

Jakob Rahr Winther

List of Publications by Year in descending order

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100
papers

5,190
citations

94433

37
h-index

88630

70
g-index

108
all docs

108
docs citations

108
times ranked

6469
citing authors

#	ARTICLE	IF	CITATIONS
1	The functional role of the autolysis loop in the regulation of factor X upon hemostatic response. <i>Journal of Thrombosis and Haemostasis</i> , 2022, 20, 589-599.	3.8	1
2	Co-evolution of drug resistance and broadened substrate recognition in HIV protease variants isolated from an <i>Escherichia coli</i> genetic selection system. <i>Biochemical Journal</i> , 2022, 479, 479-501.	3.7	1
3	Substitutional landscape of a split fluorescent protein fragment using high-density peptide microarrays. <i>PLoS ONE</i> , 2021, 16, e0241461.	2.5	1
4	Charge Interactions in a Highly Charge-Depleted Protein. <i>Journal of the American Chemical Society</i> , 2021, 143, 2500-2508.	13.7	15
5	Computational and Experimental Assessment of Backbone Templates for Computational Redesign of the Thioredoxin Fold. <i>Journal of Physical Chemistry B</i> , 2021, 125, 11141-11149.	2.6	5
6	Flash properties of <i>Gaussia luciferase</i> are the result of covalent inhibition after a limited number of cycles. <i>Protein Science</i> , 2021, 30, 638-649.	7.6	13
7	Rational Protein Engineering to Increase the Activity and Stability of IsPETase Using the PROSS Algorithm. <i>Polymers</i> , 2021, 13, 3884.	4.5	16
8	Charge Engineering Reveals the Roles of Ionizable Side Chains in Electrospray Ionization Mass Spectrometry. <i>Jacs Au</i> , 2021, 1, 2385-2393.	7.9	12
9	Mutations in a Single Signaling Pathway Allow Cell Growth in Heavy Water. <i>ACS Synthetic Biology</i> , 2020, 9, 733-748.	3.8	14
10	Improving folding properties of computationally designed proteins. <i>Protein Engineering, Design and Selection</i> , 2019, 32, 145-151.	2.1	5
11	Pulmonary effects of nanofibrillated celluloses in mice suggest that carboxylation lowers the inflammatory and acute phase responses. <i>Environmental Toxicology and Pharmacology</i> , 2019, 66, 116-125.	4.0	42
12	Steady state kinetic analysis of O-linked GalNAc glycan release catalyzed by endo- β -N-acetylgalactosaminidase. <i>Carbohydrate Research</i> , 2019, 480, 54-60.	2.3	8
13	Hacking an enzyme. <i>Nature Chemical Biology</i> , 2018, 14, 202-204.	8.0	0
14	Can a Charged Surfactant Unfold an Uncharged Protein?. <i>Biophysical Journal</i> , 2018, 115, 2081-2086.	0.5	20
15	Random Mutagenesis Analysis of the Influenza A M2 Proton Channel Reveals Novel Resistance Mutants. <i>Biochemistry</i> , 2018, 57, 5957-5968.	2.5	11
16	A Robust Proton Flux (pHlux) Assay for Studying the Function and Inhibition of the Influenza A M2 Proton Channel. <i>Biochemistry</i> , 2018, 57, 5949-5956.	2.5	15
17	Nanofibrillated cellulose causes acute pulmonary inflammation that subsides within a month. <i>Nanotoxicology</i> , 2018, 12, 729-746.	3.0	34
18	Editorial overview: A perspective on protein evolution. <i>Current Opinion in Structural Biology</i> , 2018, 48, viii-ix.	5.7	0

