

Wolfram Gronwald

List of Publications by Year in descending order

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Version: 2024-02-01

70
papers

2,870
citations

186265

28
h-index

175258

52
g-index

71
all docs

71
docs citations

71
times ranked

4984
citing authors

#	ARTICLE	IF	CITATIONS
1	A Predictive Model for Progression of CKD to Kidney Failure Based on Routine Laboratory Tests. American Journal of Kidney Diseases, 2022, 79, 217-230.e1.	1.9	21
2	Assessment of Physiological Rat Kidney Ageingâ€™ Implications for the Evaluation of Allograft Quality Prior to Renal Transplantation. Metabolites, 2022, 12, 162.	2.9	0
3	Evaluation of models for prognosing mortality in critical care patients with COVID-19: First- and second-wave data from a German university hospital. PLoS ONE, 2022, 17, e0268734.	2.5	1
4	Validation Study for Non-Invasive Prediction of IDH Mutation Status in Patients with Glioma Using In Vivo 1H-Magnetic Resonance Spectroscopy and Machine Learning. Cancers, 2022, 14, 2762.	3.7	3
5	Lactonization of the Oncometabolite D-2-Hydroxyglutarate Produces a Novel Endogenous Metabolite. Cancers, 2021, 13, 1756.	3.7	8
6	An R-Package for the Deconvolution and Integration of 1D NMR Data: MetaboDecon1D. Metabolites, 2021, 11, 452.	2.9	9
7	Cold Atmospheric Plasma Changes the Amino Acid Composition of Solutions and Influences the Anti-Tumor Effect on Melanoma Cells. International Journal of Molecular Sciences, 2021, 22, 7886.	4.1	8
8	Cytokine-specific autoantibodies shape the gut microbiome in autoimmune polyendocrine syndrome type 1. Journal of Allergy and Clinical Immunology, 2021, 148, 876-888.	2.9	9
9	Lower blood pH as a strong prognostic factor for fatal outcomes in critically ill COVID-19 patients at an intensive care unit: A multivariable analysis. PLoS ONE, 2021, 16, e0258018.	2.5	7
10	High CD206 levels in Hodgkin lymphomaâ€™educated macrophages are linked to matrixâ€™remodeling and lymphoma dissemination. Molecular Oncology, 2020, 14, 571-589.	4.6	25
11	Non-Invasive Prediction of IDH Mutation in Patients with Glioma WHO II/III/IV Based on F-18-FET PET-Guided In Vivo 1H-Magnetic Resonance Spectroscopy and Machine Learning. Cancers, 2020, 12, 3406.	3.7	17
12	Robust Metabolite Quantification from J-Compensated 2D 1H-13C-HSQC Experiments. Metabolites, 2020, 10, 449.	2.9	5
13	Results from the German Chronic Kidney Disease (GCKD) study support association of relative telomere length with mortality in a large cohort of patients with moderate chronic kidney disease. Kidney International, 2020, 98, 488-497.	5.2	16
14	Mitochondrial DNA copy number is associated with mortality and infections in a large cohort of patients with chronic kidney disease. Kidney International, 2019, 96, 480-488.	5.2	53
15	A multi-source data integration approach reveals novel associations between metabolites and renal outcomes in the German Chronic Kidney Disease study. Scientific Reports, 2019, 9, 13954.	3.3	15
16	Library Selection with a Randomized Repertoire of (Î±)-Barrel Enzymes Results in Unexpected Induction of Gene Expression. Biochemistry, 2019, 58, 4207-4217.	2.5	0
17	A Novel Metabolic Signature To Predict the Requirement of Dialysis or Renal Transplantation in Patients with Chronic Kidney Disease. Journal of Proteome Research, 2019, 18, 1796-1805.	3.7	15
18	Identification of ADGRE5 as discriminating MYC target between Burkitt lymphoma and diffuse large B-cell lymphoma. BMC Cancer, 2019, 19, 322.	2.6	8

