

# Yu Xue

## List of Publications by Year in descending order

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131  
papers

16,177  
citations

41344

49  
h-index

17592

121  
g-index

134  
all docs

134  
docs citations

134  
times ranked

30136  
citing authors

#	ARTICLE	IF	CITATIONS
1	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). <i>Autophagy</i> , 2016, 12, 1-222.	9.1	4,701
2	HemI: A Toolkit for Illustrating Heatmaps. <i>PLoS ONE</i> , 2014, 9, e111988.	2.5	963
3	IBS: an illustrator for the presentation and visualization of biological sequences. <i>Bioinformatics</i> , 2015, 31, 3359-3361.	4.1	817
4	GPS 2.0, a Tool to Predict Kinase-specific Phosphorylation Sites in Hierarchy. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1598-1608.	3.8	587
5	CSS-Palm 2.0: an updated software for palmitoylation sites prediction. <i>Protein Engineering, Design and Selection</i> , 2008, 21, 639-644.	2.1	511
6	DOG 1.0: illustrator of protein domain structures. <i>Cell Research</i> , 2009, 19, 271-273.	12.0	505
7	GPS-SUMO: a tool for the prediction of sumoylation sites and SUMO-interaction motifs. <i>Nucleic Acids Research</i> , 2014, 42, W325-W330.	14.5	417
8	Database Resources of the National Genomics Data Center, China National Center for Bioinformation in 2022. <i>Nucleic Acids Research</i> , 2022, 50, D27-D38.	14.5	364
9	AnimalTFDB 2.0: a resource for expression, prediction and functional study of animal transcription factors. <i>Nucleic Acids Research</i> , 2015, 43, D76-D81.	14.5	287
10	Inhibiting PD-L1 palmitoylation enhances T-cell immune responses against tumours. <i>Nature Biomedical Engineering</i> , 2019, 3, 306-317.	22.5	279
11	Plasma Proteomics Identify Biomarkers and Pathogenesis of COVID-19. <i>Immunity</i> , 2020, 53, 1108-1122.e5.	14.3	228
12	Systematic study of protein sumoylation: Development of a site-specific predictor of SUMOsp 2.0. <i>Proteomics</i> , 2009, 9, 3409-3412.	2.2	227
13	GPS-SNO: Computational Prediction of Protein S-Nitrosylation Sites with a Modified GPS Algorithm. <i>PLoS ONE</i> , 2010, 5, e11290.	2.5	223
14	GPS 2.1: enhanced prediction of kinase-specific phosphorylation sites with an algorithm of motif length selection. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 255-260.	2.1	217
15	GPS: a comprehensive www server for phosphorylation sites prediction. <i>Nucleic Acids Research</i> , 2005, 33, W184-W187.	14.5	215
16	PLMD: An updated data resource of protein lysine modifications. <i>Journal of Genetics and Genomics</i> , 2017, 44, 243-250.	3.9	198
17	GPS 5.0: An Update on the Prediction of Kinase-specific Phosphorylation Sites in Proteins. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 72-80.	6.9	197
18	PPSP: prediction of PK-specific phosphorylation site with Bayesian decision theory. <i>BMC Bioinformatics</i> , 2006, 7, 163.	2.6	183