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19	Positive staining for cellulose in oral pulse granuloma. <i>Oral Surgery, Oral Medicine, Oral Pathology and Oral Radiology</i> , 2017, 123, 464-467.	0.4	7
20	Exploring the antigenic response to multiplexed immunizations in a chicken model of antibody production. <i>Heliyon</i> , 2017, 3, e00267.	3.2	3
21	Endoplasmic Reticulum Transport of Glutathione by Sec61 Is Regulated by Ero1 and Bip. <i>Molecular Cell</i> , 2017, 67, 962-973.e5.	9.7	91
22	Computational Redesign of Thioredoxin Is Hypersensitive toward Minor Conformational Changes in the Backbone Template. <i>Journal of Molecular Biology</i> , 2016, 428, 4361-4377.	4.2	21
23	A Soluble, Folded Protein without Charged Amino Acid Residues. <i>Biochemistry</i> , 2016, 55, 3949-3956.	2.5	34
24	Mutational Analysis of Divalent Metal Ion Binding in the Active Site of Class II α -Mannosidase from <i>Sulfolobus solfataricus</i> . <i>Biochemistry</i> , 2015, 54, 2032-2039.	2.5	2
25	Visualization of Nanofibrillar Cellulose in Biological Tissues Using a Biotinylated Carbohydrate Binding Module of β -1,4-Glycanase. <i>Chemical Research in Toxicology</i> , 2015, 28, 1627-1635.	3.3	20
26	Catalytic site interactions in yeast OMP synthase. <i>Archives of Biochemistry and Biophysics</i> , 2014, 542, 28-38.	3.0	7
27	Rapid TaqMan-Based Quantification of Chlorophyll <i>a</i> -Containing Cyanobacteria in the Genus <i>Acaryochloris</i> . <i>Applied and Environmental Microbiology</i> , 2014, 80, 3244-3249.	3.1	9
28	Non-invasive In-cell Determination of Free Cytosolic [NAD ⁺]/[NADH] Ratios Using Hyperpolarized Glucose Show Large Variations in Metabolic Phenotypes. <i>Journal of Biological Chemistry</i> , 2014, 289, 2344-2352.	3.4	98
29	The pK_a Value and Accessibility of Cysteine Residues Are Key Determinants for Protein Substrate Discrimination by Glutaredoxin. <i>Biochemistry</i> , 2014, 53, 2533-2540.	2.5	38
30	Quantification of thiols and disulfides. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2014, 1840, 838-846.	2.4	276
31	In Silico Prediction of Mutant HIV-1 Proteases Cleaving a Target Sequence. <i>PLoS ONE</i> , 2014, 9, e95833.	2.5	12
32	Intracellular glutathione pools are heterogeneously concentrated. <i>Redox Biology</i> , 2013, 1, 508-513.	9.0	161
33	A black hole for oxidized glutathione. <i>Nature Chemical Biology</i> , 2013, 9, 69-70.	8.0	12
34	Quantifying Changes in the Cellular Thiol-Disulfide Status during Differentiation of B Cells into Antibody-Secreting Plasma Cells. <i>International Journal of Cell Biology</i> , 2013, 2013, 1-9.	2.5	6
35	Saccharopepsin. , 2013, , 128-133.		0
36	The Human Selenoprotein VCP-interacting Membrane Protein (VIMP) Is Non-globular and Harbors a Reductase Function in an Intrinsically Disordered Region. <i>Journal of Biological Chemistry</i> , 2012, 287, 26388-26399.	3.4	41

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37	Polysaccharide Effects on Calcite Growth: The Influence of Composition and Branching. <i>Crystal Growth and Design</i> , 2012, 12, 4906-4910.	3.0	30
38	Metal-Ion Dependent Catalytic Properties of <i>Sulfolobus solfataricus</i> Class II β -Mannosidase. <i>Biochemistry</i> , 2012, 51, 8039-8046.	2.5	6
39	A fluorescent probe which allows highly specific thiol labeling at low pH. <i>Analytical Biochemistry</i> , 2012, 421, 115-120.	2.4	7
40	Millisecond Dynamics in Glutaredoxin during Catalytic Turnover Is Dependent on Substrate Binding and Absent in the Resting States. <i>Journal of the American Chemical Society</i> , 2011, 133, 3034-3042.	13.7	16
41	Trisulfides in Proteins. <i>Antioxidants and Redox Signaling</i> , 2011, 15, 67-75.	5.4	53
42	Kinetic and thermodynamic properties of two barley thioredoxin h isozymes, HvTrxh1 and HvTrxh2. <i>FEBS Letters</i> , 2010, 584, 3376-3380.	2.8	15
43	Thiol-Disulfide Exchange between Glutaredoxin and Glutathione. <i>Biochemistry</i> , 2010, 49, 810-820.	2.5	39
44	Quantifying the global cellular thiol-disulfide status. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 422-427.	7.1	357
45	An introduction to methods for analyzing thiols and disulfides: Reactions, reagents, and practical considerations. <i>Analytical Biochemistry</i> , 2009, 394, 147-158.	2.4	236
46	Kinetic and Thermodynamic Aspects of Cellular Thiol-Disulfide Redox Regulation. <i>Antioxidants and Redox Signaling</i> , 2009, 11, 1047-1058.	5.4	115
47	Oxidant resistance in a yeast mutant deficient in the Sit4 phosphatase. <i>Current Genetics</i> , 2008, 53, 275-286.	1.7	5
48	Mutations in the RAM network confer resistance to the thiol oxidant 4,4'-dipyridyl disulfide. <i>Molecular Genetics and Genomics</i> , 2008, 279, 629-642.	2.1	1
49	Redox characteristics of the eukaryotic cytosol. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2008, 1783, 629-640.	4.1	159
50	High-Resolution Imaging of Redox Signaling in Live Cells Through an Oxidation-Sensitive Yellow Fluorescent Protein. <i>Science Signaling</i> , 2008, 1, pl3.	3.6	48
51	Erv2p: Characterization of the Redox Behavior of a Yeast Sulfhydryl Oxidase. <i>Biochemistry</i> , 2007, 46, 3246-3254.	2.5	30
52	Genetic Interaction between the ero1-1 and leu2 Mutations in <i>Saccharomyces cerevisiae</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2007, 71, 2934-2942.	1.3	1
53	Quantification of protein thiols and dithiols in the picomolar range using sodium borohydride and 4,4'-dithiodipyridine. <i>Analytical Biochemistry</i> , 2007, 363, 77-82.	2.4	97
54	Structure of glutaredoxin Grx1p C30S mutant from yeast. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 288-294.	2.5	39