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19	Systematic Evaluation of Non-Uniform Sampling Parameters in the Targeted Analysis of Urine Metabolites by 1H,1H 2D NMR Spectroscopy. <i>Scientific Reports</i> , 2018, 8, 4249.	3.3	26
20	Genome-Wide Association Studies of Metabolites in Patients with CKD Identify Multiple Loci and Illuminate Tubular Transport Mechanisms. <i>Journal of the American Society of Nephrology: JASN</i> , 2018, 29, 1513-1524.	6.1	39
21	Statistical Analysis of NMR Metabolic Fingerprints: Established Methods and Recent Advances. <i>Metabolites</i> , 2018, 8, 47.	2.9	32
22	Comprehensive Metaboproteomics of Burkitt's and Diffuse Large B-Cell Lymphoma Cell Lines and Primary Tumor Tissues Reveals Distinct Differences in Pyruvate Content and Metabolism. <i>Journal of Proteome Research</i> , 2017, 16, 1105-1120.	3.7	22
23	Quantification of Metabolites by NMR Spectroscopy in the Presence of Protein. <i>Journal of Proteome Research</i> , 2017, 16, 1784-1796.	3.7	24
24	Scale-Invariant Biomarker Discovery in Urine and Plasma Metabolite Fingerprints. <i>Journal of Proteome Research</i> , 2017, 16, 3596-3605.	3.7	15
25	Synergy of interleukin 10 and toll-like receptor 9 signalling in B cell proliferation: Implications for lymphoma pathogenesis. <i>International Journal of Cancer</i> , 2017, 140, 1147-1158.	5.1	5
26	Visceral adipose tissue but not subcutaneous adipose tissue is associated with urine and serum metabolites. <i>PLoS ONE</i> , 2017, 12, e0175133.	2.5	26
27	External calibration with <i>Drosophila</i> whole-cell spike-ins delivers absolute mRNA fold changes from human RNA-Seq and qPCR data. <i>BioTechniques</i> , 2017, 62, 53-61.	1.8	20
28	Evaluation of dilution and normalization strategies to correct for urinary output in HPLC-HRTOFMS metabolomics. <i>Analytical and Bioanalytical Chemistry</i> , 2016, 408, 8483-8493.	3.7	21
29	A Metabolome-Wide Association Study of Kidney Function and Disease in the General Population. <i>Journal of the American Society of Nephrology: JASN</i> , 2016, 27, 1175-1188.	6.1	159
30	Polymorphisms within the <i>APOBR</i> gene are highly associated with milk levels of prognostic ketosis biomarkers in dairy cows. <i>Physiological Genomics</i> , 2015, 47, 129-137.	2.3	22
31	Identification of Plasma Metabolites Prognostic of Acute Kidney Injury after Cardiac Surgery with Cardiopulmonary Bypass. <i>Journal of Proteome Research</i> , 2015, 14, 2897-2905.	3.7	18
32	Data Normalization of ¹ H NMR Metabolite Fingerprinting Data Sets in the Presence of Unbalanced Metabolite Regulation. <i>Journal of Proteome Research</i> , 2015, 14, 3217-3228.	3.7	32
33	Diclofenac inhibits lactate formation and efficiently counteracts local immune suppression in a murine glioma model. <i>International Journal of Cancer</i> , 2013, 132, 843-853.	5.1	77
34	Distinct metabolic differences between various human cancer and primary cells. <i>Electrophoresis</i> , 2013, 34, 2836-2847.	2.4	29
35	Analysis of human urine reveals metabolic changes related to the development of acute kidney injury following cardiac surgery. <i>Metabolomics</i> , 2013, 9, 697-707.	3.0	28
36	Correlations between Milk and Plasma Levels of Amino and Carboxylic Acids in Dairy Cows. <i>Journal of Proteome Research</i> , 2013, 12, 5223-5232.	3.7	24

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37	Current Experimental, Bioinformatic and Statistical Methods used in NMR Based Metabolomics. <i>Current Metabolomics</i> , 2013, 1, 253-268.	0.5	16
38	MetaboQuant: a tool combining individual peak calibration and outlier detection for accurate metabolite quantification in 1D ¹ H and ¹ H- ¹³ C HSQC NMR spectra. <i>BioTechniques</i> , 2013, 54, 251-256.	1.8	19
39	New Aspects of an Old Drug – Diclofenac Targets MYC and Glucose Metabolism in Tumor Cells. <i>PLoS ONE</i> , 2013, 8, e66987.	2.5	86
40	Performance Evaluation of Algorithms for the Classification of Metabolic ¹ H NMR Fingerprints. <i>Journal of Proteome Research</i> , 2012, 11, 6242-6251.	3.7	33
41	NMR Metabolomic Analysis of Dairy Cows Reveals Milk Glycerophosphocholine to Phosphocholine Ratio as Prognostic Biomarker for Risk of Ketosis. <i>Journal of Proteome Research</i> , 2012, 11, 1373-1381.	3.7	122
42	Targeting Melanoma Metastasis and Immunosuppression with a New Mode of Melanoma Inhibitory Activity (MIA) Protein Inhibition. <i>PLoS ONE</i> , 2012, 7, e37941.	2.5	23
43	Early changes in the liver-soluble proteome from mice fed a nonalcoholic steatohepatitis inducing diet. <i>Proteomics</i> , 2012, 12, 1437-1451.	2.2	26
44	State-of-the art data normalization methods improve NMR-based metabolomic analysis. <i>Metabolomics</i> , 2012, 8, 146-160.	3.0	196
45	Detection of autosomal dominant polycystic kidney disease by NMR spectroscopic fingerprinting of urine. <i>Kidney International</i> , 2011, 79, 1244-1253.	5.2	59
46	Discrimination of steatosis and NASH in mice using nuclear magnetic resonance spectroscopy. <i>Metabolomics</i> , 2011, 7, 237-246.	3.0	30
47	PROCOS: Computational analysis of protein-protein complexes. <i>Journal of Computational Chemistry</i> , 2011, 32, 2575-2586.	3.3	22
48	Comparison of serum versus plasma collection in gas chromatography – Mass spectrometry-based metabolomics. <i>Electrophoresis</i> , 2010, 31, 2365-2373.	2.4	43
49	Protein-Protein Interaction Analysis by Docking. <i>Algorithms</i> , 2009, 2, 429-436.	2.1	2
50	Residual Dipolar Couplings in Short Peptidic Foldamers: Combined Analyses of Backbone and Side-Chain Conformations and Evaluation of Structure Coordinates of Rigid Unnatural Amino Acids. <i>ChemBioChem</i> , 2009, 10, 440-444.	2.6	30
51	Chemical shift optimization in multidimensional NMR spectra by AUREMOL-SHIFTOPT. <i>Journal of Biomolecular NMR</i> , 2009, 43, 197-210.	2.8	2
52	Advances in amino acid analysis. <i>Analytical and Bioanalytical Chemistry</i> , 2009, 393, 445-452.	3.7	168
53	Infrequent cavity-forming fluctuations in HPr from <i>Staphylococcus carnosus</i> revealed by pressure- and temperature-dependent tyrosine ring flips. <i>Protein Science</i> , 2009, 13, 3104-3114.	7.6	45
54	Automated GC-MS analysis of free amino acids in biological fluids. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2008, 870, 222-232.	2.3	158