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19	SUMOSp: a web server for sumoylation site prediction. <i>Nucleic Acids Research</i> , 2006, 34, W254-W257.	14.5	179
20	Database Resources of the National Genomics Data Center, China National Center for Bioinformation in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D18-D28.	14.5	168
21	Database Resources of the National Genomics Data Center in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D24-D33.	14.5	165
22	Systematic Analysis of Protein Phosphorylation Networks From Phosphoproteomic Data. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1070-1083.	3.8	161
23	Database Resources of the BIG Data Center in 2019. <i>Nucleic Acids Research</i> , 2019, 47, D8-D14.	14.5	157
24	CPLM: a database of protein lysine modifications. <i>Nucleic Acids Research</i> , 2014, 42, D531-D536.	14.5	155
25	GPS: a novel group-based phosphorylation predicting and scoring method. <i>Biochemical and Biophysical Research Communications</i> , 2004, 325, 1443-1448.	2.1	149
26	CSS-Palm: palmitoylation site prediction with a clustering and scoring strategy (CSS). <i>Bioinformatics</i> , 2006, 22, 894-896.	4.1	130
27	PTMD: A Database of Human Disease-associated Post-translational Modifications. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 244-251.	6.9	129
28	MeMo: a web tool for prediction of protein methylation modifications. <i>Nucleic Acids Research</i> , 2006, 34, W249-W253.	14.5	123
29	Open resource of clinical data from patients with pneumonia for the prediction of COVID-19 outcomes via deep learning. <i>Nature Biomedical Engineering</i> , 2020, 4, 1197-1207.	22.5	122
30	GPS-Lipid: a robust tool for the prediction of multiple lipid modification sites. <i>Scientific Reports</i> , 2016, 6, 28249.	3.3	120
31	DrLLPS: a data resource of liquid-liquid phase separation in eukaryotes. <i>Nucleic Acids Research</i> , 2020, 48, D288-D295.	14.5	112
32	Prediction of N <sup>ɛ</sup> -acetylation on internal lysines implemented in Bayesian Discriminant Method. <i>Biochemical and Biophysical Research Communications</i> , 2006, 350, 818-824.	2.1	106
33	UUCD: a family-based database of ubiquitin and ubiquitin-like conjugation. <i>Nucleic Acids Research</i> , 2013, 41, D445-D451.	14.5	99
34	GPS-YNO2: computational prediction of tyrosine nitration sites in proteins. <i>Molecular BioSystems</i> , 2011, 7, 1197.	2.9	94
35	GPS-CCD: A Novel Computational Program for the Prediction of Calpain Cleavage Sites. <i>PLoS ONE</i> , 2011, 6, e19001.	2.5	94
36	Pyruvate Kinase M2 Activates mTORC1 by Phosphorylating AKT1S1. <i>Scientific Reports</i> , 2016, 6, 21524.	3.3	92

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37	NBA-Palm: prediction of palmitoylation site implemented in Naïve Bayes algorithm. BMC Bioinformatics, 2006, 7, 458.	2.6	88
38	GPS-PAIL: prediction of lysine acetyltransferase-specific modification sites from protein sequences. Scientific Reports, 2016, 6, 39787.	3.3	88
39	DeepNitro: Prediction of Protein Nitration and Nitrosylation Sites by Deep Learning. Genomics, Proteomics and Bioinformatics, 2018, 16, 294-306.	6.9	81
40	dbPAF: an integrative database of protein phosphorylation in animals and fungi. Scientific Reports, 2016, 6, 23534.	3.3	78
41	PhosSNP for Systematic Analysis of Genetic Polymorphisms That Influence Protein Phosphorylation. Molecular and Cellular Proteomics, 2010, 9, 623-634.	3.8	72
42	Genome of Plant Maca ( <i>Lepidium meyenii</i> ) Illuminates Genomic Basis for High-Altitude Adaptation in the Central Andes. Molecular Plant, 2016, 9, 1066-1077.	8.3	69
43	GPS-Palm: a deep learning-based graphic presentation system for the prediction of <i>S</i> -palmitoylation sites in proteins. Briefings in Bioinformatics, 2021, 22, 1836-1847.	6.5	64
44	Metformin activates chaperone-mediated autophagy and improves disease pathologies in an Alzheimer disease mouse model. Protein and Cell, 2021, 12, 769-787.	11.0	63
45	OUP accepted manuscript. Nucleic Acids Research, 2017, 45, D264-D270.	14.5	62
46	CPLA 1.0: an integrated database of protein lysine acetylation. Nucleic Acids Research, 2011, 39, D1029-D1034.	14.5	60
47	Stable Isotope Metabolic Labeling-based Quantitative Phosphoproteomic Analysis of Arabidopsis Mutants Reveals Ethylene-regulated Time-dependent Phosphoproteins and Putative Substrates of Constitutive Triple Response 1 Kinase. Molecular and Cellular Proteomics, 2013, 12, 3559-3582.	3.8	58
48	iUUCD 2.0: an update with rich annotations for ubiquitin and ubiquitin-like conjugations. Nucleic Acids Research, 2018, 46, D447-D453.	14.5	57
49	CPSS: a computational platform for the analysis of small RNA deep sequencing data. Bioinformatics, 2012, 28, 1925-1927.	4.1	55
50	A Summary of Computational Resources for Protein Phosphorylation. Current Protein and Peptide Science, 2010, 11, 485-496.	1.4	53
51	EKPD: a hierarchical database of eukaryotic protein kinases and protein phosphatases. Nucleic Acids Research, 2014, 42, D496-D502.	14.5	52
52	Mechanism of cargo recognition by retromer-linked SNX-BAR proteins. PLoS Biology, 2020, 18, e3000631.	5.6	51
53	EPSD: a well-annotated data resource of protein phosphorylation sites in eukaryotes. Briefings in Bioinformatics, 2021, 22, 298-307.	6.5	49
54	Phosphoproteome-based kinase activity profiling reveals the critical role of MAP2K2 and PLK1 in neuronal autophagy. Autophagy, 2017, 13, 1969-1980.	9.1	48

