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Citation Report

#	ARTICLE	IF	CITATIONS
2	American neurology. Neurology, 1961, 11, 843-843.	1.5	2
3	Computational Prediction of Proteinâ€“Protein Interactions. , 2004, 261, 445-468.		57
4	Transphosphorylation of E. coli Proteins during Production of Recombinant Protein Kinases Provides a Robust System to Characterize Kinase Specificity. Frontiers in Plant Science, 2012, 3, 262.	1.7	20
5	Structural and functional insights into the role of the N-terminal Mps1 TPR domain in the SAC (spindle assembly checkpoint). Biochemical Journal, 2012, 448, 321-328.	1.7	19
6	Alternative ways of modulating JAK-STAT pathway. Jak-stat, 2012, 1, 274-284.	2.2	18
7	P3DB: An Integrated Database for Plant Protein Phosphorylation. Frontiers in Plant Science, 2012, 3, 206.	1.7	50
8	Regulation of the tumor suppressor PML by sequential post-translational modifications. Frontiers in Oncology, 2012, 2, 204.	1.3	21
9	Mutational properties of amino acid residues: implications for evolvability of phosphorylatable residues. Philosophical Transactions of the Royal Society B: Biological Sciences, 2012, 367, 2584-2593.	1.8	43
10	Modification Site Localization Scoring: Strategies and Performance. Molecular and Cellular Proteomics, 2012, 11, 3-14.	2.5	100
11	Discovery of O-GlcNAc-6-phosphate Modified Proteins in Large-scale Phosphoproteomics Data. Molecular and Cellular Proteomics, 2012, 11, 1063-1069.	2.5	20
12	Discovery of O-GlcNAc-modified Proteins in Published Large-scale Proteome Data. Molecular and Cellular Proteomics, 2012, 11, 843-850.	2.5	58
13	Posttranslational Modifications of the Retinoblastoma Tumor Suppressor Protein as Determinants of Function. Genes and Cancer, 2012, 3, 619-633.	0.6	62
14	D2P2: database of disordered protein predictions. Nucleic Acids Research, 2012, 41, D508-D516.	6.5	570
15	Phosphorylation of claudin-2 on serine 208 promotes membrane retention and reduces trafficking to lysosomes. Journal of Cell Science, 2012, 125, 4902-12.	1.2	67
16	Investigation of Receptor interacting protein (RIP3)-dependent Protein Phosphorylation by Quantitative Phosphoproteomics. Molecular and Cellular Proteomics, 2012, 11, 1640-1651.	2.5	65
17	Strategies to Identify Recognition Signals and Targets of SUMOylation. Biochemistry Research International, 2012, 2012, 1-16.	1.5	34
18	Linear motifs confer functional diversity onto splice variants. Nucleic Acids Research, 2012, 40, 7123-7131.	6.5	65
19	The high mobility group box: the ultimate utility player of a cell. Trends in Biochemical Sciences, 2012, 37, 553-562.	3.7	173

#	ARTICLE	IF	CITATIONS
20	Analytical strategies for shotgun phosphoproteomics: Status and prospects. Seminars in Cell and Developmental Biology, 2012, 23, 836-842.	2.3	20
21	Multiscale Models of Breast Cancer Progression. Annals of Biomedical Engineering, 2012, 40, 2488-2500.	1.3	45
22	PTMcode: a database of known and predicted functional associations between post-translational modifications in proteins. Nucleic Acids Research, 2012, 41, D306-D311.	6.5	116
23	Charting the Landscape of Tandem BRCT Domainâ€"Mediated Protein Interactions. Science Signaling, 2012, 5, rs6.	1.6	88
24	The application of modular protein domains in proteomics. FEBS Letters, 2012, 586, 2586-2596.	1.3	37
25	The human phosphatase interactome: An intricate family portrait. FEBS Letters, 2012, 586, 2732-2739.	1.3	184
26	Functional Interplay between Caspase Cleavage and Phosphorylation Sculpts the Apoptotic Proteome. Cell, 2012, 150, 426-440.	13.5	132
27	Quantitative phosphoproteomics to characterize signaling networks. Seminars in Cell and Developmental Biology, 2012, 23, 863-871.	2.3	58
28	Mass spectrometry-based phosphoproteomics in cancer research. Frontiers in Biology, 2012, 7, 566-586.	0.7	1
29	Gains of ubiquitylation sites in highly conserved proteins in the human lineage. BMC Bioinformatics, 2012, 13, 306.	1.2	13
30	Prediction of functional phosphorylation sites by incorporating evolutionary information. Protein and Cell, 2012, 3, 675-690.	4.8	14
31	Position-Specific Analysis and Prediction for Protein Lysine Acetylation Based on Multiple Features. PLoS ONE, 2012, 7, e49108.	1.1	64
32	Mammalian Alpha Arrestins Link Activated Seven Transmembrane Receptors to Nedd4 Family E3 Ubiquitin Ligases and Interact with Beta Arrestins. PLoS ONE, 2012, 7, e50557.	1.1	58
33	Using Bacteria to Determine Protein Kinase Specificity and Predict Target Substrates. PLoS ONE, 2012, 7, e52747.	1.1	26
34	Tools to discriminate between targets of CK2 vs PLK2/PLK3 acidophilic kinases. BioTechniques, 2012, 53, 1-5.	0.8	9
35	Molecular Mechanisms of Prolactin and Its Receptor. Endocrine Reviews, 2012, 33, 504-525.	8.9	131
36	Phosphosite conservation in single domain orthologs versus paralogs: A way to combine differential regulation with redundant core functions. FEBS Letters, 2012, 586, 296-302.	1.3	3
37	NIRF/UHRF2 occupies a central position in the cell cycle network and allows coupling with the epigenetic landscape. FEBS Letters, 2012, 586, 1570-1583.	1.3	37

#	ARTICLE	IF	CITATIONS
38	Global characterization of signalling networks associated with tamoxifen resistance in breast cancer. FEBS Journal, 2013, 280, 5237-5257.	2.2	36
39	AEG-1/MTDH/LYRIC, the Beginning. Advances in Cancer Research, 2013, 120, 1-38.	1.9	55
40	Phosphoproteomic analysis of anaplastic lymphoma kinase (<scp>ALK</scp>) downstream signaling pathways identifies signal transducer and activator of transcriptionÂ3 as a functional target of activated <scp>ALK</scp> in neuroblastoma cells. FEBS Journal, 2013, 280, 5269-5282.	2.2	35
41	Tyrosine phosphorylation of the orphan receptor ESDN/DCBLD2 serves as a scaffold for the signaling adaptor CrkL. FEBS Letters, 2013, 587, 2313-2318.	1.3	15
42	Combining docking site and phosphosite predictions to find new substrates: Identification of smoothelin-like-2 (SMTNL2) as a c-Jun N-terminal kinase (JNK) substrate. Cellular Signalling, 2013, 25, 2518-2529.	1.7	28
43	Proteomics Strategies to Identify SUMO Targets and Acceptor Sites: A Survey of RNA-Binding Proteins SUMOylation. NeuroMolecular Medicine, 2013, 15, 661-676.	1.8	19
44	Profiling the Substrate Specificity of Protein Kinases by On-Bead Screening of Peptide Libraries. Biochemistry, 2013, 52, 5645-5655.	1.2	21
45	Profiling the kinome: Current capabilities and future challenges. Journal of Proteomics, 2013, 81, 43-55.	1.2	27
46	Differential phosphoproteome of the striatum from pleiotrophin knockout and midkine knockout mice treated with amphetamine: Correlations with amphetamine-induced neurotoxicity. Toxicology, 2013, 306, 147-156.	2.0	20
47	Molecular Basis of Tubulin Transport Within the Cilium by IFT74 and IFT81. Science, 2013, 341, 1009-1012.	6.0	271
48	Teaching the bioinformatics of signaling networks: an integrated approach to facilitate multi-disciplinary learning. Briefings in Bioinformatics, 2013, 14, 618-632.	3.2	15
49	Phospho-specific antibodies by design. Nature Biotechnology, 2013, 31, 889-891.	9.4	7
50	Comparative analysis of Leishmania exoproteomes: Implication for hostâ€"pathogen interactions. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 2653-2662.	1.1	8
51	Site-specific quantitative analysis of cardiac mitochondrial protein phosphorylation. Journal of Proteomics, 2013, 81, 15-23.	1.2	25
52	BAP1 is phosphorylated at serine 592 in Sâ€phase following DNA damage. FEBS Letters, 2013, 587, 3906-3911.	1.3	37
53	Hybrid Sensor Using Gold Nanoparticles and Conjugated Polyelectrolytes for Studying Sequence Rule in Proteinâ€"DNA Interactions. ACS Applied Materials & Interfaces, 2013, 5, 12725-12734.	4.0	16
54	Function and regulation of serine/threonine phosphatases in the healthy and diseased heart. Journal of Molecular and Cellular Cardiology, 2013, 64, 90-98.	0.9	101
55	A C-Terminal Acidic Domain Regulates Degradation of the Transcriptional Coactivator Bob1. Molecular and Cellular Biology, 2013, 33, 4628-4640.	1.1	8

#	ARTICLE	IF	CITATIONS
56	The role of arginine methylation in the DNA damage response. DNA Repair, 2013, 12, 459-465.	1.3	69
57	An N-terminal, 830 residues intrinsically disordered region of the cytoskeleton-regulatory protein supervillin contains Myosin II- and F-actin-binding sites. Journal of Biomolecular Structure and Dynamics, 2013, 31, 1150-1159.	2.0	9
58	Primate Transcript and Protein Expression Levels Evolve Under Compensatory Selection Pressures. Science, 2013, 342, 1100-1104.	6.0	215
59	Incorporating substrate sequence motifs and spatial amino acid composition to identify kinase-specific phosphorylation sites on protein three-dimensional structures. BMC Bioinformatics, 2013, 14, S2.	1.2	27
60	Cold shock Y-box protein-1 proteolysis autoregulates its transcriptional activities. Cell Communication and Signaling, 2013, 11, 63.	2.7	40
61	Highly homologous eEF1A1 and eEF1A2 exhibit differential post-translationalmodification with significant enrichment around localised sites of sequence variation. Biology Direct, 2013, 8, 29.	1.9	26
62	Phosphorylation of cystic fibrosis transmembrane conductance regulator (CFTR) serine-511 by the combined action of tyrosine kinases and CK2: the implication of tyrosine-512 and phenylalanine-508. Amino Acids, 2013, 45, 1423-1429.	1.2	16
63	Proteomic Strategies to Characterize Signaling Pathways. Methods in Molecular Biology, 2013, 1007, 359-377.	0.4	9
64	Phosphorylation of serine 4642 in the COOH-extremity of plectin by MNK2 and PKA modulates its interaction with intermediate filaments. Journal of Cell Science, 2013, 126, 4195-207.	1.2	28
65	RNA Polymerase II C-Terminal Domain: Tethering Transcription to Transcript and Template. Chemical Reviews, 2013, 113, 8423-8455.	23.0	146
66	Identification of complex relationship between protein kinases and substrates during the cell cycle of <scp>H</scp>e<scp>L</scp>a cells by phosphoproteomic analysis. Proteomics, 2013, 13, 1233-1246.	1.3	2
67	Systematic analysis of somatic mutations in phosphorylation signaling predicts novel cancer drivers. Molecular Systems Biology, 2013, 9, 637.	3.2	267
68	Concise Review: Pursuing Self-Renewal and Pluripotency with the Stem Cell Factor Nanog. Stem Cells, 2013, 31, 1227-1236.	1.4	87
69	Gelsolin: The tail of a molecular gymnast. Cytoskeleton, 2013, 70, 360-384.	1.0	184
70	Controlling Cholesterol Synthesis beyond 3-Hydroxy-3-methylglutaryl-CoA Reductase (HMGCR). Journal of Biological Chemistry, 2013, 288, 18707-18715.	1.6	277
71	An assignment of intrinsically disordered regions of proteins based on NMR structures. Journal of Structural Biology, 2013, 181, 29-36.	1.3	26
72	Mitochondrial Phosphorylation in Apoptosis: Flipping the Death Switch. Antioxidants and Redox Signaling, 2013, 19, 572-582.	2.5	27
73	Fat Chance! Getting a Grip on a Slippery Modification. ACS Chemical Biology, 2013, 8, 46-57.	1.6	42

#	ARTICLE	IF	CITATIONS
74	Ambra1 at the crossroad between autophagy and cell death. Oncogene, 2013, 32, 3311-3318.	2.6	81
75	Systematic characterization of the specificity of the SH2 domains of cytoplasmic tyrosine kinases. Journal of Proteomics, 2013, 81, 56-69.	1.2	8
76	Dab1 stabilizes its interaction with Cin85 by suppressing Cin85 phosphorylation at serine 587. FEBS Letters, 2013, 587, 60-66.	1.3	4
77	Toward a Comprehensive Characterization of a Human Cancer Cell Phosphoproteome. Journal of Proteome Research, 2013, 12, 260-271.	1.8	363
78	HuPho: the human phosphatase portal. FEBS Journal, 2013, 280, 379-387.	2.2	55
79	Deep proteome profiling of Trichoplax adhaerens reveals remarkable features at the origin of metazoan multicellularity. Nature Communications, 2013, 4, 1408.	5.8	50
80	Computational phosphorylation site prediction in plants using random forests and organism-specific instance weights. Bioinformatics, 2013, 29, 686-694.	1.8	46
81	Chemical proteomics and functional proteomics strategies for protein kinase inhibitor validation and protein kinase substrate identification: Applications to protein kinase CK2. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 1352-1358.	1.1	13
82	Phosphoproteomic analysis of the striatum from pleiotrophin knockout and midkine knockout mice treated with cocaine reveals regulation of oxidative stress-related proteins potentially underlying cocaine-induced neurotoxicity and neurodegeneration. Toxicology, 2013, 314, 166-173.	2.0	17
83	Role of HOXA9 and VEZF1 in Endothelial Biology. Journal of Vascular Research, 2013, 50, 265-278.	0.6	26
84	The SH2 Domain Interaction Landscape. Cell Reports, 2013, 3, 1293-1305.	2.9	110
85	Increased WD-repeat containing protein 1 in interstitial fluid from ovarian carcinomas shown by comparative proteomic analysis of malignant and healthy gynecological tissue. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 2347-2359.	1.1	24
86	IsobarPTM: A software tool for the quantitative analysis of post-translationally modified proteins. Journal of Proteomics, 2013, 90, 77-84.	1.2	19
87	Prediction of kinase-specific phosphorylational interactions using random forest. Chemometrics and Intelligent Laboratory Systems, 2013, 126, 117-122.	1.8	8
88	Structure and Intrinsic Disorder in Protein Autoinhibition. Structure, 2013, 21, 332-341.	1.6	83
89	Proteome Wide Purification and Identification of <i>O</i>-GlcNAc-Modified Proteins Using Click Chemistry and Mass Spectrometry. Journal of Proteome Research, 2013, 12, 927-936.	1.8	151
90	Structure and dynamics of molecular networks: A novel paradigm of drug discovery. , 2013, 138, 333-408.		779
91	InÂVivo SILAC-Based Proteomics Reveals Phosphoproteome Changes during Mouse Skin Carcinogenesis. Cell Reports, 2013, 3, 552-566.	2.9	90

#	ARTICLE	IF	CITATIONS
92	Unraveling the ubiquitinâ€regulated signaling networks by mass spectrometryâ€based proteomics. Proteomics, 2013, 13, 526-537.	1.3	24
93	Gads (Grb2-related adaptor downstream of Shc) is required for BCR-ABL-mediated lymphoid leukemia. Leukemia, 2013, 27, 1666-1676.	3.3	8
94	Bioinformatic survey for new physiological substrates of Cyclin-dependent kinase 5. Genomics, 2013, 101, 221-228.	1.3	13
95	Cell Death Proteomics Database: Consolidating Proteomics Data on Cell Death. Journal of Proteome Research, 2013, 12, 2206-2213.	1.8	21
96	The role of SRY-related HMG box transcription factor 4 (SOX4) in tumorigenesis and metastasis: friend or foe?. Oncogene, 2013, 32, 3397-3409.	2.6	174
97	Regulation of molecular chaperones through post-translational modifications: Decrypting the chaperone code. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2013, 1829, 443-454.	0.9	80
98	LiverAtlas: a unique integrated knowledge database for systemsâ€level research of liver and hepatic disease. Liver International, 2013, 33, 1239-1248.	1.9	20
99	Manipulation of PBF/PTTG1IP Phosphorylation Status; a Potential New Therapeutic Strategy for Improving Radioiodine Uptake in Thyroid and Other Tumors. Journal of Clinical Endocrinology and Metabolism, 2013, 98, 2876-2886.	1.8	44
100	Displacement of N/Q-rich Peptides on TiO₂ Beads Enhances the Depth and Coverage of Yeast Phosphoproteome Analyses. Journal of Proteome Research, 2013, 12, 2905-2913.	1.8	27
101	The Protein Interaction Landscape of the Human CMGC Kinase Group. Cell Reports, 2013, 3, 1306-1320.	2.9	178
102	Determination of CK2 Specificity and Substrates by Proteome-Derived Peptide Libraries. Journal of Proteome Research, 2013, 12, 3813-3821.	1.8	26
103	A spontaneous Cdt1 mutation in 129 mouse strains reveals a regulatory domain restraining replication licensing. Nature Communications, 2013, 4, 2065.	5.8	22
104	Global protein phosphorylation dynamics during deoxynivalenol-induced ribotoxic stress response in the macrophage. Toxicology and Applied Pharmacology, 2013, 268, 201-211.	1.3	38
105	RegulatING chromatin regulators: post-translational modification of the ING family of epigenetic regulators. Biochemical Journal, 2013, 450, 433-442.	1.7	13
106	Roles, regulation and inhibitors of sphingosine kinase 2. FEBS Journal, 2013, 280, 5317-5336.	2.2	145
107	A Method for Systematic Mapping of Protein Lysine Methylation Identifies Functions for HP1Î² in DNA Damage Response. Molecular Cell, 2013, 50, 723-735.	4.5	98
108	Global analysis of phosphorylation and ubiquitylation cross-talk in protein degradation. Nature Methods, 2013, 10, 676-682.	9.0	520
109	pLogo: a probabilistic approach to visualizing sequence motifs. Nature Methods, 2013, 10, 1211-1212.	9.0	384

#	Article	IF	Citations
110	Interrogating cAMP-dependent Kinase Signaling in Jurkat T Cells via a Protein Kinase A Targeted Immune-precipitation Phosphoproteomics Approach. Molecular and Cellular Proteomics, 2013, 12, 3350-3359.	2.5	48
111	Phosphoinositide-specific Phospholipase C Î² 1b (PI-PLCÎ²1b) Interactome: Affinity Purification-Mass Spectrometry Analysis of PI-PLCÎ²1b with Nuclear Protein. Molecular and Cellular Proteomics, 2013, 12, 2220-2235.	2.5	21
112	Proteome-wide Analysis of Amino Acid Variations That Influence Protein Lysine Acetylation. Journal of Proteome Research, 2013, 12, 949-958.	1.8	17
113	CDK1 stabilizes HIF-1Î± via direct phosphorylation of Ser668 to promote tumor growth. Cell Cycle, 2013, 12, 3689-3701.	1.3	84
114	AKT Facilitates EGFR Trafficking and Degradation by Phosphorylating and Activating PIKfyve. Science Signaling, 2013, 6, ra45.	1.6	87
115	Text Mining of Protein Phosphorylation Information Using a Generalizable Rule-Based Approach. , 2013, , .		1
116	Kinannote, a computer program to identify and classify members of the eukaryotic protein kinase superfamily. Bioinformatics, 2013, 29, 2387-2394.	1.8	43
117	Differential recognition of ITSN2/Ese2 by the SH2 domains of Fyn, Abl1, PLCg1 and PI3KR1 in mouse tissues. Biopolymers and Cell, 2013, 29, 424-427.	0.1	0
118	The Human Leukocyte Antigenâ€“presented Ligandome of B Lymphocytes. Molecular and Cellular Proteomics, 2013, 12, 1829-1843.	2.5	113
119	FilGAP and its close relatives: a mediator of Rhoâ€“Rac antagonism that regulates cell morphology and migration. Biochemical Journal, 2013, 453, 17-25.	1.7	77
120	The Lipid Transfer Protein StarD7: Structure, Function, and Regulation. International Journal of Molecular Sciences, 2013, 14, 6170-6186.	1.8	25
121	Using Biological Pathway Data with Paxtools. PLoS Computational Biology, 2013, 9, e1003194.	1.5	57
122	Testing for Associations between Loci and Environmental Gradients Using Latent Factor Mixed Models. Molecular Biology and Evolution, 2013, 30, 1687-1699.	3.5	627
123	A Kinome-Wide RNAi Screen in Drosophila Glia Reveals That the RIO Kinases Mediate Cell Proliferation and Survival through TORC2-Akt Signaling in Glioblastoma. PLoS Genetics, 2013, 9, e1003253.	1.5	114
124	Goliath family E3 ligases regulate the recycling endosome pathway via VAMP3 ubiquitylation. EMBO Journal, 2013, 32, 524-537.	3.5	43
125	Sumoylation at chromatin governs coordinated repression of a transcriptional program essential for cell growth and proliferation. Genome Research, 2013, 23, 1563-1579.	2.4	121
126	Pin1 promotes GR transactivation by enhancing recruitment to target genes. Nucleic Acids Research, 2013, 41, 8515-8525.	6.5	18
127	Construction of protein phosphorylation networks by data mining, text mining and ontology integration: analysis of the spindle checkpoint. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat038.	1.4	15

#	ARTICLE	IF	CITATIONS
128	Deciphering of <scp>ADP</scp>â€induced, phosphotyrosineâ€dependent signaling networks in human platelets by Srcâ€homology 2 region (SH2)â€profiling. Proteomics, 2013, 13, 1016-1027.	1.3	16
129	DAPPLE: a pipeline for the homology-based prediction of phosphorylation sites. Bioinformatics, 2013, 29, 1693-1695.	1.8	37
130	The ConsensusPathDB interaction database: 2013 update. Nucleic Acids Research, 2013, 41, D793-D800.	6.5	728
131	Early Phosphoproteomic Changes in the Mouse Spleen During Deoxynivalenol-Induced Ribotoxic Stress. Toxicological Sciences, 2013, 135, 129-143.	1.4	24
132	NDE1 and NDEL1: twin neurodevelopmental proteins with similar â€˜natureâ€™ but different â€˜nurtureâ€™. Biomolecular Concepts, 2013, 4, 447-464.	1.0	40
133	Deacetylase Rpd3 Facilitates Checkpoint Adaptation by Preventing Rad53 Overactivation. Molecular and Cellular Biology, 2013, 33, 4212-4224.	1.1	9
134	STOP gene <i>Phactr4</i> is a tumor suppressor. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E407-14.	3.3	18
135	Regulation of OSR1 and the sodium, potassium, two chloride cotransporter by convergent signals. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 18826-18831.	3.3	27
136	A genome-wide RNAi screen reveals that mRNA decapping restricts bunyaviral replication by limiting the pools of Dcp2-accessible targets for cap-snatching. Genes and Development, 2013, 27, 1511-1525.	2.7	86
137	Phosphotyrosine Signaling Proteins that Drive Oncogenesis Tend to be Highly Interconnected. Molecular and Cellular Proteomics, 2013, 12, 1204-1213.	2.5	31
138	dbPTM 3.0: an informative resource for investigating substrate site specificity and functional association of protein post-translational modifications. Nucleic Acids Research, 2013, 41, D295-D305.	6.5	179
139	Identification of O-Linked N-Acetylglucosamine (O-GlcNAc)-modified Osteoblast Proteins by Electron Transfer Dissociation Tandem Mass Spectrometry Reveals Proteins Critical for Bone Formation. Molecular and Cellular Proteomics, 2013, 12, 945-955.	2.5	63
140	The role of signalling in cellular cholesterol homeostasis. IUBMB Life, 2013, 65, 675-684.	1.5	46
141	Role of Nuclear Localization of PSMB1 in Transcriptional Activation. Bioscience, Biotechnology and Biochemistry, 2013, 77, 1785-1787.	0.6	8
142	Identification and Characterization of a Novel Human Methyltransferase Modulating Hsp70 Protein Function through Lysine Methylation. Journal of Biological Chemistry, 2013, 288, 27752-27763.	1.6	93
143	STAT2 phosphorylation and signaling. Jak-stat, 2013, 2, e25790.	2.2	46
144	The mutational landscape of phosphorylation signaling in cancer. Scientific Reports, 2013, 3, 2651.	1.6	149
145	Mammalian Target of Rapamycin Complex 1 (mTORC1)-mediated Phosphorylation Stabilizes ISCU Protein. Journal of Biological Chemistry, 2013, 288, 12901-12909.	1.6	16