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55	Cytoplasmic glutathione redox status determines survival upon exposure to the thiol-oxidant 4,4'-dipyridyl disulfide. <i>FEMS Yeast Research</i> , 2007, 7, 391-403.	2.3	21
56	The thiol oxidant dipyridyl disulfide can supply the PDI-Ero1p pathway with additional oxidative equivalents. <i>Antonie Van Leeuwenhoek</i> , 2007, 92, 463-472.	1.7	6
57	Mechanistic Insight Provided by Glutaredoxin within a Fusion to Redox-Sensitive Yellow Fluorescent Protein. <i>Biochemistry</i> , 2006, 45, 2362-2371.	2.5	58
58	Evidence That Translation Reinitiation Leads to a Partially Functional Menkes Protein Containing Two Copper-Binding Sites. <i>American Journal of Human Genetics</i> , 2006, 79, 214-229.	6.2	61
59	Crystallization of mutant forms of glutaredoxin Grx1p from yeast. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 920-922.	0.7	1
60	Measuring Intracellular Redox Conditions Using GFP-Based Sensors. <i>Antioxidants and Redox Signaling</i> , 2006, 8, 354-361.	5.4	61
61	Increasing the Reactivity of an Artificial Dithiol-Disulfide Pair through Modification of the Electrostatic Milieu. <i>Biochemistry</i> , 2005, 44, 5899-5906.	2.5	68
62	Saccharopepsin. , 2004, , 87-90.		3
63	The Contributions of Protein Disulfide Isomerase and Its Homologues to Oxidative Protein Folding in the Yeast Endoplasmic Reticulum. <i>Journal of Biological Chemistry</i> , 2004, 279, 49780-49786.	3.4	57
64	Monitoring disulfide bond formation in the eukaryotic cytosol. <i>Journal of Cell Biology</i> , 2004, 166, 337-345.	5.2	280
65	Fluorometric polyethyleneglycol-peptide hybrid substrates for quantitative assay of protein disulfide isomerase. <i>Analytical Biochemistry</i> , 2004, 333, 148-155.	2.4	7
66	Gene regulation in response to protein disulphide isomerase deficiency. <i>Yeast</i> , 2003, 20, 645-652.	1.7	6
67	Shedding light on disulfide bond formation: engineering a redox switch in green fluorescent protein. <i>EMBO Journal</i> , 2001, 20, 5853-5862.	7.8	279
68	Surprisingly high stability of barley lipid transfer protein, LTP1, towards denaturant, heat and proteases. <i>FEBS Letters</i> , 2001, 488, 145-148.	2.8	126
69	Mutation of yeast Eug1p CXXS active sites to CXXC results in a dramatic increase in protein disulphide isomerase activity. <i>Biochemical Journal</i> , 2001, 358, 269.	3.7	18
70	Mutation of yeast Eug1p CXXS active sites to CXXC results in a dramatic increase in protein disulphide isomerase activity. <i>Biochemical Journal</i> , 2001, 358, 269-274.	3.7	30
71	Production of a heterologous proteinase A by <i>Saccharomyces kluyveri</i> . <i>Applied Microbiology and Biotechnology</i> , 2001, 57, 216-219.	3.6	6
72	Functional Differences in Yeast Protein Disulfide Isomerases. <i>Journal of Cell Biology</i> , 2001, 152, 553-562.	5.2	118

