Masato Taoka

List of Publications by Year
in descending order

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88	5,524	76326	85541
papers	citations	40 h-index	71 g-index

90	90	90	7210
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Lectin affinity capture, isotope-coded tagging and mass spectrometry to identify N-linked glycoproteins. Nature Biotechnology, 2003, 21, 667-672.	17.5	637
2	Structural Analysis Reveals that Toll-like Receptor 7 Is a Dual Receptor for Guanosine and Single-Stranded RNA. Immunity, 2016, 45, 737-748.	14.3	321
3	Toll-like receptor 8 senses degradation products of single-stranded RNA. Nature Structural and Molecular Biology, 2015, 22, 109-115.	8.2	312
4	Landscape of the complete RNA chemical modifications in the human 80S ribosome. Nucleic Acids Research, 2018, 46, 9289-9298.	14.5	242
5	Molecular constituents of the postsynaptic density fraction revealed by proteomic analysis using multidimensional liquid chromatography-tandem mass spectrometry. Journal of Neurochemistry, 2003, 88, 759-768.	3.9	187
6	Dynamic RNA acetylation revealed by quantitative cross-evolutionary mapping. Nature, 2020, 583, 638-643.	27.8	175
7	14-3-3 Proteins Modulate the Expression of Epithelial Na+ Channels by Phosphorylation-dependent Interaction with Nedd4-2 Ubiquitin Ligase. Journal of Biological Chemistry, 2005, 280, 13187-13194.	3.4	170
8	14-3-3 Protein Binds to Insulin Receptor Substrate-1, One of the Binding Sites of Which Is in the Phosphotyrosine Binding Domain. Journal of Biological Chemistry, 1997, 272, 25267-25274.	3.4	141
9	Efficient production of isotopically labeled proteins by cell-free synthesis: A practical protocol. Journal of Biomolecular NMR, 2004, 30, 311-325.	2.8	124
10	Large-Scale Identification of Caenorhabditis elegans Proteins by Multidimensional Liquid Chromatographyâ^'Tandem Mass Spectrometry. Journal of Proteome Research, 2003, 2, 23-35.	3.7	118
11	Cell Surface Labeling and Mass Spectrometry Reveal Diversity of Cell Surface Markers and Signaling Molecules Expressed in Undifferentiated Mouse Embryonic Stem Cells. Molecular and Cellular Proteomics, 2005, 4, 1968-1976.	3.8	110
12	Structural Analyses of Toll-like Receptor 7 Reveal Detailed RNA Sequence Specificity and Recognition Mechanism of Agonistic Ligands. Cell Reports, 2018, 25, 3371-3381.e5.	6.4	98
13	Proteomics Reveals N-Linked Glycoprotein Diversity in Caenorhabditis elegans and Suggests an Atypical Translocation Mechanism for Integral Membrane Proteins. Molecular and Cellular Proteomics, 2007, 6, 2100-2109.	3.8	97
14	Stimulus-Coupled Interaction of Tyrosine Hydroxylase with 14-3-3 Proteinsâ€. Biochemistry, 1999, 38, 15673-15680.	2.5	93
15	Identification of Protein Substrates of Ca2+/Calmodulin-Dependent Protein Kinase II in the Postsynaptic Density by Protein Sequencing and Mass Spectrometry. Biochemical and Biophysical Research Communications, 2002, 290, 948-954.	2.1	89
16	Large-scale identification of proteins expressed in mouse embryonic stem cells. Proteomics, 2005, 5, 1346-1361.	2.2	89
17	The complete chemical structure ofSaccharomyces cerevisiaerRNA: partial pseudouridylation of U2345 in 25S rRNA by snoRNA snR9. Nucleic Acids Research, 2016, 44, 8951-8961.	14.5	87
18	Identification of functional marker proteins in the mammalian growth cone. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 17211-17216.	7.1	82