#	ARTICLE	IF	CITATIONS
146	Mutually exclusive acetylation and ubiquitylation among enzymes involved in glucose metabolism. Adipocyte, 2013, 2, 256-261.	1.3	6
148	A Preliminary Investigation on Placenta Protein Profile Reveals Only Modest Changes in Well Controlled Gestational Diabetes Mellitus. European Journal of Mass Spectrometry, 2013, 19, 211-223.	0.5	19
149	The switches.ELM Resource: A Compendium of Conditional Regulatory Interaction Interfaces. Science Signaling, 2013, 6, rs7.	1.6	101
150	Ubiquitination site preferences in anaphase promoting complex/cyclosome (APC/C) substrates. Open Biology, 2013, 3, 130097.	1.5	39
151	Aurora at the pole and equator: overlapping functions of Aurora kinases in the mitotic spindle. Open Biology, 2013, 3, 120185.	1.5	89
152	Global Screening of CK2 Kinase Substrates by an Integrated Phosphoproteomics Workflow. Scientific Reports, 2013, 3, 3460.	1.6	89
153	AMD-Associated Variants at the Chromosome 10q26 Locus and the Stability of<i>ARMS2</i>Transcripts. , 2013, 54, 5913.		12
154	Dual Coordination of Post Translational Modifications in Human Protein Networks. PLoS Computational Biology, 2013, 9, e1002933.	1.5	76
155	The Thoc1 Encoded Ribonucleoprotein Is a Substrate for the NEDD4-1 E3 Ubiquitin Protein Ligase. PLoS ONE, 2013, 8, e57995.	1.1	3
156	ATM and GLUT1-S490 Phosphorylation Regulate GLUT1 Mediated Transport in Skeletal Muscle. PLoS ONE, 2013, 8, e66027.	1.1	33
157	Celiac Anti-Type 2 Transglutaminase Antibodies Induce Phosphoproteome Modification in Intestinal Epithelial Caco-2 Cells. PLoS ONE, 2013, 8, e84403.	1.1	13
158	Direct Repair in Mammalian Cells. , 2013, , .		1
159	LAceP: Lysine Acetylation Site Prediction Using Logistic Regression Classifiers. PLoS ONE, 2014, 9, e89575.	1.1	77
160	Hsp90-Dependent Assembly of the DBC2/RhoBTB2-Cullin3 E3-Ligase Complex. PLoS ONE, 2014, 9, e90054.	1.1	16
161	Peptide Arrays for Kinome Analysis of Livestock Species. Frontiers in Veterinary Science, 2014, 1, 4.	0.9	11
162	A Comparison of the Chicken and Turkey Proteomes and Phosphoproteomes in the Development of Poultry-Specific Immuno-Metabolism Kinome Peptide Arrays. Frontiers in Veterinary Science, 2014, 1, 22.	0.9	29
163	MeCP2 post-translational modifications: a mechanism to control its involvement in synaptic plasticity and homeostasis?. Frontiers in Cellular Neuroscience, 2014, 8, 236.	1.8	81
164	Developmentally-Dynamic Murine Brain Proteomes and Phosphoproteomes Revealed by Quantitative Proteomics. Proteomes, 2014, 2, 191-207.	1.7	9

#	ARTICLE	IF	CITATIONS
165	A clathrin coat assembly role for the muniscin protein central linker revealed by TALEN-mediated gene editing. ELife, 2014, 3, .	2.8	59
166	Development of a FRET Biosensor with High Specificity for Akt. Cell Structure and Function, 2014, 39, 9-20.	0.5	36
167	Weighing up the possibilities: Controlling translation by ubiquitylation and sumoylation. Translation, 2014, 2, e959366.	2.9	3
168	A Phosphotyrosine Switch for Cargo Sequestration at Clathrin-coated Buds. Journal of Biological Chemistry, 2014, 289, 17497-17514.	1.6	2
169	Investigating co-evolution of functionally associated phosphosites in human. Molecular Genetics and Genomics, 2014, 289, 1217-1223.	1.0	0
170	Kdm3a lysine demethylase is an Hsp90 client required for cytoskeletal rearrangements during spermatogenesis. Molecular Biology of the Cell, 2014, 25, 1216-1233.	0.9	29
171	PyTMs: a useful PyMOL plugin for modeling common post-translational modifications. BMC Bioinformatics, 2014, 15, 370.	1.2	82
172	The Role of eNOS Phosphorylation in Causing Drug-induced Vascular Injury. Toxicologic Pathology, 2014, 42, 709-724.	0.9	10
173	Ultradeep Human Phosphoproteome Reveals a Distinct Regulatory Nature of Tyr and Ser/Thr-Based Signaling. Cell Reports, 2014, 8, 1583-1594.	2.9	839
174	Cancer-relevant Splicing Factor CAPERÎ± Engages the Essential Splicing Factor SF3b155 in a Specific Ternary Complex. Journal of Biological Chemistry, 2014, 289, 17325-17337.	1.6	49
175	Dynamic phosphorylation of HP1Î± regulates mitotic progression in human cells. Nature Communications, 2014, 5, 3445.	5.8	30
176	A Novel Regulatory Locus of Phosphorylation in the C Terminus of the Potassium Chloride Cotransporter KCC2 That Interferes with N-Ethylmaleimide or Staurosporine-mediated Activation*â™¦. Journal of Biological Chemistry, 2014, 289, 18668-18679.	1.6	56
177	Complexity of metastasis-associated SDF-1 ligand signaling in breast cancer stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 7503-7504.	3.3	7
178	Centralspindlin assembly and 2 phosphorylations on MgcRacGAP by Polo-like kinase 1 initiate Ect2 binding in early cytokinesis. Cell Cycle, 2014, 13, 2952-2961.	1.3	19
179	Large-scale label-free phosphoproteomics: from technology to data interpretation. Bioanalysis, 2014, 6, 2403-2420.	0.6	8
180	Human germline and pan-cancer variomes and their distinct functional profiles. Nucleic Acids Research, 2014, 42, 11570-11588.	6.5	22
181	Proteomic analysis of phosphorylation in cancer. Expert Review of Proteomics, 2014, 11, 259-267.	1.3	44
182	RLIMS-P: an online text-mining tool for literature-based extraction of protein phosphorylation information. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau081-bau081.	1.4	23

#	Article	IF	Citations
183	Proteomics of a fuzzy organelle: interphase chromatin. EMBO Journal, 2014, 33, 648-664.	3.5	58
184	Functional Divergence and Evolutionary Turnover in Mammalian Phosphoproteomes. PLoS Genetics, 2014, 10, e1004062.	1.5	41
185	Navigating the Multilayered Organization of Eukaryotic Signaling: A New Trend in Data Integration. PLoS Computational Biology, 2014, 10, e1003385.	1.5	9
186	RegPhos 2.0: an updated resource to explore protein kinaseâ€“substrate phosphorylation networks in mammals. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau034.	1.4	38
187	Network-based association of hypoxia-responsive genes with cardiovascular diseases. New Journal of Physics, 2014, 16, 105014.	1.2	14
188	Identification of developmentally-specific kinotypes and mechanisms of Varroa mite resistance through whole-organism, kinome analysis of honeybee. Frontiers in Genetics, 2014, 5, 139.	1.1	40
189	A systems-wide screen identifies substrates of the SCF ^{Î²TrCP} ubiquitin ligase. Science Signaling, 2014, 7, rs8.	1.6	49
190	CaMKII and stress mix it up in mitochondria. Frontiers in Pharmacology, 2014, 5, 67.	1.6	16
191	dbPPT: a comprehensive database of protein phosphorylation in plants. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau121.	1.4	45
192	Combining affinity proteomics and network context to identify new phosphatase substrates and adapters in growth pathways. Frontiers in Genetics, 2014, 5, 115.	1.1	13
193	PTM-SD: a database of structurally resolved and annotated posttranslational modifications in proteins. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau041-bau041.	1.4	44
194	Proteomics of the human pituitary tissue: bioanalytical methods and applications. Bioanalysis, 2014, 6, 1989-2003.	0.6	4
195	Phosphorylation of unique domains of Src family kinases. Frontiers in Genetics, 2014, 5, 181.	1.1	74
196	MoDPepInt: an interactive web server for prediction of modular domainâ€“peptide interactions. Bioinformatics, 2014, 30, 2668-2669.	1.8	37
197	Altered Transcriptional Control Networks with Trans-Differentiation of Isogenic Mutant-KRas NSCLC Models. Frontiers in Oncology, 2014, 4, 344.	1.3	15
198	A Proteome-wide Domain-centric Perspective on Protein Phosphorylation. Molecular and Cellular Proteomics, 2014, 13, 2198-2212.	2.5	5
199	Deciphering kinaseâ€“substrate relationships by analysis of domain-specific phosphorylation network. Bioinformatics, 2014, 30, 1730-1738.	1.8	17
200	Structural interrogation of phosphoproteome identified by mass spectrometry reveals allowed and disallowed regions of phosphoconformation. BMC Structural Biology, 2014, 14, 9.	2.3	9

#	ARTICLE	IF	CITATIONS
201	Prediction of human disease-specific phosphorylation sites with combined feature selection approach and support vector machine. , 2014, , .		1
202	Identification of Extracellular Signal-regulated Kinase 1 (ERK1) Direct Substrates using Stable Isotope Labeled Kinase Assay-Linked Phosphoproteomics. Molecular and Cellular Proteomics, 2014, 13, 3199-3210.	2.5	41
203	The Development and Application of a Quantitative Peptide Microarray Based Approach to Protein Interaction Domain Specificity Space. Molecular and Cellular Proteomics, 2014, 13, 3647-3662.	2.5	14
204	DYNLL2 Dynein Light Chain Binds to an Extended Linear Motif of Myosin 5a Tail That Has Structural Plasticity. Biochemistry, 2014, 53, 7107-7122.	1.2	15
205	Kinetic Analysis of BCL11B Multisite Phosphorylationâ€“Dephosphorylation and Coupled Sumoylation in Primary Thymocytes by Multiple Reaction Monitoring Mass Spectroscopy. Journal of Proteome Research, 2014, 13, 5860-5868.	1.8	16
206	Simultaneous Quantification of Protein Phosphorylation Sites using Liquid Chromatographyâ€“Tandem Mass Spectrometry-Based Targeted Proteomics: A Linear Algebra Approach for Isobaric Phosphopeptides. Journal of Proteome Research, 2014, 13, 5452-5460.	1.8	6
207	Identification of miRâ€494 direct targets involved in senescence of human diploid fibroblasts. FASEB Journal, 2014, 28, 3720-3733.	0.2	34
208	Surviving the infarct: A profile of cardiac myosin binding proteinâ€C pathogenicity, diagnostic utility, and proteomics in the ischemic myocardium. Proteomics - Clinical Applications, 2014, 8, 569-577.	0.8	11
209	PHOXTRACKâ€“a tool for interpreting comprehensive datasets of post-translational modifications of proteins. Bioinformatics, 2014, 30, 3410-3411.	1.8	22
210	Mechanism and regulation of kinesinâ€5, an essential motor for the mitotic spindle. Biology of the Cell, 2014, 106, 1-12.	0.7	60
211	Plakins, a Versatile Family of Cytolinkers: Roles in Skin Integrity and in Human Diseases. Journal of Investigative Dermatology, 2014, 134, 885-894.	0.3	103
212	Poloâ€like kinaseâ€1 triggers histone phosphorylation by Haspin in mitosis. EMBO Reports, 2014, 15, 273-281.	2.0	64
213	Distinguishing between driver and passenger mutations in individual cancer genomes by network enrichment analysis. BMC Bioinformatics, 2014, 15, 308.	1.2	68
214	ANIA: ANnotation and Integrated Analysis of the 14-3-3 interactome. Database: the Journal of Biological Databases and Curation, 2014, 2014, bat085.	1.4	51
215	P3DB 3.0: From plant phosphorylation sites to protein networks. Nucleic Acids Research, 2014, 42, D1206-D1213.	6.5	75
216	Alterations in the Cerebellar (Phospho)Proteome of a Cyclic Guanosine Monophosphate (cGMP)-dependent Protein Kinase Knockout Mouse. Molecular and Cellular Proteomics, 2014, 13, 2004-2016.	2.5	12
217	Forkhead Box P Family Members at the Crossroad Between Tolerance and Immunity: A Balancing Act. International Reviews of Immunology, 2014, 33, 94-109.	1.5	9
218	Boolean ErbB network reconstructions and perturbation simulations reveal individual drug response in different breast cancer cell lines. BMC Systems Biology, 2014, 8, 75.	3.0	36

#	ARTICLE	IF	CITATIONS
219	Tandem Mass Spectral Libraries of Peptides in Digests of Individual Proteins: Human Serum Albumin (HSA). Molecular and Cellular Proteomics, 2014, 13, 2435-2449.	2.5	21
220	A novel phosphorylation-independent interaction between SMG6 and UPF1 is essential for human NMD. Nucleic Acids Research, 2014, 42, 9217-9235.	6.5	80
221	Unraveling the Complexities of DNA-Dependent Protein Kinase Autophosphorylation. Molecular and Cellular Biology, 2014, 34, 2162-2175.	1.1	58
222	Phosphoproteomic Profiling Identifies Focal Adhesion Kinase as a Mediator of Docetaxel Resistance in Castrate-Resistant Prostate Cancer. Molecular Cancer Therapeutics, 2014, 13, 190-201.	1.9	42
223	dbGSH: a database of <i>S</i>-glutathionylation. Bioinformatics, 2014, 30, 2386-2388.	1.8	50
224	GPS-SUMO: a tool for the prediction of sumoylation sites and SUMO-interaction motifs. Nucleic Acids Research, 2014, 42, W325-W330.	6.5	417
225	Signaling regulates activity of DHCR24, the final enzyme in cholesterol synthesis. Journal of Lipid Research, 2014, 55, 410-420.	2.0	52
226	The CK1 Family: Contribution to Cellular Stress Response and Its Role in Carcinogenesis. Frontiers in Oncology, 2014, 4, 96.	1.3	200
227	Phosphoproteomic Analysis Reveals Regulatory Mechanisms at the Kidney Filtration Barrier. Journal of the American Society of Nephrology: JASN, 2014, 25, 1509-1522.	3.0	40
228	Time-resolved dissection of early phosphoproteome and ensuing proteome changes in response to TGF-Î². Science Signaling, 2014, 7, rs5.	1.6	39
229	Proteome-Wide Identification of SUMO2 Modification Sites. Science Signaling, 2014, 7, rs2.	1.6	174
230	Coordinate phosphorylation of multiple residues on single AKT1 and AKT2 molecules. Oncogene, 2014, 33, 3463-3472.	2.6	36
231	Initial description of the developing soybean seed protein Lys-NÎµ-acetylome. Journal of Proteomics, 2014, 96, 56-66.	1.2	78
232	A systems toxicology approach identifies Lyn as a key signaling phosphoprotein modulated by mercury in a B lymphocyte cell model. Toxicology and Applied Pharmacology, 2014, 276, 47-54.	1.3	16
233	EPIYA (or -like) motifs in mammalian proteins. Journal of King Saud University - Science, 2014, 26, 276-284.	1.6	4
234	Keepâ€ING balance: Tumor suppression by epigenetic regulation. FEBS Letters, 2014, 588, 2728-2742.	1.3	62
235	HMMpTM: Improving transmembrane protein topology prediction using phosphorylation and glycosylation site prediction. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 316-322.	1.1	15
236	RUBI: rapid proteomic-scale prediction of lysine ubiquitination and factors influencing predictor performance. Amino Acids, 2014, 46, 853-862.	1.2	24

#	Article	IF	Citations
237	Experimental and Computational Tools for Analysis of Signaling Networks in Primary Cells. Current Protocols in Immunology, 2014, 104, 11.11.1-11.11.23.	3.6	2
238	A â€œSYDEâ€• effect of hierarchical phosphorylation: possible relevance to the cystic fibrosis basic defect. Cellular and Molecular Life Sciences, 2014, 71, 2193-2196.	2.4	7
239	TPX2: of spindle assembly, DNA damage response, and cancer. Cellular and Molecular Life Sciences, 2014, 71, 3027-3047.	2.4	155
240	Epigenetic marking of sperm by post-translational modification of histones and protamines. Epigenetics and Chromatin, 2014, 7, 2.	1.8	149
241	Systems biology in drug discovery and development. Drug Discovery Today, 2014, 19, 113-125.	3.2	80
242	Encephalomyocarditis Virus Leader Is Phosphorylated by CK2 and Syk as a Requirement for Subsequent Phosphorylation of Cellular Nucleoporins. Journal of Virology, 2014, 88, 2219-2226.	1.5	14
243	Dynamic Changes in Ribosome-Associated Proteome and Phosphoproteome During Deoxynivalenol-Induced Translation Inhibition and Ribotoxic Stress. Toxicological Sciences, 2014, 138, 217-233.	1.4	38
244	The next level of complexity: Crosstalk of posttranslational modifications. Proteomics, 2014, 14, 513-524.	1.3	246
245	Lysine Deacetylase (KDAC) Regulatory Pathways: an Alternative Approach to Selective Modulation. ChemMedChem, 2014, 9, 511-522.	1.6	29
246	What's that gene (or protein)? Online resources for exploring functions of genes, transcripts, and proteins. Molecular Biology of the Cell, 2014, 25, 1187-1201.	0.9	13
247	The pea seedling mitochondrial NÎµ-lysine acetylome. Mitochondrion, 2014, 19, 154-165.	1.6	47
248	Role of protein tyrosine phosphatases in the modulation of insulin signaling and their implication in the pathogenesis of obesity-linked insulin resistance. Reviews in Endocrine and Metabolic Disorders, 2014, 15, 79-97.	2.6	69
249	Quantitative phosphoproteomic analysis of host responses in human lung epithelial (A549) cells during influenza virus infection. Virus Research, 2014, 179, 53-63.	1.1	21
250	Sequential Phosphoproteomic Enrichment through Complementary Metal-Directed Immobilized Metal Ion Affinity Chromatography. Analytical Chemistry, 2014, 86, 685-693.	3.2	100
251	Fine Tuning of Proteomic Technologies to Improve Biological Findings: Advancements in 2011â€“2013. Analytical Chemistry, 2014, 86, 176-195.	3.2	18
252	Aggregate-Prone R120GCRYAB Triggers Multifaceted Modifications of the Thioredoxin System. Antioxidants and Redox Signaling, 2014, 20, 2891-2906.	2.5	9
253	Methylation of the DNA/RNA-binding protein Kin17 by METTL22 affects its association with chromatin. Journal of Proteomics, 2014, 100, 115-124.	1.2	36
254	Identification of Enriched PTM Crosstalk Motifs from Large-Scale Experimental Data Sets. Journal of Proteome Research, 2014, 13, 249-259.	1.8	40

#	Article	IF	Citations
255	Turning Off AKT: PHLPP as a Drug Target. Annual Review of Pharmacology and Toxicology, 2014, 54, 537-558.	4.2	113
256	Mitotic Phosphorylation of Eukaryotic Initiation Factor 4G1 (eIF4G1) at Ser1232 by Cdk1:Cyclin B Inhibits eIF4A Helicase Complex Binding with RNA. Molecular and Cellular Biology, 2014, 34, 439-451.	1.1	35
257	Hybrid assembly of DNA-coated gold nanoparticles with water soluble conjugated polymers for studying proteinâ€"DNA interaction and ligand inhibition. RSC Advances, 2014, 4, 8883.	1.7	11
258	Regulation of transcription factor activity by interconnected post-translational modifications. Trends in Pharmacological Sciences, 2014, 35, 76-85.	4.0	176
259	The WAVE Regulatory Complex Links Diverse Receptors to the Actin Cytoskeleton. Cell, 2014, 156, 195-207.	13.5	260
260	A multiscale statistical mechanical framework integrates biophysical and genomic data to assemble cancer networks. Nature Genetics, 2014, 46, 1363-1371.	9.4	60
261	A Proteome-Scale Map of the Human Interactome Network. Cell, 2014, 159, 1212-1226.	13.5	1,199
262	Quantitative phosphoproteomic analysis of RIP3â€dependent protein phosphorylation in the course of TNFâ€induced necroptosis. Proteomics, 2014, 14, 713-724.	1.3	25
263	HOPE-Fixation of Lung Tissue Allows Retrospective Proteome and Phosphoproteome Studies. Journal of Proteome Research, 2014, 13, 5230-5239.	1.8	5
264	Heterogeneity of Pancreatic Cancer Metastases in a Single Patient Revealed by Quantitative Proteomics. Molecular and Cellular Proteomics, 2014, 13, 2803-2811.	2.5	52
265	Improving the performance of protein kinase identification via high dimensional proteinâ€"protein interactions and substrate structure data. Molecular BioSystems, 2014, 10, 694-702.	2.9	24
266	Diverse Levels of Sequence Selectivity and Catalytic Efficiency of Protein-Tyrosine Phosphatases. Biochemistry, 2014, 53, 397-412.	1.2	51
267	Global discovery of high-NaCl-induced changes of protein phosphorylation. American Journal of Physiology - Cell Physiology, 2014, 307, C442-C454.	2.1	16
268	Reconstruction of Insulin Signal Flow from Phosphoproteome and Metabolome Data. Cell Reports, 2014, 8, 1171-1183.	2.9	82
269	Role for NUP62 depletion and PYK2 redistribution in dendritic retraction resulting from chronic stress. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 16130-16135.	3.3	36
270	Using Unnatural Amino Acid Mutagenesis To Probe the Regulation of PRMT1. ACS Chemical Biology, 2014, 9, 649-655.	1.6	38
271	Uncovering global SUMOylation signaling networks in a site-specific manner. Nature Structural and Molecular Biology, 2014, 21, 927-936.	3.6	408
272	Primary cilium-associated genes mediate bone marrow stromal cell response to hypoxia. Stem Cell Research, 2014, 13, 284-299.	0.3	16

#	Article	IF	Citations
273	Asymmetric mRNA localization contributes to fidelity and sensitivity of spatially localized systems. Nature Structural and Molecular Biology, 2014, 21, 833-839.	3.6	57
274	Structure, mechanism, and regulation of soluble adenylyl cyclases â€" similarities and differences to transmembrane adenylyl cyclases. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2014, 1842, 2535-2547.	1.8	163
275	Elucidation of epithelialâ€"mesenchymal transition-related pathways in a triple-negative breast cancer cell line model by multi-omics interactome analysis. Integrative Biology (United Kingdom), 2014, 6, 1058-1068.	0.6	17
276	Studying Tumorigenesis through Network Evolution and Somatic Mutational Perturbations in the Cancer Interactome. Molecular Biology and Evolution, 2014, 31, 2156-2169.	3.5	79
277	Modulation of the Chromatin Phosphoproteome by the Haspin Protein Kinase. Molecular and Cellular Proteomics, 2014, 13, 1724-1740.	2.5	37
278	The PP4R1 subunit of protein phosphatase PP4 targets TRAF2 and TRAF6 to mediate inhibition of NF-Î°B activation. Cellular Signalling, 2014, 26, 2730-2737.	1.7	20
279	Lean Big Data integration in systems biology and systems pharmacology. Trends in Pharmacological Sciences, 2014, 35, 450-460.	4.0	85
280	Activation of diverse signalling pathways by oncogenic PIK3CA mutations. Nature Communications, 2014, 5, 4961.	5.8	72
281	Function and Regulation of the Mono-ADP-Ribosyltransferase ARTD10. Current Topics in Microbiology and Immunology, 2014, 384, 167-188.	0.7	26
282	Integrating phosphoproteomics in systems biology. Computational and Structural Biotechnology Journal, 2014, 10, 90-97.	1.9	33
283	ATP7B activity is stimulated by PKCÉ› in porcine liver. International Journal of Biochemistry and Cell Biology, 2014, 54, 60-67.	1.2	2
284	Automated hypothesis generation based on mining scientific literature. , 2014, , .		82
285	AKT1 and AKT2 Induce Distinct Phosphorylation Patterns in HL-1 Cardiac Myocytes. Journal of Proteome Research, 2014, 13, 4232-4245.	1.8	16
286	Mapping of SUMO sites and analysis of SUMOylation changes induced by external stimuli. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 12432-12437.	3.3	153
287	Ischemia in Tumors Induces Early and Sustained Phosphorylation Changes in Stress Kinase Pathways but Does Not Affect Global Protein Levels. Molecular and Cellular Proteomics, 2014, 13, 1690-1704.	2.5	323
288	Impaired exercise-induced mitochondrial biogenesis in the obese Zucker rat, despite PGC-1Î± induction, is due to compromised mitochondrial translation elongation. American Journal of Physiology - Endocrinology and Metabolism, 2014, 306, E503-E511.	1.8	27
289	A Million Peptide Motifs for the Molecular Biologist. Molecular Cell, 2014, 55, 161-169.	4.5	429
290	Unique Functional Properties of Conserved Arginine Residues in the Lentivirus Lytic Peptide Domains of the C-terminal Tail of HIV-1 gp41. Journal of Biological Chemistry, 2014, 289, 7630-7640.	1.6	9

#	Article	IF	Citations
291	A Secreted Tyrosine Kinase Acts in the Extracellular Environment. Cell, 2014, 158, 1033-1044.	13.5	111
292	Heterogeneity of glycolysis in cancers and therapeutic opportunities. Biochemical Pharmacology, 2014, 92, 12-21.	2.0	44
293	Elucidation of the evolutionary expansion of phosphorylation signaling networks using comparative phosphomotif analysis. BMC Genomics, 2014, 15, 546.	1.2	8
294	Histone H3 lysine 27 acetylation is altered in colon cancer. Clinical Proteomics, 2014, 11, 24.	1.1	72
295	Single-step Enrichment by Ti4+-IMAC and Label-free Quantitation Enables In-depth Monitoring of Phosphorylation Dynamics with High Reproducibility and Temporal Resolution. Molecular and Cellular Proteomics, 2014, 13, 2426-2434.	2.5	89
296	MiR-34a regulates therapy resistance by targeting HDAC1 and HDAC7 in breast cancer. Cancer Letters, 2014, 354, 311-319.	3.2	90
297	Impact of Digestion Conditions on Phosphoproteomics. Journal of Proteome Research, 2014, 13, 2761-2770.	1.8	59
298	Structure of the DDB1â€“CRBN E3 ubiquitin ligase in complex with thalidomide. Nature, 2014, 512, 49-53.	13.7	745
299	CK2 involvement in ESCRT-III complex phosphorylation. Archives of Biochemistry and Biophysics, 2014, 545, 83-91.	1.4	13
300	Classification of Intrinsically Disordered Regions and Proteins. Chemical Reviews, 2014, 114, 6589-6631.	23.0	1,618
301	Glucose Regulates Mitochondrial Motility via Milton Modification by O-GlcNAc Transferase. Cell, 2014, 158, 54-68.	13.5	223
302	Adrenergic Signaling Regulates Mitochondrial Ca²⁺ Uptake Through Pyk2-Dependent Tyrosine Phosphorylation of the Mitochondrial Ca²⁺ Uniporter. Antioxidants and Redox Signaling, 2014, 21, 863-879.	2.5	69
303	The UPS and downs of cholesterol homeostasis. Trends in Biochemical Sciences, 2014, 39, 527-535.	3.7	67
304	Prediction of protein post-translational modifications: main trends and methods. Russian Chemical Reviews, 2014, 83, 143-154.	2.5	6
305	Dissection of a Novel Autocrine Signaling Pathway via Quantitative Secretome and Interactome Mapping. Journal of Proteome Research, 2014, 13, 3432-3443.	1.8	5
306	Validation of the reliability of computational O-GlcNAc prediction. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 416-421.	1.1	28
307	A hydrophobic residue in position 15 of the rP2X3 receptor slows desensitization and reveals properties beneficial for pharmacological analysis and high-throughput screening. Neuropharmacology, 2014, 79, 603-615.	2.0	22
308	Identification and characterization of lysine-methylated sites on histones and non-histone proteins. Computational Biology and Chemistry, 2014, 50, 11-18.	1.1	24

