Hisashi Hirano

List of Publications by Year
in descending order

107 papers	4,118 citations	94433 37 h-index	128289 60 g-index
109 all docs	109 docs citations	109 times ranked	6497 citing authors

#	Article	IF	Citations
1	Receptor-mediated selective autophagy degrades the endoplasmic reticulum and the nucleus. Nature, 2015, 522, 359-362.	27.8	496
2	Microsequencing of proteins electrotransferred onto immobilizing matrices from polyacrylamide gel electrophoresis: Application to an insoluble protein. Electrophoresis, 1990, 11, 573-580.	2.4	214
3	Structural basis of starvation-induced assembly of the autophagy initiation complex. Nature Structural and Molecular Biology, 2014, 21, 513-521.	8.2	180
4	The Intrinsically Disordered Protein Atg13 Mediates Supramolecular Assembly of Autophagy Initiation Complexes. Developmental Cell, 2016, 38, 86-99.	7.0	161
5	Microsequence analysis of winged bean seed proteins electroblotted from two-dimensional gel. The Protein Journal, 1989, 8, 115-130.	1.1	142
6	Atg13 HORMA domain recruits Atg9 vesicles during autophagosome formation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3350-3355.	7.1	141
7	N Î±-Acetylation and Proteolytic Activity of the Yeast 20 S Proteasome. Journal of Biological Chemistry, 2000, 275, 4635-4639.	3.4	110
8	N-Terminal modifications of the 19S regulatory particle subunits of the yeast proteasome. Archives of Biochemistry and Biophysics, 2003, 409, 341-348.	3.0	86
9	Lyn Kinase Suppresses the Transcriptional Activity of IRF5 in the TLR-MyD88 Pathway to Restrain the Development of Autoimmunity. Immunity, 2016, 45, 319-332.	14.3	81
10	Electrophoretic analysis of phosphorylation of the yeast 20S proteasome. Electrophoresis, 2002, 23, 329-338.	2.4	71
11	A Peptide that Stimulates Phosphorylation of the Plant Insulin-Binding Protein. Isolation, Primary Structure and cDNA Cloning. FEBS Journal, 1994, 224, 167-172.	0.2	70
12	Involvement of Hepatitis C Virus NS5A Hyperphosphorylation Mediated by Casein Kinase I-Î± in Infectious Virus Production. Journal of Virology, 2014, 88, 7541-7555.	3.4	70
13	Proteome analysis of diploid, tetraploid and hexaploid wheat: Towards understanding genome interaction in protein expression. Proteomics, 2003, 3, 549-557.	2.2	68
14	A possible physiological function and the tertiary structure of a 4-kDa peptide in legumes. FEBS Journal, 2003, 270, 1269-1276.	0.2	64
15	Coâ€•and postâ€translational modifications of the 26S proteasome in yeast. Proteomics, 2010, 10, 2769-2779.	2.2	61
16	Varietal differences of leaf protein profiles in mulberry. Phytochemistry, 1982, 21, 1513-1518.	2.9	58
17	Microsequence analysis of theN-terminally blocked proteins immobilized on polyvinylidene difluoride membrane by Western blotting. Electrophoresis, 1993, 14, 839-846.	2.4	56
18	Proteomic search for potential diagnostic markers and therapeutic targets for ovarian clear cell adenocarcinoma. Proteomics, 2006, 6, 5880-5890.	2.2	56

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19	Biological significance of co- and post-translational modifications of the yeast 26S proteasome. Journal of Proteomics, 2016, 134, 37-46.	2.4	55
20	Role of LRP1 and ERK and cAMP Signaling Pathways in Lactoferrin-Induced Lipolysis in Mature Rat Adipocytes. PLoS ONE, 2015, 10, e0141378.	2.5	54
21	Two distinct mechanisms target the autophagy-related E3 complex to the pre-autophagosomal structure. ELife, 2019, 8, .	6.0	51
