

Yu Xue

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6894853/publications.pdf>

Version: 2024-02-01

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	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
2	Database Resources of the National Genomics Data Center, China National Center for Bioinformatics in 2022. <i>Nucleic Acids Research</i> , 2022, 50, D27-D38.	14.5	364
3	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
4	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
5	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
6	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
7	Heml 2.0: an online service for heatmap illustration. <i>Nucleic Acids Research</i> , 2022, 50, W405-W411.	14.5	24
8	iPCD: A Comprehensive Data Resource of Regulatory Proteins in Programmed Cell Death. <i>Cells</i> , 2022, 11, 2018.	4.1	0
9	GPS-Palm: a deep learning-based graphic presentation system for the prediction of <i>S</i> -palmitoylation sites in proteins. <i>Briefings in Bioinformatics</i> , 2021, 22, 1836-1847.	6.5	64
10	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
11	Database Resources of the National Genomics Data Center, China National Center for Bioinformatics in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D18-D28.	14.5	168
12	Bioinformatics Technologies in Autophagy Research. <i>Advances in Experimental Medicine and Biology</i> , 2021, 1208, 387-453.	1.6	3
13	Multi-omic profiling of plasma reveals molecular alterations in children with COVID-19. <i>Theranostics</i> , 2021, 11, 8008-8026.	10.0	27
14	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
15	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
16	Atg9-centered multi-omics integration reveals new autophagy regulators in <i>Saccharomyces cerevisiae</i> . <i>Autophagy</i> , 2021, 17, 4453-4476.	9.1	6
17	Posttranscriptional regulation of de novo lipogenesis by glucose-induced O-GlcNAcylation. <i>Molecular Cell</i> , 2021, 81, 1890-1904.e7.	9.7	39
18	Model-based analysis uncovers mutations altering autophagy selectivity in human cancer. <i>Nature Communications</i> , 2021, 12, 3258.	12.8	24

#	ARTICLE	IF	CITATIONS
19	iCAL: a new pipeline to investigate autophagy selectivity and cancer. <i>Autophagy</i> , 2021, 17, 1799-1801.	9.1	3
20	Editorial: Computational Resources for Understanding Biomacromolecular Covalent Modifications. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 728127.	3.7	0
21	Metformin activates chaperone-mediated autophagy and improves disease pathologies in an Alzheimer disease mouse model. <i>Protein and Cell</i> , 2021, 12, 769-787.	11.0	63
22	Insulin signaling regulates longevity through protein phosphorylation in <i>Caenorhabditis elegans</i> . <i>Nature Communications</i> , 2021, 12, 4568.	12.8	38
23	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
24	EPSD: a well-annotated data resource of protein phosphorylation sites in eukaryotes. <i>Briefings in Bioinformatics</i> , 2021, 22, 298-307.	6.5	49
25	Database Resources of the National Genomics Data Center in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D24-D33.	14.5	165
26	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
27	Plasma Proteomics Identify Biomarkers and Pathogenesis of COVID-19. <i>Immunity</i> , 2020, 53, 1108-1122.e5.	14.3	228
28	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
29	DrLLPS: a data resource of liquid-liquid phase separation in eukaryotes. <i>Nucleic Acids Research</i> , 2020, 48, D288-D295.	14.5	112
30	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
31	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
32	Integrated omics in <i>Drosophila</i> uncover a circadian kinome. <i>Nature Communications</i> , 2020, 11, 2710.	12.8	23
33	dbPSP 2.0, an updated database of protein phosphorylation sites in prokaryotes. <i>Scientific Data</i> , 2020, 7, 164.	5.3	20
34	Mechanism of cargo recognition by retromer-linked SNX-BAR proteins. <i>PLoS Biology</i> , 2020, 18, e3000631.	5.6	51
35	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
36	Inhibiting MARSs reduces hyperhomocysteinemia-associated neural tube and congenital heart defects. <i>EMBO Molecular Medicine</i> , 2020, 12, e9469.	6.9	21