#	Article	IF	Citations
309	Acetylated Î±-tubulin is reduced in individuals with poor sperm motility. Fertility and Sterility, 2014, 101, 95-104.e3.	0.5	58
310	A PEF/Y Substrate Recognition and Signature Motif Plays a Critical Role in DAPK-Related Kinase Activity. Chemistry and Biology, 2014, 21, 264-273.	6.2	7
311	Endothelin-1 stimulates catalase activity through the PKCÎ´-mediated phosphorylation of serine 167. Free Radical Biology and Medicine, 2014, 67, 255-264.	1.3	33
312	Chromosome 10q26 locus and age-related macular degeneration: AÂprogress update. Experimental Eye Research, 2014, 119, 1-7.	1.2	31
313	Building and exploring an integrated human kinase network: Global organization and medical entry points. Journal of Proteomics, 2014, 107, 113-127.	1.2	16
314	Characterization of the effects of phosphorylation by CK2 on the structure and binding properties of human HP1Î². FEBS Letters, 2014, 588, 1094-1099.	1.3	11
315	p38â€Mediated phosphorylation of Eps15 endocytic adaptor protein. FEBS Letters, 2014, 588, 131-137.	1.3	14
316	Identification of a Major Determinant for Serine-Threonine Kinase Phosphoacceptor Specificity. Molecular Cell, 2014, 53, 140-147.	4.5	91
317	PPP1CC2 can form a kinase/phosphatase complex with the testis-specific proteins TSSK1 and TSKS in the mouse testis. Reproduction, 2014, 147, 1-12.	1.1	26
318	Mass spectrometryâ€driven phosphoproteomics: patterning the systems biology mosaic. Wiley Interdisciplinary Reviews: Developmental Biology, 2014, 3, 83-112.	5.9	63
319	Incorporating post-translational modifications and unnatural amino acids into high-throughput modeling of protein structures. Bioinformatics, 2014, 30, 1681-1689.	1.8	8
320	Large-Scale Identification of Phosphorylation Sites for Profiling Protein Kinase Selectivity. Journal of Proteome Research, 2014, 13, 3410-3419.	1.8	52
321	AMASS: a database for investigating protein structures. Bioinformatics, 2014, 30, 1595-1600.	1.8	5
322	The structural and functional signatures of proteins that undergo multiple events of postâ€translational modification. Protein Science, 2014, 23, 1077-1093.	3.1	287
323	Signatures of Natural Selection on Mutations of Residues with Multiple Posttranslational Modifications. Molecular Biology and Evolution, 2014, 31, 1641-1645.	3.5	10
324	Short Linear Motifs: Ubiquitous and Functionally Diverse Protein Interaction Modules Directing Cell Regulation. Chemical Reviews, 2014, 114, 6733-6778.	23.0	389
325	Interplay of DNA damage and cell cycle signaling at the level of human replication protein A. DNA Repair, 2014, 21, 12-23.	1.3	15
326	Effective identification of kinase-specific phosphorylation sites based on domainâ€“domain interactions. Chemometrics and Intelligent Laboratory Systems, 2014, 136, 97-103.	1.8	4

#	ARTICLE	IF	CITATIONS
327	Sperm ubiquitination in epididymal feline semen. Theriogenology, 2014, 82, 636-642.	0.9	31
328	Phosphoproteome analysis reveals differences in phosphosite profiles between tumorigenic and non-tumorigenic epithelial cells. Journal of Proteomics, 2014, 96, 67-81.	1.2	11
329	PPISURV: a novel bioinformatics tool for uncovering the hidden role of specific genes in cancer survival outcome. Oncogene, 2014, 33, 1621-1628.	2.6	54
330	Profiling the tyrosine phosphoproteome of different mouse mammary tumour models reveals distinct, model-specific signalling networks and conserved oncogenic pathways. Breast Cancer Research, 2014, 16, 437.	2.2	13
331	Systems Medicine: from molecular features and models to the clinic in COPD. Journal of Translational Medicine, 2014, 12, S4.	1.8	23
332	Characterization and identification of protein O-GlcNAcylation sites with substrate specificity. BMC Bioinformatics, 2014, 15, S1.	1.2	27
333	A Preliminary Fastview of Mitochondrial Protein Profile from Healthy and Type 2 Diabetic Subjects. European Journal of Mass Spectrometry, 2014, 20, 307-315.	0.5	6
334	SysPTM 2.0: an updated systematic resource for post-translational modification. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau025-bau025.	1.4	58
335	Store-Operated CRAC Channels. , 2015, , 509-522.		3
336	Phosphorylation and function of DGAT1 in skeletal muscle cells. Biophysics Reports, 2015, 1, 41-50.	0.2	19
337	Cks1 proteasomal turnover is a predominant mode of regulation in breast cancer cells: Role of key tyrosines and lysines. International Journal of Oncology, 2015, 46, 395-406.	1.4	6
338	The NHERF2 sequence adjacent and upstream of the ERM-binding domain affects NHERF2â€“ezrin binding and dexamethasone stimulated NHE3 activity. Biochemical Journal, 2015, 470, 77-90.	1.7	8
339	Label-free quantitative phosphoproteomics with novel pairwise abundance normalization reveals synergistic RAS and CIP2A signaling. Scientific Reports, 2015, 5, 13099.	1.6	49
340	Integrated analysis of global proteome, phosphoproteome and glycoproteome enables complementary interpretation of disease-related protein networks. Scientific Reports, 2015, 5, 18189.	1.6	34
341	A flexible codon in genomically recoded Escherichia coli permits programmable protein phosphorylation. Nature Communications, 2015, 6, 8130.	5.8	86
342	PSEA: Kinase-specific prediction and analysis of human phosphorylation substrates. Scientific Reports, 2014, 4, 4524.	1.6	27
343	Phosphoâ€tyrosine dependent proteinâ€“protein interaction network. Molecular Systems Biology, 2015, 11, 794.	3.2	75
344	A two-layered machine learning method to identify protein O-GlcNAcylation sites with O-GlcNAc transferase substrate motifs. BMC Bioinformatics, 2015, 16, S10.	1.2	41

#	Article	IF	Citations
345	New Insights into the RNA-Binding and E3 Ubiquitin Ligase Activities of Roquins. Scientific Reports, 2015, 5, 15660.	1.6	26
346	Predicting CK2 beta-dependent substrates using linear patterns. Biochemistry and Biophysics Reports, 2015, 4, 20-27.	0.7	7
347	Phosphoproteomic analysis reveals Smarcb1 dependent EGFR signaling in Malignant Rhabdoid tumor cells. Molecular Cancer, 2015, 14, 167.	7.9	13
348	Altered regulation of PDK4 expression promotes antiestrogen resistance in human breast cancer cells. SpringerPlus, 2015, 4, 689.	1.2	26
349	A comprehensive proteomic and phosphoproteomic analysis of yeast deletion mutants of 14â€3â€3 orthologs and associated effects of rapamycin. Proteomics, 2015, 15, 474-486.	1.3	49
350	Comprehensive identification of phosphorylation sites on the Numb endocytic adaptor protein. Proteomics, 2015, 15, 434-446.	1.3	4
351	Evolution of the highly networked deubiquitinating enzymes USP4, USP15, and USP11. BMC Evolutionary Biology, 2015, 15, 230.	3.2	56
352	Confrontation of fibroblasts with cancer cells in vitro: gene network analysis of transcriptome changes and differential capacity to inhibit tumor growth. Journal of Experimental and Clinical Cancer Research, 2015, 34, 62.	3.5	11
353	Akt-mediated phosphorylation controls the activity of the Y-box protein MSY3 in skeletal muscle. Skeletal Muscle, 2015, 5, 18.	1.9	12
354	Direct Reversal Repair in Mammalian Cells. , 0, , .		3
355	Comprehensive Protein Interactome Analysis of a Key RNA Helicase: Detection of Novel Stress Granule Proteins. Biomolecules, 2015, 5, 1441-1466.	1.8	26
356	Ligand-Binding Affinity at the Insulin Receptor Isoform-A and Subsequent IR-A Tyrosine Phosphorylation Kinetics are Important Determinants of Mitogenic Biological Outcomes. Frontiers in Endocrinology, 2015, 6, 107.	1.5	25
357	Phosphoproteomic Analysis of Cell-Based Resistance to BRAF Inhibitor Therapy in Melanoma. Frontiers in Oncology, 2015, 5, 95.	1.3	26
358	Scalable Production in Human Cells and Biochemical Characterization of Full-Length Normal and Mutant Huntingtin. PLoS ONE, 2015, 10, e0121055.	1.1	38
359	The Viral G Protein-Coupled Receptor ORF74 Hijacks Î²-Arrestins for Endocytic Trafficking in Response to Human Chemokines. PLoS ONE, 2015, 10, e0124486.	1.1	17
360	Knowledge-Based Analysis for Detecting Key Signaling Events from Time-Series Phosphoproteomics Data. PLoS Computational Biology, 2015, 11, e1004403.	1.5	32
361	Synaptic Effects of Munc18-1 Alternative Splicing in Excitatory Hippocampal Neurons. PLoS ONE, 2015, 10, e0138950.	1.1	12
362	The Cardiac Stress Response Factor Ms1 Can Bind to DNA and Has a Function in the Nucleus. PLoS ONE, 2015, 10, e0144614.	1.1	4

#	Article	IF	Citations
363	Reproducible Analysis of Post-Translational Modifications in Proteomesâ€"Application to Human Mutations. PLoS ONE, 2015, 10, e0144692.	1.1	9
364	Phosphoproteomic Analysis of KSHV-Infected Cells Reveals Roles of ORF45-Activated RSK during Lytic Replication. PLoS Pathogens, 2015, 11, e1004993.	2.1	40
365	Germ-line variants identified by next generation sequencing in a panel of estrogen and cancer associated genes correlate with poor clinical outcome in Lynch syndrome patients. Oncotarget, 2015, 6, 41108-41122.	0.8	5
366	Signal Transduction Reaction Monitoring Deciphers Site-Specific PI3K-mTOR/MAPK Pathway Dynamics in Oncogene-Induced Senescence. Journal of Proteome Research, 2015, 14, 2906-2914.	1.8	33
367	Construction and Deciphering of Human Phosphorylation-Mediated Signaling Transduction Networks. Journal of Proteome Research, 2015, 14, 2745-2757.	1.8	12
368	Loss of MIG6 Accelerates Initiation and Progression of Mutant Epidermal Growth Factor Receptorâ€"Driven Lung Adenocarcinoma. Cancer Discovery, 2015, 5, 534-549.	7.7	57
369	Current strategies and findings in clinically relevant post-translational modification-specific proteomics. Expert Review of Proteomics, 2015, 12, 235-253.	1.3	147
370	Conformation-Dependent Human p52Shc Phosphorylation by Human c-Src. Biochemistry, 2015, 54, 3469-3482.	1.2	3
371	Progress and challenges in predicting protein methylation sites. Molecular BioSystems, 2015, 11, 2610-2619.	2.9	11
372	Large-scale analysis of the evolutionary histories of phosphorylation motifs in the human genome. GigaScience, 2015, 4, 21.	3.3	6
373	Comparative proteomic analysis of spermatozoa isolated by swim-up or density gradient centrifugation. Reproductive Biology and Endocrinology, 2015, 13, 36.	1.4	8
374	AKT phosphorylates H3-threonine 45 to facilitate termination of gene transcription in response to DNA damage. Nucleic Acids Research, 2015, 43, 4505-4516.	6.5	33
375	Global Phosphoproteomic Mapping of Early Mitotic Exit in Human Cells Identifies Novel Substrate Dephosphorylation Motifs. Molecular and Cellular Proteomics, 2015, 14, 2194-2212.	2.5	63
376	Phosphorylation and Alternative Splicing of 7B2 Reduce Prohormone Convertase 2 Activation. Molecular Endocrinology, 2015, 29, 756-764.	3.7	9
377	The pro-inflammatory cytokine s14-3-3Îµ is a ligand of CD13/Aminopeptidase N in cartilage. Journal of Cell Science, 2015, 128, 3250-62.	1.2	23
378	Discovery of a nucleocytoplasmic O-mannose glycoproteome in yeast. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 15648-15653.	3.3	67
379	Interleukin-2 Receptor Î² Thr-450 Phosphorylation Is a Positive Regulator for Receptor Complex Stability and Activation of Signaling Molecules. Journal of Biological Chemistry, 2015, 290, 20972-20983.	1.6	11
380	Proteomic Analysis Reveals Distinct Metabolic Differences Between Granulocyte-Macrophage Colony Stimulating Factor (GM-CSF) and Macrophage Colony Stimulating Factor (M-CSF) Grown Macrophages Derived from Murine Bone Marrow Cells*. Molecular and Cellular Proteomics, 2015, 14, 2722-2732.	2.5	23

#	ARTICLE	IF	CITATIONS
381	Phosphorylation of myosin regulatory light chain controls myosin head conformation in cardiac muscle. Journal of Molecular and Cellular Cardiology, 2015, 85, 199-206.	0.9	52
382	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
383	Phospho-iTRAQ: Assessing Isobaric Labels for the Large-Scale Study Of Phosphopeptide Stoichiometry. Journal of Proteome Research, 2015, 14, 839-849.	1.8	15
384	Crosstalk between Signaling Pathways Provided by Single and Multiple Protein Phosphorylation Sites. Journal of Molecular Biology, 2015, 427, 511-520.	2.0	47
385	Incorporating computational resources in a cancer research program. Human Genetics, 2015, 134, 467-478.	1.8	2
386	Quantitative Proteomics Analysis of CaMKII Phosphorylation and the CaMKII Interactome in the Mouse Forebrain. ACS Chemical Neuroscience, 2015, 6, 615-631.	1.7	57
387	Uncovering disease-disease relationships through the incomplete interactome. Science, 2015, 347, 1257601.	6.0	1,219
388	Integrated RNA- and protein profiling of fermentation and respiration in diploid budding yeast provides insight into nutrient control of cell growth and development. Journal of Proteomics, 2015, 119, 30-44.	1.2	5
389	A Novel Post-translational Modification of Nucleolin, SUMOylation at Lys-294, Mediates Arsenite-induced Cell Death by Regulating gadd45Î± mRNA Stability. Journal of Biological Chemistry, 2015, 290, 4784-4800.	1.6	33
390	Systematic Characterization and Prediction of Post-Translational Modification Cross-Talk *. Molecular and Cellular Proteomics, 2015, 14, 761-770.	2.5	30
391	Investigation of phosphoproteome in RAGE signaling. Proteomics, 2015, 15, 245-259.	1.3	16
392	Interactome analysis of AMP-activated protein kinase (AMPK)-Î±1 and -Î²1 in INS-1 pancreatic beta-cells by affinity purification-mass spectrometry. Scientific Reports, 2014, 4, 4376.	1.6	36
393	Mutation analysis of large tumor suppressor genes LATS1 and LATS2 supports a tumor suppressor role in human cancer. Protein and Cell, 2015, 6, 6-11.	4.8	41
394	Simultaneous dissection and comparison of <scp>IL</scp>â€2 and <scp>IL</scp>â€15 signaling pathways by global quantitative phosphoproteomics. Proteomics, 2015, 15, 520-531.	1.3	22
395	Visualization of LCâ€MS/MS proteomics data in MaxQuant. Proteomics, 2015, 15, 1453-1456.	1.3	248
396	Tyrosine phosphorylation of WW proteins. Experimental Biology and Medicine, 2015, 240, 375-382.	1.1	14
397	Differential regulation of FGFR3 by PTPN1 and PTPN2. Proteomics, 2015, 15, 419-433.	1.3	10
398	PTMcode v2: a resource for functional associations of post-translational modifications within and between proteins. Nucleic Acids Research, 2015, 43, D494-D502.	6.5	90

#	Article	IF	Citations
399	An Optimized Platform for Hydrophilic Interaction Chromatographyâ€"Immobilized Metal Affinity Chromatography Enables Deep Coverage of the Rat Liver Phosphoproteome. Journal of Proteome Research, 2015, 14, 997-1009.	1.8	22
400	Tyrosine Phosphorylation of the Lyn Src Homology 2 (SH2) Domain Modulates Its Binding Affinity and Specificity*. Molecular and Cellular Proteomics, 2015, 14, 695-706.	2.5	31
401	Affinity Proteomics for Phosphatase Interactions in Atrial Fibrillationâˆ—. Journal of the American College of Cardiology, 2015, 65, 174-176.	1.2	2
402	Human METTL20 Is a Mitochondrial Lysine Methyltransferase That Targets the Î² Subunit of Electron Transfer Flavoprotein (ETFÎ²) and Modulates Its Activity. Journal of Biological Chemistry, 2015, 290, 423-434.	1.6	48
403	The sirtuins promote Dishevelled-1 scaffolding of TIAM1, Rac activation and cell migration. Oncogene, 2015, 34, 188-198.	2.6	45
404	TAM Receptor Signaling in Immune Homeostasis. Annual Review of Immunology, 2015, 33, 355-391.	9.5	354
405	Web Resources for Mass Spectrometry-based Proteomics. Genomics, Proteomics and Bioinformatics, 2015, 13, 36-39.	3.0	17
406	Therapeutic opportunities within the DNA damage response. Nature Reviews Cancer, 2015, 15, 166-180.	12.8	442
407	MAP4-Dependent Regulation of Microtubule Formation Affects Centrosome, Cilia, and Golgi Architecture as a Central Mechanism in Growth Regulation. Human Mutation, 2015, 36, 87-97.	1.1	21
408	A DIseAse MOdule Detection (DIAMOnD) Algorithm Derived from a Systematic Analysis of Connectivity Patterns of Disease Proteins in the Human Interactome. PLoS Computational Biology, 2015, 11, e1004120.	1.5	310
409	Developing novel methods to search for substrates of protein kinases such as Rho-kinase. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 1663-1666.	1.1	15
410	Atlas of Cancer Signalling Network: a systems biology resource for integrative analysis of cancer data with Google Maps. Oncogenesis, 2015, 4, e160-e160.	2.1	129
411	Increased stability of heterogeneous ribonucleoproteins by a deacetylase inhibitor. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2015, 1849, 1095-1103.	0.9	9
412	Peptide Immunoaffinity Enrichment and Targeted Mass Spectrometry Enables Multiplex, Quantitative Pharmacodynamic Studies of Phospho-Signaling. Molecular and Cellular Proteomics, 2015, 14, 2261-2273.	2.5	56
413	Adaptation of HepG2 cells to a steady-state reduction in the content of protein phosphatase 6 (PP6) catalytic subunit. Experimental Cell Research, 2015, 335, 224-237.	1.2	2
414	Systematic investigation of hierarchical phosphorylation by protein kinase CK2. Journal of Proteomics, 2015, 118, 49-62.	1.2	64
415	Computational and statistical methods for high-throughput analysis of post-translational modifications of proteins. Journal of Proteomics, 2015, 129, 3-15.	1.2	28
416	Kinase-interacting substrate screening is a novel method to identify kinase substrates. Journal of Cell Biology, 2015, 209, 895-912.	2.3	71

#	ARTICLE	IF	CITATIONS
417	Protection against murine osteoarthritis by inhibition of the 26S proteasome and lysine-48 linked ubiquitination. Annals of the Rheumatic Diseases, 2015, 74, 1580-1587.	0.5	27
418	A Phosphoproteomic Comparison of B-RAFV600E and MKK1/2 Inhibitors in Melanoma Cells*. Molecular and Cellular Proteomics, 2015, 14, 1599-1615.	2.5	94
419	A novel role of farnesylation in targeting a mitotic checkpoint protein, human Spindly, to kinetochores. Journal of Cell Biology, 2015, 208, 881-896.	2.3	58
420	CEP63 deficiency promotes p53-dependent microcephaly and reveals a role for the centrosome in meiotic recombination. Nature Communications, 2015, 6, 7676.	5.8	96
421	Special Enrichment Strategies Greatly Increase the Efficiency of Missing Proteins Identification from Regular Proteome Samples. Journal of Proteome Research, 2015, 14, 3680-3692.	1.8	15
422	Evolutionary Constraint and Disease Associations of Post-Translational Modification Sites in Human Genomes. PLoS Genetics, 2015, 11, e1004919.	1.5	69
423	Chronic Cocaine Use Causes Changes in the Striatal Proteome Depending on the Endogenous Expression of Pleiotrophin. Chemical Research in Toxicology, 2015, 28, 1443-1454.	1.7	10
424	Crucial roles of RSK in cell motility by catalysing serine phosphorylation of EphA2. Nature Communications, 2015, 6, 7679.	5.8	106
425	Tau post-translational modifications in wild-type and human amyloid precursor protein transgenic mice. Nature Neuroscience, 2015, 18, 1183-1189.	7.1	377
426	Systematic Analysis of the Genetic Variability That Impacts SUMO Conjugation and Their Involvement in Human Diseases. Scientific Reports, 2015, 5, 10900.	1.6	11
427	Arginine methylation of HSP70 regulates retinoid acid-mediated <i>RARÎ²2</i> gene activation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E3327-36.	3.3	57
428	The Roles of Post-translational Modifications in the Context of Protein Interaction Networks. PLoS Computational Biology, 2015, 11, e1004049.	1.5	299
429	An Augmented Multiple-Protease-Based Human Phosphopeptide Atlas. Cell Reports, 2015, 11, 1834-1843.	2.9	92
430	System-wide identification of wild-type SUMO-2 conjugation sites. Nature Communications, 2015, 6, 7289.	5.8	97
431	Opposing calcium-dependent signalling pathways control skeletal muscle differentiation by regulating a chromatin remodelling enzyme. Nature Communications, 2015, 6, 7441.	5.8	36
432	SELPHI: correlation-based identification of kinase-associated networks from global phospho-proteomics data sets. Nucleic Acids Research, 2015, 43, W276-W282.	6.5	24
433	PhosphoSitePlus, 2014: mutations, PTMs and recalibrations. Nucleic Acids Research, 2015, 43, D512-D520.	6.5	2,488
434	Regulator of G Protein Signaling 14. Progress in Molecular Biology and Translational Science, 2015, 133, 169-206.	0.9	22

#	Article	IF	Citations
435	Prohibitin 2: At a communications crossroads. IUBMB Life, 2015, 67, 239-254.	1.5	136
436	Phosphorylation of Targeting Protein for Xenopus Kinesin-like Protein 2 (TPX2) at Threonine 72 in Spindle Assembly. Journal of Biological Chemistry, 2015, 290, 9122-9134.	1.6	17
437	Regulation of RAF protein kinases in ERK signalling. Nature Reviews Molecular Cell Biology, 2015, 16, 281-298.	16.1	506
438	Src family kinases interfere with dimerization of STAT5A through a phosphotyrosine-SH2 domain interaction. Cell Communication and Signaling, 2015, 13, 10.	2.7	11
439	A property-based analysis of human transcription factors. BMC Research Notes, 2015, 8, 82.	0.6	7
440	Induction of tissue- and stressor-specific kinomic responses in chickens exposed to hot and cold stresses. Poultry Science, 2015, 94, 1333-1345.	1.5	24
441	ProteomeScout: a repository and analysis resource for post-translational modifications and proteins. Nucleic Acids Research, 2015, 43, D521-D530.	6.5	42
442	Integrative analysis of kinase networks in TRAIL-induced apoptosis provides a source of potential targets for combination therapy. Science Signaling, 2015, 8, rs3.	1.6	29
443	Analysis of fast protein phosphorylation kinetics in single cells on a microfluidic chip. Lab on A Chip, 2015, 15, 726-734.	3.1	57
444	Intracellular Protein O-GlcNAc Modification Integrates Nutrient Status with Transcriptional and Metabolic Regulation. Advances in Cancer Research, 2015, 126, 137-166.	1.9	33
445	c-Src mediated tyrosine phosphorylation of plakophilin 3 as a new mechanism to control desmosome composition in cells exposed to oxidative stress. Cell and Tissue Research, 2015, 359, 799-816.	1.5	11
446	New potential eukaryotic substrates of the mycobacterial protein tyrosine phosphatase PtpA: hints of a bacterial modulation of macrophage bioenergetics state. Scientific Reports, 2015, 5, 8819.	1.6	31
447	The PI3K/AKT Pathway and Renal Cell Carcinoma. Journal of Genetics and Genomics, 2015, 42, 343-353.	1.7	267
448	Tubulation by Amphiphysin Requires Concentration-Dependent Switching from Wedging to Scaffolding. Structure, 2015, 23, 873-881.	1.6	45
449	Plasma membraneâ€"associated platforms: Dynamic scaffolds that organize membrane-associated events. Science Signaling, 2015, 8, re1.	1.6	47
450	MIMP: predicting the impact of mutations on kinase-substrate phosphorylation. Nature Methods, 2015, 12, 531-533.	9.0	75
451	dbSNO 2.0: a resource for exploring structural environment, functional and disease association and regulatory network of protein S-nitrosylation. Nucleic Acids Research, 2015, 43, D503-D511.	6.5	65
452	The human DEPhOsphorylation database DEPOD: a 2015 update. Nucleic Acids Research, 2015, 43, D531-D535.	6.5	65

