

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	Evaluation of four phosphopeptide enrichment strategies for mass spectrometry-based proteomic analysis. <i>Proteomics</i> , 2022, 22, e2100216.	1.3	12
2	Recent developments in Phos-tag electrophoresis for the analysis of phosphoproteins in proteomics. <i>Expert Review of Proteomics</i> , 2022, 19, 103-114.	1.3	2
3	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
4	Detailed Structure and Pathophysiological Roles of the IgA-Albumin Complex in Multiple Myeloma. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1766.	1.8	1
5	Basic 7S globulin in plants. <i>Journal of Proteomics</i> , 2021, 240, 104209.	1.2	15
6	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
7	Phosphorylation of Ser1452 on BRG1 inhibits the function of the SWI/SNF complex in chromatin activation. <i>Journal of Proteomics</i> , 2021, 247, 104319.	1.2	2
8	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
9	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
10	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
11	TORC1 inactivation stimulates autophagy of nucleoporin and nuclear pore complexes. <i>Journal of Cell Biology</i> , 2020, 219, .	2.3	46
12	CRMP2 dephosphorylation at S522 rather than hyperphosphorylation as an early-stage marker of Alzheimer's disease. <i>Proceedings for Annual Meeting of the Japanese Pharmacological Society</i> , 2020, 93, 2-O-068.	0.0	0
13	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
14	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
15	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
16	PIM kinases facilitate lentiviral evasion from SAMHD1 restriction via Vpx phosphorylation. <i>Nature Communications</i> , 2019, 10, 1844.	5.8	22
17	Two distinct mechanisms target the autophagy-related E3 complex to the pre-autophagosomal structure. <i>ELife</i> , 2019, 8, .	2.8	51
18	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

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19	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
20	Protein fractionation for proteomics using the SAINOME-plate. <i>Journal of Electrophoresis</i> , 2018, 62, 11-15.	0.2	1
21	In vitro mouse spermatogenesis with an organ culture method in chemically defined medium. <i>PLoS ONE</i> , 2018, 13, e0192884.	1.1	39
22	The tumour suppressor APC promotes HIV-1 assembly via interaction with Gag precursor protein. <i>Nature Communications</i> , 2017, 8, 14259.	5.8	13
23	Identification of candidate diagnostic serum biomarkers for Kawasaki disease using proteomic analysis. <i>Scientific Reports</i> , 2017, 7, 43732.	1.6	48
24	A Phos-tag-based micropipette-tip method for rapid and selective enrichment of phosphopeptides. <i>Electrophoresis</i> , 2017, 38, 2447-2455.	1.3	22
25	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
26	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
27	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
28	MZB1 in borderline resectable pancreatic cancer resected after neoadjuvant chemoradiotherapy. <i>Journal of Surgical Research</i> , 2017, 220, 391-401.	0.8	17
29	Phos-tag World: The path to the future of electrophoresis, pioneered by the Phos-tag. <i>Denki Eido</i> , 2017, 61, 45-48.	0.0	0
30	ModProt: A database for integrating laboratory and literature data concerning protein post-translational modifications. <i>Denki Eido</i> , 2017, 61, 5-8.	0.0	0
31	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
32	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
33	The Intrinsically Disordered Protein Atg13 Mediates Supramolecular Assembly of Autophagy Initiation Complexes. <i>Developmental Cell</i> , 2016, 38, 86-99.	3.1	161
34	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
35	Data for identification of GPI-anchored peptides and N-glycosylation sites in cancer cell lines. <i>Data in Brief</i> , 2016, 7, 1302-1305.	0.5	2
36	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

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37	Comprehensive behavioral study and proteomic analyses of <sc>CRMP</sc> 2â€œdeficient mice. Genes To Cells, 2016, 21, 1059-1079.	0.5	31
38	Lyn Kinase Suppresses the Transcriptional Activity of IRF5 in the TLR-MyD88 Pathway to Restrain the Development of Autoimmunity. Immunity, 2016, 45, 319-332.	6.6	81
39	Biological significance of co- and post-translational modifications of the yeast 26S proteasome. Journal of Proteomics, 2016, 134, 37-46.	1.2	55
40	Relationship between phosphorylation of sperm-specific antigen and prognosis of lung adenocarcinoma. Journal of Proteomics, 2016, 139, 60-66.	1.2	13
41	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.	1.2	22
42	ModProt: a database for integrating laboratory and literature data about protein post-translational modifications. Journal of Electrophoresis, 2016, 60, 1-4.	0.2	3
43	Role of LRP1 and ERK and cAMP Signaling Pathways in Lactoferrin-Induced Lipolysis in Mature Rat Adipocytes. PLoS ONE, 2015, 10, e0141378.	1.1	54
44	Receptor-mediated selective autophagy degrades the endoplasmic reticulum and the nucleus. Nature, 2015, 522, 359-362.	13.7	496
45	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.	1.2	19
46	Identification of Tyrosine-Phosphorylated Proteins Upregulated during Epithelialâ€œMesenchymal Transition Induced with TGF-Î². Journal of Proteome Research, 2015, 14, 4127-4136.	1.8	19
47	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.	3.3	141
48	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
49	Two-dimensional electrophoresis of post-translationally modified proteins (modforms). Denki Eido, 2015, 59, 126-128.	0.0	0
50	Phosphoproteome analysis of <i>Lotus japonicus</i> seeds. Proteomics, 2014, 14, 116-120.	1.3	10
51	Structural basis of starvation-induced assembly of the autophagy initiation complex. Nature Structural and Molecular Biology, 2014, 21, 513-521.	3.6	180
52	Proteomic Analysis of Proteins Related to Prognosis of Lung Adenocarcinoma. Journal of Proteome Research, 2014, 13, 4686-4694.	1.8	27
53	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.	1.8	16
54	Involvement of Hepatitis C Virus NS5A Hyperphosphorylation Mediated by Casein Kinase IÎ± in Infectious Virus Production. Journal of Virology, 2014, 88, 7541-7555.	1.5	70