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19	V-1, a Protein Expressed Transiently during Murine Cerebellar Development, Regulates Actin Polymerization via Interaction with Capping Protein. Journal of Biological Chemistry, 2003, 278, 5864-5870.	3.4	80
20	Ariadne: a database search engine for identification and chemical analysis of RNA using tandem mass spectrometry data. Nucleic Acids Research, 2009, 37, e47-e47.	14.5	79
21	Large-scale Identification of N-Glycosylated Proteins of Mouse Tissues and Construction of a Glycoprotein Database, GlycoProtDB. Journal of Proteome Research, 2012, 11, 4553-4566.	3.7	77
22	Only a Small Subset of the Horizontally Transferred Chromosomal Genes in Escherichia coli Are Translated into Proteins. Molecular and Cellular Proteomics, 2004, 3, 780-787.	3.8	75
23	Proteomic Analysis of in Vivo 14-3-3 Interactions in the Yeast Saccharomyces cerevisiae. Biochemistry, 2007, 46, 7781-7792.	2.5	75
24	FANCD2 Binds CtIP and Regulates DNA-End Resection during DNA Interstrand Crosslink Repair. Cell Reports, 2014, 7, 1039-1047.	6.4	73
25	Replication stress induces accumulation of FANCD2 at central region of large fragile genes. Nucleic Acids Research, 2018, 46, 2932-2944.	14.5	70
26	A mass spectrometry-based method for comprehensive quantitative determination of post-transcriptional RNA modifications: the complete chemical structure ofSchizosaccharomyces pomberibosomal RNAs. Nucleic Acids Research, 2015, 43, e115-e115.	14.5	69
27	Atomic resolution snapshot of Leishmania ribosome inhibition by the aminoglycoside paromomycin. Nature Communications, 2017, 8, 1589.	12.8	66
28	Matrix assisted laser desorption/ionization-time of flight-mass spectrometry analysis of proteins detected by anti-phosphotyrosine antibody on two-dimensional-gels of fibrolast cell lysates after tumor necrosis factor-l± stimulation. Electrophoresis, 2000, 21, 1890-1898.	2.4	62
29	STEM:Â A Software Tool for Large-Scale Proteomic Data Analyses. Journal of Proteome Research, 2005, 4, 1826-1831.	3.7	59
30	14-3-3 Mediates Phosphorylation-Dependent Inhibition of the Interaction between the Ubiquitin E3 Ligase Nedd4-2 and Epithelial Na+ Channels. Biochemistry, 2006, 45, 6733-6740.	2.5	58
31	Profiling ofCaenorhabditis elegans proteins using two-dimensional gel electrophoresis and matrix assisted laser desorption/ionization-time of flight-mass spectrometry. Electrophoresis, 2000, 21, 1755-1765.	2.4	55
32	Phosphorylation-Dependent Interaction of Kinesin Light Chain 2 and the 14-3-3 Protein. Biochemistry, 2002, 41, 5566-5572.	2.5	54
33	Isomerase Pin1 Stimulates Dephosphorylation of Tau Protein at Cyclin-dependent Kinase (Cdk5)-dependent Alzheimer Phosphorylation Sites. Journal of Biological Chemistry, 2013, 288, 7968-7977.	3.4	52
34	<scp>FANCD</scp>2 protects genome stability by recruiting <scp>RNA</scp> processing enzymes to resolve Râ€loops during mild replication stress. FEBS Journal, 2019, 286, 139-150.	4.7	51
35	Phosphorylation of Drebrin by Cyclin-Dependent Kinase 5 and Its Role in Neuronal Migration. PLoS ONE, 2014, 9, e92291.	2.5	51
36	An analytical platform for mass spectrometry-based identification and chemical analysis of RNA in ribonucleoprotein complexes. Nucleic Acids Research, 2009, 37, e140-e140.	14.5	50

