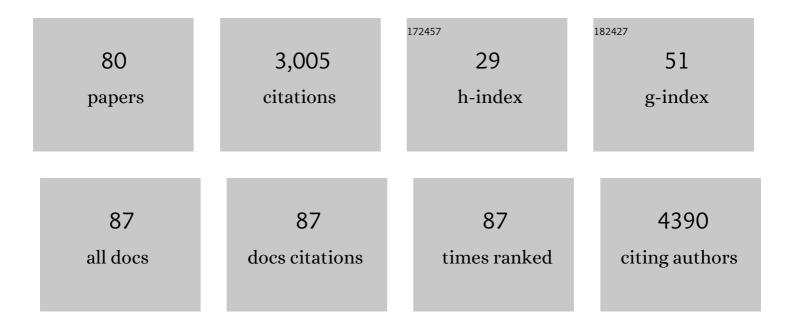
List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A Diverse Family of Proteins Containing Tumor Necrosis Factor Receptor-associated Factor Domains. Journal of Biological Chemistry, 2001, 276, 24242-24252.	3.4	192
2	Expression of Genes Involved in Oxidative Stress Responses in Airway Epithelial Cells of Smokers with Chronic Obstructive Pulmonary Disease. American Journal of Respiratory and Critical Care Medicine, 2007, 175, 577-586.	5.6	191
3	Ion Channel Activity of the BH3 Only Bcl-2 Family Member, BID. Journal of Biological Chemistry, 1999, 274, 21932-21936.	3.4	174
4	BAR: An apoptosis regulator at the intersection of caspases and Bcl-2 family proteins. Proceedings of the United States of America, 2000, 97, 2597-2602.	7.1	172
5	ADPâ€ribosyltransferases, an update on function and nomenclature. FEBS Journal, 2022, 289, 7399-7410.	4.7	150
6	Protein AMPylation by an Evolutionarily Conserved Pseudokinase. Cell, 2018, 175, 809-821.e19.	28.9	149
7	PAAD – a new protein domain associated with apoptosis, cancer and autoimmune diseases. Trends in Biochemical Sciences, 2001, 26, 85-87.	7.5	129
8	Bacterial pseudokinase catalyzes protein polyglutamylation to inhibit the SidE-family ubiquitin ligases. Science, 2019, 364, 787-792.	12.6	111
9	CADD, a Chlamydia Protein That Interacts with Death Receptors. Journal of Biological Chemistry, 2002, 277, 9633-9636.	3.4	84
10	Saturated BLAST: an automated multiple intermediate sequence search used to detect distant homology. Bioinformatics, 2000, 16, 1105-1110.	4.1	69
11	TNF-α-induced self expression in human lung endothelial cells is inhibited by native and oxidized α1-antitrypsin. International Journal of Biochemistry and Cell Biology, 2008, 40, 258-271.	2.8	62
12	Novel Higher-Order Epigenetic Regulation of the <i>Bdnf</i> Gene upon Seizures. Journal of Neuroscience, 2013, 33, 2507-2511.	3.6	62
13	A Novel Protein Kinase-Like Domain in a Selenoprotein, Widespread in the Tree of Life. PLoS ONE, 2012, 7, e32138.	2.5	61
14	FAM46 proteins are novel eukaryotic non-canonical poly(A) polymerases. Nucleic Acids Research, 2016, 44, 3534-3548.	14.5	60
15	From fold predictions to function predictions: Automation of functional site conservation analysis for functional genome predictions. Protein Science, 1999, 8, 1104-1115.	7.6	59
16	Phosphorylation of spore coat proteins by a family of atypical protein kinases. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E3482-91.	7.1	56
17	A Bacterial Effector Mimics a Host HSP90 Client to Undermine Immunity. Cell, 2019, 179, 205-218.e21.	28.9	53
18	Genome-wide functional analyses of plant coiled–coil NLR-type pathogen receptors reveal essential roles of their N-terminal domain in oligomerization, networking, and immunity. PLoS Biology, 2018, 16, e2005821.	5.6	52

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19	Metabolic control of BRISC–SHMT2 assembly regulates immune signalling. Nature, 2019, 570, 194-199.	27.8	51
20	Novel conserved hydrolase domain in the CLCA family of alleged calcium-activated chloride channels. Proteins: Structure, Function and Bioinformatics, 2006, 63, 424-439.	2.6	49
21	Isolated Calcium-Binding Loops of EF-Hand Proteins Can Dimerize To Form a Native-Like Structure. Biochemistry, 1997, 36, 680-687.	2.5	44
22	Quantitative proteomics identifies brain acid soluble protein 1 (BASP1) as a prognostic biomarker candidate in pancreatic cancer tissue. EBioMedicine, 2019, 43, 282-294.	6.1	43
23	A Novel Predicted Calcium-Regulated Kinase Family Implicated in Neurological Disorders. PLoS ONE, 2013, 8, e66427.	2.5	40
24	YAP1 is an independent prognostic marker in pancreatic cancer and associated with extracellular matrix remodeling. Journal of Translational Medicine, 2020, 18, 77.	4.4	40
25	LTK is an ER-resident receptor tyrosine kinase that regulates secretion. Journal of Cell Biology, 2019, 218, 2470-2480.	5.2	39
26	Proteomic analyses identify prognostic biomarkers for pancreatic ductal adenocarcinoma. Oncotarget, 2018, 9, 9789-9807.	1.8	38