#	Article	IF	Citations
453	Testing whether Metazoan Tyrosine Loss Was Driven by Selection against Promiscuous Phosphorylation. Molecular Biology and Evolution, 2015, 32, 144-152.	3.5	9
454	Identifying novel targets of oncogenic EGF receptor signaling in lung cancer through global phosphoproteomics. Proteomics, 2015, 15, 340-355.	1.3	42
455	A Mechanism of Global Shape-dependent Recognition and Phosphorylation of Filamin by Protein Kinase A. Journal of Biological Chemistry, 2015, 290, 8527-8538.	1.6	14
456	Quantitative Phosphoproteomics Analysis Reveals a Key Role of Insulin Growth Factor 1 Receptor (IGF1R) Tyrosine Kinase in Human Sperm Capacitation*. Molecular and Cellular Proteomics, 2015, 14, 1104-1112.	2.5	70
457	Selective detection of tyrosine-containing proximally phosphorylated motifs using an antenna-free Tb³⁺ luminescent sensor. Chemical Communications, 2015, 51, 6675-6677.	2.2	8
458	Cavin family proteins and the assembly of caveolae. Journal of Cell Science, 2015, 128, 1269-1278.	1.2	181
459	Communication between the N and C Termini Is Required for Copper-stimulated Ser/Thr Phosphorylation of Cu(I)-ATPase (ATP7B). Journal of Biological Chemistry, 2015, 290, 8803-8819.	1.6	29
460	Large-scale determination of absolute phosphorylation stoichiometries in human cells by motif-targeting quantitative proteomics. Nature Communications, 2015, 6, 6622.	5.8	139
461	Pin1: Intimate involvement with the regulatory protein kinase networks in the global phosphorylation landscape. Biochimica Et Biophysica Acta - General Subjects, 2015, 1850, 2077-2086.	1.1	22
462	Global Phosphoproteomic Analysis of Human Skeletal Muscle Reveals a Network of Exercise-Regulated Kinases and AMPK Substrates. Cell Metabolism, 2015, 22, 922-935.	7.2	333
463	Informatics and Analytical Tools for Glycan Analysis and the Development of Biotherapeutics. , 2015, , 173-192.		1
464	SH2-PLA: a sensitive in-solution approach for quantification of modular domain binding by proximity ligation and real-time PCR. BMC Biotechnology, 2015, 15, 60.	1.7	6
465	Motifs of VDAC2 required for mitochondrial Bak import and tBid-induced apoptosis. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5590-9.	3.3	63
466	Positive-unlabeled ensemble learning for kinase substrate prediction from dynamic phosphoproteomics data. Bioinformatics, 2016, 32, 252-259.	1.8	34
467	Degree of Recruitment of DOT1L to MLL-AF9 Defines Level of H3K79 Di- and Tri-methylation on Target Genes and Transformation Potential. Cell Reports, 2015, 11, 808-820.	2.9	98
468	FAIMS and Phosphoproteomics of Fibroblast Growth Factor Signaling: Enhanced Identification of Multiply Phosphorylated Peptides. Journal of Proteome Research, 2015, 14, 5077-5087.	1.8	23
469	A comprehensive quantitative phosphoproteome analysis of rice in response to bacterial blight. BMC Plant Biology, 2015, 15, 163.	1.6	55
470	Discovery of Chemical Inhibitors of Human Bromodomains. Chemical Reviews, 2015, 115, 11625-11668.	23.0	93

#	Article	IF	Citations
471	The exploration of amino acid variants co-occurring with post-translational modifications. , 2015, , .		0
472	PhosphOrtholog: a web-based tool for cross-species mapping of orthologous protein post-translational modifications. BMC Genomics, 2015, 16, 617.	1.2	20
473	Avoiding abundance bias in the functional annotation of posttranslationally modified proteins. Nature Methods, 2015, 12, 1003-1004.	9.0	60
474	TransVar: a multilevel variant annotator for precision genomics. Nature Methods, 2015, 12, 1002-1003.	9.0	67
475	Global Analysis of Protein Expression and Phosphorylation Levels in Nicotine-Treated Pancreatic Stellate Cells. Journal of Proteome Research, 2015, 14, 4246-4256.	1.8	51
476	Role for Tyrosine Phosphorylation of A-kinase Anchoring Protein 8 (AKAP8) in Its Dissociation from Chromatin and the Nuclear Matrix. Journal of Biological Chemistry, 2015, 290, 10891-10904.	1.6	20
477	Integrating proteomics with electrochemistry for identifying kinase biomarkers. Chemical Science, 2015, 6, 4756-4766.	3.7	30
478	Regulation of Catalytic and Non-catalytic Functions of the Drosophila Ste20 Kinase Slik by Activation Segment Phosphorylation. Journal of Biological Chemistry, 2015, 290, 20960-20971.	1.6	13
479	Robust production of recombinant phosphoproteins using cell-free protein synthesis. Nature Communications, 2015, 6, 8168.	5.8	106
480	A Positive Feedback Loop between Akt and mTORC2 via SIN1 Phosphorylation. Cell Reports, 2015, 12, 937-943.	2.9	232
481	mapDIA: Preprocessing and statistical analysis of quantitative proteomics data from data independent acquisition mass spectrometry. Journal of Proteomics, 2015, 129, 108-120.	1.2	149
482	Lysine Acetylation of CREBH Regulates Fasting-Induced Hepatic Lipid Metabolism. Molecular and Cellular Biology, 2015, 35, 4121-4134.	1.1	41
483	A novel method for predicting post-translational modifications on serine and threonine sites by using site-modification network profiles. Molecular BioSystems, 2015, 11, 3092-3100.	2.9	16
484	Proteogenomics Dashboard for the Human Proteome Project. Journal of Proteome Research, 2015, 14, 3738-3749.	1.8	11
485	mTOR regulates MAPKAPK2 translation to control the senescence-associated secretory phenotype. Nature Cell Biology, 2015, 17, 1205-1217.	4.6	552
486	Nonenzymatic Protein Acetylation Detected by NAPPA Protein Arrays. ACS Chemical Biology, 2015, 10, 2034-2047.	1.6	47
487	RLIMS-P 2.0: A Generalizable Rule-Based Information Extraction System for Literature Mining of Protein Phosphorylation Information. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 17-29.	1.9	42
488	PhosphoPath: Visualization of Phosphosite-centric Dynamics in Temporal Molecular Networks. Journal of Proteome Research, 2015, 14, 4332-4341.	1.8	56

#	ARTICLE	IF	CITATIONS
489	Analysis of Phosphorylation-dependent Protein Interactions of Adhesion and Degranulation Promoting Adaptor Protein (ADAP) Reveals Novel Interaction Partners Required for Chemokine-directed T cell Migration. Molecular and Cellular Proteomics, 2015, 14, 2961-2972.	2.5	8
490	The Inner Centromere Protein (INCENP) Coil Is a Single Î±-Helix (SAH) Domain That Binds Directly to Microtubules and Is Important for Chromosome Passenger Complex (CPC) Localization and Function in Mitosis. Journal of Biological Chemistry, 2015, 290, 21460-21472.	1.6	56
491	Evaluation of Kinase Activity Profiling Using Chemical Proteomics. ACS Chemical Biology, 2015, 10, 2743-2752.	1.6	32
492	Receptor sequestration in response to Î²-arrestin-2 phosphorylation by ERK1/2 governs steady-state levels of GPCR cell-surface expression. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5160-8.	3.3	39
493	Computational Phosphorylation Network Reconstruction: Methods and Resources. Methods in Molecular Biology, 2015, 1306, 177-194.	0.4	2
494	Beyond single modification: Reanalysis of the acetylproteome of human sperm reveals widespread multiple modifications. Journal of Proteomics, 2015, 126, 296-302.	1.2	11
495	Prediction of human diseaseâ€associated phosphorylation sites with combined feature selection approach and support vector machine. IET Systems Biology, 2015, 9, 155-163.	0.8	11
496	EGF-receptor specificity for phosphotyrosine-primed substrates provides signal integration with Src. Nature Structural and Molecular Biology, 2015, 22, 983-990.	3.6	36
497	Antibody-based detection of protein phosphorylation status to track the efficacy of novel therapies using nanogram protein quantities from stem cells and cell lines. Nature Protocols, 2015, 10, 149-168.	5.5	21
498	Folic acid deficiency induces premature hearing loss through mechanisms involving cochlear oxidative stress and impairment of homocysteine metabolism. FASEB Journal, 2015, 29, 418-432.	0.2	49
499	Impact of regulatory variation from RNA to protein. Science, 2015, 347, 664-667.	6.0	399
500	Accurate in silico identification of species-specific acetylation sites by integrating protein sequence-derived and functional features. Scientific Reports, 2014, 4, 5765.	1.6	71
501	Computational phosphoproteomics: From identification to localization. Proteomics, 2015, 15, 950-963.	1.3	24
502	Non-histone protein methylation as a regulator of cellular signalling and function. Nature Reviews Molecular Cell Biology, 2015, 16, 5-17.	16.1	403
503	Bioinformatics approaches for the functional interpretation of protein lists: From ontology term enrichment to network analysis. Proteomics, 2015, 15, 981-996.	1.3	27
504	Comparative phosphoproteomic analysis of mammalian glomeruli reveals conserved podocin C-terminal phosphorylation as a determinant of slit diaphragm complex architecture. Proteomics, 2015, 15, 1326-1331.	1.3	21
505	Case study: using sequence homology to identify putative phosphorylation sites in an evolutionarily distant species (honeybee). Briefings in Bioinformatics, 2015, 16, 820-829.	3.2	5
506	Exploring human 40S ribosomal proteins binding to the 18S rRNA fragment containing major 3â€²-terminal domain. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 101-109.	1.1	8

#	Article	IF	Citations
507	Survey of phosphorylation near drug binding sites in the Protein Data Bank (PDB) and their effects. Proteins: Structure, Function and Bioinformatics, 2015, 83, 25-36.	1.5	18
508	Nanomechanical Property Maps of Breast Cancer Cells As Determined by Multiharmonic Atomic Force Microscopy Reveal Syk-Dependent Changes in Microtubule Stability Mediated by MAP1B. Biochemistry, 2015, 54, 60-68.	1.2	39
509	Combined experimental and bioinformatics analysis for the prediction and identification of VHR/DUSP3 nuclear targets related to DNA damage and repair. Integrative Biology (United Kingdom), 2015, 7, 73-89.	0.6	11
510	Integration of conventional quantitative and phosphoâ€proteomics reveals new elements in activated Jurkat Tâ€cell receptor pathway maintenance. Proteomics, 2015, 15, 25-33.	1.3	10
511	An ERK/Cdk5 axis controls the diabetogenic actions of PPARÎ³. Nature, 2015, 517, 391-395.	13.7	251
512	Substrate Trapping Proteomics Reveals Targets of the Î²TrCP2/FBXW11 Ubiquitin Ligase. Molecular and Cellular Biology, 2015, 35, 167-181.	1.1	55
513	Making proteomics data accessible and reusable: Current state of proteomics databases and repositories. Proteomics, 2015, 15, 930-950.	1.3	181
514	Chromo Domain Proteins. , 2016, , 113-125.		0
515	Bringing the Signal into the Nucleus. , 2016, , 441-476.		3
516	Induction of Macrophage Function in Human THP-1 Cells Is Associated with Rewiring of MAPK Signaling and Activation of MAP3K7 (TAK1) Protein Kinase. Frontiers in Cell and Developmental Biology, 2016, 4, 21.	1.8	54
517	Phosphoproteome Discovery in Human Biological Fluids. Proteomes, 2016, 4, 37.	1.7	15
518	Feature-based classification of human transcription factors into hypothetical sub-classes related to regulatory function. BMC Bioinformatics, 2016, 17, 459.	1.2	15
519	Phosphoproteome Analysis of Invasion and Metastasis-Related Factors in Pancreatic Cancer Cells. PLoS ONE, 2016, 11, e0152280.	1.1	21
520	Computational Analysis of the Predicted Evolutionary Conservation of Human Phosphorylation Sites. PLoS ONE, 2016, 11, e0152809.	1.1	9
521	Threonine 89 Is an Important Residue of Profilin-1 That Is Phosphorylatable by Protein Kinase A. PLoS ONE, 2016, 11, e0156313.	1.1	11
522	Protein lysine methylation by seven-Î²-strand methyltransferases. Biochemical Journal, 2016, 473, 1995-2009.	1.7	92
523	A Role for the Chromatinâ€Remodeling Factor<i>BAZ1A</i>in Neurodevelopment. Human Mutation, 2016, 37, 964-975.	1.1	29
524	Identification of differentially expressed three novel transcript variants of mouse <scp>ARNT</scp> gene. IUBMB Life, 2016, 68, 122-135.	1.5	8

#	ARTICLE	IF	CITATIONS
525	MALDIâ€TOF and nESI Orbitrap MS/MS identify orthogonal parts of the phosphoproteome. Proteomics, 2016, 16, 1447-1456.	1.3	13
526	Quantitative proteomics suggests metabolic reprogramming during ETHE1 deficiency. Proteomics, 2016, 16, 1166-1176.	1.3	12
527	Common errors in mass spectrometryâ€based analysis of postâ€translational modifications. Proteomics, 2016, 16, 700-714.	1.3	106
528	Commercially available antibodies can be applied in quantitative multiplexed peptide immunoaffinity enrichment targeted mass spectrometry assays. Proteomics, 2016, 16, 2141-2145.	1.3	17
529	KinasePA: Phosphoproteomics data annotation using hypothesis driven kinase perturbation analysis. Proteomics, 2016, 16, 1868-1871.	1.3	27
530	Variation Interpretation Predictors: Principles, Types, Performance, and Choice. Human Mutation, 2016, 37, 579-597.	1.1	109
531	DAPPLE 2: a Tool for the Homology-Based Prediction of Post-Translational Modification Sites. Journal of Proteome Research, 2016, 15, 2760-2767.	1.8	20
532	Global analysis of phosphoproteome dynamics in embryonic development of zebrafish (<i>Danio) Tj ETQq1 1 0.784314 rgBT /Overloc	1.3	19
533	Temporal Regulation of the Bacillus subtilis Acetylome and Evidence for a Role of MreB Acetylation in Cell Wall Growth. MSystems, 2016, 1, .	1.7	35
534	Quantitative Phosphoproteomic Study Reveals that Protein Kinase A Regulates Neural Stem Cell Differentiation Through Phosphorylation of Catenin Beta-1 and Glycogen Synthase Kinase 3Î². Stem Cells, 2016, 34, 2090-2101.	1.4	17
535	Nuclear PKC-Î¸ facilitates rapid transcriptional responses in human memory CD4+ T cells <i>via</i> p65 and H2B phosphorylation. Journal of Cell Science, 2016, 129, 2448-61.	1.2	11
536	PHLPPing through history: a decade in the life of PHLPP phosphatases. Biochemical Society Transactions, 2016, 44, 1675-1682.	1.6	73
537	PTM Tracker: A system for determining trends of PTM modification sites relative to protein domains. , 2016, , .		0
538	A disease module detection algorithm for lung adenocarcinoma tumor network with significance of connections and network controllability methodology. , 2016, , .		1
539	Endocytosis of Cargo Proteins: LDL. , 2016, , 418-432.		0
540	Phosphoproteomics: Approaches, Developments, and Challenges. , 2016, , 177-186.		4
541	PredPhos: an ensemble framework for structure-based prediction of phosphorylation sites. Journal of Biological Research, 2016, 23, 12.	2.2	11
542	Quantitative deep mapping of the cultured podocyte proteome uncovers shifts in proteostatic mechanisms during differentiation. American Journal of Physiology - Cell Physiology, 2016, 311, C404-C417.	2.1	31

#	ARTICLE	IF	CITATIONS
543	Characterization and phosphoproteomic analysis of a human immortalized podocyte model of Fabry disease generated using CRISPR/Cas9 technology. American Journal of Physiology - Renal Physiology, 2016, 311, F1015-F1024.	1.3	19
544	Driver gene classification reveals a substantial overrepresentation of tumor suppressors among very large chromatin-regulating proteins. Scientific Reports, 2016, 6, 38988.	1.6	22
545	Quantitative profiling of spreading-coupled protein tyrosine phosphorylation in migratory cells. Scientific Reports, 2016, 6, 31811.	1.6	6
546	Modern Proteomics â€“ Sample Preparation, Analysis and Practical Applications. Advances in Experimental Medicine and Biology, 2016, , .	0.8	13
547	Identification, Quantification, and Site Localization of Protein Posttranslational Modifications via Mass Spectrometry-Based Proteomics. Advances in Experimental Medicine and Biology, 2016, 919, 345-382.	0.8	51
548	Pooledâ€matrix protein interaction screens using Barcode Fusion Genetics. Molecular Systems Biology, 2016, 12, 863.	3.2	102
549	The exploration of network motifs as potential drug targets from post-translational regulatory networks. Scientific Reports, 2016, 6, 20558.	1.6	13
550	Prioritizing functional phosphorylation sites based on multiple feature integration. Scientific Reports, 2016, 6, 24735.	1.6	30
551	Regulation of divalent metal transporter-1 by serine phosphorylation. Biochemical Journal, 2016, 473, 4243-4254.	1.7	15
552	A tale of two paralogs: human Transformer2 proteins with differential RNA-binding affinities. Journal of Biomolecular Structure and Dynamics, 2016, 34, 1979-1986.	2.0	5
553	Deep Proteomics of Breast Cancer Cells Reveals that Metformin Rewires Signaling Networks Away from a Pro-growth State. Cell Systems, 2016, 2, 159-171.	2.9	76
554	A metabolic labeling approach for glycoproteomic analysis reveals altered glycoprotein expression upon GALNT3 knockdown in ovarian cancer cells. Journal of Proteomics, 2016, 145, 91-102.	1.2	21
555	Global-scale profiling of differential expressed lysine acetylated proteins in colorectal cancer tumors and paired liver metastases. Journal of Proteomics, 2016, 142, 24-32.	1.2	28
556	Post-Translational Modifications in sperm Proteome: The Chemistry of Proteome diversifications in the Pathophysiology of male factor infertility. Biochimica Et Biophysica Acta - General Subjects, 2016, 1860, 1450-1465.	1.1	57
557	Poly-ubiquitination in TNFR1-mediated necroptosis. Cellular and Molecular Life Sciences, 2016, 73, 2165-2176.	2.4	130
558	Controllability analysis of the directed human protein interaction network identifies disease genes and drug targets. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 4976-4981.	3.3	249
559	Quantitative phosphoproteomics-based molecular network description for high-resolution kinase-substrate interactome analysis. Bioinformatics, 2016, 32, 2083-2088.	1.8	18
560	AGC1/2, the mitochondrial aspartate-glutamate carriers. Biochimica Et Biophysica Acta - Molecular Cell Research, 2016, 1863, 2394-2412.	1.9	72

#	Article	IF	Citations
561	Parallel Regulation of von Hippel-Lindau Disease by pVHL-Mediated Degradation of B-Myb and Hypoxia-Inducible Factor Î±. Molecular and Cellular Biology, 2016, 36, 1803-1817.	1.1	20
562	Structural aspects of small-molecule inhibition of methyllysine reader proteins. Future Medicinal Chemistry, 2016, 8, 1681-1702.	1.1	4
563	Nonhistone Lysine Methylation in the Regulation of Cancer Pathways. Cold Spring Harbor Perspectives in Medicine, 2016, 6, a026435.	2.9	98
564	Identification of Protein Kinase Substrates by the Kinaseâ€Interacting Substrate Screening (KISS) Approach. Current Protocols in Cell Biology, 2016, 72, 14.16.1-14.16.12.	2.3	8
565	Glycogen synthase kinase-3-mediated phosphorylation of serine 73 targets sterol response element binding protein-1c (SREBP-1c) for proteasomal degradation. Bioscience Reports, 2016, 36, e00284.	1.1	19
566	Combined Antibody/Lectin Enrichment Identifies Extensive Changes in the <i>O-</i>GlcNAc Sub-proteome upon Oxidative Stress. Journal of Proteome Research, 2016, 15, 4318-4336.	1.8	50
567	Global proteomic analysis of lysine acetylation in zebrafish (<i>Danio rerio</i>) embryos. Electrophoresis, 2016, 37, 3137-3145.	1.3	14
568	DHCR7: A vital enzyme switch between cholesterol and vitamin D production. Progress in Lipid Research, 2016, 64, 138-151.	5.3	120
569	Approaches to Study Phosphatases. ACS Chemical Biology, 2016, 11, 2944-2961.	1.6	73
570	K-CLASP: A Tool to Identify Phosphosite Specific Kinases and Interacting Proteins. ACS Chemical Biology, 2016, 11, 3251-3255.	1.6	17
571	Prediction of kinase-specific phosphorylation sites through an integrative model of protein context and sequence. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2016, 1864, 1599-1608.	1.1	16
572	Oâ€Glc<scp>NA</scp>cylation: a bridge between glucose and cell differentiation. Journal of Cellular and Molecular Medicine, 2016, 20, 769-781.	1.6	32
573	Multisite tyrosine phosphorylation of the Nâ€terminus of Mint1/X11Î± by Src kinase regulates the trafficking of amyloid precursor protein. Journal of Neurochemistry, 2016, 137, 518-527.	2.1	24
574	Live imaging of transforming growth factorâ€Î² activated kinase 1 activation in Lewis lung carcinoma 3<scp>LL</scp> cells implanted into syngeneic mice and treated with polyinosinic:polycytidylic acid. Cancer Science, 2016, 107, 644-652.	1.7	10
575	Phosphoproteomics to Characterize Host Response During Influenza A Virus Infection of Human Macrophages. Molecular and Cellular Proteomics, 2016, 15, 3203-3219.	2.5	66
576	Functional characterization of EI24-induced autophagy in the degradation of RING-domain E3 ligases. Autophagy, 2016, 12, 2038-2053.	4.3	28
577	Roles and regulation of protein phosphatase 2A (PP2A) in the heart. Journal of Molecular and Cellular Cardiology, 2016, 101, 127-133.	0.9	69
578	A phosphotyrosine switch regulates organic cation transporters. Nature Communications, 2016, 7, 10880.	5.8	100

#	Article	IF	Citations
579	Ultra-deep tyrosine phosphoproteomics enabled by a phosphotyrosine superbinder. Nature Chemical Biology, 2016, 12, 959-966.	3.9	141
580	The mitochondrial Ca2+ uniporter: regulation by auxiliary subunits and signal transduction pathways. American Journal of Physiology - Cell Physiology, 2016, 311, C67-C80.	2.1	24
581	Glucose-regulated and drug-perturbed phosphoproteome reveals molecular mechanisms controlling insulin secretion. Nature Communications, 2016, 7, 13250.	5.8	74
582	Phosphorylation of STAT2 on Serine-734 negatively regulates the IFNÎ±-induced antiviral response. Journal of Cell Science, 2016, 129, 4190-4199.	1.2	13
583	Coupling an EML4-ALKâ€"centric interactome with RNA interference identifies sensitizers to ALK inhibitors. Science Signaling, 2016, 9, rs12.	1.6	27
584	miR-625-3p regulates oxaliplatin resistance by targeting MAP2K6-p38 signalling in human colorectal adenocarcinoma cells. Nature Communications, 2016, 7, 12436.	5.8	82
585	Proteome-wide analysis of arginine monomethylation reveals widespread occurrence in human cells. Science Signaling, 2016, 9, rs9.	1.6	241
586	Protein Kinase C in Oncogenic Transformation and Cell Polarity. , 2016, , 529-588.		3
587	Identification of Protein Thiazolidination as a Novel Molecular Signature for Oxidative Stress and Formaldehyde Exposure. Chemical Research in Toxicology, 2016, 29, 1865-1871.	1.7	27
588	KAT2A/KAT2B-targeted acetylome reveals a role for PLK4 acetylation in preventing centrosome amplification. Nature Communications, 2016, 7, 13227.	5.8	84
589	Frequent mutations in acetylation and ubiquitination sites suggest novel driver mechanisms of cancer. Genome Medicine, 2016, 8, 55.	3.6	51
590	Endophenotype Network Models: Common Core of Complex Diseases. Scientific Reports, 2016, 6, 27414.	1.6	72
592	Quantitative Proteomics Reveals the Dynamics of Protein Phosphorylation in Human Bronchial Epithelial Cells during Internalization, Phagosomal Escape, and Intracellular Replication of <i>Staphylococcus aureus</i>. Journal of Proteome Research, 2016, 15, 4369-4386.	1.8	8
593	Network-based in silico drug efficacy screening. Nature Communications, 2016, 7, 10331.	5.8	394
594	Computational Methods in Mass Spectrometry-Based Proteomics. Advances in Experimental Medicine and Biology, 2016, 939, 63-89.	0.8	12
595	GlycoMinestruct: a new bioinformatics tool for highly accurate mapping of the human N-linked and O-linked glycoproteomes by incorporating structural features. Scientific Reports, 2016, 6, 34595.	1.6	69
596	EP4 Receptorâ€"Associated Protein in Macrophages Protects against Bleomycin-Induced Pulmonary Inflammation in Mice. Journal of Immunology, 2016, 197, 4436-4443.	0.4	7
597	A homology-based pipeline for global prediction of post-translational modification sites. Scientific Reports, 2016, 6, 25801.	1.6	4

#	Article	IF	Citations
598	A rapid and cost-effective fluorescence detection in tube (FDIT) method to analyze protein phosphorylation. Plant Methods, 2016, 12, 43.	1.9	14
599	The harmonizome: a collection of processed datasets gathered to serve and mine knowledge about genes and proteins. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw100.	1.4	1,085
600	Systems-wide Identification of cis-Regulatory Elements in Proteins. Cell Systems, 2016, 2, 89-100.	2.9	22
601	Structural Basis of the Recruitment of Ubiquitin-specific Protease USP15 by Spliceosome Recycling Factor SART3. Journal of Biological Chemistry, 2016, 291, 17283-17292.	1.6	24
602	ProVizâ€"a web-based visualization tool to investigate the functional and evolutionary features of protein sequences. Nucleic Acids Research, 2016, 44, W11-W15.	6.5	68
603	Large-scale profiling of protein kinases for cellular signaling studies by mass spectrometry and other techniques. Journal of Pharmaceutical and Biomedical Analysis, 2016, 130, 264-272.	1.4	10
604	A systematic exploration of the associations between amino acid variants and post-translational modifications. Neurocomputing, 2016, 206, 13-18.	3.5	1
605	Chemical genetic discovery of PARP targets reveals a role for PARP-1 in transcription elongation. Science, 2016, 353, 45-50.	6.0	302
606	ATRIP Deacetylation by SIRT2 Drives ATR Checkpoint Activation by Promoting Binding to RPA-ssDNA. Cell Reports, 2016, 14, 1435-1447.	2.9	54
607	Regulation of Platelet Derived Growth Factor Signaling by Leukocyte Common Antigen-related (LAR) Protein Tyrosine Phosphatase: A Quantitative Phosphoproteomics Study. Molecular and Cellular Proteomics, 2016, 15, 1823-1836.	2.5	10
608	Individualized network-based drug repositioning infrastructure for precision oncology in the panomics era. Briefings in Bioinformatics, 2016, 18, bbw051.	3.2	57
609	The deubiquitinase Usp27x stabilizes the <scp>BH</scp>3â€only protein Bim and enhances apoptosis. EMBO Reports, 2016, 17, 724-738.	2.0	40
610	Global quantitative analysis of phosphorylation underlying phencyclidine signaling and sensorimotor gating in the prefrontal cortex. Molecular Psychiatry, 2016, 21, 205-215.	4.1	13
611	Aberrant lysine acetylation in tumorigenesis: Implications in the development of therapeutics. , 2016, 162, 98-119.		65
612	Trans-Omics: How To Reconstruct Biochemical Networks Across Multiple â€˜Omicâ€™ Layers. Trends in Biotechnology, 2016, 34, 276-290.	4.9	221
613	Decreased N-TAF1 expression in X-Linked Dystonia-Parkinsonism patient-specific neural stem cells. DMM Disease Models and Mechanisms, 2016, 9, 451-62.	1.2	36
614	The Shp2-induced epithelial disorganization defect is reversed by HDAC6 inhibition independent of Cdc42. Nature Communications, 2016, 7, 10420.	5.8	6
615	Global proteomic analysis of protein acetylation affecting metabolic regulation in Daphnia pulex. Biochimie, 2016, 121, 219-227.	1.3	10