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73	The Potency and Specificity of the Interaction between the IA3 Inhibitor and Its Target Aspartic Proteinase from <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2001, 276, 2023-2030.	3.4	37
74	Barley Lipid Transfer Protein, LTP1, Contains a New Type of Lipid-like Post-translational Modification*. <i>Journal of Biological Chemistry</i> , 2001, 276, 33547-33553.	3.4	36
75	Thiol Alkylation below Neutral pH. <i>Analytical Biochemistry</i> , 2000, 286, 308-310.	2.4	29
76	The aspartic proteinase from <i>Saccharomyces cerevisiae</i> folds its own inhibitor into a helix. <i>Nature Structural Biology</i> , 2000, 7, 113-117.	9.7	87
77	Protein oxidation: prime suspect found "not guilty". <i>Nature Cell Biology</i> , 1999, 1, E57-E58.	10.3	11
78	Ligand recognition and domain structure of Vps10p, a vacuolar protein sorting receptor in <i>Saccharomyces cerevisiae</i> . <i>FEBS Journal</i> , 1999, 260, 461-469.	0.2	65
79	Functional properties of the two redox-active sites in yeast protein disulphide isomerase in Vitro and in Vivo 1 Edited by G. Von Heijne. <i>Journal of Molecular Biology</i> , 1999, 286, 1229-1239.	4.2	29
80	Preparation of fluorescence quenched libraries containing interchain disulphide bonds for studies of protein disulphide isomerases. <i>Journal of Peptide Science</i> , 1998, 4, 128-137.	1.4	15
81	A High-Affinity Inhibitor of Yeast Carboxypeptidase Y Is Encoded by TFS1 and Shows Homology to a Family of Lipid Binding Proteins. <i>Biochemistry</i> , 1998, 37, 3351-3357.	2.5	54
82	Kinetic Analysis of the Mechanism and Specificity of Protein-disulfide Isomerase Using Fluorescence-quenched Peptides. <i>Journal of Biological Chemistry</i> , 1998, 273, 24992-24999.	3.4	22
83	Active Site Mutations in Yeast Protein Disulfide Isomerase Cause Dithiothreitol Sensitivity and a Reduced Rate of Protein Folding in the Endoplasmic Reticulum. <i>Journal of Cell Biology</i> , 1997, 138, 1229-1238.	5.2	76
84	Mechanism and ion-dependence of <i>in vitro</i> autoactivation of yeast proteinase A: possible implications for compartmentalized activation <i>in vivo</i> . <i>Biochemical Journal</i> , 1997, 326, 339-344.	3.7	19
85	Mutational Analysis of the Vacuolar Sorting Signal of Procarboxypeptidase Y in Yeast Shows a Low Requirement for Sequence Conservation. <i>Journal of Biological Chemistry</i> , 1996, 271, 841-846.	3.4	18
86	Exchange of Regions of the Carboxypeptidase Y Propeptide. Sequence Specificity and Function in Folding in Vivo. <i>FEBS Journal</i> , 1996, 242, 29-35.	0.2	9
87	Review: Biosynthesis and function of yeast vacuolar proteases. <i>Yeast</i> , 1996, 12, 1-16.	1.7	162
88	Multiple Pathways for Vacuolar Sorting of Yeast Proteinase A. <i>Journal of Biological Chemistry</i> , 1996, 271, 11865-11870.	3.4	59
89	Random Substitution of Large Parts of the Propeptide of Yeast Proteinase A. <i>Journal of Biological Chemistry</i> , 1995, 270, 8602-8609.	3.4	28
90	Why is DsbA such an oxidizing disulfide catalyst?. <i>Cell</i> , 1995, 83, 947-955.	28.9	300

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91	Active-site residues of procarboxypeptidase Y are accessible to chemical modification. BBA - Proteins and Proteomics, 1994, 1205, 289-293.	2.1	4
92	pH-dependent processing of yeast procarboxypeptidase Y by proteinase A in vivo and in vitro. FEBS Journal, 1994, 220, 19-27.	0.2	47
93	The pro region required for folding of carboxypeptidase Y is a partially folded domain with little regular structural core. Biochemistry, 1993, 32, 12160-12166.	2.5	27
94	Autoactivation of proteinase A initiates activation of yeast vacuolar zymogens. FEBS Journal, 1992, 207, 277-283.	0.2	68
95	Yeast carboxypeptidase Y requires glycosylation for efficient intracellular transport, but not for vacuolar sorting, in vivo stability, or activity. FEBS Journal, 1991, 197, 681-689.	0.2	81
96	Propeptide of carboxypeptidase Y provides a chaperone-like function as well as inhibition of the enzymatic activity.. Proceedings of the National Academy of Sciences of the United States of America, 1991, 88, 9330-9334.	7.1	195
97	Yeast carboxypeptidase Y vacuolar targeting signal is defined by four propeptide amino acids.. Journal of Cell Biology, 1990, 111, 361-368.	5.2	152
98	The free sulfhydryl group (Cys341) of carboxypeptidase Y: Functional effects of mutational substitutions. Carlsberg Research Communications, 1987, 52, 263-273.	1.8	17
99	Mutational replacement of methionine by arginine in the Sâ€²1 substrate binding site of yeast carboxypeptidase. Carlsberg Research Communications, 1986, 51, 459-465.	1.8	4
100	Increased hydrophobicity of the Sâ€²1 binding site in carboxypeptidase Y obtained by site-directed mutagenesis. Carlsberg Research Communications, 1985, 50, 273-284.	1.8	22