27	Surface Map Comparison: Studying Function Diversity of Homologous Proteins. Journal of Molecular Biology, 2001, 309, 793-806.	4.2	36
28	Identification and Characterization of DEDD2, a Death Effector Domain-containing Protein. Journal of Biological Chemistry, 2002, 277, 7501-7508.	3.4	36
29	Comparative Proteomic Analysis of Extracellular Vesicles Isolated by Acoustic Trapping or Differential Centrifugation. Analytical Chemistry, 2016, 88, 8577-8586.	6.5	36
30	Clinical protein science in translational medicine targeting malignant melanoma. Cell Biology and Toxicology, 2019, 35, 293-332.	5.3	33
31	Structural Diversity in a Family of Homologous Proteins. Journal of Molecular Biology, 1996, 258, 349-366.	4.2	32
32	Pseudo-DUBs as allosteric activators and molecular scaffolds of protein complexes. Biochemical Society Transactions, 2018, 46, 453-466.	3.4	29
33	Correlation of histopathologic characteristics to protein expression and function in malignant melanoma. PLoS ONE, 2017, 12, e0176167.	2.5	27
34	A widespread peroxiredoxin-like domain present in tumor suppression- and progression-implicated proteins. BMC Genomics, 2010, 11, 590.	2.8	26
35	Fold Predictions for Bacterial Genomes. Journal of Structural Biology, 2001, 134, 219-231.	2.8	25
36	Uncharacterized/hypothetical proteins in biomedical 'omics' experiments: is novelty being swept under the carpet?. Briefings in Functional Genomics & Proteomics, 2008, 7, 283-290.	3.8	25

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37	Multiple Model Approach: Exploring the Limits of Comparative Modeling. Journal of Molecular Modeling, 1998, 4, 294-309.	1.8	24
38	The dead phosphatases society: a review of the emerging roles of pseudophosphatases. FEBS Journal, 2020, 287, 4198-4220.	4.7	22
39	The Human Melanoma Proteome Atlas—Complementing the melanoma transcriptome. Clinical and Translational Medicine, 2021, 11, e451.	4.0	20
40	Analysis of Alpha-Synuclein in Malignant Melanoma – Development of a SRM Quantification Assay. PLoS ONE, 2014, 9, e110804.	2.5	20
41	Probabilistic Approach to Predicting Substrate Specificity of Methyltransferases. PLoS Computational Biology, 2014, 10, e1003514.	3.2	19
42	A Protein Deep Sequencing Evaluation of Metastatic Melanoma Tissues. PLoS ONE, 2015, 10, e0123661.	2.5	19
43	PEAK3/C19orf35 pseudokinase, a new NFK3 kinase family member, inhibits CrkII through dimerization. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 15495-15504.	7.1	19
44	CLCAs - A Family of Metalloproteases of Intriguing Phylogenetic Distribution and with Cases of Substituted Catalytic Sites. PLoS ONE, 2013, 8, e62272.	2.5	19
45	TheHelicobacter pylori genome: From sequence analysis to structural and functional predictions. Proteins: Structure, Function and Bioinformatics, 1999, 36, 20-30.	2.6	18
46	Structural and mechanistic basis for protein glutamylation by the kinase fold. Molecular Cell, 2021, 81, 4527-4539.e8.	9.7	18
47	A Legionella effector kinase is activated by host inositol hexakisphosphate. Journal of Biological Chemistry, 2020, 295, 6214-6224.	3.4	17
48	The Hidden Story of Heterogeneous B-raf V600E Mutation Quantitative Protein Expression in Metastatic Melanoma—Association with Clinical Outcome and Tumor Phenotypes. Cancers, 2019, 11, 1981.	3.7	16
49	Dynamic remodeling of host membranes by self-organizing bacterial effectors. Science, 2021, 372, 935-941.	12.6	16
50	A Legionella effector ADP-ribosyltransferase inactivates glutamate dehydrogenase. Journal of Biological Chemistry, 2021, 296, 100301.	3.4	15
51	Structural and functional characterization of annexin 1 from Medicago truncatula. Plant Physiology and Biochemistry, 2013, 73, 56-62.	5.8	14
52	The human melanoma proteome atlas—Defining the molecular pathology. Clinical and Translational Medicine, 2021, 11, e473.	4.0	14
53	Bioinformatics Analysis of Bacterial Annexins – Putative Ancestral Relatives of Eukaryotic Annexins. PLoS ONE, 2014, 9, e85428.	2.5	14
54	STYX: a versatile pseudophosphatase. Biochemical Society Transactions, 2017, 45, 449-456.	3.4	13

