

Hisashi Hirano

List of Publications by Year in descending order

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107
papers

4,118
citations

94381

37
h-index

128225

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. <i>Nature</i> , 2015, 522, 359-362.	13.7	496
2	Microsequencing of proteins electrotransferred onto immobilizing matrices from polyacrylamide gel electrophoresis: Application to an insoluble protein. <i>Electrophoresis</i> , 1990, 11, 573-580.	1.3	214
3	Structural basis of starvation-induced assembly of the autophagy initiation complex. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 513-521.	3.6	180
4	The Intrinsically Disordered Protein Atg13 Mediates Supramolecular Assembly of Autophagy Initiation Complexes. <i>Developmental Cell</i> , 2016, 38, 86-99.	3.1	161
5	Microsequence analysis of winged bean seed proteins electroblotted from two-dimensional gel. <i>The Protein Journal</i> , 1989, 8, 115-130.	1.1	142
6	Atg13 HORMA domain recruits Atg9 vesicles during autophagosome formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3350-3355.	3.3	141
7	N ¹ -Acetylation and Proteolytic Activity of the Yeast 20 S Proteasome. <i>Journal of Biological Chemistry</i> , 2000, 275, 4635-4639.	1.6	110
8	N-Terminal modifications of the 19S regulatory particle subunits of the yeast proteasome. <i>Archives of Biochemistry and Biophysics</i> , 2003, 409, 341-348.	1.4	86
9	Lyn Kinase Suppresses the Transcriptional Activity of IRF5 in the TLR-MyD88 Pathway to Restrain the Development of Autoimmunity. <i>Immunity</i> , 2016, 45, 319-332.	6.6	81
10	Electrophoretic analysis of phosphorylation of the yeast 20S proteasome. <i>Electrophoresis</i> , 2002, 23, 329-338.	1.3	71
11	A Peptide that Stimulates Phosphorylation of the Plant Insulin-Binding Protein. Isolation, Primary Structure and cDNA Cloning. <i>FEBS Journal</i> , 1994, 224, 167-172.	0.2	70
12	Involvement of Hepatitis C Virus NS5A Hyperphosphorylation Mediated by Casein Kinase I ¹ in Infectious Virus Production. <i>Journal of Virology</i> , 2014, 88, 7541-7555.	1.5	70
13	Proteome analysis of diploid, tetraploid and hexaploid wheat: Towards understanding genome interaction in protein expression. <i>Proteomics</i> , 2003, 3, 549-557.	1.3	68
14	A possible physiological function and the tertiary structure of a 4-kDa peptide in legumes. <i>FEBS Journal</i> , 2003, 270, 1269-1276.	0.2	64
15	Co ¹ - and post ¹ -translational modifications of the 26S proteasome in yeast. <i>Proteomics</i> , 2010, 10, 2769-2779.	1.3	61
16	Varietal differences of leaf protein profiles in mulberry. <i>Phytochemistry</i> , 1982, 21, 1513-1518.	1.4	58
17	Microsequence analysis of the N-terminally blocked proteins immobilized on polyvinylidene difluoride membrane by Western blotting. <i>Electrophoresis</i> , 1993, 14, 839-846.	1.3	56
18	Proteomic search for potential diagnostic markers and therapeutic targets for ovarian clear cell adenocarcinoma. <i>Proteomics</i> , 2006, 6, 5880-5890.	1.3	56

