

Satoko Akashi

List of Publications by Year in descending order

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79
papers

2,409
citations

257357

24
h-index

223716

46
g-index

86
all docs

86
docs citations

86
times ranked

3228
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative study of H ₃ O ⁺ (aq) and NH ₄ ⁺ (aq) on electrophoresis, protonating ability, and sodiation of proteins. <i>International Journal of Mass Spectrometry</i> , 2022, 471, 116728.	0.7	5
2	Metal distribution in Cu/Zn-superoxide dismutase revealed by native mass spectrometry. <i>Free Radical Biology and Medicine</i> , 2022, 183, 60-68.	1.3	8
3	Structural plasticity of a designer protein sheds light on α -propeller protein evolution. <i>FEBS Journal</i> , 2021, 288, 530-545.	2.2	13
4	Single-Cell Native Mass Spectrometry of Human Erythrocytes. <i>Analytical Chemistry</i> , 2021, 93, 6583-6588.	3.2	9
5	Native Mass Spectrometry of Protein and DNA Complexes Prepared in Nonvolatile Buffers. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 711-718.	1.2	15
6	Screening of protein-ligand interactions under crude conditions by native mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , 2020, 412, 4037-4043.	1.9	10
7	Mass Spectrometric Characterization of Histone H3 Isolated from <i>in-Vitro</i> Reconstituted and Acetylated Nucleosome Core Particle. <i>Mass Spectrometry</i> , 2020, 9, A0090-A0090.	0.2	1
8	Structural visualization of key steps in nucleosome reorganization by human FACT. <i>Scientific Reports</i> , 2019, 9, 10183.	1.6	42
9	Rapid and Definitive Analysis of In Vitro DNA Methylation by Nano-electrospray Ionization Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 2335-2346.	1.2	3
10	Application of the NZ α 1 Fab as a crystallization chaperone for PA tag α 1 inserted target proteins. <i>Protein Science</i> , 2019, 28, 823-836.	3.1	26
11	Structural analysis and taste evaluation of β -glutamyl peptides comprising sulfur-containing amino acids. <i>Bioscience, Biotechnology and Biochemistry</i> , 2018, 82, 383-394.	0.6	18
12	The crystal structure and oligomeric form of Escherichia coli l, d -carboxypeptidase A. <i>Biochemical and Biophysical Research Communications</i> , 2018, 499, 594-599.	1.0	6
13	Structural Diversity of Nucleosomes Characterized by Native Mass Spectrometry. <i>Analytical Chemistry</i> , 2018, 90, 8217-8226.	3.2	15
14	Methyl-selective isotope labeling using β -ketoisovalerate for the yeast <i>Pichia pastoris</i> recombinant protein expression system. <i>Journal of Biomolecular NMR</i> , 2018, 71, 213-223.	1.6	17
15	Photoinduced <i>in vivo</i> Magnetic Resonance Imaging (MRI) with Rapid CO Release from an MnCO ₃ -Protein Needle Composite. <i>Chemistry - A European Journal</i> , 2018, 24, 11578-11583.	1.7	3
16	Crystal structure of the overlapping dinucleosome composed of hexasome and octasome. <i>Science</i> , 2017, 356, 205-208.	6.0	77
17	3D structural analysis of protein <i>mannosyl kinase</i> , <i>POMK</i> , a causative gene product of dystroglycanopathy. <i>Genes To Cells</i> , 2017, 22, 348-359.	0.5	23
18	Comprehensive Characterization of Relationship Between Higher-Order Structure and Fc γ Rn Binding Affinity of Stress-Exposed Monoclonal Antibodies. <i>Pharmaceutical Research</i> , 2016, 33, 994-1002.	1.7	15

