

Yunhuang Yang

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

651
citations

759233

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all docs

39
docs citations

39
times ranked

488
citing authors

#	ARTICLE	IF	CITATIONS
1	Mass spectrometry-based strategies for single-cell metabolomics. <i>Mass Spectrometry Reviews</i> , 2023, 42, 67-94.	5.4	27
2	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. <i>Analytical and Bioanalytical Chemistry</i> , 2022, 414, 497-506.	3.7	3
3	Development of a biotinylated nanobody for sensitive detection of aflatoxin B1 in cereal via ELISA. <i>Talanta</i> , 2022, 239, 123125.	5.5	28
4	A fast microfluidic mixer enabling rapid preparation of homogeneous PEG and bicelle media for RDC in NMR analysis. <i>Chemical Engineering Journal</i> , 2022, 431, 133817.	12.7	5
5	Enhancing the detection sensitivity of nanobody against aflatoxin B1 through structure-guided modification. <i>International Journal of Biological Macromolecules</i> , 2022, 194, 188-197.	7.5	8
6	NMR-Based Metabolomics in Cancer Research. <i>Advances in Experimental Medicine and Biology</i> , 2021, 1280, 201-218.	1.6	6
7	NMR-Based Methods for Protein Analysis. <i>Analytical Chemistry</i> , 2021, 93, 1866-1879.	6.5	43
8	Expression, purification and characterization of the RhoA-binding domain of human SHIP2 in E.coli. <i>Protein Expression and Purification</i> , 2021, 180, 105821.	1.3	5
9	G-triplex: A new type of CRISPR-Cas12a reporter enabling highly sensitive nucleic acid detection. <i>Biosensors and Bioelectronics</i> , 2021, 187, 113292.	10.1	52
10	Quantitative Proteomic Analysis for High- and Low-Aflatoxin-Yield <i>Aspergillus flavus</i> Strains Isolated From Natural Environments. <i>Frontiers in Microbiology</i> , 2021, 12, 741875.	3.5	4
11	Structural Investigations on the SH3b Domains of <i>Clostridium perfringens</i> Autolysin through NMR Spectroscopy and Structure Simulation Enlighten the Cell Wall Binding Function. <i>Molecules</i> , 2021, 26, 5716.	3.8	3
12	Structural Insight into the Binding of TGIF1 to SIN3A PAH2 Domain through a C-Terminal Amphipathic Helix. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12631.	4.1	5
13	Solution NMR structure of CGL2373, a polyketide cyclase-like protein from <i>Corynebacterium glutamicum</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 237-241.	2.6	1
14	Hyperpolarized Xe NMR signal advancement by metal-organic framework entrapment in aqueous solution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 17558-17563.	7.1	175
15	Structural basis of DNA binding to human YB-1 cold shock domain regulated by phosphorylation. <i>Nucleic Acids Research</i> , 2020, 48, 9361-9371.	14.5	30
16	Naked-eye based point-of-care detection of E.coli O157: H7 by a signal-amplified microfluidic aptasensor. <i>Analytica Chimica Acta</i> , 2020, 1130, 20-28.	5.4	32
17	CRISPR-Cas12a <i>trans</i> -cleaves DNA G-quadruplexes. <i>Chemical Communications</i> , 2020, 56, 12526-12529.	4.1	40
18	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

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19	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
20	Microfluidic triple-gradient generator for efficient screening of chemical space. <i>Talanta</i> , 2019, 204, 569-575.	5.5	8
21	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. <i>Nucleic Acids Research</i> , 2019, 48, 432-444.	14.5	4
22	Backbone and side chain resonance assignments of the C-terminal domain of human TGIF1. <i>Biomolecular NMR Assignments</i> , 2019, 13, 357-360.	0.8	1
23	Free-base porphyrins as CEST MRI contrast agents with highly upfield shifted labile protons. <i>Magnetic Resonance in Medicine</i> , 2019, 82, 577-585.	3.0	14
24	Uncorrelated Effect of Interdomain Contact on Pin1 Isomerase Activity Reveals Positive Catalytic Cooperativity. <i>Journal of Physical Chemistry Letters</i> , 2019, 10, 1272-1278.	4.6	10
25	Safety analysis of edible oil products via Raman spectroscopy. <i>Talanta</i> , 2019, 191, 324-332.	5.5	56
26	Solution NMR structure of CHU_1110 from <i>Cytophaga hutchinsonii</i> , an AHSA1 protein potentially involved in metal ion stress response. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 91-95.	2.6	1
27	Chemical shift assignments of a camelid nanobody against aflatoxin B1. <i>Biomolecular NMR Assignments</i> , 2019, 13, 75-78.	0.8	3
28	Structural insights into the impact of two holoprosencephaly-related mutations on human TGIF1 homeodomain. <i>Biochemical and Biophysical Research Communications</i> , 2018, 496, 575-581.	2.1	7
29	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
30	Characterization of the interaction interface and conformational dynamics of human TGIF1 homeodomain upon the binding of consensus DNA. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2018, 1866, 1021-1028.	2.3	2
31	Chemical shift assignments of CHU_1110: an AHSA1-like protein from <i>Cytophaga hutchinsonii</i> . <i>Biomolecular NMR Assignments</i> , 2018, 12, 155-158.	0.8	1
32	Chemical shift assignments of RHE_RS02845, a NTF2-like domain-containing protein from <i>Rhizobium etli</i> . <i>Biomolecular NMR Assignments</i> , 2018, 12, 249-252.	0.8	1
33	Solution structure of SHIP2 SH2 domain and its interaction with a phosphotyrosine peptide from c-MET. <i>Archives of Biochemistry and Biophysics</i> , 2018, 656, 31-37.	3.0	5
34	Nanobody Technology for Mycotoxin Detection in the Field of Food Safety: Current Status and Prospects. <i>Toxins</i> , 2018, 10, 180.	3.4	35
35	Solution NMR structure of RHE_CH02687 from <i>Rhizobium etli</i> : A novel flavonoid-binding protein. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 951-956.	2.6	4
36	Solution NMR structure of zinc finger 4 and 5 from human INSM1, an essential regulator of neuroendocrine differentiation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 957-962.	2.6	4

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37	Chemical shift assignments of polyketide cyclase_like protein CGL2373 from <i>Corynebacterium glutamicum</i> . <i>Biomolecular NMR Assignments</i> , 2017, 11, 289-292.	0.8	2
38	Chemical shift assignments of the homodimer protein SP_0782 (7â€“79) from <i>Streptococcus pneumoniae</i> . <i>Biomolecular NMR Assignments</i> , 2016, 10, 341-344.	0.8	2
39	¹ H NMR spectroscopic evidence of interaction between ibuprofen and lipoproteins in human blood plasma. <i>Analytical Biochemistry</i> , 2004, 324, 292-297.	2.4	23