22	Technical aspects of functional proteomics in plants. Phytochemistry, 2004, 65, 1487-1498.	2.9	50
23	NÎ±-Acetylation of yeast ribosomal proteins and its effect on protein synthesis. Journal of Proteomics, 2011, 74, 431-441.	2.4	50
24	Structural Basis for Inhibition of Xyloglucan-specific Endo-Î²-1,4-glucanase (XEG) by XEG-Protein Inhibitor. Journal of Biological Chemistry, 2012, 287, 18710-18716.	3.4	49
25	Style-specific and developmentally regulated accumulation of a glycosylated thaumatin/PR5-like protein in Japanese pear (Pyrus serotina Rehd.). Planta, 1998, 205, 514-521.	3.2	48
26	Changes in the Proteome of Xylem Sap in Brassica oleracea in Response to Fusarium oxysporum Stress. Frontiers in Plant Science, 2016, 7, 31.	3.6	48
27	Identification of candidate diagnostic serum biomarkers for Kawasaki disease using proteomic analysis. Scientific Reports, 2017, 7, 43732.	3.3	48
28	Identification of the 19S regulatory particle subunits from the rice 26S proteasome. FEBS Journal, 2002, 269, 1474-1483.	0.2	47
29	Crystal structure of basic 7S globulin, a xyloglucanâ€specific endoâ€Î²â€1,4â€glucanase inhibitor proteinâ€like protein from soybean lacking inhibitory activity against endoâ€Î²â€glucanase. FEBS Journal, 2011, 278, 1944-1954.	4.7	47
30	Amino acid residues on the surface of soybean 4-kDa peptide involved in the interaction with its binding protein. FEBS Journal, 2003, 270, 2583-2592.	0.2	46
31	N-Myristoylation of the Rpt2 Subunit Regulates Intracellular Localization of the Yeast 26S Proteasome. Biochemistry, 2012, 51, 8856-8866.	2.5	46
32	TORC1 inactivation stimulates autophagy of nucleoporin and nuclear pore complexes. Journal of Cell Biology, 2020, 219, .	5.2	46
33	Plant basic 7 S globulin-like proteins have insulin and insulin-like growth factor binding activity. FEBS Letters, 1991, 294, 210-212.	2.8	44
34	Proteome approaches to characterize seed storage proteins related to ditelocentric chromosomes in common wheat (Triticum aestivum L.). Proteomics, 2002, 2, 1146-1155.	2.2	44
35	Wheat proteomics: Relationship between fine chromosome deletion and protein expression. Proteomics, 2003, 3, 307-316.	2.2	44
36	Soybean basic 7 S globulin represents a protein widely distributed in legume species. FEBS Letters, 1987, 226, 145-149.	2.8	42

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37	Efficient peptide mapping and its application to identify embryo proteins in rice proteome analysis. Electrophoresis, 2002, 23, 647-654.	2.4	40
38	In vitro mouse spermatogenesis with an organ culture method in chemically defined medium. PLoS ONE, 2018, 13, e0192884.	2.5	39
39	Assessing matrix assisted laser desorption/ ionization-time of flight-mass spectrometry as a means of rapid embryo protein identification in rice. Electrophoresis, 2003, 24, 1319-1329.	2.4	38
40	Proteomic analysis of exosome-enriched fractions derived from cerebrospinal fluid of amyotrophic lateral sclerosis patients. Neuroscience Research, 2020, 160, 43-49.	1.9	38
41	Characterization of multiple alternative forms of heterogeneous nuclear ribonucleoprotein K by phosphateâ€affinity electrophoresis. Proteomics, 2010, 10, 3884-3895.	2.2	36
42	Sequence of a cDNA encoding soybean bask 7S globulin. Nucleic Acids Research, 1989, 17, 8868-8868.	14.5	35
43	Deblocking and Subsequent Microsequence Analysis of NÎ±-Blocked Proteins Electroblotted onto PVDF Membrane1. Journal of Biochemistry, 1992, 111, 754-757.	1.7	35