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55	Computational prediction of methylation types of covalently modified lysine and arginine residues in proteins. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw041.	6.5	47
56	A genome-wide analysis of sumoylation-related biological processes and functions in human nucleus. <i>FEBS Letters</i> , 2005, 579, 3369-3375.	2.8	46
57	Mal-Lys: prediction of lysine malonylation sites in proteins integrated sequence-based features with mRMR feature selection. <i>Scientific Reports</i> , 2016, 6, 38318.	3.3	46
58	dbPPT: a comprehensive database of protein phosphorylation in plants. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau121.	3.0	45
59	Enhanced Purification of Ubiquitinated Proteins by Engineered Tandem Hybrid Ubiquitin-binding Domains (ThUBDs). <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1381-1396.	3.8	44
60	GPS-ARM: Computational Analysis of the APC/C Recognition Motif by Predicting D-Boxes and KEN-Boxes. <i>PLoS ONE</i> , 2012, 7, e34370.	2.5	44
61	OUP accepted manuscript. <i>Nucleic Acids Research</i> , 2017, 45, D397-D403.	14.5	42
62	Information Commons for Rice (IC4R). <i>Nucleic Acids Research</i> , 2016, 44, D1172-D1180.	14.5	41
63	THANATOS: an integrative data resource of proteins and post-translational modifications in the regulation of autophagy. <i>Autophagy</i> , 2018, 14, 296-310.	9.1	41
64	GPS-PUP: computational prediction of pupylation sites in prokaryotic proteins. <i>Molecular BioSystems</i> , 2011, 7, 2737.	2.9	40
65	Systematic analysis of the in situ crosstalk of tyrosine modifications reveals no additional natural selection on multiply modified residues. <i>Scientific Reports</i> , 2014, 4, 7331.	3.3	39
66	Pan-Cancer Analysis Reveals the Functional Importance of Protein Lysine Modification in Cancer Development. <i>Frontiers in Genetics</i> , 2018, 9, 254.	2.3	39
67	Posttranscriptional regulation of de novo lipogenesis by glucose-induced O-GlcNAcylation. <i>Molecular Cell</i> , 2021, 81, 1890-1904.e7.	9.7	39
68	Systematic Analysis of the Phosphoproteome and Kinase-substrate Networks in the Mouse Testis. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3626-3638.	3.8	38
69	Insulin signaling regulates longevity through protein phosphorylation in <i>Caenorhabditis elegans</i> . <i>Nature Communications</i> , 2021, 12, 4568.	12.8	38
70	Comparative Analysis of Fruit Ripening-Related miRNAs and Their Targets in Blueberry Using Small RNA and Degradome Sequencing. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2767.	4.1	36
71	An integrative multi-omics approach uncovers the regulatory role of CDK7 and CDK4 in autophagy activation induced by silica nanoparticles. <i>Autophagy</i> , 2021, 17, 1426-1447.	9.1	33
72	Predicting lysine malonylation sites of proteins using sequence and predicted structural features. <i>Journal of Computational Chemistry</i> , 2018, 39, 1757-1763.	3.3	30