#	ARTICLE	IF	CITATIONS
616	Identification of Phosphorylation Consensus Sequences and Endogenous Neuronal Substrates of the Psychiatric Risk Kinase TNIK. Journal of Pharmacology and Experimental Therapeutics, 2016, 356, 410-423.	1.3	33
617	Effects of MacroH2A and H2A.Z on Nucleosome Dynamics as Elucidated by Molecular Dynamics Simulations. Biophysical Journal, 2016, 110, 327-337.	0.2	50
618	Structural basis for the regulatory role of the PPxY motifs in the thioredoxin-interacting protein TXNIP. Biochemical Journal, 2016, 473, 179-187.	1.7	36
619	Germline BAP1 Mutational Landscape of Asbestos-Exposed Malignant Mesothelioma Patients with Family History of Cancer. Cancer Research, 2016, 76, 206-215.	0.4	93
620	Mining Large Scale Tandem Mass Spectrometry Data for Protein Modifications Using Spectral Libraries. Journal of Proteome Research, 2016, 15, 721-731.	1.8	26
621	Evolution of disorder in Mediator complex and its functional relevance. Nucleic Acids Research, 2016, 44, 1591-1612.	6.5	55
622	Bioluminescent kinase strips: A novel approach to targeted and flexible kinase inhibitor profiling. Analytical Biochemistry, 2016, 495, 9-20.	1.1	6
623	A Phosphotyrosine Switch Controls the Association of Histone Mark Readers with Methylated Proteins. Biochemistry, 2016, 55, 1631-1634.	1.2	7
624	IKAP: A heuristic framework for inference of kinase activities from Phosphoproteomics data. Bioinformatics, 2016, 32, 424-431.	1.8	62
625	Slack sodium-activated potassium channel membrane expression requires p38 mitogen-activated protein kinase phosphorylation. Neuropharmacology, 2016, 103, 279-289.	2.0	8
626	Oncogenic Gene Fusion FGFR3-TACC3 Is Regulated by Tyrosine Phosphorylation. Molecular Cancer Research, 2016, 14, 458-469.	1.5	69
627	Regulation of peroxisome dynamics by phosphorylation. Biochimica Et Biophysica Acta - Molecular Cell Research, 2016, 1863, 1027-1037.	1.9	41
628	Quantitative Proteomics by Mass Spectrometry. Methods in Molecular Biology, 2016, 1410, v.	0.4	6
629	The phosphoproteome of human Jurkat T cell clones upon costimulation with anti-CD3/anti-CD28 antibodies. Journal of Proteomics, 2016, 131, 190-198.	1.2	19
630	Extended-Synaptotagmins (E-Syts); the extended story. Pharmacological Research, 2016, 107, 48-56.	3.1	23
631	Deubiquitylation of Protein Cargo Is Not an Essential Step in Exosome Formation. Molecular and Cellular Proteomics, 2016, 15, 1556-1571.	2.5	49
632	The current state of the art of quantitative phosphoproteomics and its applications to diabetes research. Expert Review of Proteomics, 2016, 13, 421-433.	1.3	26
633	Uncovering Phosphorylation-Based Specificities through Functional Interaction Networks. Molecular and Cellular Proteomics, 2016, 15, 236-245.	2.5	68

#	ARTICLE	IF	CITATIONS
634	Evidence supporting a critical contribution of intrinsically disordered regions to the biochemical behavior of full-length human HP1Î³. Journal of Molecular Modeling, 2016, 22, 12.	0.8	16
635	Identification of significantly mutated regions across cancer types highlights a rich landscape of functional molecular alterations. Nature Genetics, 2016, 48, 117-125.	9.4	80
636	Immobilized Metal Affinity Chromatography Coupled to Multiple Reaction Monitoring Enables Reproducible Quantification of Phospho-signaling. Molecular and Cellular Proteomics, 2016, 15, 726-739.	2.5	46
637	The upstreams and downstreams of H3K79 methylation by DOT1L. Chromosoma, 2016, 125, 593-605.	1.0	86
638	Characterization of Ambra1 in asexual cycle of a non-vertebrate chordate, the colonial tunicate Botryllus schlosseri, and phylogenetic analysis of the protein group in Bilateria. Molecular Phylogenetics and Evolution, 2016, 95, 46-57.	1.2	5
639	Exploring the phosphoproteome profiles duringXenopusegg activation by calcium stimulation using a fully automated phosphopeptide purification system. Journal of Biochemistry, 2016, 159, 407-419.	0.9	1
640	Proteomic analysis of O-GlcNAcylated proteins in invasive ductal breast carcinomas with and without lymph node metastasis. Amino Acids, 2016, 48, 365-374.	1.2	18
641	Regulation of RIPK1's cell death function by phosphorylation. Cell Cycle, 2016, 15, 5-6.	1.3	16
642	Changes in Protein Expression and Lysine Acetylation Induced by Decreased Glutathione Levels in Astrocytes. Molecular and Cellular Proteomics, 2016, 15, 493-505.	2.5	16
643	Phosphoproteomics in the Age of Rapid and Deep Proteome Profiling. Analytical Chemistry, 2016, 88, 74-94.	3.2	217
644	Advances in computational approaches for prioritizing driver mutations and significantly mutated genes in cancer genomes. Briefings in Bioinformatics, 2016, 17, 642-656.	3.2	120
645	The role of Plk3 in oncogenesis. Oncogene, 2016, 35, 135-147.	2.6	79
646	An Efficient Semi-supervised Learning Approach to Predict SH2 Domain Mediated Interactions. Methods in Molecular Biology, 2017, 1555, 83-97.	0.4	0
647	Polyanhydride Nanoparticle Interactions with Host Serum Proteins and Their Effects on Bone Marrow Derived Macrophage Activation. ACS Biomaterials Science and Engineering, 2017, 3, 160-168.	2.6	7
648	ESA-UbiSite: accurate prediction of human ubiquitination sites by identifying a set of effective negatives. Bioinformatics, 2017, 33, 661-668.	1.8	37
649	S.Âpombe Uba1-Ubc15 Structure Reveals a Novel Regulatory Mechanism of Ubiquitin E2 Activity. Molecular Cell, 2017, 65, 699-714.e6.	4.5	40
650	O-GlcNAcylation of STAT5 controls tyrosine phosphorylation and oncogenic transcription in STAT5-dependent malignancies. Leukemia, 2017, 31, 2132-2142.	3.3	47
651	SH2 Domains. Methods in Molecular Biology, 2017, , .	0.4	1

#	ARTICLE	IF	CITATIONS
652	Extracellular Signal-Regulated Kinases 1 and 2 Phosphorylate Gab2 To Promote a Negative-Feedback Loop That Attenuates Phosphoinositide 3-Kinase/Akt Signaling. Molecular and Cellular Biology, 2017, 37, .	1.1	17
653	Stress-induced O-GlcNAcylation: an adaptive process of injured cells. Biochemical Society Transactions, 2017, 45, 237-249.	1.6	89
654	Technological advances for interrogating the human kinome. Biochemical Society Transactions, 2017, 45, 65-77.	1.6	26
655	The nonreceptor tyrosine kinase c-Src attenuates SCF(Î²-TrCP) E3-ligase activity abrogating Taz proteasomal degradation. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 1678-1683.	3.3	42
656	Decreased Mitochondrial Pyruvate Transport Activity in the Diabetic Heart. Journal of Biological Chemistry, 2017, 292, 4423-4433.	1.6	44
657	Hormonally up-regulated neu-associated kinase: A novel target for breast cancer progression. Pharmacological Research, 2017, 119, 188-194.	3.1	5
658	Multiplexed Phosphoproteomic Profiling Using Titanium Dioxide and Immunoaffinity Enrichments Reveals Complementary Phosphorylation Events. Journal of Proteome Research, 2017, 16, 1506-1514.	1.8	52
659	The SUV39H1 Protein Lysine Methyltransferase Methylates Chromatin Proteins Involved in Heterochromatin Formation and VDJ Recombination. ACS Chemical Biology, 2017, 12, 958-968.	1.6	26
660	Regulation of DENND3, the exchange factor for the small GTPase Rab12 through an intramolecular interaction. Journal of Biological Chemistry, 2017, 292, 7274-7282.	1.6	20
661	Peroxisomes. Methods in Molecular Biology, 2017, , .	0.4	3
662	Identification of protein features encoded by alternative exons using Exon Ontology. Genome Research, 2017, 27, 1087-1097.	2.4	45
663	Study of Peroxisomal Protein Phosphorylation by Functional Proteomics. Methods in Molecular Biology, 2017, 1595, 267-289.	0.4	3
664	Tspan2: a tetraspanin protein involved in oligodendrogenesis and cancer metastasis. Biochemical Society Transactions, 2017, 45, 465-475.	1.6	29
665	Hyper-O-GlcNAcylation activates nuclear factor Îº-light-chain-enhancer of activated B cells (NF-ÎºB) signaling through interplay with phosphorylation and acetylation. Journal of Biological Chemistry, 2017, 292, 9150-9163.	1.6	53
666	Assessment of roles for the Rho-specific guanine nucleotide dissociation inhibitor Ly-GDI in platelet function: a spatial systems approach. American Journal of Physiology - Cell Physiology, 2017, 312, C527-C536.	2.1	21
667	Into the linker's DENN: A tyrosine's control of autophagy. Journal of Biological Chemistry, 2017, 292, 7283-7284.	1.6	11
668	Phosphoproteome Analysis Reveals Differential Mode of Action of Sorafenib in Wildtype and Mutated FLT3 Acute Myeloid Leukemia (AML) Cells. Molecular and Cellular Proteomics, 2017, 16, 1365-1376.	2.5	8
669	A Proteomic Approach to Analyze the Aspirin-mediated Lysine Acetylome. Molecular and Cellular Proteomics, 2017, 16, 310-326.	2.5	45

#	ARTICLE	IF	CITATIONS
670	Methylation of human eukaryotic elongation factor alpha (eEF1A) by a member of a novel protein lysine methyltransferase family modulates mRNA translation. Nucleic Acids Research, 2017, 45, 8239-8254.	6.5	44
671	Argininosuccinate synthase 1 is an intrinsic Akt repressor transactivated by p53. Science Advances, 2017, 3, e1603204.	4.7	40
672	Site-specific incorporation of phosphotyrosine using an expanded genetic code. Nature Chemical Biology, 2017, 13, 842-844.	3.9	82
673	Hepatitis B virus X proteinâ€“elevated MSL2 modulates hepatitis B virus covalently closed circular DNA by inducing degradation of APOBEC3B to enhance hepatocarcinogenesis. Hepatology, 2017, 66, 1413-1429.	3.6	50
674	Tissue-Specific Signaling Networks Rewired by Major Somatic Mutations in Human Cancer Revealed by Proteome-Wide Discovery. Cancer Research, 2017, 77, 2810-2821.	0.4	29
675	SIRT4 Is a Lysine Deacylase that Controls Leucine Metabolism and Insulin Secretion. Cell Metabolism, 2017, 25, 838-855.e15.	7.2	259
676	Architecture and mechanism of the central gear in an ancient molecular timer. Journal of the Royal Society Interface, 2017, 14, 20161065.	1.5	7
677	PTMOracle: A Cytoscape App for Covisualizing and Coanalyzing Post-Translational Modifications in Protein Interaction Networks. Journal of Proteome Research, 2017, 16, 1988-2003.	1.8	17
678	SCFFBXO17 E3 ligase modulates inflammation by regulating proteasomal degradation of glycogen synthase kinase-3Î² in lung epithelia. Journal of Biological Chemistry, 2017, 292, 7452-7461.	1.6	25
679	Deciphering the Acute Cellular Phosphoproteome Response to Irradiation with X-rays, Protons and Carbon Ions. Molecular and Cellular Proteomics, 2017, 16, 855-872.	2.5	27
680	Engineering Small Molecule Responsive Split Protein Kinases. Methods in Molecular Biology, 2017, 1596, 307-319.	0.4	0
681	Insights regarding fungal phosphoproteomic analysis. Fungal Genetics and Biology, 2017, 104, 38-44.	0.9	6
682	Collapsin response mediator protein 2: high-resolution crystal structure sheds light on small-molecule binding, post-translational modifications, and conformational flexibility. Amino Acids, 2017, 49, 747-759.	1.2	22
683	Proteome-Scale Investigation of Protein Allosteric Regulation Perturbed by Somatic Mutations in 7,000 Cancer Genomes. American Journal of Human Genetics, 2017, 100, 5-20.	2.6	72
684	Impaired liver regeneration in aged mice can be rescued by silencing Hippo core kinases MST1 and MST2. EMBO Molecular Medicine, 2017, 9, 46-60.	3.3	98
685	Age-Dependent Effects of Acute Alcohol Administration in the Hippocampal Phosphoproteome. Chemical Research in Toxicology, 2017, 30, 2165-2173.	1.7	5
686	Site-specific identification and quantitation of endogenous SUMO modifications under native conditions. Nature Communications, 2017, 8, 1171.	5.8	92
687	Sendai virus recruits cellular villin to remodel actin cytoskeleton during fusion with hepatocytes. Molecular Biology of the Cell, 2017, 28, 3801-3814.	0.9	6

#	Article	IF	Citations
688	Phosphoproteomics Profiling of Nonsmall Cell Lung Cancer Cells Treated with a Novel Phosphatase Activator. Proteomics, 2017, 17, 1700214.	1.3	21
689	Strategy Based on Deglycosylation, Multiprotease, and Hydrophilic Interaction Chromatography for Large-Scale Profiling of Protein Methylation. Analytical Chemistry, 2017, 89, 12909-12917.	3.2	24
690	MAPPIN: a method for annotating, predicting pathogenicity and mode of inheritance for nonsynonymous variants. Nucleic Acids Research, 2017, 45, 10393-10402.	6.5	15
691	Regulation of mitosis-meiosis transition by the ubiquitin ligase Î²-TrCP in male germ cells. Development (Cambridge), 2017, 144, 4137-4147.	1.2	17
692	Bonding-induced emission of silyl-protected copper nanoclusters for luminescence turn-on detection of trace water in organic solvents. Analyst, The, 2017, 142, 4613-4617.	1.7	28
693	Recent advances in phosphoproteomics and application to neurological diseases. Analyst, The, 2017, 142, 4373-4387.	1.7	33
694	Alternative splicing discriminates molecular subtypes and has prognostic impact in diffuse large B-cell lymphoma. Blood Cancer Journal, 2017, 7, e596-e596.	2.8	14
695	Systematic and Quantitative Assessment of Hydrogen Peroxide Reactivity With Cysteines Across Human Proteomes. Molecular and Cellular Proteomics, 2017, 16, 1815-1828.	2.5	61
696	Defining Human Tyrosine Kinase Phosphorylation Networks Using Yeast as an In Vivo Model Substrate. Cell Systems, 2017, 5, 128-139.e4.	2.9	20
697	Identification of Missing Proteins in the Phosphoproteome of Kidney Cancer. Journal of Proteome Research, 2017, 16, 4364-4373.	1.8	19
698	eIF4B phosphorylation at Ser504 links synaptic activity with protein translation in physiology and pathology. Scientific Reports, 2017, 7, 10563.	1.6	14
699	Uncovering human METTL12 as a mitochondrial methyltransferase that modulates citrate synthase activity through metabolite-sensitive lysine methylation. Journal of Biological Chemistry, 2017, 292, 17950-17962.	1.6	27
700	Dual Specificity Phosphatase 5â€Substrate Interaction: A Mechanistic Perspective. , 2017, 7, 1449-1461.		16
701	Phosphoproteome-based kinase activity profiling reveals the critical role of MAP2K2 and PLK1 in neuronal autophagy. Autophagy, 2017, 13, 1969-1980.	4.3	48
702	PP2A-Bâ€² holoenzyme substrate recognition, regulation and role in cytokinesis. Cell Discovery, 2017, 3, 17027.	3.1	68
703	Using ALoFT to determine the impact of putative loss-of-function variants in protein-coding genes. Nature Communications, 2017, 8, 382.	5.8	40
704	PhosphoPredict: A bioinformatics tool for prediction of human kinase-specific phosphorylation substrates and sites by integrating heterogeneous feature selection. Scientific Reports, 2017, 7, 6862.	1.6	72
705	A compendium of ERK targets. FEBS Letters, 2017, 591, 2607-2615.	1.3	128

#	ARTICLE	IF	CITATIONS
706	MusiteDeep: a deep-learning framework for general and kinase-specific phosphorylation site prediction. Bioinformatics, 2017, 33, 3909-3916.	1.8	205
707	MARCKS-related protein regulates cytoskeletal organization at cell-cell and cell-substrate contacts in epithelial cells. Journal of Cell Science, 2018, 131, .	1.2	7
708	Quantitative Phosphoproteomics Reveals a Role for Collapsin Response Mediator Protein 2 in PDGF-Induced Cell Migration. Scientific Reports, 2017, 7, 3970.	1.6	8
709	Transgelin-2: A potential oncogenic factor. Tumor Biology, 2017, 39, 101042831770265.	0.8	31
710	Linking functions: an additional role for an intrinsically disordered linker domain in the transcriptional coactivator CBP. Scientific Reports, 2017, 7, 4676.	1.6	39
711	Genotype-phenotype evaluation of MED13L defects in the light of a novel truncating and a recurrent missense mutation. European Journal of Medical Genetics, 2017, 60, 451-464.	0.7	34
712	In silico re-identification of properties of drug target proteins. BMC Bioinformatics, 2017, 18, 248.	1.2	26
713	GLADIATOR: a global approach for elucidating disease modules. Genome Medicine, 2017, 9, 48.	3.6	23
714	The KSEA App: a web-based tool for kinase activity inference from quantitative phosphoproteomics. Bioinformatics, 2017, 33, 3489-3491.	1.8	181
715	Regulation of mRNA capping in the cell cycle. RNA Biology, 2017, 14, 11-14.	1.5	15
716	Posttranslational Mechanisms of Zinc Signaling. , 2017, , 273-281.		1
717	Multi-OMIC profiling of survival and metabolic signaling networks in cells subjected to photodynamic therapy. Cellular and Molecular Life Sciences, 2017, 74, 1133-1151.	2.4	34
718	Phosphorylation regulates activity of 7-dehydrocholesterol reductase (DHCR7), a terminal enzyme of cholesterol synthesis. Journal of Steroid Biochemistry and Molecular Biology, 2017, 165, 363-368.	1.2	26
719	Molecular property diagnostic suite (MPDS): Development of disease-specific open source web portals for drug discovery. SAR and QSAR in Environmental Research, 2017, 28, 913-926.	1.0	11
720	Emerging and Diverse Functions of the EphA2 Noncanonical Pathway in Cancer Progression. Biological and Pharmaceutical Bulletin, 2017, 40, 1616-1624.	0.6	60
721	Mechanisms for DNAâ€'damaging agentâ€'induced inactivation of ErbB2 and ErbB3 via the ERK and p38 signaling pathways. Oncology Letters, 2018, 15, 1758-1762.	0.8	2
722	Protein Kinase CK2: Intricate Relationships within Regulatory Cellular Networks. Pharmaceuticals, 2017, 10, 27.	1.7	84
723	A Comprehensive Gene Expression Meta-analysis Identifies Novel Immune Signatures in Rheumatoid Arthritis Patients. Frontiers in Immunology, 2017, 8, 74.	2.2	35

#	ARTICLE	IF	CITATIONS
724	Interplay between Janus Kinase/Signal Transducer and Activator of Transcription Signaling Activated by Type I Interferons and Viral Antagonism. Frontiers in Immunology, 2017, 8, 1758.	2.2	106
725	A Novel Phosphorylation Site-Kinase Network-Based Method for the Accurate Prediction of Kinase-Substrate Relationships. BioMed Research International, 2017, 2017, 1-11.	0.9	9
726	The ESRP1-GPR137 axis contributes to intestinal pathogenesis. ELife, 2017, 6, .	2.8	24
727	Constitutive and activation-dependent phosphorylation of lymphocyte phosphatase-associated phosphoprotein (LPAP). PLoS ONE, 2017, 12, e0182468.	1.1	10
728	PRmePRed: A protein arginine methylation prediction tool. PLoS ONE, 2017, 12, e0183318.	1.1	28
729	Recent Advances in Substrate Identification of Protein Kinases in Plants and Their Role in Stress Management. Current Genomics, 2017, 18, 523-541.	0.7	3
731	Co-occurring protein phosphorylation are functionally associated. PLoS Computational Biology, 2017, 13, e1005502.	1.5	26
732	The M-phase specific hyperphosphorylation of Staufen2 involved the cyclin-dependent kinase CDK1. BMC Cell Biology, 2017, 18, 25.	3.0	4
733	Inferring Methionine Sulfoxidation and serine Phosphorylation crosstalk from Phylogenetic analyses. BMC Evolutionary Biology, 2017, 17, 171.	3.2	4
734	Structural prediction of the interaction of the tumor suppressor p27KIP1 with cyclin A/CDK2 identifies a novel catalytically relevant determinant. BMC Bioinformatics, 2017, 18, 15.	1.2	5
735	LiverWiki: a wiki-based database for human liver. BMC Bioinformatics, 2017, 18, 452.	1.2	4
736	SLiMSearch: a framework for proteome-wide discovery and annotation of functional modules in intrinsically disordered regions. Nucleic Acids Research, 2017, 45, W464-W469.	6.5	87
737	Protein kinase C: perfectly balanced. Critical Reviews in Biochemistry and Molecular Biology, 2018, 53, 208-230.	2.3	207
738	<i>O</i>-GlcNAc Transferase Recognizes Protein Substrates Using an Asparagine Ladder in the Tetratricopeptide Repeat (TPR) Superhelix. Journal of the American Chemical Society, 2018, 140, 3510-3513.	6.6	79
739	A proteomics landscape of circadian clock in mouse liver. Nature Communications, 2018, 9, 1553.	5.8	115
740	Pseudotargeted MS Method for the Sensitive Analysis of Protein Phosphorylation in Protein Complexes. Analytical Chemistry, 2018, 90, 6214-6221.	3.2	14
741	Phosphorylation of xeroderma pigmentosum group C regulates ultraviolet-induced DNA damage repair. Nucleic Acids Research, 2018, 46, 5050-5060.	6.5	17
742	Berberine induced modulation of PHLPP2-Akt-MST1 kinase signaling is coupled with mitochondrial impairment and hepatoma cell death. Toxicology and Applied Pharmacology, 2018, 347, 92-103.	1.3	14

#	ARTICLE	IF	CITATIONS
743	Impact of the Anticancer Drug NT157 on Tyrosine Kinase Signaling Networks. Molecular Cancer Therapeutics, 2018, 17, 931-942.	1.9	15
744	A single Nâ€terminal phosphomimic disrupts TDPâ€43 polymerization, phase separation, and RNA splicing. EMBO Journal, 2018, 37, .	3.5	297
745	O-GlcNAcPRED-II: an integrated classification algorithm for identifying O-GlcNAcylation sites based on fuzzy undersampling and a <i>K</i>-means PCA oversampling technique. Bioinformatics, 2018, 34, 2029-2036.	1.8	128
746	Glycogen synthase kinaseâ€3Î² regulation: another kinase gets in on the AKT. FEBS Letters, 2018, 592, 535-536.	1.3	1
747	Identifying Novel Signaling Pathways: An Exercise Scientists Guide to Phosphoproteomics. Exercise and Sport Sciences Reviews, 2018, 46, 76-85.	1.6	5
748	Gene Network Analysis of Interstitial Macrophages After Treatment with Induced Pluripotent Stem Cells Secretome (iPSC-cm) in the Bleomycin Injured Rat Lung. Stem Cell Reviews and Reports, 2018, 14, 412-424.	5.6	14
749	Measuring phenotype-phenotype similarity through the interactome. BMC Bioinformatics, 2018, 19, 114.	1.2	32
750	Computational Prediction of Protein O-GlcNAc Modification. Methods in Molecular Biology, 2018, 1754, 235-246.	0.4	5
751	Systematic characterization of panâ€cancer mutation clusters. Molecular Systems Biology, 2018, 14, e7974.	3.2	39
752	Small proline-rich protein 2B drives stress-dependent p53 degradation and fibroblast proliferation in heart failure. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3436-E3445.	3.3	30
753	Mining protein phosphorylation information from biomedical literature using NLP parsing and Support Vector Machines. Computer Methods and Programs in Biomedicine, 2018, 160, 57-64.	2.6	4
754	Regulation of the Hsp90 system. Biochimica Et Biophysica Acta - Molecular Cell Research, 2018, 1865, 889-897.	1.9	48
755	<i>In situ</i> simultaneous profiling of phosphorylation and ubiquitination by single excitation-duplexed luminescence resonance energy transfer. Chemical Communications, 2018, 54, 3648-3651.	2.2	4
756	Vertebrate GAF/ThPOK: emerging functions in chromatin architecture and transcriptional regulation. Cellular and Molecular Life Sciences, 2018, 75, 623-633.	2.4	13
757	Transcriptional and post-translational regulation of Arc in synaptic plasticity. Seminars in Cell and Developmental Biology, 2018, 77, 3-9.	2.3	35
758	Src homology 2 domains enhance tyrosine phosphorylation in vivo by protecting binding sites in their target proteins from dephosphorylation. Journal of Biological Chemistry, 2018, 293, 623-637.	1.6	23
759	Multivalent Interactions with Fbw7 and Pin1 Facilitate Recognition of c-Jun by the SCFFbw7 Ubiquitin Ligase. Structure, 2018, 26, 28-39.e2.	1.6	29
760	Integrating Protein Localization with Automated Signaling Pathway Reconstruction. , 2018, , .		1