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37	Glial Dysfunction Causes Age-Related Memory Impairment in Drosophila. Neuron, 2014, 84, 753-763.	8.1	50
38	Adenovirus E4orf6 targets pp32/LANP to control the fate of ARE-containing mRNAs by perturbing the CRM1-dependent mechanism. Journal of Cell Biology, 2005, 170, 15-20.	5.2	47
39	TDP-43 stabilises the processing intermediates of mitochondrial transcripts. Scientific Reports, 2017, 7, 7709.	3.3	45
40	Direct Identification of Human Cellular MicroRNAs by Nanoflow Liquid Chromatographyâ€“High-Resolution Tandem Mass Spectrometry and Database Searching. Analytical Chemistry, 2015, 87, 2884-2891.	6.5	43
41	Transcriptomic and Proteomic Analysis of a 14-3-3 Gene-Deficient Yeast. Biochemistry, 2004, 43, 6149-6158.	2.5	40
42	Protein profiling of rat cerebella during development. Electrophoresis, 2000, 21, 1872-1879.	2.4	39
43	Identification of Proteins Enriched in Rice Egg or Sperm Cells by Single-Cell Proteomics. PLoS ONE, 2013, 8, e69578.	2.5	39
44	Phosphorylation of Adult Type Sept5 (CDCrel-1) by Cyclin-dependent Kinase 5 Inhibits Interaction with Syntaxin-1. Journal of Biological Chemistry, 2007, 282, 7869-7876.	3.4	38
45	Denaturing reversed phase liquid chromatographic separation of non-coding ribonucleic acids on macro-porous polystyrene-divinylbenzene resins. Journal of Chromatography A, 2013, 1312, 87-92.	3.7	36
46	Functional Evolution of Duplicated Odorant-Binding Protein Genes, Obp57d and Obp57e, in Drosophila. PLoS ONE, 2012, 7, e29710.	2.5	34
47	A rat cerebellar protein containing the cdc10/SWI6 motif. FEBS Journal, 1992, 207, 615-620.	0.2	33
48	Role of fruA and csgA Genes in Gene Expression during Development of Myxococcus xanthus. Journal of Biological Chemistry, 2002, 277, 26753-26760.	3.4	33
49	14-3-3 proteins sequester a pool of soluble TRIM32 ubiquitin ligase to repress autoubiquitination and cytoplasmic body formation. Journal of Cell Science, 2013, 126, 2014-26.	2.0	33
50	In Vivo and in Vitro Phosphorylation at Ser-493 in the Glutamate (E)-segment of Neurofilament-H Subunit by Glycogen Synthase Kinase 3Î². Journal of Biological Chemistry, 2002, 277, 36032-36039.	3.4	32
51	Redox proteins are constitutively secreted by skeletal muscle. Journal of Physiological Sciences, 2014, 64, 401-409.	2.1	32
52	Identification of truncated forms of U1 snRNA reveals a novel RNA degradation pathway during snRNP biogenesis. Nucleic Acids Research, 2014, 42, 2708-2724.	14.5	31
53	Poly(A)-specific ribonuclease regulates the processing of small-subunit rRNAs in human cells. Nucleic Acids Research, 2017, 45, 3437-3447.	14.5	30
54	Multiplicity of 5â€² Cap Structures Present on Short RNAs. PLoS ONE, 2014, 9, e102895.	2.5	29

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55	Automated two-dimensional liquid chromatographic system for mapping proteins in highly complex mixtures. Journal of Chromatography A, 1991, 588, 115-123.	3.7	28
56	Rab2a and Rab27a cooperatively regulate transition from granule maturation to exocytosis through the dual effector Noc2. Journal of Cell Science, 2017, 130, 541-550.	2.0	27
57	A mass spectrometry-based method for direct determination of pseudouridine in RNA. Nucleic Acids Research, 2016, 44, e59-e59.	14.5	27
58	TDP-43 regulates site-specific 2â€²-O-methylation of U1 and U2 snRNAs via controlling the Cajal body localization of a subset of C/D scaRNAs. Nucleic Acids Research, 2019, 47, 2487-2505.	14.5	25
59	The ER cholesterol sensor SCAP promotes CARTS biogenesis at ERâ€“Golgi membrane contact sites. Journal of Cell Biology, 2021, 220, .	5.2	25
60	Global PROTOMAP Profiling to Search for Biomarkers of Early-Recurrent Hepatocellular Carcinoma. Journal of Proteome Research, 2014, 13, 4847-4858.	3.7	23
61	Automated high-resolution two-dimensional liquid chromatographic system for the rapid and sensitive separation of complex peptide mixtures. Journal of Chromatography A, 1990, 515, 313-320.	3.7	22
62	In-Gel Digestion for Mass Spectrometric Characterization of RNA from Fluorescently Stained Polyacrylamide Gels. Analytical Chemistry, 2010, 82, 7795-7803.	6.5	22
63	14â€³â€³ Proteins directly regulate Ca²⁺/calmodulinâ€dependent protein kinase kinase Î± through phosphorylationâ€dependent multisite binding. FEBS Letters, 2008, 582, 661-665.	2.8	21
64	Quantitative and combinatory determination of in situ phosphorylation of tau and its FTDP-17 mutants. Scientific Reports, 2016, 6, 33479.	3.3	21
65	Method for Direct Mass-Spectrometry-Based Identification of Monomethylated RNA Nucleoside Positional Isomers and Its Application to the Analysis of Leishmania rRNA. Analytical Chemistry, 2019, 91, 15634-15643.	6.5	21
66	DKC1 Overexpression Induces a More Aggressive Cellular Behavior and Increases Intrinsic Ribosomal Activity in Immortalized Mammary Gland Cells. Cancers, 2020, 12, 3512.	3.7	21
67	Identification of a cuticle protein with unique repeated motifs in the silkworm, Bombyx mori. Insect Biochemistry and Molecular Biology, 2013, 43, 344-351.	2.7	20
68	RNA Cytidine Acetyltransferase of Small-Subunit Ribosomal RNA: Identification of Acetylation Sites and the Responsible Acetyltransferase in Fission Yeast, Schizosaccharomyces pombe. PLoS ONE, 2014, 9, e112156.	2.5	20
69	Novel Essential Gene Involved in 16S rRNA Processing in Escherichia coli. Journal of Molecular Biology, 2015, 427, 955-965.	4.2	19
70	Cryo-EM structure of the highly atypical cytoplasmic ribosome of Euglena gracilis. Nucleic Acids Research, 2020, 48, 11750-11761.	14.5	19
71	Re-examination of a Î±-chymotrypsin-solubilized laccase in the pupal cuticle of the silkworm, Bombyx mori: Insights into the regulation system for laccase activation during the ecdysis process. Insect Biochemistry and Molecular Biology, 2014, 55, 61-69.	2.7	18
72	Regulation of the interaction of Disabledâ€1 with CIN85 by phosphorylation with Cyclinâ€dependent kinase 5. Genes To Cells, 2007, 12, 1315-1327.	1.2	17