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73	Phosphorylation of SNX27 by MAPK11/14 links cellular stress signaling pathways with endocytic recycling. <i>Journal of Cell Biology</i> , 2021, 220, .	5.2	30
74	Proteome-wide prediction of PKA phosphorylation sites in eukaryotic kingdom. <i>Genomics</i> , 2008, 92, 457-463.	2.9	29
75	Systematic analysis of the Plk-mediated phosphoregulation in eukaryotes. <i>Briefings in Bioinformatics</i> , 2013, 14, 344-360.	6.5	29
76	HybridSucc: A Hybrid-learning Architecture for General and Species-specific Succinylation Site Prediction. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 194-207.	6.9	28
77	The E3 ubiquitin ligase HECTD3 regulates ubiquitination and degradation of Tara. <i>Biochemical and Biophysical Research Communications</i> , 2008, 367, 805-812.	2.1	27
78	MiCroKit 3.0: an integrated database of midbody, centrosome and kinetochore. <i>Nucleic Acids Research</i> , 2010, 38, D155-D160.	14.5	27
79	Systematic characterization of small RNAome during zebrafish early developmental stages. <i>BMC Genomics</i> , 2014, 15, 117.	2.8	27
80	Multi-omic profiling of plasma reveals molecular alterations in children with COVID-19. <i>Theranostics</i> , 2021, 11, 8008-8026.	10.0	27
81	Prediction of novel pre-microRNAs with high accuracy through boosting and SVM. <i>Bioinformatics</i> , 2011, 27, 1436-1437.	4.1	26
82	A general user interface for prediction servers of proteins' post-translational modification sites. <i>Nature Protocols</i> , 2006, 1, 1318-1321.	12.0	25
83	Comprehensive and Reliable Phosphorylation Site Mapping of Individual Phosphoproteins by Combination of Multiple Stage Mass Spectrometric Analysis with a Target-Decoy Database Search. <i>Analytical Chemistry</i> , 2009, 81, 5794-5805.	6.5	25
84	Model-based analysis uncovers mutations altering autophagy selectivity in human cancer. <i>Nature Communications</i> , 2021, 12, 3258.	12.8	24
85	Heml 2.0: an online service for heatmap illustration. <i>Nucleic Acids Research</i> , 2022, 50, W405-W411.	14.5	24
86	dbPSP: a curated database for protein phosphorylation sites in prokaryotes. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav031.	3.0	23
87	MiCroKiTS 4.0: a database of midbody, centrosome, kinetochore, telomere and spindle. <i>Nucleic Acids Research</i> , 2015, 43, D328-D334.	14.5	23
88	Integrated omics in <i>Drosophila</i> uncover a circadian kinome. <i>Nature Communications</i> , 2020, 11, 2710.	12.8	23
89	Phosphoproteomic Analysis of the Highly-Metastatic Hepatocellular Carcinoma Cell Line, MHCC97-H. <i>International Journal of Molecular Sciences</i> , 2015, 16, 4209-4225.	4.1	22
90	iEKPD 2.0: an update with rich annotations for eukaryotic protein kinases, protein phosphatases and proteins containing phosphoprotein-binding domains. <i>Nucleic Acids Research</i> , 2019, 47, D344-D350.	14.5	22

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91	Inhibiting MARSs reduces hyperhomocysteinemia-associated neural tube and congenital heart defects. <i>EMBO Molecular Medicine</i> , 2020, 12, e9469.	6.9	21
92	dbPSP 2.0, an updated database of protein phosphorylation sites in prokaryotes. <i>Scientific Data</i> , 2020, 7, 164.	5.3	20
93	CPLM 4.0: an updated database with rich annotations for protein lysine modifications. <i>Nucleic Acids Research</i> , 2022, 50, D451-D459.	14.5	20
94	Dysbindin as a novel biomarker for pancreatic ductal adenocarcinoma identified by proteomic profiling. <i>International Journal of Cancer</i> , 2016, 139, 1821-1829.	5.1	19
95	DeepPhagy: a deep learning framework for quantitatively measuring autophagy activity in <i>Saccharomyces cerevisiae</i> . <i>Autophagy</i> , 2020, 16, 626-640.	9.1	18
96	Reconfiguring phosphorylation signaling by genetic polymorphisms affects cancer susceptibility. <i>Journal of Molecular Cell Biology</i> , 2015, 7, 187-202.	3.3	17
97	Phosphoproteomics-based network medicine. <i>FEBS Journal</i> , 2013, 280, 5696-5704.	4.7	16
98	WocEA: The visualization of functional enrichment results in word clouds. <i>Journal of Genetics and Genomics</i> , 2018, 45, 415-417.	3.9	16
99	Precision Medicine: What Challenges Are We Facing?. <i>Genomics, Proteomics and Bioinformatics</i> , 2016, 14, 253-261.	6.9	15
100	A new method for classifying different phenotypes of kidney transplantation. <i>Cell Biology and Toxicology</i> , 2016, 32, 323-332.	5.3	14
101	Post-mortem tissue proteomics reveals the pathogenesis of multi-organ injuries of COVID-19. <i>National Science Review</i> , 2021, 8, nwab143.	9.5	14
102	Computational Prediction of Post-Translational Modification Sites in Proteins. , 0, , .		13
103	Computational Analysis of Phosphoproteomics: Progresses and Perspectives. <i>Current Protein and Peptide Science</i> , 2011, 12, 591-601.	1.4	13
104	Precipitate-Supported Thermal Proteome Profiling Coupled with Deep Learning for Comprehensive Screening of Drug Target Proteins. <i>ACS Chemical Biology</i> , 2022, 17, 252-262.	3.4	13
105	Enhancing autophagy maturation with CCZ1-MON1A complex alleviates neuropathology and memory defects in Alzheimer disease models. <i>Theranostics</i> , 2022, 12, 1738-1755.	10.0	13
106	Phosphoproteome Analysis Reveals Phosphorylation Underpinnings in the Brains of Nurse and Forager Honeybees ( <i>Apis mellifera</i> ). <i>Scientific Reports</i> , 2017, 7, 1973.	3.3	11
107	Computationally characterizing and comprehensive analysis of zinc-binding sites in proteins. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 171-180.	2.3	10
108	GPS-PBS: A Deep Learning Framework to Predict Phosphorylation Sites that Specifically Interact with Phosphoprotein-Binding Domains. <i>Cells</i> , 2020, 9, 1266.	4.1	10