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19	Biological significance of co- and post-translational modifications of the yeast 26S proteasome. <i>Journal of Proteomics</i> , 2016, 134, 37-46.	1.2	55
20	Role of LRP1 and ERK and cAMP Signaling Pathways in Lactoferrin-Induced Lipolysis in Mature Rat Adipocytes. <i>PLoS ONE</i> , 2015, 10, e0141378.	1.1	54
21	Two distinct mechanisms target the autophagy-related E3 complex to the pre-autophagosomal structure. <i>ELife</i> , 2019, 8, .	2.8	51
22	Technical aspects of functional proteomics in plants. <i>Phytochemistry</i> , 2004, 65, 1487-1498.	1.4	50
23	N ^ε -Acetylation of yeast ribosomal proteins and its effect on protein synthesis. <i>Journal of Proteomics</i> , 2011, 74, 431-441.	1.2	50
24	Structural Basis for Inhibition of Xyloglucan-specific Endo-β-1,4-glucanase (XEG) by XEG-Protein Inhibitor. <i>Journal of Biological Chemistry</i> , 2012, 287, 18710-18716.	1.6	49
25	Style-specific and developmentally regulated accumulation of a glycosylated thaumatin/PR5-like protein in Japanese pear (<i>Pyrus serotina</i> Rehd.). <i>Planta</i> , 1998, 205, 514-521.	1.6	48
26	Changes in the Proteome of Xylem Sap in Brassica oleracea in Response to Fusarium oxysporum Stress. <i>Frontiers in Plant Science</i> , 2016, 7, 31.	1.7	48
27	Identification of candidate diagnostic serum biomarkers for Kawasaki disease using proteomic analysis. <i>Scientific Reports</i> , 2017, 7, 43732.	1.6	48
28	Identification of the 19S regulatory particle subunits from the rice 26S proteasome. <i>FEBS Journal</i> , 2002, 269, 1474-1483.	0.2	47
29	Crystal structure of basic 7S globulin, a xyloglucan-specific endo-β-1,4-glucanase inhibitor protein-like protein from soybean lacking inhibitory activity against endo-β-1,4-glucanase. <i>FEBS Journal</i> , 2011, 278, 1944-1954.	2.2	47
30	Amino acid residues on the surface of soybean 4-kDa peptide involved in the interaction with its binding protein. <i>FEBS Journal</i> , 2003, 270, 2583-2592.	0.2	46
31	N-Myristoylation of the Rpt2 Subunit Regulates Intracellular Localization of the Yeast 26S Proteasome. <i>Biochemistry</i> , 2012, 51, 8856-8866.	1.2	46
32	TORC1 inactivation stimulates autophagy of nucleoporin and nuclear pore complexes. <i>Journal of Cell Biology</i> , 2020, 219, .	2.3	46
33	Plant basic 7 S globulin-like proteins have insulin and insulin-like growth factor binding activity. <i>FEBS Letters</i> , 1991, 294, 210-212.	1.3	44
34	Proteome approaches to characterize seed storage proteins related to ditelocentric chromosomes in common wheat (<i>Triticum aestivum</i> L.). <i>Proteomics</i> , 2002, 2, 1146-1155.	1.3	44
35	Wheat proteomics: Relationship between fine chromosome deletion and protein expression. <i>Proteomics</i> , 2003, 3, 307-316.	1.3	44
36	Soybean basic 7 S globulin represents a protein widely distributed in legume species. <i>FEBS Letters</i> , 1987, 226, 145-149.	1.3	42

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37	Efficient peptide mapping and its application to identify embryo proteins in rice proteome analysis. <i>Electrophoresis</i> , 2002, 23, 647-654.	1.3	40
38	In vitro mouse spermatogenesis with an organ culture method in chemically defined medium. <i>PLoS ONE</i> , 2018, 13, e0192884.	1.1	39
39	Assessing matrix assisted laser desorption/ ionization-time of flight-mass spectrometry as a means of rapid embryo protein identification in rice. <i>Electrophoresis</i> , 2003, 24, 1319-1329.	1.3	38
40	Proteomic analysis of exosome-enriched fractions derived from cerebrospinal fluid of amyotrophic lateral sclerosis patients. <i>Neuroscience Research</i> , 2020, 160, 43-49.	1.0	38
41	Characterization of multiple alternative forms of heterogeneous nuclear ribonucleoprotein K by phosphate α affinity electrophoresis. <i>Proteomics</i> , 2010, 10, 3884-3895.	1.3	36
42	Sequence of a cDNA encoding soybean basic 7S globulin. <i>Nucleic Acids Research</i> , 1989, 17, 8868-8868.	6.5	35
43	Deblocking and Subsequent Microsequence Analysis of N α -Blocked Proteins Electroblotted onto PVDF Membrane. <i>Journal of Biochemistry</i> , 1992, 111, 754-757.	0.9	35
44	Two-dimensional gel electrophoresis using immobilized pH gradient tube gels. <i>Electrophoresis</i> , 2000, 21, 440-445.	1.3	35
45	Interaction of a 43-kDa Receptor-like Protein with a 4-kDa Hormone-like Peptide in Soybean. <i>Biochemistry</i> , 2004, 43, 12105-12112.	1.2	35
46	Characterization of proteins released from legume seeds in hot water. <i>Phytochemistry</i> , 1992, 31, 731-735.	1.4	32
47	Primary structural features of the 20S proteasome subunits of rice (<i>Oryza sativa</i>). <i>Gene</i> , 2000, 250, 61-66.	1.0	32
48	Comprehensive behavioral study and proteomic analyses of CRMP2-deficient mice. <i>Genes To Cells</i> , 2016, 21, 1059-1079.	0.5	31
49	Protein Kinase Activity and Insulin-binding Activity in Plant Basic 7S Globulin. <i>Bioscience, Biotechnology and Biochemistry</i> , 1994, 58, 1705-1706.	0.6	27
50	Proteomic Analysis of Proteins Related to Prognosis of Lung Adenocarcinoma. <i>Journal of Proteome Research</i> , 2014, 13, 4686-4694.	1.8	27
51	Identification of three phosphorylation sites in the β 7 subunit of the yeast 20S proteasome in vivo using mass spectrometry. <i>Archives of Biochemistry and Biophysics</i> , 2004, 431, 9-15.	1.4	23
52	Clinical Significance of Tissue Factor Pathway Inhibitor 2, a Serum Biomarker Candidate for Ovarian Clear Cell Carcinoma. <i>PLoS ONE</i> , 2016, 11, e0165609.	1.1	23
53	N-Myristoylation of the Rpt2 subunit of the yeast 26S proteasome is implicated in the subcellular compartment-specific protein quality control system. <i>Journal of Proteomics</i> , 2016, 130, 33-41.	1.2	22
54	A Phos α tag α based micropipette α tip method for rapid and selective enrichment of phosphopeptides. <i>Electrophoresis</i> , 2017, 38, 2447-2455.	1.3	22

