-164.	0.8	2
105	A PilT N-terminus domain protein SSO1118 from hyperthemophilic archaeon Sulfolobus solfataricus P2. Journal of Biomolecular NMR, 2013, 57, 363-368.	2.8	2
106	Solution structure of a unicellular microalgae-derived translationally controlled tumor protein revealed both conserved features and structural diversity. Archives of Biochemistry and Biophysics, 2019, 665, 23-29.	3.0	2
107	Resonance assignments for the tandem PWWP-ARID domains of human RBBP1. Biomolecular NMR Assignments, 2019, 13, 177-181.	0.8	2
108	Structural Basis for Selective Oxidation of Phosphorylated Ethylphenols by Cytochrome P450 Monooxygenase Crej. Applied and Environmental Microbiology, 2021, 87, .	3.1	2

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109	The Native-like Interactions between SNase121 and SNase( $111\hat{a}^{\circ}$ '143) Fragments Induce the Recovery of Their Native-like Structures and the Ability to Degrade DNA. Biochemistry, 2009, 48, 8692-8703.	2.5	1
110	Structure determination of archaea-specific ribosomal protein L46a reveals a novel protein fold. Biochemical and Biophysical Research Communications, 2014, 450, 67-72.	2.1	1
111	1H, 15N and 13C resonance assignments of translationally-controlled tumor protein from photosynthetic microalga Nannochloropsis oceanica. Biomolecular NMR Assignments, 2015, 9, 325-328.	0.8	1
112	Deactivation of Mclâ€1 by Dualâ€Function Smallâ€Molecule Inhibitors Targeting the Bclâ€2 Homology 3 Domain and Facilitating Mclâ€1 Ubiquitination. Angewandte Chemie, 2016, 128, 14462-14468.	2.0	1
113	Modeling of the [E43S]SNase-ssDNA–Cd2+ complex: Structural insight into the action of nuclease on ssDNA. Archives of Biochemistry and Biophysics, 2013, 532, 103-113.	3.0	0
114	Resonance assignments of a VapC family toxin from Clostridium thermocellum. Biomolecular NMR Assignments, 2016, 10, 367-371.	0.8	0
115	Low stability of the reduced state of <i>Mycobacterium tuberculosis</i> NrdH redoxin. FEBS Letters, 2016, 590, 387-395.	2.8	0
116	Titelbild: Deactivation of Mcl-1 by Dual-Function Small-Molecule Inhibitors Targeting the Bcl-2 Homology 3 Domain and Facilitating Mcl-1 Ubiquitination (Angew. Chem. 46/2016). Angewandte Chemie, 2016, 128, 14387-14387.	2.0	0
117	Backbone and side-chain 1H, 15N and 13C resonance assignments of two Sac10b family members Mvo10b and Mth10bTQQA from archaea. Biomolecular NMR Assignments, 2017, 11, 269-273.	0.8	0
118	Solution structure of an archaeal DUF61 family protein SSO0941 encoded by a gene in the operon of box C/D RNA protein complexes. Journal of Structural Biology, 2018, 203, 179-184.	2.8	0
119	NMR chemical shift assignments of a module of unknown function in the cellulosomal secondary scaffoldin ScaF from Clostridium thermocellum. Biomolecular NMR Assignments, 2021, 15, 329-334.	0.8	O