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109	GPS-Uber: a hybrid-learning framework for prediction of general and E3-specific lysine ubiquitination sites. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	10
110	GPS-MBA: Computational Analysis of MHC Class II Epitopes in Type 1 Diabetes. <i>PLoS ONE</i> , 2012, 7, e33884.	2.5	9
111	Computational Analyses of TBC Protein Family in Eukaryotes. <i>Protein and Peptide Letters</i> , 2008, 15, 505-509.	0.9	8
112	Correlated expression of retrocopies and parental genes in zebrafish. <i>Molecular Genetics and Genomics</i> , 2016, 291, 723-737.	2.1	7
113	PTMsnP: A Web Server for the Identification of Driver Mutations That Affect Protein Post-translational Modification. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 593661.	3.7	7
114	Atg9-centered multi-omics integration reveals new autophagy regulators in <i>Saccharomyces cerevisiae</i> . <i>Autophagy</i> , 2021, 17, 4453-4476.	9.1	6
115	Analysis of phosphorylation sites on autophagy proteins. <i>Protein and Cell</i> , 2015, 6, 698-701.	11.0	5
116	Identification of rare variants in cardiac sodium channel $\beta$ 4-subunit gene SCN4B associated with ventricular tachycardia. <i>Molecular Genetics and Genomics</i> , 2019, 294, 1059-1071.	2.1	5
117	Ray Wu, fifth business or father of DNA sequencing?. <i>Protein and Cell</i> , 2016, 7, 467-470.	11.0	4
118	A novel genome-wide full-length kinesin prediction analysis reveals additional mammalian kinesins. <i>Science Bulletin</i> , 2006, 51, 1836-1847.	1.7	3
119	An efficient site-directed mutagenesis method for ColE1-type ori plasmid. <i>Analytical Biochemistry</i> , 2007, 363, 151-153.	2.4	3
120	Bioinformatics Technologies in Autophagy Research. <i>Advances in Experimental Medicine and Biology</i> , 2021, 1208, 387-453.	1.6	3
121	iCAL: a new pipeline to investigate autophagy selectivity and cancer. <i>Autophagy</i> , 2021, 17, 1799-1801.	9.1	3
122	Bioinformaticians wrestling with the big biomedical data. <i>Journal of Genetics and Genomics</i> , 2017, 44, 223-225.	3.9	2
123	Bioinformatics Commons: The Cornerstone of Life and Health Sciences. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 223-225.	6.9	2
124	The Potential Effect of Pests on Forest Fire: Flammability of Mongolian Pine Bark with Resinosis on Boles. <i>Forests</i> , 2021, 12, 365.	2.1	2
125	Design and Performance Analysis of 3-D Markov-Chain-Model-Based Fair Spectrum-Sharing Access for IoT Services. <i>IEEE Internet of Things Journal</i> , 2022, 9, 15756-15770.	8.7	2
126	Computational Identification of Protein Kinases and Kinase-Specific Substrates in Plants. <i>Methods in Molecular Biology</i> , 2015, 1306, 195-205.	0.9	1



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127	Ubiquitin and Ubiquitin-Like Conjugations in Complex Diseases: A Computational Perspective. <i>Translational Bioinformatics</i> , 2013, , 171-187.	0.0	1
128	Editorial: Computational Resources for Understanding Biomacromolecular Covalent Modifications. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 728127.	3.7	0
129	Proteome-Wide Analysis of Amino Acid Absence in Composition and Plasticity. <i>Lecture Notes in Computer Science</i> , 2008, , 167-178.	1.3	0
130	The human kinaseâ€substrate phosphorylation network rewired by genetic polymorphisms is heavily associated with cancers (984.3). <i>FASEB Journal</i> , 2014, 28, 984.3.	0.5	0
131	iPCD: A Comprehensive Data Resource of Regulatory Proteins in Programmed Cell Death. <i>Cells</i> , 2022, 11, 2018.	4.1	0