44	Two-dimensional gel electrophoresis using immobilized pH gradient tube gels. Electrophoresis, 2000, 21, 440-445.	2.4	35
45	Interaction of a 43-kDa Receptor-like Protein with a 4-kDa Hormone-like Peptide in Soybean. Biochemistry, 2004, 43, 12105-12112.	2.5	35
46	Characterization of proteins released from legume seeds in hot water. Phytochemistry, 1992, 31, 731-735.	2.9	32
47	Primary structural features of the 20S proteasome subunits of rice (Oryza sativa). Gene, 2000, 250, 61-66.	2.2	32
48	Comprehensive behavioral study and proteomic analyses of <scp>CRMP</scp>2â€deficient mice. Genes To Cells, 2016, 21, 1059-1079.	1.2	31
49	Protein Kinase Activity and Insulin-binding Activity in Plant Basic 7S Globulin. Bioscience, Biotechnology and Biochemistry, 1994, 58, 1705-1706.	1.3	27
50	Proteomic Analysis of Proteins Related to Prognosis of Lung Adenocarcinoma. Journal of Proteome Research, 2014, 13, 4686-4694.	3.7	27
51	Identification of three phosphorylation sites in the Î±7 subunit of the yeast 20S proteasome in vivo using mass spectrometry. Archives of Biochemistry and Biophysics, 2004, 431, 9-15.	3.0	23
52	Clinical Significance of Tissue Factor Pathway Inhibitor 2, a Serum Biomarker Candidate for Ovarian Clear Cell Carcinoma. PLoS ONE, 2016, 11, e0165609.	2.5	23
53	N-Myristoylation of the Rpt2 subunit of the yeast 26S proteasome is implicated in the subcellular compartment-specific protein quality control system. Journal of Proteomics, 2016, 130, 33-41.	2.4	22
54	A Phosâ€tagâ€based micropipetteâ€tip method for rapid and selective enrichment of phosphopeptides. Electrophoresis, 2017, 38, 2447-2455.	2.4	22

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55	PIM kinases facilitate lentiviral evasion from SAMHD1 restriction via Vpx phosphorylation. Nature Communications, 2019, 10, 1844.	12.8	22
56	Mass Spectrometric Identification of Glycosylphosphatidylinositol-Anchored Peptides. Journal of Proteome Research, 2013, 12, 4617-4626.	3.7	20
57	N-Terminal methylation of proteasome subunit Rpt1 in yeast. Proteomics, 2013, 13, 3167-3174.	2.2	20
58	Common Repository of FBS Proteins (cRFP) To Be Added to a Search Database for Mass Spectrometric Analysis of Cell Secretome. Journal of Proteome Research, 2019, 18, 3800-3806.	3.7	20
59	Augmentation of multiple protein kinase activities associated with secondary imatinib resistance in gastrointestinal stromal tumors as revealed by quantitative phosphoproteome analysis. Journal of Proteomics, 2015, 115, 132-142.	2.4	19
60	Identification of Tyrosine-Phosphorylated Proteins Upregulated during Epithelialâ€"Mesenchymal Transition Induced with TGF-Î². Journal of Proteome Research, 2015, 14, 4127-4136.	3.7	19
61	Shank2 Binds to aPKC and Controls Tight Junction Formation with Rap1 Signaling during Establishment of Epithelial Cell Polarity. Cell Reports, 2020, 31, 107407.	6.4	19
62	Varietal differences of leaf protein profiles in mulberry. Phytochemistry, 1982, 21, 1513-1518.	2.9	19
63	Mass Spectrometric Analysis of Posttranslational Modifications of a Carrot Extracellular Glycoproteinâ€. Biochemistry, 2004, 43, 6281-6292.	2.5	18
64	Proteome and behavioral alterations in phosphorylation-deficient mutant Collapsin Response Mediator Protein2 knock-in mice. Neurochemistry International, 2018, 119, 207-217.	3.8	18