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19	Structure and assembly mechanisms of toxic human islet amyloid polypeptide oligomers associated with copper. <i>Chemical Science</i> , 2016, 7, 5398-5406.	3.7	38
20	Effect of charge on the conformation of highly basic peptides including the tail regions of histone proteins by ion mobility mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , 2016, 408, 6637-6648.	1.9	4
21	C-terminal acidic domain of histone chaperone human NAP1 is an efficient binding assistant for histone H2A/H2B, but not H3/H4. <i>Genes To Cells</i> , 2016, 21, 252-263.	0.5	21
22	Mass Spectrometric Approach for Characterizing the Disordered Tail Regions of the Histone H2A/H2B Dimer. <i>Analytical Chemistry</i> , 2015, 87, 2220-2227.	3.2	10
23	Charge-neutralization effect of the tail regions on the histone H2A/H2B dimer structure. <i>Protein Science</i> , 2015, 24, 1224-1231.	3.1	4
24	Stability of the H2B2B3 crystallin heterodimer to increased oxidation by radical probe and ion mobility mass spectrometry. <i>Journal of Structural Biology</i> , 2015, 189, 20-27.	1.3	7
25	Characterization of Stress-Exposed Granulocyte Colony Stimulating Factor Using ELISA and Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2014, 25, 1747-1754.	1.2	3
26	The Crystal Structure of the Active Domain of Anopheles Anti-platelet Protein, a Powerful Anti-coagulant, in Complex with an Antibody. <i>Journal of Biological Chemistry</i> , 2014, 289, 16303-16312.	1.6	10
27	Characterisation of an intrinsically disordered protein complex of Swi5/Sfr1 by ion mobility mass spectrometry and small-angle X-ray scattering. <i>Analyst</i> , 2013, 138, 1441-1449.	1.7	31
28	Gas-Phase Structure of the Histone Multimers Characterized by Ion Mobility Mass Spectrometry and Molecular Dynamics Simulation. <i>Analytical Chemistry</i> , 2013, 85, 4165-4171.	3.2	22
29	Conclusive Evidence of the Reconstituted Hexasome Proven by Native Mass Spectrometry. <i>Biochemistry</i> , 2013, 52, 5155-5157.	1.2	26
30	Function of homo- and hetero-oligomers of human nucleoplasmin/nucleophosmin family proteins NPM1, NPM2 and NPM3 during sperm chromatin remodeling. <i>Nucleic Acids Research</i> , 2012, 40, 4861-4878.	6.5	67
31	Crystal Structures of Penicillin-Binding Protein 3 (PBP3) from Methicillin-Resistant <i>Staphylococcus aureus</i> in the Apo and Cefotaxime-Bound Forms. <i>Journal of Molecular Biology</i> , 2012, 423, 351-364.	2.0	48
32	Impact of limited oxidation on protein ion mobility and structure of importance to footprinting by radical probe mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2012, 26, 226-230.	0.7	25
33	Homology-modelled structure of the H2B2B3 crystallin heterodimer studied by ion mobility and radical probe MS. <i>FEBS Journal</i> , 2011, 278, 4044-4054.	2.2	14
34	Structural and biochemical analyses of the human PAD4 variant encoded by a functional haplotype gene. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 112-118.	2.5	14
35	Fission Yeast Swi5-Sfr1 Protein Complex, an Activator of Rad51 Recombinase, Forms an Extremely Elongated Dogleg-shaped Structure. <i>Journal of Biological Chemistry</i> , 2011, 286, 43569-43576.	1.6	22
36	Deimination stabilizes histone H2A/H2B dimers as revealed by electrospray ionization mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2010, 45, 900-908.	0.7	20

