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List of Publications by Year in descending order

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70
papers

3,582
citations

159585

30
h-index

138484

58
g-index

76
all docs

76
docs citations

76
times ranked

4333
citing authors

#	ARTICLE	IF	CITATIONS
1	Conformational Studies of Oligosaccharides and Glycopeptides: Complementarity of NMR, X-ray Crystallography, and Molecular Modelling. <i>Chemical Reviews</i> , 2002, 102, 371-386.	47.7	400
2	Statistical analysis of the protein environment of N-glycosylation sites: implications for occupancy, structure, and folding. <i>Glycobiology</i> , 2003, 14, 103-114.	2.5	391
3	Coiled-Coil Domain-Dependent Homodimerization of Intracellular Barley Immune Receptors Defines a Minimal Functional Module for Triggering Cell Death. <i>Cell Host and Microbe</i> , 2011, 9, 187-199.	11.0	269
4	Harmonicities in slow protein dynamics. <i>Chemical Physics</i> , 2000, 261, 25-37.	1.9	197
5	Nucleocytoplasmic Distribution Is Required for Activation of Resistance by the Potato NB-LRR Receptor Rx1 and Is Balanced by Its Functional Domains. <i>Plant Cell</i> , 2011, 22, 4195-4215.	6.6	140
6	A statistical analysis of N- and O-glycan linkage conformations from crystallographic data. <i>Glycobiology</i> , 1999, 9, 343-352.	2.5	125
7	Mutations at Critical N-Glycosylation Sites Reduce Tyrosinase Activity by Altering Folding and Quality Control. <i>Journal of Biological Chemistry</i> , 2000, 275, 8169-8175.	3.4	113
8	A Secreted SPRY Domain-Containing Protein (SPRYSEC) from the Plant-Parasitic Nematode <i>Globodera rostochiensis</i> Interacts with a CC-NB-LRR Protein from a Susceptible Tomato. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 330-340.	2.6	109
9	A <i>Caenorhabditis elegans</i> Wild Type Defies the Temperature-Size Rule Owing to a Single Nucleotide Polymorphism in tra-3. <i>PLoS Genetics</i> , 2007, 3, e34.	3.5	104
10	Transposon molecular domestication and the evolution of the RAG recombinase. <i>Nature</i> , 2019, 569, 79-84.	27.8	100
11	The solution NMR structure of glucosylated N-glycans involved in the early stages of glycoprotein biosynthesis and folding. <i>EMBO Journal</i> , 1997, 16, 4302-4310.	7.8	91
12	In Planta Secretion of a Calreticulin by Migratory and Sedentary Stages of Root-Knot Nematode. <i>Molecular Plant-Microbe Interactions</i> , 2005, 18, 1277-1284.	2.6	91
13	Tyrosinase Folding and Copper Loading in Vivo: A Crucial Role for Calnexin and β -Glucosidase II. <i>Biochemical and Biophysical Research Communications</i> , 1999, 261, 720-725.	2.1	82
14	Structural aspects of glycomes with a focus on N-glycosylation and glycoprotein folding. <i>Current Opinion in Structural Biology</i> , 2006, 16, 600-607.	5.7	79
15	Inhibition of N-Glycan Processing in B16 Melanoma Cells Results in Inactivation of Tyrosinase but Does Not Prevent Its Transport to the Melanosome. <i>Journal of Biological Chemistry</i> , 1997, 272, 15796-15803.	3.4	76
16	Structural Determinants at the Interface of the ARC2 and Leucine-Rich Repeat Domains Control the Activation of the Plant Immune Receptors Rx1 and Gpa2. <i>Plant Physiology</i> , 2013, 162, 1510-1528.	4.8	73
17	Radially Softening Diffusive Motions in a Globular Protein. <i>Biophysical Journal</i> , 2001, 81, 1666-1676.	0.5	72
18	Mutations in dopachrome tautomerase (Dct) affect eumelanin/pheomelanin synthesis, but do not affect intracellular trafficking of the mutant protein. <i>Biochemical Journal</i> , 2005, 391, 249-259.	3.7	66