65	The role of glycosylation in the function of a 48-kDa glycoprotein from carrot. Biochemical and Biophysical Research Communications, 2005, 328, 144-149.	2.1	17
66	The effects of heat stress on morphological properties and intracellular signaling of denervated and intact soleus muscles in rats. Physiological Reports, 2017, 5, e13350.	1.7	17
67	MZB1 in borderline resectable pancreatic cancer resected after neoadjuvant chemoradiotherapy. Journal of Surgical Research, 2017, 220, 391-401.	1.6	17
68	Mass spectrometric analysis of expression of ATPase subunits encoded by duplicated genes in the 19S regulatory particle of rice 26S proteasome. Archives of Biochemistry and Biophysics, 2004, 421, 34-41.	3.0	16
69	Mass Spectrometric Analysis of the Phosphorylation Levels of the SWI/SNF Chromatin Remodeling/Tumor Suppressor Proteins ARID1A and Brg1 in Ovarian Clear Cell Adenocarcinoma Cell Lines. Journal of Proteome Research, 2014, 13, 4959-4969.	3.7	16
70	Matrix metalloproteinase-7 induces homotypic tumor cell aggregation via proteolytic cleavage of the membrane-bound Kunitz-type inhibitor HAI-1. Journal of Biological Chemistry, 2017, 292, 20769-20784.	3.4	16
71	Wildâ€type p53 enhances annexinâ€ƒIV gene expression in ovarian clear cell adenocarcinoma. FEBS Journal, 2011, 278, 1470-1483.	4.7	15
72	Phosphoproteome analysis demonstrates the potential role of THRAP3 phosphorylation in androgenâ€independent prostate cancer cell growth. Proteomics, 2016, 16, 1069-1078.	2.2	15

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73	Basic 7S globulin in plants. Journal of Proteomics, 2021, 240, 104209.	2.4	15
74	Identification of glycosylphosphatidylinositol-anchored proteins and Ï‰-sites using TiO2-based affinity purification followed by hydrogen fluoride treatment. Journal of Proteomics, 2016, 139, 77-83.	2.4	13
75	Relationship between phosphorylation of sperm-specific antigen and prognosis of lung adenocarcinoma. Journal of Proteomics, 2016, 139, 60-66.	2.4	13
76	The tumour suppressor APC promotes HIV-1 assembly via interaction with Gag precursor protein. Nature Communications, 2017, 8, 14259.	12.8	13
77	Proteomic analysis of aortic smooth muscle cell secretions reveals an association of myosin heavy chain 11 with abdominal aortic aneurysm. American Journal of Physiology - Heart and Circulatory Physiology, 2018, 315, H1012-H1018.	3.2	13
78	Network-guided analysis of hippocampal proteome identifies novel proteins that colocalize with AÎ² in a mice model of early-stage Alzheimerâ€™s disease. Neurobiology of Disease, 2019, 132, 104603.	4.4	13
79	Evaluation of four phosphopeptide enrichment strategies for mass spectrometryâ€based proteomic analysis. Proteomics, 2022, 22, e2100216.	2.2	12
80	Phosphoproteome analysis of Lotus japonicus seeds. Proteomics, 2014, 14, 116-120.	2.2	10
81	Increase in constitutively active MEK1 species by introduction of MEK1 mutations identified in cancers. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2019, 1867, 62-70.	2.3	10
82	Screening of rice genes from the cDNA catalog using the data obtained by protein sequencing. The Protein Journal, 1997, 16, 533-536.	1.1	9
83	Effects of microgravity exposure and fructo-oligosaccharide ingestion on the proteome of soleus and extensor digitorum longus muscles in developing mice. Npj Microgravity, 2021, 7, 34.	3.7	8