#	ARTICLE	IF	CITATIONS
37	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
38	Identification of rare variants in cardiac sodium channel β 4-subunit gene SCN4B associated with ventricular tachycardia. <i>Molecular Genetics and Genomics</i> , 2019, 294, 1059-1071.	2.1	5
39	Inhibiting PD-L1 palmitoylation enhances T-cell immune responses against tumours. <i>Nature Biomedical Engineering</i> , 2019, 3, 306-317.	22.5	279
40	Database Resources of the BIG Data Center in 2019. <i>Nucleic Acids Research</i> , 2019, 47, D8-D14.	14.5	157
41	iEKP2.0: 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
42	WocEA: The visualization of functional enrichment results in word clouds. <i>Journal of Genetics and Genomics</i> , 2018, 45, 415-417.	3.9	16
43	iUUCD 2.0: an update with rich annotations for ubiquitin and ubiquitin-like conjugations. <i>Nucleic Acids Research</i> , 2018, 46, D447-D453.	14.5	57
44	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
45	PTMD: A Database of Human Disease-associated Post-translational Modifications. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 244-251.	6.9	129
46	Bioinformatics Commons: The Cornerstone of Life and Health Sciences. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 223-225.	6.9	2
47	DeepNitro: Prediction of Protein Nitration and Nitrosylation Sites by Deep Learning. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 294-306.	6.9	81
48	Predicting lysine ϵ -malonylation sites of proteins using sequence and predicted structural features. <i>Journal of Computational Chemistry</i> , 2018, 39, 1757-1763.	3.3	30
49	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
50	OUP accepted manuscript. <i>Nucleic Acids Research</i> , 2017, 45, D397-D403.	14.5	42
51	OUP accepted manuscript. <i>Nucleic Acids Research</i> , 2017, 45, D264-D270.	14.5	62
52	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
53	PLMD: An updated data resource of protein lysine modifications. <i>Journal of Genetics and Genomics</i> , 2017, 44, 243-250.	3.9	198
54	Bioinformaticians wrestling with the big biomedical data. <i>Journal of Genetics and Genomics</i> , 2017, 44, 223-225.	3.9	2

#	ARTICLE	IF	CITATIONS
55	Phosphoproteome-based kinase activity profiling reveals the critical role of MAP2K2 and PLK1 in neuronal autophagy. <i>Autophagy</i> , 2017, 13, 1969-1980.	9.1	48
56	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
57	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
58	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
59	GPS-PAIL: prediction of lysine acetyltransferase-specific modification sites from protein sequences. <i>Scientific Reports</i> , 2016, 6, 39787.	3.3	88
60	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
61	Genome of Plant Maca (<i>Lepidium meyenii</i>) Illuminates Genomic Basis for High-Altitude Adaptation in the Central Andes. <i>Molecular Plant</i> , 2016, 9, 1066-1077.	8.3	69
62	Pyruvate Kinase M2 Activates mTORC1 by Phosphorylating AKT1S1. <i>Scientific Reports</i> , 2016, 6, 21524.	3.3	92
63	Precision Medicine: What Challenges Are We Facing?. <i>Genomics, Proteomics and Bioinformatics</i> , 2016, 14, 253-261.	6.9	15
64	GPS-Lipid: a robust tool for the prediction of multiple lipid modification sites. <i>Scientific Reports</i> , 2016, 6, 28249.	3.3	120
65	dbPAF: an integrative database of protein phosphorylation in animals and fungi. <i>Scientific Reports</i> , 2016, 6, 23534.	3.3	78
66	A new method for classifying different phenotypes of kidney transplantation. <i>Cell Biology and Toxicology</i> , 2016, 32, 323-332.	5.3	14
67	Ray Wu, fifth business or father of DNA sequencing?. <i>Protein and Cell</i> , 2016, 7, 467-470.	11.0	4
68	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). <i>Autophagy</i> , 2016, 12, 1-222.	9.1	4,701
69	Correlated expression of retrocopies and parental genes in zebrafish. <i>Molecular Genetics and Genomics</i> , 2016, 291, 723-737.	2.1	7
70	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
71	Information Commons for Rice (IC4R). <i>Nucleic Acids Research</i> , 2016, 44, D1172-D1180.	14.5	41
72	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