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55	Urinary Metabolite Quantification Employing 2D NMR Spectroscopy. <i>Analytical Chemistry</i> , 2008, 80, 9288-9297.	6.5	123
56	Structure of the Leech Protein Saratin and Characterization of Its Binding to Collagen. <i>Journal of Molecular Biology</i> , 2008, 381, 913-927.	4.2	36
57	Combined chemical shift changes and amino acid specific chemical shift mapping of protein-protein interactions. <i>Journal of Biomolecular NMR</i> , 2007, 39, 275-289.	2.8	200
58	AUREMOL-RFAC-3D, combination of R-factors and their use for automated quality assessment of protein solution structures. <i>Journal of Biomolecular NMR</i> , 2006, 37, 15-30.	2.8	11
59	Improved simulation of NOESY spectra by RELAX-JT2 including effects of J-coupling, transverse relaxation and chemical shift anisotropy. <i>Journal of Biomolecular NMR</i> , 2004, 30, 121-131.	2.8	12
60	Automated structure determination of proteins by NMR spectroscopy. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2004, 44, 33-96.	7.5	98
61	Structure Determination and Ligand Interactions of the PDZ2b Domain of PTP-Bas (hPTP1E): Splicing-induced Modulation of Ligand Specificity. <i>Journal of Molecular Biology</i> , 2003, 334, 143-155.	4.2	29
62	Automated assignment of NOESY NMR spectra using a knowledge based method (KNOWNOE). <i>Journal of Biomolecular NMR</i> , 2002, 23, 271-287.	2.8	53
63	Solution NMR structure of the cold-shock protein from the hyperthermophilic bacterium <i>Thermotoga maritima</i> . <i>FEBS Journal</i> , 2001, 268, 2527-2539.	0.2	97
64	Overcoming the problems associated with poor spectra quality of the protein kinase Byr2 using residual dipolar couplings. <i>Protein Science</i> , 2001, 10, 1260-1263.	7.6	2
65	Solution Structure of the Ras Binding Domain of the Protein Kinase Byr2 from <i>Schizosaccharomyces pombe</i> . <i>Structure</i> , 2001, 9, 1029-1041.	3.3	52
66	RFAC, a program for automated NMR R-factor estimation. <i>Journal of Biomolecular NMR</i> , 2000, 17, 137-151.	2.8	50
67	CAMRA: chemical shift based computer aided protein NMR assignments. <i>Journal of Biomolecular NMR</i> , 1998, 12, 395-405.	2.8	46
68	Unusual β -sheet periodicity in small cyclic peptides. <i>Nature Structural Biology</i> , 1998, 5, 284-288.	9.7	111
69	Assessment by ^1H NMR Spectroscopy of the Structural Behaviour of Human Parathyroid-Hormone-Related Protein(1 - 34) and Its Close Relationship with the N-Terminal Fragments of Human Parathyroid Hormone in Solution. <i>Biological Chemistry</i> , 1997, 378, 1501-8.	2.5	13
70	ORB, a homology-based program for the prediction of protein NMR chemical shifts. <i>Journal of Biomolecular NMR</i> , 1997, 10, 165-179.	2.8	18