84	OsPAA2 , a distinct Î±1 subunit gene for the 20S proteasome in rice (Oryza sativa L.). Gene, 2001, 272, 19-23.	2.2	7
85	Serum Quantitative Proteomic Analysis Reveals Soluble EGFR To Be a Marker of Insulin Resistance in Male Mice and Humans. Endocrinology, 2017, 158, 4152-4164.	2.8	7
86	Phos-tag diagonal electrophoresis precisely detects the mobility change of phosphoproteins in Phos-tag SDS-PAGE. Journal of Proteomics, 2021, 231, 104005.	2.4	6
87	Mass spectrometric characterization of proteins transferred from polyacrylamide gels to membrane filters. FEBS Journal, 2011, 278, 3807-3814.	4.7	5
88	Proteomic analysis revealed different responses to hypergravity of soleus and extensor digitorum longus muscles in mice. Journal of Proteomics, 2020, 217, 103686.	2.4	5
89	On-Chip Identification and Interaction Analysis of Gel-Resolved Proteins Using a Diamond-like Carbon-Coated Plate. Journal of Proteome Research, 2007, 6, 2315-2322.	3.7	4
90	ModProt: a database for integrating laboratory and literature data about protein post-translational modifications. Journal of Electrophoresis, 2016, 60, 1-4.	0.4	3

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91	Data for identification of GPI-anchored peptides and ï‰-sites in cancer cell lines. Data in Brief, 2016, 7, 1302-1305.	1.0	2
92	Phosphorylation of Ser1452 on BRG1 inhibits the function of the SWI/SNF complex in chromatin activation. Journal of Proteomics, 2021, 247, 104319.	2.4	2
93	Two-dimensional gel electrophoresis using immobilized pH gradient tube gels. Electrophoresis, 2000, 21, 440-445.	2.4	2
94	Recent developments in Phos-tag electrophoresis for the analysis of phosphoproteins in proteomics. Expert Review of Proteomics, 2022, 19, 103-114.	3.0	2
95	Protein fractionation for proteomics using the SAINOME-plate. Journal of Electrophoresis, 2018, 62, 11-15.	0.4	1
96	Detailed Structure and Pathophysiological Roles of the IgA-Albumin Complex in Multiple Myeloma. International Journal of Molecular Sciences, 2021, 22, 1766.	4.1	1
97	Analyses of Wheat Seed Proteome: Exploring Protein-Protein Interactions by Manipulating Genome Composition. Principles and Practice, 2004, , 49-66.	0.3	1
98	Two-dimensional Phos-tag affinity electrophoresis. Seibutsu Butsuri Kagaku, 2012, 56, s21-s24.	0.1	1
99	Phosphopeptide shotgun analysis using mass spectrometry and Phos-tag agarose beads. Seibutsu Butsuri Kagaku, 2012, 56, s25-s28.	0.1	1
100	2-DE based comparative quantitative analysis of phosphoprotein using Pro-Q Diamond staining and common internal standard. Denki Eido, 2015, 59, 1-7.	0.0	1
101	Technical Aspects of Functional Proteomics in Plants. ChemInform, 2004, 35, no.	0.0	0
102	Cereal Proteomics. , 2007, , 87-104.		0
103	N-Terminal Sequencing of N-Terminally Modified Proteins. Springer Protocols, 2009, , 1063-1074.	0.3	0
104	Two-dimensional electrophoresis of post-translationally modified proteins (modforms). Denki Eido, 2015, 59, 126-128.	0.0	0
105	Phos-tag World: The path to the future of electrophoresis, pioneered by the Phos-tag. Denki Eido, 2017, 61, 45-48.	0.0	0
106	ModProt: A database for integrating laboratory and literature data concerning protein post-translational modifications. Denki Eido, 2017, 61, 5-8.	0.0	0
107	CRMP2 dephosphorylation at S522 rather than hyperphosphorylation as an early-stage marker of Alzheimer's disease. Proceedings for Annual Meeting of the Japanese Pharmacological Society, 2020, 93, 2-O-068.	0.0	0