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55	PIM kinases facilitate lentiviral evasion from SAMHD1 restriction via Vpx phosphorylation. <i>Nature Communications</i> , 2019, 10, 1844.	5.8	22
56	Mass Spectrometric Identification of Glycosylphosphatidylinositol-Anchored Peptides. <i>Journal of Proteome Research</i> , 2013, 12, 4617-4626.	1.8	20
57	N-Terminal methylation of proteasome subunit Rpt1 in yeast. <i>Proteomics</i> , 2013, 13, 3167-3174.	1.3	20
58	Common Repository of FBS Proteins (cRFP) To Be Added to a Search Database for Mass Spectrometric Analysis of Cell Secretome. <i>Journal of Proteome Research</i> , 2019, 18, 3800-3806.	1.8	20
59	Augmentation of multiple protein kinase activities associated with secondary imatinib resistance in gastrointestinal stromal tumors as revealed by quantitative phosphoproteome analysis. <i>Journal of Proteomics</i> , 2015, 115, 132-142.	1.2	19
60	Identification of Tyrosine-Phosphorylated Proteins Upregulated during Epithelial to Mesenchymal Transition Induced with TGF- β 2. <i>Journal of Proteome Research</i> , 2015, 14, 4127-4136.	1.8	19
61	Shank2 Binds to aPKC and Controls Tight Junction Formation with Rap1 Signaling during Establishment of Epithelial Cell Polarity. <i>Cell Reports</i> , 2020, 31, 107407.	2.9	19
62	Varietal differences of leaf protein profiles in mulberry. <i>Phytochemistry</i> , 1982, 21, 1513-1518.	1.4	19
63	Mass Spectrometric Analysis of Posttranslational Modifications of a Carrot Extracellular Glycoprotein. <i>Biochemistry</i> , 2004, 43, 6281-6292.	1.2	18
64	Proteome and behavioral alterations in phosphorylation-deficient mutant Collapsin Response Mediator Protein2 knock-in mice. <i>Neurochemistry International</i> , 2018, 119, 207-217.	1.9	18
65	The role of glycosylation in the function of a 48-kDa glycoprotein from carrot. <i>Biochemical and Biophysical Research Communications</i> , 2005, 328, 144-149.	1.0	17
66	The effects of heat stress on morphological properties and intracellular signaling of denervated and intact soleus muscles in rats. <i>Physiological Reports</i> , 2017, 5, e13350.	0.7	17
67	MZB1 in borderline resectable pancreatic cancer resected after neoadjuvant chemoradiotherapy. <i>Journal of Surgical Research</i> , 2017, 220, 391-401.	0.8	17
68	Mass spectrometric analysis of expression of ATPase subunits encoded by duplicated genes in the 19S regulatory particle of rice 26S proteasome. <i>Archives of Biochemistry and Biophysics</i> , 2004, 421, 34-41.	1.4	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. <i>Journal of Proteome Research</i> , 2014, 13, 4959-4969.	1.8	16
70	Matrix metalloproteinase-7 induces homotypic tumor cell aggregation via proteolytic cleavage of the membrane-bound Kunitz-type inhibitor HAI-1. <i>Journal of Biological Chemistry</i> , 2017, 292, 20769-20784.	1.6	16
71	Wild-type p53 enhances annexin IV gene expression in ovarian clear cell adenocarcinoma. <i>FEBS Journal</i> , 2011, 278, 1470-1483.	2.2	15
72	Phosphoproteome analysis demonstrates the potential role of THRAP3 phosphorylation in androgen-independent prostate cancer cell growth. <i>Proteomics</i> , 2016, 16, 1069-1078.	1.3	15