#	ARTICLE	IF	CITATIONS
761	Critical observations that shaped our understanding of the function(s) of intracellular glycosylation (Oâ€Glc<scp>NA</scp>c). FEBS Letters, 2018, 592, 3950-3975.	1.3	38
762	SignaLink: Multilayered Regulatory Networks. Methods in Molecular Biology, 2018, 1819, 53-73.	0.4	17
763	Engineering Improved Antiphosphotyrosine Antibodies Based on an Immunoconvergent Binding Motif. Journal of the American Chemical Society, 2018, 140, 16615-16624.	6.6	20
764	A resource of variant effect predictions of single nucleotide variants in model organisms. Molecular Systems Biology, 2018, 14, e8430.	3.2	84
765	Systematic characterization and prediction of post-translational modification cross-talk between proteins. Bioinformatics, 2019, 35, 2626-2633.	1.8	12
766	Single-Cell Imaging of Metastatic Potential of Cancer Cells. IScience, 2018, 10, 53-65.	1.9	20
767	SETting up Methylation in Mammalian Cells: Role of Histone Methyltransferases in Disease and Development. , 2018, , 197-258.		0
768	Lysine Acetylation Regulates Alanyl-tRNA Synthetase Activity in Escherichia coli. Genes, 2018, 9, 473.	1.0	10
769	Multiple phosphorylation sites on Î³â€tubulin are essential and contribute to the biogenesis of basal bodies in <i>Tetrahymena</i>. Journal of Cellular Physiology, 2018, 233, 8648-8665.	2.0	4
770	Application of Proteomics Technologies in Oil Palm Research. Protein Journal, 2018, 37, 473-499.	0.7	7
771	Phosphoregulation of the intracellular termini of K+-Clâˆ' cotransporter 2 (KCC2) enables flexible control of its activity. Journal of Biological Chemistry, 2018, 293, 16984-16993.	1.6	22
772	Role of novel histone modifications in cancer. Oncotarget, 2018, 9, 11414-11426.	0.8	88
773	Substrate priming enhances phosphorylation by the budding yeast kinases Kin1 and Kin2. Journal of Biological Chemistry, 2018, 293, 18353-18364.	1.6	3
774	SUMOgo: Prediction of sumoylation sites on lysines by motif screening models and the effects of various post-translational modifications. Scientific Reports, 2018, 8, 15512.	1.6	28
775	Oncogenic activation of PI3K induces progenitor cell differentiation to suppress epidermal growth. Nature Cell Biology, 2018, 20, 1256-1266.	4.6	45
776	Src kinase phosphorylates Notch1 to inhibit MAML binding. Scientific Reports, 2018, 8, 15515.	1.6	15
777	Dynamic disulfide exchange in a crystallin protein in the human eye lens promotes cataract-associated aggregation. Journal of Biological Chemistry, 2018, 293, 17997-18009.	1.6	49
779	Exome-wide analysis identifies three low-frequency missense variants associated with pancreatic cancer risk in Chinese populations. Nature Communications, 2018, 9, 3688.	5.8	32

#	ARTICLE	IF	CITATIONS
780	Systems-wide Analysis of Serine ADP-Ribosylation Reveals Widespread Occurrence and Site-Specific Overlap with Phosphorylation. Cell Reports, 2018, 24, 2493-2505.e4.	2.9	123
781	CPSNF: Classification of Protein Structure with Novel Features. , 2018, , .		0
782	IPSNN: Identification of Protein Structure based Neural Network. , 2018, , .		0
783	ActiveDriverDB: human disease mutations and genome variation in post-translational modification sites of proteins. Nucleic Acids Research, 2018, 46, D901-D910.	6.5	82
784	Structural basis of O-GlcNAc recognition by mammalian 14-3-3 proteins. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 5956-5961.	3.3	50
785	Integration of protein phosphorylation, acetylation, and methylation data sets to outline lung cancer signaling networks. Science Signaling, 2018, 11, .	1.6	40
786	Network-Based Disease Module Discovery by a Novel Seed Connector Algorithm with Pathobiological Implications. Journal of Molecular Biology, 2018, 430, 2939-2950.	2.0	41
787	Differentially expressed novel alternatively spliced transcript variant of tumor suppressor Stk11 gene in mouse. Gene, 2018, 668, 146-154.	1.0	5
788	Cisplatinâ€‘induced nonâ€‘canonical endocytosis of EGFR via p38 phosphorylation of the Câ€‘terminal region containing Serâ€‘1015 in nonâ€‘small cell lung cancer cells. Oncology Letters, 2018, 15, 9251-9256.	0.8	10
789	Pi-Pi contacts are an overlooked protein feature relevant to phase separation. ELife, 2018, 7, .	2.8	571
790	Site-specific characterization of endogenous SUMOylation across species and organs. Nature Communications, 2018, 9, 2456.	5.8	139
791	Identification and expression of alternatively spliced novel isoforms of cancer associated MYD88 lacking death domain in mouse. Molecular Biology Reports, 2018, 45, 699-711.	1.0	6
792	EGF Regulates the Interaction of Tks4 with Src through Its SH2 and SH3 Domains. Biochemistry, 2018, 57, 4186-4196.	1.2	17
793	EviNet: a web platform for network enrichment analysis with flexible definition of gene sets. Nucleic Acids Research, 2018, 46, W163-W170.	6.5	22
794	Cofilin and profilin: partners in cancer aggressiveness. Biophysical Reviews, 2018, 10, 1323-1335.	1.5	39
795	Phosphorylation of synaptic GTPase-activating protein (synGAP) by polo-like kinase (Plk2) alters the ratio of its GAP activity toward HRas, Rap1 and Rap2 GTPases. Biochemical and Biophysical Research Communications, 2018, 503, 1599-1604.	1.0	14
796	PhoPepMass: A database and search tool assisting human phosphorylation peptide identification from mass spectrometry data. Journal of Genetics and Genomics, 2018, 45, 381-388.	1.7	1
797	Evaluation of functionality for serine and threonine phosphorylation with different evolutionary ages in human and mouse. BMC Genomics, 2018, 19, 431.	1.2	9

#	ARTICLE	IF	CITATIONS
798	Connexin43 Carboxyl-Terminal Domain Directly Interacts with Î²-Catenin. International Journal of Molecular Sciences, 2018, 19, 1562.	1.8	28
799	Radio-sensitizing effects of VE-821 and beyond: Distinct phosphoproteomic and metabolomic changes after ATR inhibition in irradiated MOLT-4 cells. PLoS ONE, 2018, 13, e0199349.	1.1	8
800	Proximal Pathway Enrichment Analysis for Targeting Comorbid Diseases via Network Endopharmacology. Pharmaceuticals, 2018, 11, 61.	1.7	32
801	KSIBW: Predicting Kinase-Substrate Interactions Based on Bi-random Walk. Lecture Notes in Computer Science, 2018, , 151-162.	1.0	0
802	Î²-Amyloid Induces Pathology-Related Patterns of Tau Hyperphosphorylation at Synaptic Terminals. Journal of Neuropathology and Experimental Neurology, 2018, 77, 814-826.	0.9	46
803	Affinity switching of the LEDGF/p75 IBD interactome is governed by kinase-dependent phosphorylation. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E7053-E7062.	3.3	27
804	An integrative functional genomics framework for effective identification of novel regulatory variants in genomeâ€“phenome studies. Genome Medicine, 2018, 10, 7.	3.6	29
805	Protein phosphatase 2A is crucial for sarcomere organization in<i>Caenorhabditis elegans</i>striated muscle. Molecular Biology of the Cell, 2018, 29, 2084-2097.	0.9	14
806	Discerning evolutionary trends in post-translational modification and the effect of intrinsic disorder: Analysis of methylation, acetylation and ubiquitination sites in human proteins. PLoS Computational Biology, 2018, 14, e1006349.	1.5	31
807	PTM-ssMP: A Web Server for Predicting Different Types of Post-translational Modification Sites Using Novel Site-specific Modification Profile. International Journal of Biological Sciences, 2018, 14, 946-956.	2.6	45
808	A Methodological Assessment and Characterization of Genetically-Driven Variation in Three Human Phosphoproteomes. Scientific Reports, 2018, 8, 12106.	1.6	2
809	Conservation of kinase-phosphorylation site pairings: Evidence for an evolutionarily dynamic phosphoproteome. PLoS ONE, 2018, 13, e0202036.	1.1	6
810	Genetic Analysis of Rare Human Variants of Regulators of G Protein Signaling Proteins and Their Role in Human Physiology and Disease. Pharmacological Reviews, 2018, 70, 446-474.	7.1	53
811	In vivo brain GPCR signaling elucidated by phosphoproteomics. Science, 2018, 360, .	6.0	105
812	Simultaneous precise editing of multiple genes in human cells. Nucleic Acids Research, 2019, 47, e116-e116.	6.5	85
813	Identification of lysine methylation in the core GTPase domain by GoMADScan. PLoS ONE, 2019, 14, e0219436.	1.1	6
814	A STAT3-based gene signature stratifies glioma patients for targeted therapy. Nature Communications, 2019, 10, 3601.	5.8	67
815	Proteomic Analysis of Lipid Rafts from RBL-2H3 Mast Cells. International Journal of Molecular Sciences, 2019, 20, 3904.	1.8	6

#	Article	IF	Citations
816	Phosphorylation of a serine/proline-rich motif in oxysterol binding protein-related protein 4L (ORP4L) regulates cholesterol and vimentin binding. PLoS ONE, 2019, 14, e0214768.	1.1	9
817	Phosphoproteomics reveals conserved exerciseâ€stimulated signaling and AMPK regulation of storeâ€operated calcium entry. EMBO Journal, 2019, 38, e102578.	3.5	54
818	Identification of candidate disease genes in patients with common variable immunodeficiency. Quantitative Biology, 2019, 7, 190-201.	0.3	2
819	Reconstructing signaling pathways using regular language constrained paths. Bioinformatics, 2019, 35, i624-i633.	1.8	7
820	Global view of the RAF-MEK-ERK module and its immediate downstream effectors. Scientific Reports, 2019, 9, 10865.	1.6	12
821	Interactome of the Autoimmune Risk Protein ANKRD55. Frontiers in Immunology, 2019, 10, 2067.	2.2	13
822	Wordsworth and Robespierre. Essays in Criticism, 2019, 69, 16-36.	0.0	0
823	Extracellular phosphorylation drives the formation of neuronal circuitry. Nature Chemical Biology, 2019, 15, 1035-1042.	3.9	22
824	N-GlycositeAtlas: a database resource for mass spectrometry-based human N-linked glycoprotein and glycosylation site mapping. Clinical Proteomics, 2019, 16, 35.	1.1	56
825	Post-translational Modifications of Nucleotide Excision Repair Proteins and Their Role in the DNA Repair. Biochemistry (Moscow), 2019, 84, 1008-1020.	0.7	12
826	The human organic cation transporter OCT1 and its role as a target for drug responses. Drug Metabolism Reviews, 2019, 51, 389-407.	1.5	18
827	T cell receptor signaling results in ERK-dependent Ser163 phosphorylation of lymphocyte phosphatase-associated phosphoprotein. Biochemical and Biophysical Research Communications, 2019, 519, 559-565.	1.0	0
828	Oncogenic Mutations Rewire Signaling Pathways by Switching Protein Recruitment to Phosphotyrosine Sites. Cell, 2019, 179, 543-560.e26.	13.5	65
829	De novo identification of essential protein domains from CRISPR-Cas9 tiling-sgRNA knockout screens. Nature Communications, 2019, 10, 4541.	5.8	44
830	Structural insights into the tyrosine phosphorylationâ€"mediated inhibition of SH3 domainâ€"ligand interactions. Journal of Biological Chemistry, 2019, 294, 4608-4620.	1.6	12
831	Illuminating the dark phosphoproteome. Science Signaling, 2019, 12, .	1.6	219
832	KSIMC: Predicting Kinaseâ€"Substrate Interactions Based on Matrix Completion. International Journal of Molecular Sciences, 2019, 20, 302.	1.8	3
833	iProteinDB: An Integrative Database of <i>Drosophila</i> Post-translational Modifications. G3: Genes, Genomes, Genetics, 2019, 9, 1-11.	0.8	24

#	Article	IF	Citations
834	Parathyroid hormone initiates dynamic NHERF1 phosphorylation cycling and conformational changes that regulate NPT2A-dependent phosphate transport. Journal of Biological Chemistry, 2019, 294, 4546-4571.	1.6	22
835	Research progress in protein posttranslational modification site prediction. Briefings in Functional Genomics, 2019, 18, 220-229.	1.3	39
836	DOC2B promotes insulin sensitivity in mice via a novel KLC1-dependent mechanism in skeletal muscle. Diabetologia, 2019, 62, 845-859.	2.9	17
837	Regulated Phosphosignaling Associated with Breast Cancer Subtypes and Druggability*. Molecular and Cellular Proteomics, 2019, 18, 1630-1650.	2.5	14
838	Human FAM173A is a mitochondrial lysine-specific methyltransferase that targets adenine nucleotide translocase and affects mitochondrial respiration. Journal of Biological Chemistry, 2019, 294, 11654-11664.	1.6	18
839	Mapping connections in signaling networks with ambiguous modularity. Npj Systems Biology and Applications, 2019, 5, 19.	1.4	9
840	Analysis and prediction of human acetylation using a cascade classifier based on support vector machine. BMC Bioinformatics, 2019, 20, 346.	1.2	12
841	Multiomics Profiling Establishes the Polypharmacology of FDA-Approved CDK4/6 Inhibitors and the Potential for Differential Clinical Activity. Cell Chemical Biology, 2019, 26, 1067-1080.e8.	2.5	151
842	Posttranslational Modifications Associated With Cancer and Their Therapeutic Implications. , 2019, , 203-227.		1
843	Progesterone induced Warburg effect in HEK293 cells is associated with post-translational modifications and proteasomal degradation of progesterone receptor membrane component 1. Journal of Steroid Biochemistry and Molecular Biology, 2019, 191, 105376.	1.2	24
844	Multi-omic Profiling Reveals Dynamics of the Phased Progression of Pluripotency. Cell Systems, 2019, 8, 427-445.e10.	2.9	111
845	Crystal Structures of Protein-Bound Cyclic Peptides. Chemical Reviews, 2019, 119, 9861-9914.	23.0	65
846	Footprint-based functional analysis of multiomic data. Current Opinion in Systems Biology, 2019, 15, 82-90.	1.3	39
847	Exon Inclusion Modulates Conformational Plasticity and Autoinhibition of the Intersectin 1 SH3A Domain. Structure, 2019, 27, 977-987.e5.	1.6	4
848	Conserved phosphorylation hotspots in eukaryotic protein domain families. Nature Communications, 2019, 10, 1977.	5.8	39
849	RAD51D splice variants and cancer-associated mutations reveal XRCC2 interaction to be critical for homologous recombination. DNA Repair, 2019, 76, 99-107.	1.3	13
850	GlyStruct: glycation prediction using structural properties of amino acid residues. BMC Bioinformatics, 2019, 19, 547.	1.2	31
851	Post-transcriptional regulatory patterns revealed by protein-RNA interactions. Scientific Reports, 2019, 9, 4302.	1.6	21

#	ARTICLE	IF	CITATIONS
852	Proteasome Dependent Actin Remodeling Facilitates Antigen Extraction at the Immune Synapse of B Cells. Frontiers in Immunology, 2019, 10, 225.	2.2	35
853	DYRK1A regulates the recruitment of 53BP1 to the sites of DNA damage in part through interaction with RNF169. Cell Cycle, 2019, 18, 531-551.	1.3	32
854	Prediction of response to anti-cancer drugs becomes robust via network integration of molecular data. Scientific Reports, 2019, 9, 2379.	1.6	11
855	Epigenetic Effects of Curcumin in Cancer Prevention. , 2019, , 107-128.		12
856	The arginine methyltransferase PRMT5 and PRMT1 distinctly regulate the degradation of anti-apoptotic protein CFLARL in human lung cancer cells. Journal of Experimental and Clinical Cancer Research, 2019, 38, 64.	3.5	36
857	Visualization and Analysis of Epiproteome Dynamics. Journal of Molecular Biology, 2019, 431, 1519-1539.	2.0	10
858	Murine xenograft bioreactors for human immunopeptidome discovery. Scientific Reports, 2019, 9, 18558.	1.6	9
859	Phosphoproteomic analysis sheds light on intracellular signaling cascades triggered by Formyl-Peptide Receptor 2. Scientific Reports, 2019, 9, 17894.	1.6	31
860	Integrating protein localization with automated signaling pathway reconstruction. BMC Bioinformatics, 2019, 20, 505.	1.2	4
861	ERK1/2 Phosphorylation of FHOD Connects Signaling and Nuclear Positioning Alternations in Cardiac Laminopathy. Developmental Cell, 2019, 51, 602-616.e12.	3.1	28
862	Friend or foeâ€"Post-translational modifications as regulators of phase separation and RNP granule dynamics. Journal of Biological Chemistry, 2019, 294, 7137-7150.	1.6	275
863	Multisite Phosphorylation of S6K1 Directs a Kinase Phospho-code that Determines Substrate Selection. Molecular Cell, 2019, 73, 446-457.e6.	4.5	36
864	MoMo: discovery of statistically significant post-translational modification motifs. Bioinformatics, 2019, 35, 2774-2782.	1.8	131
865	Comprehensive analysis of kinase-oriented phospho-signalling pathways. Journal of Biochemistry, 2019, 165, 301-307.	0.9	9
866	Clinically Relevant Post-Translational Modification Analysesâ€"Maturing Workflows and Bioinformatics Tools. International Journal of Molecular Sciences, 2019, 20, 16.	1.8	50
867	Phosphorylation of Cx43 residue Y313 by Src contributes to blocking the interaction with Drebrin and disassembling gap junctions. Journal of Molecular and Cellular Cardiology, 2019, 126, 36-49.	0.9	22
868	DeepPhos: prediction of protein phosphorylation sites with deep learning. Bioinformatics, 2019, 35, 2766-2773.	1.8	132
869	qPhos: a database of protein phosphorylation dynamics in humans. Nucleic Acids Research, 2019, 47, D451-D458.	6.5	44

#	Article	IF	Citations
870	Lysine methylation by the mitochondrial methyltransferase FAM173B optimizes the function of mitochondrial ATP synthase. Journal of Biological Chemistry, 2019, 294, 1128-1141.	1.6	18
871	Structure-based prediction of post-translational modification cross-talk within proteins using complementary residue- and residue pair-based features. Briefings in Bioinformatics, 2020, 21, 609-620.	3.2	13
872	Lysine methyltransferase SETD6 modifies histones on a glycine-lysine motif. Epigenetics, 2020, 15, 26-31.	1.3	6
873	IP₃ Receptor Plasticity Underlying Diverse Functions. Annual Review of Physiology, 2020, 82, 151-176.	5.6	31
874	Tackling the complexities of orphan GPCR ligand discovery with rationally assisted approaches. , 2020, , 295-334.		2
875	Human muscle pathology is associated with altered phosphoprotein profile of mitochondrial proteins in the skeletal muscle. Journal of Proteomics, 2020, 211, 103556.	1.2	8
876	Phosphoproteomics and Bioinformatics Analyses Reveal Key Roles of GSK-3 and AKAP4 in Mouse Sperm Capacitation. International Journal of Molecular Sciences, 2020, 21, 7283.	1.8	4
877	Stat2 stability regulation: an intersection between immunity and carcinogenesis. Experimental and Molecular Medicine, 2020, 52, 1526-1536.	3.2	27
878	Network-based characterization of diseaseâ€“disease relationships in terms of drugs and therapeutic targets. Bioinformatics, 2020, 36, i516-i524.	1.8	13
879	Profilin: many facets of a small protein. Biophysical Reviews, 2020, 12, 827-849.	1.5	38
880	The Polyglutamine Expansion at the N-Terminal of Huntingtin Protein Modulates the Dynamic Configuration and Phosphorylation of the C-Terminal HEAT Domain. Structure, 2020, 28, 1035-1050.e8.	1.6	24
881	The ZSWIM8 ubiquitin ligase mediates target-directed microRNA degradation. Science, 2020, 370, .	6.0	138
882	DeepTL-Ubi: A novel deep transfer learning method for effectively predicting ubiquitination sites of multiple species. Methods, 2021, 192, 103-111.	1.9	18
883	Network-based modeling of drug effects on disease module in systemic sclerosis. Scientific Reports, 2020, 10, 13393.	1.6	9
884	Network-principled deep generative models for designing drug combinations as graph sets. Bioinformatics, 2020, 36, i445-i454.	1.8	24
885	The Chemical Biology of Reversible Lysine Post-translational Modifications. Cell Chemical Biology, 2020, 27, 953-969.	2.5	76
886	A Progressive Loss of phosphoSer138-Profilin Aligns with Symptomatic Course in the R6/2 Mouse Model of Huntingtonâ€™s Disease: Possible Sex-Dependent Signaling. Cellular and Molecular Neurobiology, 2022, 42, 871-888.	1.7	2
887	Microchip-Based Structure Determination of Disease-Relevant p53. Analytical Chemistry, 2020, 92, 15558-15564.	3.2	9

#	ARTICLE	IF	CITATIONS
888	Resolving the Interactome of the Human Macrophage Immunometabolism Regulator (MACIR) with Enhanced Membrane Protein Preparation and Affinity Proteomics. Proteomics, 2020, 20, e2000062.	1.3	4
889	Amyloid beta regulates ER exit sites formation through Oâ€GlcNAcylation triggered by disrupted calcium homeostasis. Biology of the Cell, 2020, 112, 439-451.	0.7	9
890	Everything you ever wanted to know about PKA regulation and its involvement in mammalian sperm capacitation. Molecular and Cellular Endocrinology, 2020, 518, 110992.	1.6	19
891	A novel subnetwork representation learning method for uncovering disease-disease relationships. Methods, 2021, 192, 77-84.	1.9	17
892	Deep proteomics and phosphoproteomics reveal novel biological pathways perturbed by morphine, morphineâ€3â€glucuronide and morphineâ€6â€glucuronide in human astrocytes. Journal of Neuroscience Research, 2022, 100, 220-236.	1.3	10
893	Dynamic remodelling of the human host cell proteome and phosphoproteome upon enterovirus infection. Nature Communications, 2020, 11, 4332.	5.8	27
894	Targeting Phosphotyrosine in Native Proteins with Conditional, Bispecific Antibody Traps. Journal of the American Chemical Society, 2020, 142, 17703-17713.	6.6	7
895	Intrinsic Disorder in Human Proteins Encoded by Core Duplicon Gene Families. Journal of Physical Chemistry B, 2020, 124, 8050-8070.	1.2	4
896	<i>In Silico</i> Identification of Potential Phosphorylation in the Cytoplasmic Domain of Epithelial Cell Adhesion Molecule. ACS Omega, 2020, 5, 30808-30816.	1.6	2
897	Hyperactive CDK2 Activity in Basal-like Breast Cancer Imposes a Genome Integrity Liability that Can Be Exploited by Targeting DNA Polymerase Îµ. Molecular Cell, 2020, 80, 682-698.e7.	4.5	25
898	GasPhos: Protein Phosphorylation Site Prediction Using a New Feature Selection Approach with a GA-Aided Ant Colony System. International Journal of Molecular Sciences, 2020, 21, 7891.	1.8	8
899	Staurosporine and NEM mainly impair WNK-SPAK/OSR1 mediated phosphorylation of KCC2 and NKCC1. PLoS ONE, 2020, 15, e0232967.	1.1	14
900	Hypomorphic CAMKK2 in EA.hy926 endothelial cells causes abnormal transferrin trafficking, iron homeostasis and glucose metabolism. Biochimica Et Biophysica Acta - Molecular Cell Research, 2020, 1867, 118763.	1.9	13
901	A Comprehensive Analysis of Symmetric Arginine Dimethylation in Colorectal Cancer Tissues Using Immunoaffinity Enrichment and Mass Spectrometry. Proteomics, 2020, 20, e1900367.	1.3	5
902	In-depth mining of the immunopeptidome of an acute myeloid leukemia cell line using complementary ligand enrichment and data acquisition strategies. Molecular Immunology, 2020, 123, 7-17.	1.0	18
903	CAMKK2-CAMK4 signaling regulates transferrin trafficking, turnover, and ironÂhomeostasis. Cell Communication and Signaling, 2020, 18, 80.	2.7	9
904	Phosphorylation of ACTN4 Leads to Podocyte Vulnerability and Proteinuric Glomerulosclerosis. Journal of the American Society of Nephrology: JASN, 2020, 31, 1479-1495.	3.0	19
905	Intrinsic Disorder in Tetratricopeptide Repeat Proteins. International Journal of Molecular Sciences, 2020, 21, 3709.	1.8	9