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37	Guidelines for reporting the use of capillary electrophoresis in proteomics. <i>Nature Biotechnology</i> , 2010, 28, 654-655.	9.4	24
38	Structure of the N-terminal Regulatory Domain of a Plant NADPH Oxidase and Its Functional Implications. <i>Journal of Biological Chemistry</i> , 2010, 285, 1435-1445.	1.6	129
39	Crystal Structure of Human REV7 in Complex with a Human REV3 Fragment and Structural Implication of the Interaction between DNA Polymerase η and REV1. <i>Journal of Biological Chemistry</i> , 2010, 285, 12299-12307.	1.6	110
40	The nature of the TRAP α -Anti-TRAP complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 2176-2181.	3.3	27
41	A Self-Assembled Protein Nanotube with High Aspect Ratio. <i>Small</i> , 2009, 5, 2077-2084.	5.2	73
42	Purification, crystallization and initial X-ray diffraction study of human REV7 in complex with a REV3 fragment. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 1302-1305.	0.7	24
43	RNA and Protein Complexes of trp RNA-Binding Attenuation Protein Characterized by Mass Spectrometry. <i>Analytical Chemistry</i> , 2009, 81, 2218-2226.	3.2	13
44	Thermal unfolding of proteins probed by laser spray mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2008, 22, 1430-1436.	0.7	14
45	Structural characterization of human general transcription factor TFIIF in solution. <i>Protein Science</i> , 2008, 17, 389-400.	3.1	6
46	Crystal Structures of the Clock Protein EA4 from the Silkworm <i>Bombyx mori</i> . <i>Journal of Molecular Biology</i> , 2008, 377, 630-635.	2.0	26
47	A Mass Spectrometric Approach to the Study of DNA-Binding Proteins: Interaction of Human TRF2 with Telomeric DNA. <i>Biochemistry</i> , 2008, 47, 1797-1807.	1.2	39
48	1P016 EA4 is a protein with a built-in self-timer (Proteins-structure and structure-function) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 302 Td	0.0	0
49	Dynamic Allostery in the Ring Protein TRAP. <i>Journal of Molecular Biology</i> , 2007, 371, 154-167.	2.0	24
50	Denaturation of α -lactalbumin and ubiquitin studied by electrospray and laser spray. <i>Rapid Communications in Mass Spectrometry</i> , 2007, 21, 1635-1643.	0.7	10
51	Top-down analysis of basic proteins by microchip capillary electrophoresis mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2006, 20, 1932-1938.	0.7	36
52	Evaluation of binding affinity of protein-mutant dna complexes in solution by laser spray mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2006, 17, 611-620.	1.2	16
53	Investigation of molecular interaction within biological macromolecular complexes by mass spectrometry. <i>Medicinal Research Reviews</i> , 2006, 26, 339-368.	5.0	27
54	Stability analysis for double-stranded DNA oligomers and their noncovalent complexes with drugs by laser spray. <i>Journal of Mass Spectrometry</i> , 2006, 41, 1086-1095.	0.7	18