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73	Basic 7S globulin in plants. <i>Journal of Proteomics</i> , 2021, 240, 104209.	1.2	15
74	Identification of glycosylphosphatidylinositol-anchored proteins and N-glycosylation sites using TiO ₂ -based affinity purification followed by hydrogen fluoride treatment. <i>Journal of Proteomics</i> , 2016, 139, 77-83.	1.2	13
75	Relationship between phosphorylation of sperm-specific antigen and prognosis of lung adenocarcinoma. <i>Journal of Proteomics</i> , 2016, 139, 60-66.	1.2	13
76	The tumour suppressor APC promotes HIV-1 assembly via interaction with Gag precursor protein. <i>Nature Communications</i> , 2017, 8, 14259.	5.8	13
77	Proteomic analysis of aortic smooth muscle cell secretions reveals an association of myosin heavy chain 11 with abdominal aortic aneurysm. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2018, 315, H1012-H1018.	1.5	13
78	Network-guided analysis of hippocampal proteome identifies novel proteins that colocalize with A β in a mice model of early-stage Alzheimer's disease. <i>Neurobiology of Disease</i> , 2019, 132, 104603.	2.1	13
79	Evaluation of four phosphopeptide enrichment strategies for mass spectrometry-based proteomic analysis. <i>Proteomics</i> , 2022, 22, e2100216.	1.3	12
80	Phosphoproteome analysis of <i>Lotus japonicus</i> seeds. <i>Proteomics</i> , 2014, 14, 116-120.	1.3	10
81	Increase in constitutively active MEK1 species by introduction of MEK1 mutations identified in cancers. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2019, 1867, 62-70.	1.1	10
82	Screening of rice genes from the cDNA catalog using the data obtained by protein sequencing. <i>The Protein Journal</i> , 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. <i>Npj Microgravity</i> , 2021, 7, 34.	1.9	8
84	OsPAA2, a distinct β 1 subunit gene for the 20S proteasome in rice (<i>Oryza sativa</i> L.). <i>Gene</i> , 2001, 272, 19-23.	1.0	7
85	Serum Quantitative Proteomic Analysis Reveals Soluble EGFR To Be a Marker of Insulin Resistance in Male Mice and Humans. <i>Endocrinology</i> , 2017, 158, 4152-4164.	1.4	7
86	Phos-tag diagonal electrophoresis precisely detects the mobility change of phosphoproteins in Phos-tag SDS-PAGE. <i>Journal of Proteomics</i> , 2021, 231, 104005.	1.2	6
87	Mass spectrometric characterization of proteins transferred from polyacrylamide gels to membrane filters. <i>FEBS Journal</i> , 2011, 278, 3807-3814.	2.2	5
88	Proteomic analysis revealed different responses to hypergravity of soleus and extensor digitorum longus muscles in mice. <i>Journal of Proteomics</i> , 2020, 217, 103686.	1.2	5
89	On-Chip Identification and Interaction Analysis of Gel-Resolved Proteins Using a Diamond-like Carbon-Coated Plate. <i>Journal of Proteome Research</i> , 2007, 6, 2315-2322.	1.8	4
90	ModProt: a database for integrating laboratory and literature data about protein post-translational modifications. <i>Journal of Electrophoresis</i> , 2016, 60, 1-4.	0.2	3

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91	Data for identification of GPI-anchored peptides and i%o-sites in cancer cell lines. Data in Brief, 2016, 7, 1302-1305.	0.5	2
92	Phosphorylation of Ser1452 on BRG1 inhibits the function of the SWI/SNF complex in chromatin activation. Journal of Proteomics, 2021, 247, 104319.	1.2	2
93	Two-dimensional gel electrophoresis using immobilized pH gradient tube gels. Electrophoresis, 2000, 21, 440-445.	1.3	2
94	Recent developments in Phos-tag electrophoresis for the analysis of phosphoproteins in proteomics. Expert Review of Proteomics, 2022, 19, 103-114.	1.3	2
95	Protein fractionation for proteomics using the SAINOME-plate. Journal of Electrophoresis, 2018, 62, 11-15.	0.2	1
96	Detailed Structure and Pathophysiological Roles of the IgA-Albumin Complex in Multiple Myeloma. International Journal of Molecular Sciences, 2021, 22, 1766.	1.8	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.	0.1	0
102	Cereal Proteomics. , 2007, , 87-104.		0
103	N-Terminal Sequencing of N-Terminally Modified Proteins. Springer Protocols, 2009, , 1063-1074.	0.1	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