

Yunhuang Yang

List of Publications by Year in descending order

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papers

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all docs

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docs citations

39
times ranked

488
citing authors

#	ARTICLE	IF	CITATIONS
1	Hyperpolarized Xe NMR signal advancement by metal-organic framework entrapment in aqueous solution. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 17558-17563.	7.1	175
2	Safety analysis of edible oil products via Raman spectroscopy. Talanta, 2019, 191, 324-332.	5.5	56
3	G-triplex: A new type of CRISPR-Cas12a reporter enabling highly sensitive nucleic acid detection. Biosensors and Bioelectronics, 2021, 187, 113292.	10.1	52
4	NMR-Based Methods for Protein Analysis. Analytical Chemistry, 2021, 93, 1866-1879.	6.5	43
5	CRISPR-Cas12a <i>trans</i> -cleaves DNA G-quadruplexes. Chemical Communications, 2020, 56, 12526-12529.	4.1	40
6	Nanobody Technology for Mycotoxin Detection in the Field of Food Safety: Current Status and Prospects. Toxins, 2018, 10, 180.	3.4	35
7	Naked-eye based point-of-care detection of E.coli O157: H7 by a signal-amplified microfluidic aptasensor. Analytica Chimica Acta, 2020, 1130, 20-28.	5.4	32
8	Structural basis of DNA binding to human YB-1 cold shock domain regulated by phosphorylation. Nucleic Acids Research, 2020, 48, 9361-9371.	14.5	30
9	Development of a biotinylated nanobody for sensitive detection of aflatoxin B1 in cereal via ELISA. Talanta, 2022, 239, 123125.	5.5	28
10	Mass spectrometry-based strategies for single-cell metabolomics. Mass Spectrometry Reviews, 2023, 42, 67-94.	5.4	27
11	¹ H NMR spectroscopic evidence of interaction between ibuprofen and lipoproteins in human blood plasma. Analytical Biochemistry, 2004, 324, 292-297.	2.4	23
12	Free-base porphyrins as CEST MRI contrast agents with highly upfield shifted labile protons. Magnetic Resonance in Medicine, 2019, 82, 577-585.	3.0	14
13	Uncorrelated Effect of Interdomain Contact on Pin1 Isomerase Activity Reveals Positive Catalytic Cooperativity. Journal of Physical Chemistry Letters, 2019, 10, 1272-1278.	4.6	10
14	Microfluidic triple-gradient generator for efficient screening of chemical space. Talanta, 2019, 204, 569-575.	5.5	8
15	Enhancing the detection sensitivity of nanobody against aflatoxin B1 through structure-guided modification. International Journal of Biological Macromolecules, 2022, 194, 188-197.	7.5	8
16	Structural insights into the impact of two holoprosencephaly-related mutations on human TGIF1 homeodomain. Biochemical and Biophysical Research Communications, 2018, 496, 575-581.	2.1	7
17	NMR-Based Metabolomics in Cancer Research. Advances in Experimental Medicine and Biology, 2021, 1280, 201-218.	1.6	6
18	Solution structure of SHIP2 SH2 domain and its interaction with a phosphotyrosine peptide from c-MET. Archives of Biochemistry and Biophysics, 2018, 656, 31-37.	3.0	5