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73	Macrophage migration inhibitory factor diminishes muscle glucose transport induced by insulin and AICAR in a muscle type-dependent manner. Biochemical and Biophysical Research Communications, 2014, 444, 496-501.	2.1	17
74	Direct Determination of Pseudouridine in RNA by Mass Spectrometry Coupled with Stable Isotope Labeling. Analytical Chemistry, 2020, 92, 11349-11356.	6.5	14
75	Intracellular cAMP controls a physical association of V-1 with CapZ in cultured mammalian endocrine cells. Biochemical and Biophysical Research Communications, 2005, 331, 181-186.	2.1	11
76	Truncated forms of U2 snRNA (U2-tfs) are shunted toward a novel uridylylation pathway that differs from the degradation pathway for U1-tfs. RNA Biology, 2018, 15, 261-268.	3.1	10
77	Efficient and cost effective production of active-form human PKB using silkworm larvae. Scientific Reports, 2015, 4, 6016.	3.3	9
78	Low-fluence blue light-induced phosphorylation of Zmphot1 mediates the first positive phototropism. Journal of Experimental Botany, 2019, 70, 5929-5941.	4.8	9
79	RNase MRP Cleaves Pre-tRNASer-Met in the tRNA Maturation Pathway. PLoS ONE, 2014, 9, e112488.	2.5	8
80	BTB-ZF Protein Znf131 Regulates Cell Growth of Developing and Mature T Cells. Journal of Immunology, 2015, 195, 982-993.	0.8	7
81	A Sensitive Microbead-Based Organic Media-Assisted Method for Proteomics Sample Preparation from Dilute and Denaturing Solutions. ACS Applied Materials & Interfaces, 2017, 9, 42661-42667.	8.0	7
82	An Ionic Liquid-Based Sample Preparation Method for Next-Stage Aggregate Proteomic Analysis. Analytical Chemistry, 2019, 91, 13494-13500.	6.5	7
83	Sequential two-step chromatographic purification of infectious poliovirus using ceramic fluoroapatite and ceramic hydroxyapatite columns. PLoS ONE, 2019, 14, e0222199.	2.5	7
84	The proteasome factor Bag101 binds to Rad22 and suppresses homologous recombination. Scientific Reports, 2013, 3, 2022.	3.3	6
85	TRIM32-Cytoplasmic-Body Formation Is an ATP-Consuming Process Stimulated by HSP70 in Cells. PLoS ONE, 2017, 12, e0169436.	2.5	6
86	Presence of a novel inhibitor of capping protein in neutrophil extract. Cytoskeleton, 2005, 62, 232-243.	4.4	5
87	Matrix assisted laser desorption/ionization-time of flight-mass spectrometry analysis of proteins detected by anti-phosphotyrosine antibody on two-dimensional-gels of fibrolast cell lysates after tumor necrosis factor-Î± stimulation. Electrophoresis, 2000, 21, 1890-1898.	2.4	5
88	Subunit Composition of Ribosome in the <i>yqgF</i> Mutant Is Deficient in pre-16S rRNA Processing of <i>Escherichia coli</i>. Journal of Molecular Microbiology and Biotechnology, 2018, 28, 179-182.	1.0	3