#	Article	IF	Citations
906	dBMHCC: A comprehensive hepatocellular carcinoma (HCC) biomarker database provides a reliable prediction system for novel HCC phosphorylated biomarkers. PLoS ONE, 2020, 15, e0234084.	1.1	11
907	Scop3P: A Comprehensive Resource of Human Phosphosites within Their Full Context. Journal of Proteome Research, 2020, 19, 3478-3486.	1.8	19
908	Phosphorylation Sites in Protein Kinases and Phosphatases Regulated by Formyl Peptide Receptor 2 Signaling. International Journal of Molecular Sciences, 2020, 21, 3818.	1.8	18
909	From Beef to Bees: High-Throughput Kinome Analysis to Understand Host Responses of Livestock Species to Infectious Diseases and Industry-Associated Stress. Frontiers in Immunology, 2020, 11, 765.	2.2	6
910	Quantitative phosphoproteomics to unravel the cellular response to chemical stressors with different modes of action. Archives of Toxicology, 2020, 94, 1655-1671.	1.9	16
911	Lysine Acetylation Reshapes the Downstream Signaling Landscape of Vav1 in Lymphocytes. Cells, 2020, 9, 609.	1.8	6
912	TGFBR2 mediated phosphorylation of BUB1 at Ser-318 is required for transforming growth factor-Î² signaling. Neoplasia, 2020, 22, 163-178.	2.3	12
913	The cytosolic isoform of glutaredoxin 2 promotes cell migration and invasion. Biochimica Et Biophysica Acta - General Subjects, 2020, 1864, 129599.	1.1	7
914	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. Cell, 2020, 182, 200-225.e35.	13.5	410
915	Protein Phosphorylation Dynamics: Unexplored Because of Current Methodological Limitations. BioEssays, 2020, 42, 1900149.	1.2	1
916	The Shb scaffold binds the Nck adaptor protein, p120 RasGAP, and Chimaerins and thereby facilitates heterotypic cell segregation by the receptor EphB2. Journal of Biological Chemistry, 2020, 295, 3932-3944.	1.6	6
917	FUNMarker: Fusion Network-Based Method to Identify Prognostic and Heterogeneous Breast Cancer Biomarkers. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2483-2491.	1.9	10
918	Why and how to investigate the role of protein phosphorylation in ZIP and ZnT zinc transporter activity and regulation. Cellular and Molecular Life Sciences, 2020, 77, 3085-3102.	2.4	30
919	Ring Finger Protein 11 acts on ligandâ€activated EGFR via the direct interaction with the UIM region of ANKRD13 protein family. FEBS Journal, 2020, 287, 3526-3550.	2.2	12
920	Analysis of Interactions Stabilized by Fusicoccin A Reveals an Expanded Suite of Potential 14â€“3â€“3 Binding Partners. ACS Chemical Biology, 2020, 15, 305-310.	1.6	11
921	Effects of Intermittent versus Chronic-Moderate Ethanol Administration during Adolescence in the Adult Hippocampal Phosphoproteome. Chemical Research in Toxicology, 2020, 33, 448-460.	1.7	3
922	Advances in defining signaling networks for the establishment of neuronal polarity. Current Opinion in Cell Biology, 2020, 63, 76-87.	2.6	12
923	BCAT2-mediated BCAA catabolism is critical for development of pancreatic ductal adenocarcinoma. Nature Cell Biology, 2020, 22, 167-174.	4.6	117

#	ARTICLE	IF	CITATIONS
924	Analyzing Protein Disorder with IUPred2A. Current Protocols in Bioinformatics, 2020, 70, e99.	25.8	233
925	Post-translational Modification Crosstalk and Hotspots in Sirtuin Interactors Implicated in Cardiovascular Diseases. Frontiers in Genetics, 2020, 11, 356.	1.1	25
926	Emerging links between endosomal pH and cancer. Cancer and Metastasis Reviews, 2020, 39, 519-534.	2.7	49
927	Multiphosphorylated peptides: importance, synthetic strategies, and applications for studying biological mechanisms. Organic and Biomolecular Chemistry, 2020, 18, 3405-3422.	1.5	11
928	Differential dephosphorylation of CTP:phosphocholine cytidylyltransferase upon translocation to nuclear membranes and lipid droplets. Molecular Biology of the Cell, 2020, 31, 1047-1059.	0.9	10
929	Emerging evidence for cellâ€autonomous axon guidance. Development Growth and Differentiation, 2020, 62, 391-397.	0.6	4
930	Bioinformatics Methods for Mass Spectrometry-Based Proteomics Data Analysis. International Journal of Molecular Sciences, 2020, 21, 2873.	1.8	134
931	Shank2 Binds to aPKC and Controls Tight Junction Formation with Rap1 Signaling during Establishment of Epithelial Cell Polarity. Cell Reports, 2020, 31, 107407.	2.9	19
932	Proteogenomic Characterization of Ovarian HGSC Implicates Mitotic Kinases, Replication Stress in Observed Chromosomal Instability. Cell Reports Medicine, 2020, 1, 100004.	3.3	46
933	Proteome and Phosphoproteome Analysis of Brown Adipocytes Reveals That RICTOR Loss Dampens Global Insulin/AKT Signaling. Molecular and Cellular Proteomics, 2020, 19, 1104-1119.	2.5	9
934	Bioinformatics toolbox for exploring protein phosphorylation network. Briefings in Bioinformatics, 2021, 22, .	3.2	7
935	PHLPPing the Script: Emerging Roles of PHLPP Phosphatases in Cell Signaling. Annual Review of Pharmacology and Toxicology, 2021, 61, 723-743.	4.2	16
936	DeepPSP: A Globalâ€"Local Information-Based Deep Neural Network for the Prediction of Protein Phosphorylation Sites. Journal of Proteome Research, 2021, 20, 346-356.	1.8	25
937	Transcriptional co-activators YAP/TAZ: Potential therapeutic targets for metastatic breast cancer. Biomedicine and Pharmacotherapy, 2021, 133, 110956.	2.5	23
938	Phosphorylation of the RB C-terminus regulates condensin II release from chromatin. Journal of Biological Chemistry, 2021, 296, 100108.	1.6	6
939	Role of histone acetyltransferase inhibitors in cancer therapy. Advances in Protein Chemistry and Structural Biology, 2021, 125, 149-191.	1.0	12
940	Optoproteomics elucidates the interactome of L-type amino acid transporter 3 (LAT3). Chemical Communications, 2021, 57, 4734-4737.	2.2	2
941	GuidePro: a multi-source ensemble predictor for prioritizing sgRNAs in CRISPR/Cas9 protein knockouts. Bioinformatics, 2021, 37, 134-136.	1.8	7

#	ARTICLE	IF	CITATIONS
942	Lung cancer molecular mutations and abnormal glycosylation as biomarkers for early diagnosis. Cancer Treatment and Research Communications, 2021, 27, 100311.	0.7	11
943	Charting protein dephosphorylation triggered by Toll-like receptor (TLR) signaling in macrophages and its role in health and disease. International Review of Cell and Molecular Biology, 2021, 361, 211-243.	1.6	0
944	New insights into the molecular mechanisms of axon guidance receptor regulation and signaling. Current Topics in Developmental Biology, 2021, 142, 147-196.	1.0	44
945	Proteome-wide identification of NEDD8 modification sites reveals distinct proteomes for canonical and atypical NEDDylation. Cell Reports, 2021, 34, 108635.	2.9	35
946	Network-based systems pharmacology reveals heterogeneity in LCK and BCL2 signaling and therapeutic sensitivity of T-cell acute lymphoblastic leukemia. Nature Cancer, 2021, 2, 284-299.	5.7	70
947	Virus systems biology: Proteomics profiling of dynamic protein networks during infection. Advances in Virus Research, 2021, 109, 1-29.	0.9	5
948	Posttranslational modifications in systems biology. Advances in Protein Chemistry and Structural Biology, 2021, 127, 93-126.	1.0	16
949	Development and biological applications of sulfurâ€“triazole exchange (SuTEx) chemistry. RSC Chemical Biology, 2021, 2, 322-337.	2.0	18
950	Pro-Resolving FPR2 Agonists Regulate NADPH Oxidase-Dependent Phosphorylation of HSP27, OSR1, and MARCKS and Activation of the Respective Upstream Kinases. Antioxidants, 2021, 10, 134.	2.2	15
951	KinPred: A unified and sustainable approach for harnessing proteome-level human kinase-substrate predictions. PLoS Computational Biology, 2021, 17, e1008681.	1.5	10
954	PhosR enables processing and functional analysis of phosphoproteomic data. Cell Reports, 2021, 34, 108771.	2.9	48
956	System-wide identification and prioritization of enzyme substrates by thermal analysis. Nature Communications, 2021, 12, 1296.	5.8	44
957	Human RecQ Helicases in DNA Double-Strand Break Repair. Frontiers in Cell and Developmental Biology, 2021, 9, 640755.	1.8	38
958	Spatiotemporal dissection of the cell cycle with single-cell proteogenomics. Nature, 2021, 590, 649-654.	13.7	104
959	Regulation of OATP1B1 Function by Tyrosine Kinaseâ€“mediated Phosphorylation. Clinical Cancer Research, 2021, 27, 4301-4310.	3.2	24
960	Phosphoproteomics-Based Characterization of Prostaglandin E2 Signaling in T Cells. Molecular Pharmacology, 2021, 99, 370-382.	1.0	2
961	Regulation of N-glycosylation and secretion of Isthmin-1 by its C-mannosylation. Biochimica Et Biophysica Acta - General Subjects, 2021, 1865, 129840.	1.1	13
962	A Review of Small-Molecule Inhibitors of One-Carbon Enzymes: SHMT2 and MTHFD2 in the Spotlight. ACS Pharmacology and Translational Science, 2021, 4, 624-646.	2.5	30

#	ARTICLE	IF	CITATIONS
965	Proteomicsâ€based interrogation of the kinome and its implications for precision oncology. Proteomics, 2021, 21, 2000161.	1.3	4
966	Large-scale identification of protein histidine methylation in human cells. NAR Genomics and Bioinformatics, 2021, 3, lqab045.	1.5	12
967	A comprehensive review of the imbalance classification of protein post-translational modifications. Briefings in Bioinformatics, 2021, 22, .	3.2	26
968	Proteomic analysis of tyrosine phosphorylation induced by exogenous expression of oncogenic kinase fusions identified in lung adenocarcinoma. Proteomics, 2021, 21, e2000283.	1.3	1
970	multiSLIDE is a web server for exploring connected elements of biological pathways in multi-omics data. Nature Communications, 2021, 12, 2279.	5.8	12
971	ERK1/2: An Integrator of Signals That Alters Cardiac Homeostasis and Growth. Biology, 2021, 10, 346.	1.3	17
973	NIDM: network impulsive dynamics on multiplex biological network for disease-gene prediction. Briefings in Bioinformatics, 2021, 22, .	3.2	19
974	The Arp2/3 Inhibitory Protein Arpin Is Required for Intestinal Epithelial Barrier Integrity. Frontiers in Cell and Developmental Biology, 2021, 9, 625719.	1.8	12
975	Ovalbumin Antigen-Specific Activation of Human T Cell Receptor Closely Resembles Soluble Antibody Stimulation as Revealed by BOOST Phosphotyrosine Proteomics. Journal of Proteome Research, 2021, 20, 3330-3344.	1.8	4
976	Prognostic relevance of the hexosamine biosynthesis pathway activation in leiomyosarcoma. Npj Genomic Medicine, 2021, 6, 30.	1.7	8
978	Mechanism of p38 MAPKâ€"induced EGFR endocytosis and its crosstalk with ligand-induced pathways. Journal of Cell Biology, 2021, 220, .	2.3	19
979	Ecm29-Dependent Proteasome Localization Regulates Cytoskeleton Remodeling at the Immune Synapse. Frontiers in Cell and Developmental Biology, 2021, 9, 650817.	1.8	8
980	Metabolomics bridging proteomics along metabolites/oncometabolites and protein modifications: Paving the way toward integrative multiomics. Journal of Pharmaceutical and Biomedical Analysis, 2021, 199, 114031.	1.4	8
981	Evaluating Mechanisms of IDH1 Regulation through Site-Specific Acetylation Mimics. Biomolecules, 2021, 11, 740.	1.8	3
982	A data-independent acquisition-based global phosphoproteomics system enables deep profiling. Nature Communications, 2021, 12, 2539.	5.8	44
983	AP-3â€"dependent targeting of flippase ATP8A1 to lamellar bodies suppresses activation of YAP in alveolar epithelial type 2 cells. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	16
984	DHODH and cancer: promising prospects to be explored. Cancer & Metabolism, 2021, 9, 22.	2.4	71
985	Copy number aberrations drive kinase rewiring, leading to genetic vulnerabilities in cancer. Cell Reports, 2021, 35, 109155.	2.9	10

#	Article	IF	Citations
986	Cereblon Regulates the Proteotoxicity of Tau by Tuning the Chaperone Activity of DNAJA1. Journal of Neuroscience, 2021, 41, 5138-5156.	1.7	5
987	On the Need to Tell Apart Fraternal Twins eEF1A1 and eEF1A2, and Their Respective Outfits. International Journal of Molecular Sciences, 2021, 22, 6973.	1.8	15
988	Protocol for the processing and downstream analysis of phosphoproteomic data with PhosR. STAR Protocols, 2021, 2, 100585.	0.5	7
989	Loss of GSK-3Î² mediated phosphorylation in HtrA2 contributes to uncontrolled cell death with Parkinsonian phenotype. International Journal of Biological Macromolecules, 2021, 180, 97-111.	3.6	3
990	Targeted mass-spectrometry-based assays enable multiplex quantification of receptor tyrosine kinase, MAP kinase, and AKT signaling. Cell Reports Methods, 2021, 1, 100015.	1.4	10
991	Tyrosine Phosphoproteomics of Patient-Derived Xenografts Reveals Ephrin Type-B Receptor 4 Tyrosine Kinase as a Therapeutic Target in Pancreatic Cancer. Cancers, 2021, 13, 3404.	1.7	2
993	Proteomic strategies for characterizing ubiquitin-like modifications. Nature Reviews Methods Primers, 2021, 1, .	11.8	6
994	Possible Therapeutic Strategy Involving the Purine Synthesis Pathway Regulated by ITK in Tongue Squamous Cell Carcinoma. Cancers, 2021, 13, 3333.	1.7	4
995	Oxygen-dependent changes in binding partners and post-translational modifications regulate the abundance and activity of HIF-1Î±/2Î±. Science Signaling, 2021, 14, .	1.6	26
996	Post-Translational Modifications Modulate Proteinopathies of TDP-43, FUS and hnRNP-A/B in Amyotrophic Lateral Sclerosis. Frontiers in Molecular Biosciences, 2021, 8, 693325.	1.6	16
998	The secreted tyrosine kinase VLK is essential for normal platelet activation and thrombus formation. Blood, 2022, 139, 104-117.	0.6	6
999	Exploiting polypharmacology to dissect host kinases and kinase inhibitors that modulate endothelial barrier integrity. Cell Chemical Biology, 2021, , .	2.5	9
1000	Global identification of phospho-dependent SCF substrates reveals a FBXO22 phosphodegron and an ERK-FBXO22-BAG3 axis in tumorigenesis. Cell Death and Differentiation, 2022, 29, 1-13.	5.0	22
1001	Regulation of ubiquitin and ubiquitinâ€like modifiers by phosphorylation. FEBS Journal, 2022, 289, 4797-4810.	2.2	9
1002	A global map of associations between types of protein posttranslational modifications and human genetic diseases. IScience, 2021, 24, 102917.	1.9	7
1003	A proteogenomic portrait of lung squamous cell carcinoma. Cell, 2021, 184, 4348-4371.e40.	13.5	170
1004	A histone modifier, ASXL1, interacts with NONO and is involved in paraspeckle formation in hematopoietic cells. Cell Reports, 2021, 36, 109576.	2.9	15
1005	Mitotic WNT signalling orchestrates neurogenesis in the developing neocortex. EMBO Journal, 2021, 40, e108041.	3.5	26

#	Article	IF	Citations
1006	Role of protein phosphatase 2A in kidney disease (Review). Experimental and Therapeutic Medicine, 2021, 22, 1236.	0.8	9
1007	FHL2 anchors mitochondria to actin and adapts mitochondrial dynamics to glucose supply. Journal of Cell Biology, 2021, 220, .	2.3	31
1008	Kinase-Catalyzed Biotinylation to Map Cell Signaling Pathways: Application to Epidermal Growth Factor Signaling. Journal of Proteome Research, 2021, 20, 4852-4861.	1.8	3
1009	The Î±-Arrestin ARRDC3 Is an Emerging Multifunctional Adaptor Protein in Cancer. Antioxidants and Redox Signaling, 2022, 36, 1066-1079.	2.5	8
1010	Structural Insights into Protein Regulation by Phosphorylation and Substrate Recognition of Protein Kinases/Phosphatases. Life, 2021, 11, 957.	1.1	23
1013	The genome of the naturally evolved obesity-prone Ossabaw miniature pig. IScience, 2021, 24, 103081.	1.9	9
1014	CAMKK2 regulates mitochondrial function by controlling succinate dehydrogenase expression, post-translational modification, megacomplex assembly, and activity in a cell-type-specific manner. Cell Communication and Signaling, 2021, 19, 98.	2.7	8
1015	Intrinsic Disorder in Human RNA-Binding Proteins. Journal of Molecular Biology, 2021, 433, 167229.	2.0	23
1016	Antisense overlapping long non-coding RNA regulates coding arachidonate 12-lipoxygenase gene by translational interference. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2021, 1866, 158987.	1.2	2
1018	Proteomic Interrogation in Cancer Biomarker. Advances in Experimental Medicine and Biology, 2021, 1187, 305-322.	0.8	2
1019	Decoding Post-Translational Modification Crosstalk With Proteomics. Molecular and Cellular Proteomics, 2021, 20, 100129.	2.5	92
1021	A Practical Recipe to Survey Phosphoproteomes. Methods in Molecular Biology, 2014, 1156, 389-405.	0.4	1
1022	Computational Prediction of Protein-Protein Interactions. Methods in Molecular Biology, 2015, 1278, 57-75.	0.4	37
1023	From Phosphosites to Kinases. Methods in Molecular Biology, 2016, 1355, 307-321.	0.4	21
1024	Screening One-Bead-One-Compound Peptide Libraries for Optimal Kinase Substrates. Methods in Molecular Biology, 2016, 1360, 169-181.	0.4	1
1025	Using the CPTAC Assay Portal to Identify and Implement Highly Characterized Targeted Proteomics Assays. Methods in Molecular Biology, 2016, 1410, 223-236.	0.4	33
1026	SH2 Binding Site Protection Assay: A Method for Identification of SH2 Domain Interaction Partners by Exploiting SH2 Mediated Phosphosite Protection. Methods in Molecular Biology, 2017, 1555, 477-492.	0.4	2
1027	Bioinformatics Analysis of PTM-Modified Protein Interaction Networks and Complexes. Methods in Molecular Biology, 2017, 1558, 321-332.	0.4	2

#	Article	IF	Citations
1028	Mapping Biological Networks from Quantitative Data-Independent Acquisition Mass Spectrometry: Data to Knowledge Pipelines. Methods in Molecular Biology, 2017, 1558, 395-413.	0.4	7
1029	Cross-Species PTM Mapping from Phosphoproteomic Data. Methods in Molecular Biology, 2017, 1558, 459-469.	0.4	2
1030	Impact of Nonsynonymous Single-Nucleotide Variations on Post-Translational Modification Sites in Human Proteins. Methods in Molecular Biology, 2017, 1558, 159-190.	0.4	2
1031	Expression of Recombinant Phosphoproteins for Signal Transduction Studies. Methods in Molecular Biology, 2017, 1636, 71-78.	0.4	3
1032	Chaperones and Multitasking Proteins in the Nucleolus. , 2013, , 149-172.		7
1033	Deacetylation by SIRT3 Relieves Inhibition of Mitochondrial Protein Function. , 2016, , 105-138.		3
1034	Post-translational Mechanisms of Zinc Signalling in Cancer. , 2019, , 319-345.		1
1035	Systems Biology and Integrated Computational Methods for Cancer-Associated Mutation Analysis. , 2020, , 335-362.		3
1036	DNA damage response and repair pathway modulation by non-histone protein methylation: implications in neurodegeneration. Journal of Cell Communication and Signaling, 2020, 14, 31-45.	1.8	14
1037	Regulation of the Î±-ketoglutarate dehydrogenasecomplex during hibernation in a small mammal, the Richardson's ground squirrel (Urocitellus richardsonii). Biochimica Et Biophysica Acta - Proteins and Proteomics, 2020, 1868, 140448.	1.1	3
1038	PRISMOID: a comprehensive 3D structure database for post-translational modifications and mutations with functional impact. Briefings in Bioinformatics, 2020, 21, 1069-1079.	3.2	38
1051	A systems immunology approach identifies the collective impact of 5 miRs in Th2 inflammation. JCI Insight, 2018, 3, .	2.3	10
1052	Impaired plasma membrane localization of ubiquitin ligase complex underlies 3-M syndrome development. Journal of Clinical Investigation, 2019, 129, 4393-4407.	3.9	14
1053	Proteome-wide identification of arginine methylation in colorectal cancer tissues from patients. Proteome Science, 2020, 18, 6.	0.7	18
1054	Rapamycin-insensitive mTORC1 activity controls eIF4E:4E-BP1 binding. F1000Research, 2012, 1, 4.	0.8	33
1055	SwissPalm: Protein Palmitoylation database. F1000Research, 2015, 4, 261.	0.8	209
1056	Prediction of Functionally Important Phospho-Regulatory Events in Xenopus laevis Oocytes. PLoS Computational Biology, 2015, 11, e1004362.	1.5	14
1057	Systematic identification of phosphorylation-mediated protein interaction switches. PLoS Computational Biology, 2017, 13, e1005462.	1.5	44

#	ARTICLE	IF	CITATIONS
1058	Accurate prediction of kinase-substrate networks using knowledge graphs. PLoS Computational Biology, 2020, 16, e1007578.	1.5	19
1059	Anillin Phosphorylation Controls Timely Membrane Association and Successful Cytokinesis. PLoS Genetics, 2017, 13, e1006511.	1.5	29
1060	Protein Phosphorylation Profiling Using an In Situ Proximity Ligation Assay: Phosphorylation of AURKA-Elicited EGFR-Thr654 and EGFR-Ser1046 in Lung Cancer Cells. PLoS ONE, 2013, 8, e55657.	1.1	14
1061	Semi-Supervised Prediction of SH2-Peptide Interactions from Imbalanced High-Throughput Data. PLoS ONE, 2013, 8, e62732.	1.1	27
1062	Adaptor Proteins Intersectin 1 and 2 Bind Similar Proline-Rich Ligands but Are Differentially Recognized by SH2 Domain-Containing Proteins. PLoS ONE, 2013, 8, e70546.	1.1	15
1063	Structural Propensities of Human Ubiquitination Sites: Accessibility, Centrality and Local Conformation. PLoS ONE, 2013, 8, e83167.	1.1	10
1064	Deriving a Mutation Index of Carcinogenicity Using Protein Structure and Protein Interfaces. PLoS ONE, 2014, 9, e84598.	1.1	22
1065	JMJD6 Regulates ERÎ± Methylation on Arginine. PLoS ONE, 2014, 9, e87982.	1.1	70
1066	Inhibitor of Apoptosis-Stimulating Protein of p53 (iASPP) Is Required for Neuronal Survival after Axonal Injury. PLoS ONE, 2014, 9, e94175.	1.1	28
1067	Phosphokinase Antibody Arrays on Dendron-Coated Surface. PLoS ONE, 2014, 9, e96456.	1.1	5
1068	FMRP S499 Is Phosphorylated Independent of mTORC1-S6K1 Activity. PLoS ONE, 2014, 9, e96956.	1.1	30
1069	Inferring Protein Modulation from Gene Expression Data Using Conditional Mutual Information. PLoS ONE, 2014, 9, e109569.	1.1	21
1070	Identification of the PLK2-Dependent Phosphopeptidome by Quantitative Proteomics. PLoS ONE, 2014, 9, e111018.	1.1	9
1071	Binding of Kif23-iso1/CHO1 to 14-3-3 Is Regulated by Sequential Phosphorylations at Two LATS Kinase Consensus Sites. PLoS ONE, 2015, 10, e0117857.	1.1	12
1072	A Multi-Omics Approach Identifies Key Hubs Associated with Cell Type-Specific Responses of Airway Epithelial Cells to Staphylococcal Alpha-Toxin. PLoS ONE, 2015, 10, e0122089.	1.1	15
1073	Dynamic Alterations to Î±-Actinin Accompanying Sarcomere Disassembly and Reassembly during Cardiomyocyte Mitosis. PLoS ONE, 2015, 10, e0129176.	1.1	21
1074	Bioinformatics Knowledge Map for Analysis of Beta-Catenin Function in Cancer. PLoS ONE, 2015, 10, e0141773.	1.1	12
1075	Glucose Regulated Protein 78 Phosphorylation in Sperm Undergoes Dynamic Changes during Maturation. PLoS ONE, 2015, 10, e0141858.	1.1	12

#	Article	IF	Citations
1076	The Functional Significance of Posttranslational Modifications on Polo-Like Kinase 1 Revealed by Chemical Genetic Complementation. PLoS ONE, 2016, 11, e0150225.	1.1	10
1077	The Functional Human C-Terminome. PLoS ONE, 2016, 11, e0152731.	1.1	11
1078	Improved Species-Specific Lysine Acetylation Site Prediction Based on a Large Variety of Features Set. PLoS ONE, 2016, 11, e0155370.	1.1	26
1079	Unraveling Kinase Activation Dynamics Using Kinase-Substrate Relationships from Temporal Large-Scale Phosphoproteomics Studies. PLoS ONE, 2016, 11, e0157763.	1.1	14
1080	Sequence- and Structure-Based Analysis of Tissue-Specific Phosphorylation Sites. PLoS ONE, 2016, 11, e0157896.	1.1	10
1081	Integrative proteomics reveals principles of dynamic phosphosignaling networks in human erythropoiesis. Molecular Systems Biology, 2020, 16, e9813.	3.2	21
1082	PreImplantation factor (PIF) therapy provides comprehensive protection against radiation induced pathologies. Oncotarget, 2016, 7, 58975-58994.	0.8	17
1083	PIF* promotes brain re-myelination locally while regulating systemic inflammation- clinically relevant multiple sclerosis <i>M.smegmatis</i> model. Oncotarget, 2017, 8, 21834-21851.	0.8	17
1084	Quantitative network mapping of the human kinome interactome reveals new clues for rational kinase inhibitor discovery and individualized cancer therapy. Oncotarget, 2014, 5, 3697-3710.	0.8	96
1085	CIPPN: computational identification of protein pupylation sites by using neural network. Oncotarget, 2017, 8, 108867-108879.	0.8	16
1086	CDK1 phosphorylation of TAZ in mitosis inhibits its oncogenic activity. Oncotarget, 2015, 6, 31399-31412.	0.8	28
1087	Protein Post-Translational Modification Crosstalk in Acute Myeloid Leukemia Calls for Action. Current Medicinal Chemistry, 2019, 26, 5317-5337.	1.2	8
1088	Review of Progress in Predicting Protein Methylation Sites. Current Organic Chemistry, 2019, 23, 1663-1670.	0.9	8
1089	A Comparative Analysis and Review of lysyl Residues Affected by Posttranslational Modifications. Current Genomics, 2015, 16, 128-138.	0.7	12
1090	CYLD-Mediated Signaling and Diseases. Current Drug Targets, 2015, 16, 284-294.	1.0	74
1091	Towards Computational Models of Identifying Protein Ubiquitination Sites. Current Drug Targets, 2019, 20, 565-578.	1.0	7
1092	The extracellular kinome. Kinome, 2012, 1, 1-3.	0.5	1
1093	The Role of Hypoxia-Inducible Factor Post-Translational Modifications in Regulating Its Localisation, Stability, and Activity. International Journal of Molecular Sciences, 2021, 22, 268.	1.8	58