#	ARTICLE	IF	CITATIONS
19	Expression, purification and characterization of the RhoA-binding domain of human SHIP2 in E.coli. Protein Expression and Purification, 2021, 180, 105821.	1.3	5
20	Structural Insight into the Binding of TGIF1 to SIN3A PAH2 Domain through a C-Terminal Amphipathic Helix. International Journal of Molecular Sciences, 2021, 22, 12631.	4.1	5
21	A fast microfluidic mixer enabling rapid preparation of homogeneous PEG and bicelle media for RDC in NMR analysis. Chemical Engineering Journal, 2022, 431, 133817.	12.7	5
22	Solution NMR structure of RHE_CH02687 from <i>Rhizobium etli</i> : A novel flavonoid-binding protein. Proteins: Structure, Function and Bioinformatics, 2017, 85, 951-956.	2.6	4
23	Solution NMR structure of zinc finger 4 and 5 from human INSM1, an essential regulator of neuroendocrine differentiation. Proteins: Structure, Function and Bioinformatics, 2017, 85, 957-962.	2.6	4
24	Structural insight into the length-dependent binding of ssDNA by SP_0782 from <i>Streptococcus pneumoniae</i> , reveals a divergence in the DNA-binding interface of PC4-like proteins. Nucleic Acids Research, 2019, 48, 432-444.	14.5	4
25	Quantitative Proteomic Analysis for High- and Low-Aflatoxin-Yield <i>Aspergillus flavus</i> Strains Isolated From Natural Environments. Frontiers in Microbiology, 2021, 12, 741875.	3.5	4
26	Chemical shift assignments of a camelid nanobody against aflatoxin B1. Biomolecular NMR Assignments, 2019, 13, 75-78.	0.8	3
27	An auxiliary binding interface of SHIP2-SH2 for Y292-phosphorylated Fc γ RIIB reveals diverse recognition mechanisms for tyrosine-phosphorylated receptors involved in different cell signaling pathways. Analytical and Bioanalytical Chemistry, 2022, 414, 497-506.	3.7	3
28	Structural Investigations on the SH3b Domains of <i>Clostridium perfringens</i> Autolysin through NMR Spectroscopy and Structure Simulation Enlighten the Cell Wall Binding Function. Molecules, 2021, 26, 5716.	3.8	3
29	Chemical shift assignments of the homodimer protein SP_0782 (7â€“79) from <i>Streptococcus pneumoniae</i> . Biomolecular NMR Assignments, 2016, 10, 341-344.	0.8	2
30	Chemical shift assignments of polyketide cyclase _{like} protein CGL2373 from <i>Corynebacterium glutamicum</i> . Biomolecular NMR Assignments, 2017, 11, 289-292.	0.8	2
31	Characterization of the interaction interface and conformational dynamics of human TGIF1 homeodomain upon the binding of consensus DNA. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2018, 1866, 1021-1028.	2.3	2
32	Chemical shift assignments of CHU_1110: an AHSA1-like protein from <i>Cytophaga hutchinsonii</i> . Biomolecular NMR Assignments, 2018, 12, 155-158.	0.8	1
33	Chemical shift assignments of RHE_RS02845, a NTF2-like domain-containing protein from <i>Rhizobium etli</i> . Biomolecular NMR Assignments, 2018, 12, 249-252.	0.8	1
34	Backbone and side chain resonance assignments of the C-terminal domain of human TGIF1. Biomolecular NMR Assignments, 2019, 13, 357-360.	0.8	1
35	Solution NMR structure of CHU_1110 from <i>Cytophaga hutchinsonii</i> , an AHSA1 protein potentially involved in metal ion stress response. Proteins: Structure, Function and Bioinformatics, 2019, 87, 91-95.	2.6	1
36	Solution NMR structure of CGL2373, a polyketide cyclase _{like} protein from <i>Corynebacterium glutamicum</i> . Proteins: Structure, Function and Bioinformatics, 2020, 88, 237-241.	2.6	1

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37	Mutation of leucine 20 causes a change of local conformation indirectly impairing the DNA binding of SP_0782 from <i>Streptococcus pneumoniae</i> . <i>Biochemical and Biophysical Research Communications</i> , 2020, 524, 103-108.	2.1	1
38	Chemical shift assignments of Mb1858 (24-155), a FHA domain-containing protein from <i>Mycobacterium bovis</i> . <i>Biomolecular NMR Assignments</i> , 2018, 12, 1-4.	0.8	0
39	Solution NMR structure and ligand identification of human Gas7 SH3 domain reveal a typical SH3 fold but a non-canonical ligand-binding mode. <i>Biochemical and Biophysical Research Communications</i> , 2019, 516, 1190-1195.	2.1	0