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19	Origin, distribution and 3D-modeling of Gr-EXPB1, an expansin from the potato cyst nematode <i>Globodera rostochiensis</i> . <i>FEBS Letters</i> , 2005, 579, 2451-2457.	2.8	56
20	Tyrosinase and Glycoprotein Folding: Roles of Chaperones That Recognize Glycans. <i>Biochemistry</i> , 2000, 39, 5229-5237.	2.5	53
21	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. <i>PLoS Biology</i> , 2018, 16, e2005821.	5.6	52
22	Ancient diversity of splicing motifs and protein surfaces in the wild emmer wheat (<i>Triticum</i>). <i>PLoS Pathology</i> , 2012, 13, 276-287.	4.2	45
23	Protein specific N-glycosylation of tyrosinase and tyrosinase-related protein-1 in B16 mouse melanoma cells. <i>Biochemical Journal</i> , 1999, 344, 659-665.	3.7	42
24	Cell death triggering and effector recognition by Sw-5 SD-CNL proteins from resistant and susceptible tomato isolines to <i>Tomato spotted wilt virus</i> . <i>Molecular Plant Pathology</i> , 2016, 17, 1442-1454.	4.2	42
25	N-Glycosylation Processing and Glycoprotein Folding: Lessons from the Tyrosinase-Related Proteins. <i>Chemical Reviews</i> , 2000, 100, 4697-4712.	47.7	41
26	An LRR/Malectin Receptor-Like Kinase Mediates Resistance to Non-adapted and Adapted Powdery Mildew Fungi in Barley and Wheat. <i>Frontiers in Plant Science</i> , 2016, 7, 1836.	3.6	39
27	Structural and functional characterization of a novel, host penetration-related pectate lyase from the potato cyst nematode <i>Globodera rostochiensis</i> . <i>Molecular Plant Pathology</i> , 2007, 8, 293-305.	4.2	37
28	Random mutagenesis of the nucleotide-binding domain of <i>NRC1</i> (<i>NB-LRR</i> Required for Hypersensitive Response-Associated Cell Death 1), a downstream signalling nucleotide-binding, leucine-rich repeat (<i>NB-LRR</i>) protein, identifies gain-of-function mutations in the nucleotide-binding pocket. <i>New Phytologist</i> , 2015, 208, 210-223.	7.3	37
29	SPRYSEC Effectors: A Versatile Protein-Binding Platform to Disrupt Plant Innate Immunity. <i>Frontiers in Plant Science</i> , 2016, 7, 1575.	3.6	37
30	Tyrosinase Degradation Is Prevented when EDEM1 Lacks the Intrinsically Disordered Region. <i>PLoS ONE</i> , 2012, 7, e42998.	2.5	34
31	Small-angle neutron scattering by a strongly denatured protein: analysis using random polymer theory. <i>Biophysical Journal</i> , 1997, 72, 335-342.	0.5	33
32	LRRpredictor: A New LRR Motif Detection Method for Irregular Motifs of Plant NLR Proteins Using an Ensemble of Classifiers. <i>Genes</i> , 2020, 11, 286.	2.4	33
33	An N-Linked Glycan Modulates the Interaction between the CD1d Heavy Chain and β 2-Microglobulin. <i>Journal of Biological Chemistry</i> , 2006, 281, 40369-40378.	3.4	28
34	Excluded volume in the configurational distribution of a strongly denatured protein. <i>Protein Science</i> , 1998, 7, 1396-1403.	7.6	27
35	RAG and HMGB1 create a large bend in the 23RSS in the V(D)J recombination synaptic complexes. <i>Nucleic Acids Research</i> , 2013, 41, 2437-2454.	14.5	23
36	Roles of the C-terminal domains of topoisomerase $\text{III}\alpha$ and topoisomerase $\text{III}\beta$ in regulation of the decatenation checkpoint. <i>Nucleic Acids Research</i> , 2017, 45, 5995-6010.	14.5	23