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55	Improved survival prognostication of node-positive malignant melanoma patients utilizing shotgun proteomics guided by histopathological characterization and genomic data. Scientific Reports, 2019, 9, 5154.	3.3	12
56	Genomic positions of co-expressed genes: echoes of chromosome organisation in gene expression data. BMC Research Notes, 2013, 6, 229.	1.4	11
57	Alpha-1-acid glycoprotein 1 is upregulated in pancreatic ductal adenocarcinoma and confers a poor prognosis. Translational Research, 2019, 212, 67-79.	5.0	11
58	Labeling of heterochronic ribosomes reveals C1ORF109 and SPATA5 control a late step in human ribosome assembly. Cell Reports, 2022, 38, 110597.	6.4	11
59	Feasibility Study on Measuring Selected Proteins in Malignant Melanoma Tissue by SRM Quantification. Journal of Proteome Research, 2014, 13, 1315-1326.	3.7	9
60	A novel predicted ADP-ribosyltransferase-like family conserved in eukaryotic evolution. PeerJ, 2021, 9, e11051.	2.0	9
61	The expanding world of protein kinase-like families in bacteria: forty families and counting. Biochemical Society Transactions, 2020, 48, 1337-1352.	3.4	9
62	Intersection of selenoproteins and kinase signalling. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 1279-1284.	2.3	8
63	Global pentapeptide statistics are far away from expected distributions. Scientific Reports, 2018, 8, 15178.	3.3	7
64	Short-term effect of pharmacologically induced alterations in testosterone levels on common blood biomarkers in a controlled healthy human model. Scandinavian Journal of Clinical and Laboratory Investigation, 2020, 80, 25-31.	1.2	7
65	Phosphoproteomic insights into processes influenced by the kinase-like protein DIA1/C3orf58. PeerJ, 2018, 6, e4599.	2.0	7
66	A novel conserved family of Macro-like domains—putative new players in ADP-ribosylation signaling. PeerJ, 2019, 7, e6863.	2.0	7
67	Bioinformatics Analysis of Oligosaccharide Phosphorylation Effect on the Stabilization of the β-Amylase Ligand Complex. Journal of Carbohydrate Chemistry, 2008, 27, 479-495.	1.1	6
68	An Approach to Predicting Hematopoietic Stem Cell Transplantation Outcome Using HLA-Mismatch Information Mapped on Protein Structure Data. Biology of Blood and Marrow Transplantation, 2009, 15, 1014-1025.	2.0	6
69	Workflow for large-scale analysis of melanoma tissue samples. EuPA Open Proteomics, 2015, 8, 78-84.	2.5	4
70	A pilot proteomic study reveals different protein profiles related to testosterone and gonadotropin changes in a short-term controlled healthy human cohort. Journal of Proteomics, 2020, 220, 103768.	2.4	4
71	Distinct Protein Classes in Human Red Cell Proteome Revealed by Similarity of Phylogenetic Profiles. PLoS ONE, 2013, 8, e54471.	2.5	3
72	Novel protein markers of androgen activity in humans: proteomic study of plasma from young chemically castrated men. ELife, 2022, 11, .	6.0	3

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73	Methods for discovering catalytic activities for pseudokinases. Methods in Enzymology, 2022, 667, 575-610.	1.0	3
74	From fold to function predictions: an apoptosis regulator protein BID. Computers & Chemistry, 2000, 24, 511-517.	1.2	2
75	Looking for chromosome spatial organization rules in microarray gene expression data. BMC Bioinformatics, 2009, 10, .	2.6	2
76	The <i>Legionella pneumophila</i> effector Lpg1137 is a homologue of mitochondrial SLC25 carrier proteins, not of known serine proteases. PeerJ, 2017, 5, e3849.	2.0	2
77	Short-Term Effect of Induced Alterations in Testosterone Levels on Fasting Plasma Amino Acid Levels in Healthy Young Men. Life, 2021, 11, 1276.	2.4	2
78	A novel predicted calcium-regulated kinase family implicated in neurological disorders. Nature Precedings, 2012, , .	0.1	1
79	The Helicobacter pylori genome: From sequence analysis to structural and functional predictions. Proteins: Structure, Function and Bioinformatics, 1999, 36, 20-30.	2.6	1
80	Alpha-1-acid glycoprotein 1 (AGP1) as a novel biomarker for pancreatic cancer Journal of Clinical Oncology, 2019, 37, e15708-e15708.	1.6	1