#	ARTICLE	IF	CITATIONS
1094	Serum Protein Profile in Women With Pregnancy Morbidity Associated With Antiphospholipid Syndrome. Journal of Human Reproductive Sciences, 2017, 10, 10-17.	0.4	6
1095	Computational comparison of two new fusion proteins for multiple sclerosis. Research in Pharmaceutical Sciences, 2018, 13, 394.	0.6	5
1096	Weighing up the possibilities: Controlling translation by ubiquitylation and sumoylation. Translation, 2014, 2, e29211.	2.9	1
1097	A Proteomic Approach to Screening of Dynamic Changes in Detergent-Resistant Membranes from Activated Human Primary T Cells. Journal of Proteomics and Bioinformatics, 2013, 06, .	0.4	7
1098	Prediction of Protein Acetylation Sites using Kernel Naive Bayes Classifier Based on Protein Sequences Profiling. Bioinformation, 2018, 14, 213-218.	0.2	10
1099	Ancestral resurrection reveals evolutionary mechanisms of kinase plasticity. ELife, 2014, 3, .	2.8	53
1100	Huntingtinâ€™s spherical solenoid structure enables polyglutamine tract-dependent modulation of its structure and function. ELife, 2016, 5, e11184.	2.8	52
1101	Time-resolved multimodal analysis of Src Homology 2 (SH2) domain binding in signaling by receptor tyrosine kinases. ELife, 2016, 5, e11835.	2.8	20
1102	Rewiring MAP kinases in Saccharomyces cerevisiae to regulate novel targets through ubiquitination. ELife, 2016, 5, .	2.8	11
1103	Context-enriched interactome powered by proteomics helps the identification of novel regulators of macrophage activation. ELife, 2018, 7, .	2.8	11
1104	Determination of host proteins composing the microenvironment of coronavirus replicase complexes by proximity-labeling. ELife, 2019, 8, .	2.8	157
1105	Prediction of post-translational modification sites using multiple kernel support vector machine. PeerJ, 2017, 5, e3261.	0.9	12
1106	ksrMKL: a novel method for identification of kinaseâ€“substrate relationships using multiple kernel learning. PeerJ, 2017, 5, e4182.	0.9	5
1107	Phosphoproteomic insights into processes influenced by the kinase-like protein DIA1/C3orf58. PeerJ, 2018, 6, e4599.	0.9	7
1109	Mass Spectrometry-Based Phosphoproteomics and Systems Biology: Approaches to Study T Lymphocyte Activation and Exhaustion. Journal of Molecular Biology, 2021, 433, 167318.	2.0	5
1110	Structure, Activity and Function of the Dual Protein Lysine and Protein N-Terminal Methyltransferase METTL13. Life, 2021, 11, 1121.	1.1	4
1111	Locally Adjust Networks Based on Connectivity and Semantic Similarities for Disease Module Detection. Frontiers in Genetics, 2021, 12, 726596.	1.1	1
1112	Proteomics analysis identifies PEA-15 as an endosomal phosphoprotein that regulates Î±5Î²1 integrin endocytosis. Scientific Reports, 2021, 11, 19830.	1.6	2

#	Article	IF	Citations
1113	HUPHO: the human phosphatase portal. EMBnet Journal, 2012, 18, 55.	0.2	0
1114	Domain-context information for the improvement of phosphorylation site prediction. EMBnet Journal, 2012, 18, 120.	0.2	0
1115	Cell Signalling Technology Antibodies. Materials and Methods, 0, 2, .	0.0	0
1116	Bioinformatics for Proteomics: Opportunities at the Interface Between the Scientists, Their Experiments, and the Community. Methods in Molecular Biology, 2014, 1156, 239-248.	0.4	0
1117	Zinc Signaling and Cancer. , 2014, , 285-313.		2
1118	Systems-Wide Analysis of Protein Ubiquitylation: We Finally Have the Tiger by the Tail. , 2014, , 367-391.		0
1119	TACC2 (transforming, acidic coiled-coil containing protein 2). Atlas of Genetics and Cytogenetics in Oncology and Haematology, 2014, , .	0.1	0
1121	Investigating Signaling Processes in Membrane Trafficking. Methods in Molecular Biology, 2015, 1270, 81-90.	0.4	0
1122	Cellular Zinc Signalling Is Triggered by CK2. , 2015, , 141-157.		2
1125	Gold Nanoparticle-Based FÃ¶rster Resonance Energy Transfer (FRET) Analysis of Estrogen Receptor: DNA Interaction. Methods in Molecular Biology, 2016, 1366, 219-232.	0.4	1
1126	The Diverse Requirements of ARS2 in nuclear cap-binding complex-dependent RNA Processing. RNA & Disease (Houston, Tex), 0, , .	1.0	1
1129	High-Throughput Quantification of SH2 Domainâ€“Phosphopeptide Interactions with Celluloseâ€“Peptide Conjugate Microarrays. Methods in Molecular Biology, 2017, 1555, 375-394.	0.4	1
1131	Multi-Omics Profiling Establishes the Polypharmacology of FDA Approved CSK4/6 Inhibitors and Its Impact on Drug Response. SSRN Electronic Journal, 0, , .	0.4	1
1146	Advances in Mass Spectrometry-Based Proteomics and Its Application in Cancer Research. , 2019, , 89-112.		0
1151	Selected Reaction Monitoring of Kinase Activity-Targeted Phosphopeptides. Chromatography, 2019, 40, 39-47.	0.8	5
1163	Identifying Disease Modules Based on Connectivity and Semantic Similarities. Communications in Computer and Information Science, 2020, , 26-40.	0.4	1
1164	IMRPS: Inserted and Modified Residues in Protein Structures. A database. Journal of Applied Crystallography, 2020, 53, 569-573.	1.9	1
1166	Lysine acetylation regulates the interaction between proteins and membranes. Nature Communications, 2021, 12, 6466.	5.8	27

#	ARTICLE	IF	CITATIONS
1168	BioKG. , 2020, , .		24
1171	Purification and Regulation of Pyruvate Kinase from the Foot Muscle of the Anoxia and Freeze Tolerant Marine Snail, Littorina littorea. Protein Journal, 2020, 39, 531-541.	0.7	5
1172	Kinaseâ€"substrate Edge Biomarkers Provide A More Accurate Prognostic Prediction in ER-negative Breast Cancer. Genomics, Proteomics and Bioinformatics, 2020, 18, 525-538.	3.0	0
1173	Computational methods and opportunities for phosphorylation network medicine. Translational Cancer Research, 2014, 3, 266-278.	0.4	8
1175	Systems biology and big data analytics. , 2022, , 425-442.		0
1176	Targeted Mass Spectrometry Enables Multiplexed Quantification of Immunomodulatory Proteins in Clinical Biospecimens. Frontiers in Immunology, 2021, 12, 765898.	2.2	13
1178	Multiomic characterization of oncogenic signaling mediated by wild-type and mutant RIT1. Science Signaling, 2021, 14, eabc4520.	1.6	6
1179	The Spliced Leader RNA Silencing (SLS) Pathway in Trypanosoma brucei Is Induced by Perturbations of Endoplasmic Reticulum, Golgi Complex, or Mitochondrial Protein Factors: Functional Analysis of SLS-Inducing Kinase PK3. MBio, 2021, 12, e0260221.	1.8	2
1180	Overexpression of Lin28A in neural progenitor cells in vivo does not lead to brain tumor formation but results in reduced spine density. Acta Neuropathologica Communications, 2021, 9, 185.	2.4	5
1181	Cholesterol Regulates the Tumor Adaptive Resistance to MAPK Pathway Inhibition. Journal of Proteome Research, 2021, 20, 5379-5391.	1.8	4
1182	Diet high in branched-chain amino acid promotes PDAC development by USP1-mediated BCAT2 stabilization. National Science Review, 2022, 9, .	4.6	15
1184	Predicting Kinase-Substrate Interactions in Medulloblastoma Subtypes. , 2020, , .		0
1185	Aberrant TDPâ€43 phosphorylation: a key wind gap from TDPâ€43 to TDPâ€43 proteinopathy. , 2021, 7, 119-131.		0
1186	Advanced Glycation End-Products (AGEs) of Lysine and Effects of Anti-TCR/Anti-TNF-Î± Antibody-Based Therapy in the LEW.1AR1-iddm Rat, an Animal Model of Human Type 1 Diabetes. International Journal of Molecular Sciences, 2022, 23, 1541.	1.8	1
1187	Erythropoietin Interacts with Specific S100 Proteins. Biomolecules, 2022, 12, 120.	1.8	8
1188	multiFLEX-LF: A Computational Approach to Quantify the Modification Stoichiometries in Label-Free Proteomics Data Sets. Journal of Proteome Research, 2022, 21, 899-909.	1.8	1
1189	Integrin-linked kinase (ILK): the known vs. the unknown and perspectives. Cellular and Molecular Life Sciences, 2022, 79, 100.	2.4	28
1190	Computational analyses of mechanism of action (MoA): data, methods and integration. RSC Chemical Biology, 2022, 3, 170-200.	2.0	32

#	ARTICLE	IF	CITATIONS
1191	Functions and Regulation of Translation Elongation Factors. Frontiers in Molecular Biosciences, 2021, 8, 816398.	1.6	19
1192	Proteomeâ€scale mapping of binding sites in the unstructured regions of the human proteome. Molecular Systems Biology, 2022, 18, e10584.	3.2	33
1193	Cytoplasmic switch of ARS2 isoforms promotes nonsense-mediated mRNA decay and arsenic sensitivity. Nucleic Acids Research, 2022, 50, 1620-1638.	6.5	2
1194	Structure-based prediction of HDAC6 substrates validated by enzymatic assay reveals determinants of promiscuity and detects new potential substrates. Scientific Reports, 2022, 12, 1788.	1.6	7
1195	The aqueous humor proteome is intrinsically disordered. Biochemistry and Biophysics Reports, 2022, 29, 101202.	0.7	0
1196	EMBER: multi-label prediction of kinase-substrate phosphorylation events through deep learning. Bioinformatics, 2022, 38, 2119-2126.	1.8	11
1197	Metadherin (AEG-1/MTDH/LYRIC) expression: Significance in malignancy and crucial role in colorectal cancer. Advances in Clinical Chemistry, 2022, 106, 235-280.	1.8	15
1199	Phosphoproteome of signaling by ErbB2 in ovarian cancer cells. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2022, 1870, 140768.	1.1	3
1201	PhosPiR: an automated phosphoproteomic pipeline in R. Briefings in Bioinformatics, 2022, 23, .	3.2	7
1202	åŸºäºŽç½‘ç»œå’ŒåŸºå›å·®å¼‚è¡¨è¾¾ä¿¡æ¯çš„ç™Œç—‡è‡´ç—…åŸºå›é¢„æµ‹. Scientia Sinica Vitae, 2022, , .	0.1	0
1203	A human kinase yeast array for the identification of kinases modulating phosphorylationâ€dependent proteinâ€“protein interactions. Molecular Systems Biology, 2022, 18, e10820.	3.2	9
1204	Resources for computational prediction of intrinsic disorder in proteins. Methods, 2022, 204, 132-141.	1.9	17
1205	Epitope-based peptide vaccine design and elucidation of novel compounds against 3C like protein of SARS-CoV-2. PLoS ONE, 2022, 17, e0264700.	1.1	10
1207	Temporal dynamics from phosphoproteomics using endoscopic biopsy specimens provides new therapeutic targets in stage IV gastric cancer. Scientific Reports, 2022, 12, 4419.	1.6	4
1208	Protein methylation in mitochondria. Journal of Biological Chemistry, 2022, 298, 101791.	1.6	18
1209	RIF1 acts in DNA repair through phosphopeptide recognition of 53BP1. Molecular Cell, 2022, 82, 1359-1371.e9.	4.5	14
1210	DOC2b Enhances Î²-Cell Function via a Novel Tyrosine Phosphorylation-Dependent Mechanism. Diabetes, 2022, 71, 1246-1260.	0.3	4
1211	Evaluation of Jumonji C lysine demethylase substrate preference to guide identification of in vitro substrates. STAR Protocols, 2022, 3, 101271.	0.5	2

#	Article	IF	Citations
1212	KANPHOS: A Database of Kinase-Associated Neural Protein Phosphorylation in the Brain. Cells, 2022, 11, 47.	1.8	8
1213	Identification of transcriptional regulatory network associated with response of host epithelial cells to SARS-CoV-2. Scientific Reports, 2021, 11, 23928.	1.6	2
1214	Genetic encoding of a nonhydrolyzable phosphotyrosine analog in mammalian cells. Chemical Communications, 2022, 58, 5897-5900.	2.2	7
1215	STE20 phosphorylation of AMPK-related kinases revealed by biochemical purifications combined with genetics. Journal of Biological Chemistry, 2022, 298, 101928.	1.6	5
1216	Molecular characterization of linker and loop-mediated structural modulation and hinge motion in the C4-C5 domains of cMyBPC. Journal of Structural Biology, 2022, 214, 107856.	1.3	5
1217	Identification of Phosphorylation and Other Post-Translational Modifications in the Central C4C5 Domains of Murine Cardiac Myosin Binding Protein C. ACS Omega, 2022, 7, 14189-14202.	1.6	4
1218	An atlas of posttranslational modifications on RNA binding proteins. Nucleic Acids Research, 2022, 50, 4329-4339.	6.5	8
1235	What Is Parvalbumin for?. Biomolecules, 2022, 12, 656.	1.8	15
1237	Extracellular phosphoprotein regulation is affected by culture system scale-down. Biochimica Et Biophysica Acta - General Subjects, 2022, 1866, 130165.	1.1	1
1238	Allosteric regulation controls actin-bundling properties of human plastins. Nature Structural and Molecular Biology, 2022, 29, 519-528.	3.6	11
1239	Src kinase: An attractive therapeutic target for prostate cancer. , 2022, , 479-503.		0
1240	Probing lysine posttranslational modifications by unnatural amino acids. Chemical Communications, 2022, 58, 7216-7231.	2.2	15
1241	Identifying Candidate Flavonoids for Non-Alcoholic Fatty Liver Disease by Network-Based Strategy. Frontiers in Pharmacology, 0, 13, .	1.6	4
1242	Time-resolved phosphoproteome and proteome analysis reveals kinase signaling on master transcription factors during myogenesis. IScience, 2022, 25, 104489.	1.9	4
1245	Posttranslational Regulation of Inflammasomes, Its Potential as Biomarkers and in the Identification of Novel Drugs Targets. Frontiers in Cell and Developmental Biology, 0, 10, .	1.8	5
1246	Quantitative phosphoproteomics reveal cellular responses from caffeine, coumarin and quercetin in treated HepG2 cells. Toxicology and Applied Pharmacology, 2022, 449, 116110.	1.3	4
1247	Time-resolved quantitative phosphoproteomics reveals cellular responses induced by caffeine and coumarin. Toxicology and Applied Pharmacology, 2022, 449, 116115.	1.3	4
1248	Mini-review: Recent advances in post-translational modification site prediction based on deep learning. Computational and Structural Biotechnology Journal, 2022, 20, 3522-3532.	1.9	13

#	ARTICLE	IF	CITATIONS
1249	VEGFR endocytosis: Implications for angiogenesis. Progress in Molecular Biology and Translational Science, 2023, , 109-139.	0.9	1
1251	Englerin A Rewires Phosphosignaling via Hsp27 Hyperphosphorylation to Induce Cytotoxicity in Renal Cancer Cells. Journal of Proteome Research, 2022, 21, 1948-1960.	1.8	3
1252	Hepatitis C Virus Infection and Intrinsic Disorder in the Signaling Pathways Induced by Toll-Like Receptors. Biology, 2022, 11, 1091.	1.3	4
1253	KSTAR: An algorithm to predict patient-specific kinase activities from phosphoproteomic data. Nature Communications, 2022, 13, .	5.8	6
1254	Revisiting the multisite phosphorylation that produces the M-phase supershift of key mitotic regulators. Molecular Biology of the Cell, 2022, 33, .	0.9	2
1256	Co-expression network analysis of human tau-transgenic mice reveals protein modules associated with tau-induced pathologies. IScience, 2022, 25, 104832.	1.9	9
1257	Intrinsically disordered BMP4 morphogen and the beak of the finch: Co-option of an ancient axial patterning system. International Journal of Biological Macromolecules, 2022, 219, 366-373.	3.6	5
1258	PeSA 2.0: A software tool for peptide specificity analysis implementing positive and negative motifs and motif-based peptide scoring. Computational Biology and Chemistry, 2022, 101, 107753.	1.1	2
1259	Bioinformatics Resources, Tools, and Strategies in Designing Therapeutic Proteins. , 2022, , 91-123.		0
1260	Intrinsic Disorder in BAP1 and Its Association with Uveal Melanoma. Genes, 2022, 13, 1703.	1.0	7
1262	Canonical structural-binding modes in the calmodulinâ€"target protein complexes. Journal of Biomolecular Structure and Dynamics, 2023, 41, 7582-7594.	2.0	1
1263	Phosphoproteomics of extracellular vesicles integrated with multiomics analysis reveals novel kinase networks for lung cancer. Molecular Carcinogenesis, 2022, 61, 1116-1127.	1.3	2
1264	CARM1-mediated methylation of ASXL2 impairs tumor-suppressive function of MLL3/COMPASS. Science Advances, 2022, 8, .	4.7	4
1265	Characterization of KDM5 lysine demethylase family substrate preference and identification of novel substrates. Journal of Biochemistry, 2023, 173, 31-42.	0.9	2
1266	Thirty years of molecular dynamics simulations on posttranslational modifications of proteins. Physical Chemistry Chemical Physics, 2022, 24, 26371-26397.	1.3	9
1267	Structural and functional investigation of the human snRNP assembly factor AAR2 in complex with the RNase H-like domain of PRPF8. Acta Crystallographica Section D: Structural Biology, 2022, 78, 1373-1383.	1.1	1
1269	Testisâ€specific serine kinase 3 is required for sperm morphogenesis and male fertility. Andrology, 2023, 11, 826-839.	1.9	7
1271	Identification and molecular modeling of novel endogenous activator proteins of Sirt-1: an <i>in silico</i> study. Journal of Biomolecular Structure and Dynamics, 0, , 1-16.	2.0	1

#	Article	IF	Citations
1272	Predictive functional, statistical and structural analysis of CSNK2A1 and CSNK2B variants linked to neurodevelopmental diseases. Frontiers in Molecular Biosciences, 0, 9, .	1.6	2
1273	Host protein kinases required for SARS-CoV-2 nucleocapsid phosphorylation and viral replication. Science Signaling, 2022, 15, .	1.6	26
1274	Looking at the Pathogenesis of the Rabies Lyssavirus Strain Pasteur Vaccins through a Prism of the Disorder-Based Bioinformatics. Biomolecules, 2022, 12, 1436.	1.8	0
1276	Bioinformatics tools and data resources for assay development of fluid protein biomarkers. Biomarker Research, 2022, 10, .	2.8	8
1277	Phosphotyrosine Profiling Using SILAC. Methods in Molecular Biology, 2023, , 117-125.	0.4	0
1279	Inhibition of USP1 reverses the chemotherapy resistance through destabilization of MAX in the relapsed/refractory B-cell lymphoma. Leukemia, 0, , .	3.3	1
1280	Intrinsic disorder and posttranslational modification: an evolutionary perspective. , 2023, , 377-396.		0
1281	Customized synthesis of phosphoprotein bearing phosphoserine or its nonhydrolyzable analog. Synthetic and Systems Biotechnology, 2023, 8, 69-78.	1.8	1
1282	Intrinsic Disorder as a Natural Preservative: High Levels of Intrinsic Disorder in Proteins Found in the 2600-Year-Old Human Brain. Biology, 2022, 11, 1704.	1.3	3
1283	Evolutionary Divergence of Phosphorylation to Regulate Interactive Protein Networks in Lower and Higher Species. International Journal of Molecular Sciences, 2022, 23, 14429.	1.8	4
1284	Enhanced access to the human phosphoproteome with genetically encoded phosphothreonine. Nature Communications, 2022, 13, .	5.8	4
1285	dSCOPE: a software to detect sequences critical for liquidâ€“liquid phase separation. Briefings in Bioinformatics, 2023, 24, .	3.2	8
1286	A Genetically Encoded Magnetic Resonance Imaging Reporter Enables Sensitive Detection and Tracking of Spontaneous Metastases in Deep Tissues. Cancer Research, 2023, 83, 673-685.	0.4	12
1287	PICALM and Alzheimerâ€™s Disease: An Update and Perspectives. Cells, 2022, 11, 3994.	1.8	19
1288	DisCanVis: Visualizing integrated structural and functional annotations to better understand the effect of cancer mutations located within disordered proteins. Protein Science, 2023, 32, .	3.1	1
1289	Systemic structural analysis of alterations reveals a common structural basis of driver mutations in cancer. NAR Cancer, 2023, 5, .	1.6	1
1290	Phosphorylation mutation impairs the promoting effect of spastin on neurite outgrowth without affecting its microtubule severing ability. European Journal of Histochemistry, 2022, 67, .	0.6	0
1291	Applications of deep learning in understanding gene regulation. Cell Reports Methods, 2023, 3, 100384.	1.4	13

#	Article	IF	Citations
1292	Genetic encoding of 3â€nitroâ€tyrosine reveals the impacts of 14â€3â€3 nitration on client binding and dephosphorylation. Protein Science, 2023, 32, .	3.1	2
1293	Liaisons dangereuses: Intrinsic Disorder in Cellular Proteins Recruited to Viral Infection-Related Biocondensates. International Journal of Molecular Sciences, 2023, 24, 2151.	1.8	5
1294	HEAT SHOCK PROTEIN 90.6 interacts with carbon and nitrogen metabolism components during seed development. Plant Physiology, 2023, 191, 2316-2333.	2.3	4
1295	Phosphoproteomic analysis of metformin signaling in colorectal cancer cells elucidates mechanism of action and potential therapeutic opportunities. Clinical and Translational Medicine, 2023, 13, .	1.7	7
1296	mNeuCode Empowers Targeted Proteome Analysis of Arginine Dimethylation. Analytical Chemistry, 2023, 95, 3684-3693.	3.2	2
1297	Translation regulation of specific mRNAs by RPS26 C-terminal RNA-binding tail integrates energy metabolism and AMPK-mTOR signaling. Nucleic Acids Research, 2023, 51, 4415-4428.	6.5	0
1298	Protein phosphorylation database and prediction tools. Briefings in Bioinformatics, 2023, 24, .	3.2	3
1299	Structural remodeling of AAA+ ATPase p97 by adaptor protein ASPL facilitates posttranslational methylation by METTL21D. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	6
1300	Phosformer: an explainable transformer model for protein kinase-specific phosphorylation predictions. Bioinformatics, 2023, 39, .	1.8	6
1301	Systematic Assessment of Protein C-Termini Mutated in Human Disorders. Biomolecules, 2023, 13, 355.	1.8	0
1303	Coordinated activation of c-Src and FOXM1 drives tumor cell proliferation and breast cancer progression. Journal of Clinical Investigation, 2023, 133, .	3.9	6
1305	The language of posttranslational modifications and deciphering it from proteomics data. , 2023, , 109-136.		1
1306	Coâ€translational Installation of Posttranslational Modifications by Nonâ€canonical Amino Acid Mutagenesis. ChemBioChem, 2023, 24, .	1.3	1
1307	Automated assembly of molecular mechanisms at scale from text mining and curated databases. Molecular Systems Biology, 2023, 19, .	3.2	9
1308	Human seven-Î²-strand (METTL) methyltransferasesÂ-Âconquering the universe of protein lysine methylation. Journal of Biological Chemistry, 2023, 299, 104661.	1.6	6
1309	Glutathionylation on RNA-binding proteins: a regulator of liquidâ€'liquid phase separation in the pathogenesis of amyotrophic lateral sclerosis. Experimental and Molecular Medicine, 0, , .	3.2	1
1310	Exploration of O-GlcNAc transferase glycosylation sites reveals a target sequence compositional bias. Journal of Biological Chemistry, 2023, 299, 104629.	1.6	1
1311	Biomolecular condensates: insights into early and late steps of the HIV-1 replication cycle. Retrovirology, 2023, 20, .	0.9	4

#	ARTICLE	IF	CITATIONS
1312	The lysophosphatidic acid-regulated signal transduction network in ovarian cancer cells and its role in actomyosin dynamics, cell migration and entosis. Theranostics, 2023, 13, 1921-1948.	4.6	2
1313	Cellular stress induces non-canonical activation of the receptor tyrosine kinase EphA2 through the p38-MK2-RSK signaling pathway. Journal of Biological Chemistry, 2023, 299, 104699.	1.6	1
1314	Computational Analysis Reveals Distinctive Interaction of miRNAs with Target Genes in the Pathogenesis of Chronic Kidney Disease. Genes, 2023, 14, 898.	1.0	0
1345	Tutorial: a guide for the selection of fast and accurate computational tools for the prediction of intrinsic disorder in proteins. Nature Protocols, 2023, 18, 3157-3172.	5.5	4
1356	Tumor-suppressive functions of protein lysine methyltransferases. Experimental and Molecular Medicine, 2023, 55, 2475-2497.	3.2	0