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37	Protein specific N-glycosylation of tyrosinase and tyrosinase-related protein-1 in B16 mouse melanoma cells. <i>Biochemical Journal</i> , 1999, 344, 659.	3.7	20
38	Three-Dimensional Modeling and Diversity Analysis Reveals Distinct AVR Recognition Sites and Evolutionary Pathways in Wild and Domesticated Wheat Pm3 R Genes. <i>Molecular Plant-Microbe Interactions</i> , 2014, 27, 835-845.	2.6	19
39	Identification of RAG-like transposons in protostomes suggests their ancient bilaterian origin. <i>Mobile DNA</i> , 2020, 11, 17.	3.6	19
40	C-Terminus Glycans with Critical Functional Role in the Maturation of Secretory Glycoproteins. <i>PLoS ONE</i> , 2011, 6, e19979.	2.5	19
41	Mapping and Quantitation of the Interaction between the Recombination Activating Gene Proteins RAG1 and RAG2. <i>Journal of Biological Chemistry</i> , 2015, 290, 11802-11817.	3.4	18
42	Heavy metal accumulation by <i>Saccharomyces cerevisiae</i> cells armed with metal binding hexapeptides targeted to the inner face of the plasma membrane. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 5749-5763.	3.6	18
43	Distinct Roles of Non-Overlapping Surface Regions of the Coiled-Coil Domain in the Potato Immune Receptor Rx1. <i>Plant Physiology</i> , 2018, 178, 1310-1331.	4.8	18
44	Structure–function analysis of ZAR1 immune receptor reveals key molecular interactions for activity. <i>Plant Journal</i> , 2020, 101, 352-370.	5.7	18
45	Change in backbone torsion angle distribution on protein folding. <i>Protein Science</i> , 2000, 9, 1129-1136.	7.6	12
46	Interface Analysis of the Complex between ERK2 and PTP-SL. <i>PLoS ONE</i> , 2009, 4, e5432.	2.5	12
47	Identification of an unusually sulfated tetrasaccharide chondroitin/dermatan motif in mouse brain by combining chip–nanoelectrospray multistage ²–MS⁴ and high resolution ⁴-MS. <i>Electrophoresis</i> , 2013, 34, 1581-1592.	2.4	12
48	The architecture of the 12RSS in V(D)J recombination signal and synaptic complexes. <i>Nucleic Acids Research</i> , 2015, 43, 917-931.	14.5	11
49	Clonal lineage of high grade serous ovarian cancer in a patient with neurofibromatosis type 1. <i>Gynecologic Oncology Reports</i> , 2018, 23, 41-44.	0.6	11
50	Collective dynamics of a photosynthetic protein probed by neutron spin-echo spectroscopy and molecular dynamics simulation. <i>Physica B: Condensed Matter</i> , 2000, 276-278, 514-515.	2.7	10
51	Gangliosidome of human anencephaly: A high resolution multistage mass spectrometry study. <i>Biochimie</i> , 2019, 163, 142-151.	2.6	9
52	Immunoaffinity Chromatography on Antibodies Immobilized on Nitrocellulose Powder. <i>Analytical Biochemistry</i> , 1995, 229, 299-303.	2.4	8
53	Evaluation of a neural networks QSAR method based on ligand representation using substituent descriptors. <i>Journal of Molecular Graphics and Modelling</i> , 2006, 25, 37-45.	2.4	8
54	Profiling Optimal Conditions for Capturing EDEM Proteins Complexes in Melanoma Using Mass Spectrometry. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1140, 155-167.	1.6	8

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55	Inhibition of N-glycan processing modulates the network of EDEM3 interactors. <i>Biochemical and Biophysical Research Communications</i> , 2017, 486, 978-984.	2.1	7
56	Human caudate nucleus exhibits a highly complex ganglioside pattern as revealed by high-resolution multistage Orbitrap MS. <i>Journal of Carbohydrate Chemistry</i> , 2019, 38, 531-551.	1.1	7
57	Affinity Proteomics and Deglycoproteomics Uncover Novel EDEM2 Endogenous Substrates and an Integrative ERAD Network. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100125.	3.8	7
58	EDEM3 Domains Cooperate to Perform Its Overall Cell Functioning. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2172.	4.1	7
59	Robosample: A rigid-body molecular simulation program based on robot mechanics. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129616.	2.4	5
60	Tyrosine 656 in topoisomerase III ^β is important for the catalytic activity of the enzyme: Identification based on artifactual +80â€œDa modification at this site. <i>Proteomics</i> , 2011, 11, 829-842.	2.2	4
61	Liquid-like and solid-like motions in proteins. <i>Journal of Molecular Liquids</i> , 2002, 98-99, 383-400.	4.9	3
62	Identification and structural characterization of novel O- and N-glycoforms in the urine of a Schindler disease patient by Orbitrap mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2015, 50, 1044-1056.	1.6	3
63	A natural diversity screen in <i>Arabidopsis thaliana</i> reveals determinants for HopZ1a recognition in the ZAR1-ZED1 immune complex. <i>Plant, Cell and Environment</i> , 2021, 44, 629-644.	5.7	3
64	The Design of New HIV-IN Tethered Bifunctional Inhibitors Using Multiple Microdomain Targeted Docking. <i>Current Medicinal Chemistry</i> , 2019, 26, 2574-2600.	2.4	3
65	Motions in native and denatured proteins. <i>Physica B: Condensed Matter</i> , 1997, 241-243, 1110-1114.	2.7	2
66	The Glycosylation of Tyrosinase in Melanoma Cells and the Effect on Antigen Presentation. <i>Advances in Experimental Medicine and Biology</i> , 2003, 535, 257-269.	1.6	2
67	Mass Spectrometry for Cancer Biomarkers. , 0, , .		2
68	Deep Learning in the Quest for Compound Nomination for Fighting COVID-19. <i>Current Medicinal Chemistry</i> , 2021, 28, 5699-5732.	2.4	2
69	Purification and partial characterization of a lectin from <i>Datura innoxia</i> seeds. <i>Phytochemistry</i> , 1993, 34, 343-348.	2.9	1
70	Abstract 2526: Tyrosine 656 in topoisomerase III ^β is important for the catalytic activity. , 2011, , .		0