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55	Mass Spectrometric Identification of Glycosylphosphatidylinositol-Anchored Peptides. <i>Journal of Proteome Research</i> , 2013, 12, 4617-4626.	1.8	20
56	N-Terminal methylation of proteasome subunit Rpt1 in yeast. <i>Proteomics</i> , 2013, 13, 3167-3174.	1.3	20
57	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
58	N-Myristoylation of the Rpt2 Subunit Regulates Intracellular Localization of the Yeast 26S Proteasome. <i>Biochemistry</i> , 2012, 51, 8856-8866.	1.2	46
59	Two-dimensional Phos-tag affinity electrophoresis. <i>Seibutsu Butsuri Kagaku</i> , 2012, 56, s21-s24.	0.1	1
60	Phosphopeptide shotgun analysis using mass spectrometry and Phos-tag agarose beads. <i>Seibutsu Butsuri Kagaku</i> , 2012, 56, s25-s28.	0.1	1
61	Wild-type p53 enhances annexin IV gene expression in ovarian clear cell adenocarcinoma. <i>FEBS Journal</i> , 2011, 278, 1470-1483.	2.2	15
62	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
63	Mass spectrometric characterization of proteins transferred from polyacrylamide gels to membrane filters. <i>FEBS Journal</i> , 2011, 278, 3807-3814.	2.2	5
64	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
65	Co- and post-translational modifications of the 26S proteasome in yeast. <i>Proteomics</i> , 2010, 10, 2769-2779.	1.3	61
66	Characterization of multiple alternative forms of heterogeneous nuclear ribonucleoprotein K by phosphate affinity electrophoresis. <i>Proteomics</i> , 2010, 10, 3884-3895.	1.3	36
67	N-Terminal Sequencing of N-Terminally Modified Proteins. <i>Springer Protocols</i> , 2009, , 1063-1074.	0.1	0
68	Cereal Proteomics. , 2007, , 87-104.		0
69	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
70	Proteomic search for potential diagnostic markers and therapeutic targets for ovarian clear cell adenocarcinoma. <i>Proteomics</i> , 2006, 6, 5880-5890.	1.3	56
71	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
72	Technical Aspects of Functional Proteomics in Plants. <i>ChemInform</i> , 2004, 35, no.	0.1	0

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73	Technical aspects of functional proteomics in plants. <i>Phytochemistry</i> , 2004, 65, 1487-1498.	1.4	50
74	Mass Spectrometric Analysis of Posttranslational Modifications of a Carrot Extracellular Glycoprotein. <i>Biochemistry</i> , 2004, 43, 6281-6292.	1.2	18
75	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
76	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
77	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
78	Analyses of Wheat Seed Proteome: Exploring Protein-Protein Interactions by Manipulating Genome Composition. <i>Principles and Practice</i> , 2004, , 49-66.	0.3	1
79	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
80	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
81	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
82	Wheat proteomics: Relationship between fine chromosome deletion and protein expression. <i>Proteomics</i> , 2003, 3, 307-316.	1.3	44
83	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
84	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
85	Electrophoretic analysis of phosphorylation of the yeast 20S proteasome. <i>Electrophoresis</i> , 2002, 23, 329-338.	1.3	71
86	Efficient peptide mapping and its application to identify embryo proteins in rice proteome analysis. <i>Electrophoresis</i> , 2002, 23, 647-654.	1.3	40
87	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
88	Identification of the 19S regulatory particle subunits from the rice 26S proteasome. <i>FEBS Journal</i> , 2002, 269, 1474-1483.	0.2	47
89	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
90	Two-dimensional gel electrophoresis using immobilized pH gradient tube gels. <i>Electrophoresis</i> , 2000, 21, 440-445.	1.3	35

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91	N ^ε -Acetylation and Proteolytic Activity of the Yeast 20 S Proteasome. <i>Journal of Biological Chemistry</i> , 2000, 275, 4635-4639.	1.6	110
92	Primary structural features of the 20S proteasome subunits of rice (<i>Oryza sativa</i>). <i>Gene</i> , 2000, 250, 61-66.	1.0	32
93	Two-dimensional gel electrophoresis using immobilized pH gradient tube gels. <i>Electrophoresis</i> , 2000, 21, 440-445.	1.3	2
94	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
95	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
96	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
97	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
98	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
99	Deblocking and Subsequent Microsequence Analysis of N ^ε -Blocked Proteins Electroblotted onto PVDF Membrane. <i>Journal of Biochemistry</i> , 1992, 111, 754-757.	0.9	35
100	Characterization of proteins released from legume seeds in hot water. <i>Phytochemistry</i> , 1992, 31, 731-735.	1.4	32
101	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
102	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
103	Sequence of a cDNA encoding soybean basic 7S globulin. <i>Nucleic Acids Research</i> , 1989, 17, 8868-8868.	6.5	35
104	Microsequence analysis of winged bean seed proteins electroblotted from two-dimensional gel. <i>The Protein Journal</i> , 1989, 8, 115-130.	1.1	142
105	Soybean basic 7 S globulin represents a protein widely distributed in legume species. <i>FEBS Letters</i> , 1987, 226, 145-149.	1.3	42
106	Varietal differences of leaf protein profiles in mulberry. <i>Phytochemistry</i> , 1982, 21, 1513-1518.	1.4	58
107	Varietal differences of leaf protein profiles in mulberry. <i>Phytochemistry</i> , 1982, 21, 1513-1518.	1.4	19