#	ARTICLE	IF	CITATIONS
73	Phosphoproteomic Analysis of the Highly-Metastatic Hepatocellular Carcinoma Cell Line, MHCC97-H. International Journal of Molecular Sciences, 2015, 16, 4209-4225.	4.1	22
74	IBS: an illustrator for the presentation and visualization of biological sequences. Bioinformatics, 2015, 31, 3359-3361.	4.1	817
75	Reconfiguring phosphorylation signaling by genetic polymorphisms affects cancer susceptibility. Journal of Molecular Cell Biology, 2015, 7, 187-202.	3.3	17
76	MiCroKiTS 4.0: a database of midbody, centrosome, kinetochore, telomere and spindle. Nucleic Acids Research, 2015, 43, D328-D334.	14.5	23
77	AnimalTFDB 2.0: a resource for expression, prediction and functional study of animal transcription factors. Nucleic Acids Research, 2015, 43, D76-D81.	14.5	287
78	Analysis of phosphorylation sites on autophagy proteins. Protein and Cell, 2015, 6, 698-701.	11.0	5
79	Computational Identification of Protein Kinases and Kinase-Specific Substrates in Plants. Methods in Molecular Biology, 2015, 1306, 195-205.	0.9	1
80	dbPPT: a comprehensive database of protein phosphorylation in plants. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau121.	3.0	45
81	Systematic Analysis of the Phosphoproteome and Kinase-substrate Networks in the Mouse Testis. Molecular and Cellular Proteomics, 2014, 13, 3626-3638.	3.8	38
82	GPS-SUMO: a tool for the prediction of sumoylation sites and SUMO-interaction motifs. Nucleic Acids Research, 2014, 42, W325-W330.	14.5	417
83	Heml: A Toolkit for Illustrating Heatmaps. PLoS ONE, 2014, 9, e111988.	2.5	963
84	Systematic characterization of small RNAome during zebrafish early developmental stages. BMC Genomics, 2014, 15, 117.	2.8	27
85	EKPD: a hierarchical database of eukaryotic protein kinases and protein phosphatases. Nucleic Acids Research, 2014, 42, D496-D502.	14.5	52
86	CPLM: a database of protein lysine modifications. Nucleic Acids Research, 2014, 42, D531-D536.	14.5	155
87	Computationally characterizing and comprehensive analysis of zinc-binding sites in proteins. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 171-180.	2.3	10
88	Systematic analysis of the in situ crosstalk of tyrosine modifications reveals no additional natural selection on multiply modified residues. Scientific Reports, 2014, 4, 7331.	3.3	39
89	The human kinase-substrate phosphorylation network rewired by genetic polymorphisms is heavily associated with cancers (984.3). FASEB Journal, 2014, 28, 984.3.	0.5	0
90	Systematic analysis of the Plk-mediated phosphoregulation in eukaryotes. Briefings in Bioinformatics, 2013, 14, 344-360.	6.5	29

#	ARTICLE	IF	CITATIONS
91	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. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3559-3582.	3.8	58
92	UUUCD: a family-based database of ubiquitin and ubiquitin-like conjugation. <i>Nucleic Acids Research</i> , 2013, 41, D445-D451.	14.5	99
93	Phosphoproteomics-based network medicine. <i>FEBS Journal</i> , 2013, 280, 5696-5704.	4.7	16
94	Ubiquitin and Ubiquitin-Like Conjugations in Complex Diseases: A Computational Perspective. <i>Translational Bioinformatics</i> , 2013, , 171-187.	0.0	1
95	CPSS: a computational platform for the analysis of small RNA deep sequencing data. <i>Bioinformatics</i> , 2012, 28, 1925-1927.	4.1	55
96	Systematic Analysis of Protein Phosphorylation Networks From Phosphoproteomic Data. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1070-1083.	3.8	161
97	GPS-MBA: Computational Analysis of MHC Class II Epitopes in Type 1 Diabetes. <i>PLoS ONE</i> , 2012, 7, e33884.	2.5	9
98	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
99	GPS-PUP: computational prediction of pupylation sites in prokaryotic proteins. <i>Molecular BioSystems</i> , 2011, 7, 2737.	2.9	40
100	GPS-YNO2: computational prediction of tyrosine nitration sites in proteins. <i>Molecular BioSystems</i> , 2011, 7, 1197.	2.9	94
101	GPS-CCD: A Novel Computational Program for the Prediction of Calpain Cleavage Sites. <i>PLoS ONE</i> , 2011, 6, e19001.	2.5	94
102	CPLA 1.0: an integrated database of protein lysine acetylation. <i>Nucleic Acids Research</i> , 2011, 39, D1029-D1034.	14.5	60
103	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
104	Prediction of novel pre-microRNAs with high accuracy through boosting and SVM. <i>Bioinformatics</i> , 2011, 27, 1436-1437.	4.1	26
105	Computational Analysis of Phosphoproteomics: Progresses and Perspectives. <i>Current Protein and Peptide Science</i> , 2011, 12, 591-601.	1.4	13
106	GPS-SNO: Computational Prediction of Protein S-Nitrosylation Sites with a Modified GPS Algorithm. <i>PLoS ONE</i> , 2010, 5, e11290.	2.5	223
107	PhosSNP for Systematic Analysis of Genetic Polymorphisms That Influence Protein Phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 623-634.	3.8	72
108	MiCroKit 3.0: an integrated database of midbody, centrosome and kinetochore. <i>Nucleic Acids Research</i> , 2010, 38, D155-D160.	14.5	27