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55	Evaluation of protein-DNA binding affinity by electrospray ionization mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2005, 16, 116-125.	1.2	25
56	Investigation of molecular size of transcription factor TFIIIE in solution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 633-641.	1.5	11
57	Comparative Study of Laser Spray and Electrospray Using an Orthogonal TOF Mass Spectrometer. <i>Journal of the Mass Spectrometry Society of Japan</i> , 2005, 53, 100-107.	0.0	1
58	Selective dissociation of non-covalent bonds in biological molecules by laser spray. <i>Journal of Mass Spectrometry</i> , 2004, 39, 1053-1058.	0.7	24
59	Solvent accessibility of the thrombin-thrombomodulin interface ¹¹ Edited by M. F. Moody. <i>Journal of Molecular Biology</i> , 2001, 306, 575-589.	2.0	106
60	Structure of melittin bound to phospholipid micelles studied using hydrogen-deuterium exchange and electrospray ionization Fourier transform ion cyclotron resonance mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2001, 12, 1247-1253.	1.2	28
61	Characterization of the interface structure of enzyme-inhibitor complex by using hydrogen-deuterium exchange and electrospray ionization Fourier transform ion cyclotron resonance mass spectrometry. <i>Protein Science</i> , 2000, 9, 2497-2505.	3.1	50
62	Observation of Hydrogen-Deuterium Exchange of Ubiquitin by Direct Analysis of Electrospray Capillary-Skimmer Dissociation with Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. <i>Analytical Chemistry</i> , 1999, 71, 4974-4980.	3.2	57
63	Collision-Induced Dissociation Spectra Obtained by Fourier Transform Ion Cyclotron Resonance Mass Spectrometry Using a ¹³ C, ¹⁵ N-Doubly Depleted Protein. <i>Analytical Chemistry</i> , 1998, 70, 3333-3336.	3.2	10
64	Conformational Changes of Proteins Observed by Hydrogen/Deuterium Exchange and Electrospray Ionization Mass Spectrometry.. <i>Journal of the Mass Spectrometry Society of Japan</i> , 1998, 46, 75-82.	0.0	3
65	Structural Characterization of Mouse Monoclonal Antibody 13-1 against a Porphyrin Derivative: Identification of a Disulfide Bond in CDR-H3 of Mab13-1. <i>Biochemical and Biophysical Research Communications</i> , 1997, 240, 566-572.	1.0	8
66	Characterization of the Structural Difference between Active and Inactive Forms of the Ras Protein by Chemical Modification Followed by Mass Spectrometric Peptide Mapping. <i>Analytical Biochemistry</i> , 1997, 248, 15-25.	1.1	21
67	Studies on the Protein Structures by Mass Spectrometry.. <i>Journal of the Mass Spectrometry Society of Japan</i> , 1997, 45, 1-23.	0.0	1
68	Characterization of mouse switch variant antibodies by matrix-assisted laser desorption ionization mass spectrometry and electrospray ionization mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 1996, 7, 707-721.	1.2	16
69	Annonaceous Acetogenins from the Seeds of <i>Annona squamosa</i> . Adjacent Bis-tetrahydrofuranic Acetogenins.. <i>Chemical and Pharmaceutical Bulletin</i> , 1994, 42, 1163-1174.	0.6	83
70	Structural studies of polyhydroxybis(tetrahydrofuran)acetogenins from <i>Annona squamosa</i> using the combination of chemical derivatization and precursor-ion scanning mass spectrometry. <i>Organic Mass Spectrometry</i> , 1993, 28, 1516-1524.	1.3	11
71	Investigation of the interaction between enzyme and inhibitor by the combination of chemical modification, electrospray ionization mass spectrometry and frit-fast atom bombardment liquid chromatography/mass spectrometry. <i>Biological Mass Spectrometry</i> , 1993, 22, 124-132.	0.5	16
72	Rapid confirmation and revision of the primary structure of bovine serum albumin by ESIMS and frit-FAB LC/MS. <i>Biochemical and Biophysical Research Communications</i> , 1990, 173, 639-646.	1.0	510

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73	The primary structure of human EGF produced by genetic engineering, studied by high-performance tandem mass spectrometry. <i>Biochemical and Biophysical Research Communications</i> , 1989, 163, 1100-1106.	1.0	6
74	Determination of the primary structure of paim II, an $\hat{\pm}$ -amylase inhibitor from <i>Streptomyces corchorushii</i> , by high-performance tandem mass spectrometry. <i>Biochemical and Biophysical Research Communications</i> , 1989, 158, 514-519.	1.0	9
75	Histidine microenvironment analyses of recombinant human interleukin-2 by fast atom bombardment mass spectrometry and proton magnetic resonance spectrometry.. <i>Analytical Sciences</i> , 1989, 5, 759-761.	0.8	6
76	A determination of the positions of disulphide bonds in Paim I, $\hat{\pm}$ -amylase inhibitor from <i>Streptomyces corchorushii</i> , using fast atom bombardment mass spectrometry. <i>Biomedical & Environmental Mass Spectrometry</i> , 1988, 15, 541-546.	1.6	23
77	Primary structure of Paim I, an α -amylase inhibitor from <i>Streptomyces corchorushii</i> , as determined by the combination of Edman degradation and fast atom bombardment mass spectrometry. <i>Biochemistry</i> , 1987, 26, 6483-6488.	1.2	41
78	Field desorption tandem mass spectrometry of anthracycline antibiotics, cosmomycin A, B, C and D. <i>Biomedical & Environmental Mass Spectrometry</i> , 1987, 14, 305-312.	1.6	12
79	Total synthesis of (+)-tryptoquivaline. <i>Tetrahedron Letters</i> , 1984, 25, 3865-3868.	0.7	20