#	ARTICLE	IF	CITATIONS
109	A Summary of Computational Resources for Protein Phosphorylation. <i>Current Protein and Peptide Science</i> , 2010, 11, 485-496.	1.4	53
110	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
111	DOG 1.0: illustrator of protein domain structures. <i>Cell Research</i> , 2009, 19, 271-273.	12.0	505
112	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
113	Proteome-wide prediction of PKA phosphorylation sites in eukaryotic kingdom. <i>Genomics</i> , 2008, 92, 457-463.	2.9	29
114	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
115	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
116	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
117	Computational Analyses of TBC Protein Family in Eukaryotes. <i>Protein and Peptide Letters</i> , 2008, 15, 505-509.	0.9	8
118	Proteome-Wide Analysis of Amino Acid Absence in Composition and Plasticity. <i>Lecture Notes in Computer Science</i> , 2008, , 167-178.	1.3	0
119	An efficient site-directed mutagenesis method for ColE1-type ori plasmid. <i>Analytical Biochemistry</i> , 2007, 363, 151-153.	2.4	3
120	MeMo: a web tool for prediction of protein methylation modifications. <i>Nucleic Acids Research</i> , 2006, 34, W249-W253.	14.5	123
121	Prediction of N ^ε -acetylation on internal lysines implemented in Bayesian Discriminant Method. <i>Biochemical and Biophysical Research Communications</i> , 2006, 350, 818-824.	2.1	106
122	A general user interface for prediction servers of proteins' post-translational modification sites. <i>Nature Protocols</i> , 2006, 1, 1318-1321.	12.0	25
123	A novel genome-wide full-length kinesin prediction analysis reveals additional mammalian kinesins. <i>Science Bulletin</i> , 2006, 51, 1836-1847.	1.7	3
124	PPSP: prediction of PK-specific phosphorylation site with Bayesian decision theory. <i>BMC Bioinformatics</i> , 2006, 7, 163.	2.6	183
125	NBA-Palm: prediction of palmitoylation site implemented in Na ⁺ -ve Bayes algorithm. <i>BMC Bioinformatics</i> , 2006, 7, 458.	2.6	88
126	SUMOsp: a web server for sumoylation site prediction. <i>Nucleic Acids Research</i> , 2006, 34, W254-W257.	14.5	179

#	ARTICLE	IF	CITATIONS
127	CSS-Palm: palmitoylation site prediction with a clustering and scoring strategy (CSS). <i>Bioinformatics</i> , 2006, 22, 894-896.	4.1	130
128	GPS: a comprehensive www server for phosphorylation sites prediction. <i>Nucleic Acids Research</i> , 2005, 33, W184-W187.	14.5	215
129	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
130	GPS: a novel group-based phosphorylation predicting and scoring method. <i>Biochemical and Biophysical Research Communications</i> , 2004, 325, 1443-1448.	2.1	149
131	Computational Prediction of Post-Translational Modification Sites in Proteins. , 0, , .		13