

Johannes Graumann

List of Publications by Year in descending order

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Version: 2024-02-01

84
papers

6,459
citations

117625

34
h-index

71685

76
g-index

97
all docs

97
docs citations

97
times ranked

11030
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenetic scores for the circulating proteome as tools for disease prediction. <i>ELife</i> , 2022, 11, .	6.0	37
2	Noncanonical HIPPO/MST Signaling via BUB3 and FOXO Drives Pulmonary Vascular Cell Growth and Survival. <i>Circulation Research</i> , 2022, 130, 760-778.	4.5	19
3	Arachidonic acid, a clinically adverse mediator in the ovarian cancer microenvironment, impairs JAK-STAT signaling in macrophages by perturbing lipid raft structures. <i>Molecular Oncology</i> , 2022, 16, 3146-3166.	4.6	9
4	Depletion of cardiolipin induces major changes in energy metabolism in <i>Trypanosoma brucei</i> bloodstream forms. <i>FASEB Journal</i> , 2021, 35, e21176.	0.5	8
5	Insulin-promoted mobilization of GLUT4 from a perinuclear storage site requires RAB10. <i>Molecular Biology of the Cell</i> , 2021, 32, 57-73.	2.1	21
6	Phosphoproteomics identify arachidonic-acid-regulated signal transduction pathways modulating macrophage functions with implications for ovarian cancer. <i>Theranostics</i> , 2021, 11, 1377-1395.	10.0	22
7	Complexity of the eukaryotic dolichol-linked oligosaccharide scramblase suggested by activity correlation profiling mass spectrometry. <i>Scientific Reports</i> , 2021, 11, 1411.	3.3	13
8	Positioning of nucleosomes containing γ -H2AX precedes active DNA demethylation and transcription initiation. <i>Nature Communications</i> , 2021, 12, 1072.	12.8	30
9	Revealing the role of the human blood plasma proteome in obesity using genetic drivers. <i>Nature Communications</i> , 2021, 12, 1279.	12.8	50
10	SIRT1 promotes lipid metabolism and mitochondrial biogenesis in adipocytes and coordinates adipogenesis by targeting key enzymatic pathways. <i>Scientific Reports</i> , 2021, 11, 8177.	3.3	77
11	Metabolic syndrome and the plasma proteome: from association to causation. <i>Cardiovascular Diabetology</i> , 2021, 20, 111.	6.8	19
12	Plasma Proteomics of Renal Function: A Transethnic Meta-Analysis and Mendelian Randomization Study. <i>Journal of the American Society of Nephrology: JASN</i> , 2021, 32, 1747-1763.	6.1	16
13	Protein kinase N2 mediates flow-induced endothelial NOS activation and vascular tone regulation. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	27
14	The E3 ubiquitin-protein ligase Rbx1 regulates cardiac wall morphogenesis in zebrafish. <i>Developmental Biology</i> , 2021, 480, 1-12.	2.0	3
15	The multicellular signalling network of ovarian cancer metastases. <i>Clinical and Translational Medicine</i> , 2021, 11, e633.	4.0	14
16	A PhotoClick cholesterol-based quantitative proteomics screen for cytoplasmic sterol-binding proteins in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2020, 37, 15-25.	1.7	4
17	Epigenetics meets proteomics in an epigenome-wide association study with circulating blood plasma protein traits. <i>Nature Communications</i> , 2020, 11, 15.	12.8	57
18	Deciphering the Plasma Proteome of Type 2 Diabetes. <i>Diabetes</i> , 2020, 69, 2766-2778.	0.6	34

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19	Stimulation of glycolysis promotes cardiomyocyte proliferation after injury in adult zebrafish. <i>EMBO Reports</i> , 2020, 21, e49752.	4.5	62
20	Modulation of Mammalian Cardiomyocyte Cytokinesis by the Extracellular Matrix. <i>Circulation Research</i> , 2020, 127, 896-907.	4.5	37
21	Effect of induced hypoglycemia on inflammation and oxidative stress in type 2 diabetes and control subjects. <i>Scientific Reports</i> , 2020, 10, 4750.	3.3	69
22	Digenic inheritance of mutations in EPHA2 and SLC26A4 in Pendred syndrome. <i>Nature Communications</i> , 2020, 11, 1343.	12.8	22
23	Tumor-associated macrophages promote ovarian cancer cell migration by secreting transforming growth factor beta induced (TGFB1) and tenascin C. <i>Cell Death and Disease</i> , 2020, 11, 249.	6.3	78
24	Lin28B configures INO80 to regulate muscle stem cell numbers and skeletal muscle hypertrophy. <i>EMBO Journal</i> , 2020, 39, e105098.	7.8	20
25	multicrispr: gRNA design for prime editing and parallel targeting of thousands of targets. <i>Life Science Alliance</i> , 2020, 3, e202000757.	2.8	21
26	Susceptibility of microtubule-associated protein 1 light chain 3 ² (MAP1LC3B/LC3B) knockout mice to lung injury and fibrosis. <i>FASEB Journal</i> , 2019, 33, 12392-12408.	0.5	13
27	A Systems-level Characterization of the Differentiation of Human Embryonic Stem Cells into Mesenchymal Stem Cells*[S]. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1950-1966.	3.8	13
28	Fine-Mapping of the Human Blood Plasma N-Glycome onto Its Proteome. <i>Metabolites</i> , 2019, 9, 122.	2.9	10
29	Mechanical Forces Regulate Cardiomyocyte Myofilament Maturation via the VCL-SSH1-CFL Axis. <i>Developmental Cell</i> , 2019, 51, 62-77.e5.	7.0	35
30	Cardiolipin depletion-induced changes in the Trypanosoma brucei proteome. <i>FASEB Journal</i> , 2019, 33, 13161-13175.	0.5	11
31	Characterization of mast cell-derived rRNA-containing microvesicles and their inflammatory impact on endothelial cells. <i>FASEB Journal</i> , 2019, 33, 5457-5467.	0.5	17
32	Small molecule-mediated chemical knockdown of MuRF1/MuRF2 and attenuation of diaphragm dysfunction in chronic heart failure. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2019, 10, 1102-1115.	7.3	35
33	Remodeling of ER plasma membrane contact sites but not STIM1 phosphorylation inhibits Ca ²⁺ influx in mitosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 10392-10401.	7.1	26
34	MARMoSET – Extracting Publication-ready Mass Spectrometry Metadata from RAW Files. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1700-1702.	3.8	21
35	Dual-platform affinity proteomics identifies links between the recurrence of ovarian carcinoma and proteins released into the tumor microenvironment. <i>Theranostics</i> , 2019, 9, 6601-6617.	10.0	36
36	Multi-platform Affinity Proteomics Identify Proteins Linked to Metastasis and Immune Suppression in Ovarian Cancer Plasma. <i>Frontiers in Oncology</i> , 2019, 9, 1150.	2.8	47

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37	Epigenetic therapy of novel tumour suppressor ZAR1 and its cancer biomarker function. <i>Clinical Epigenetics</i> , 2019, 11, 182.	4.1	15
38	Cell type-selective pathways and clinical associations of lysophosphatidic acid biosynthesis and signaling in the ovarian cancer microenvironment. <i>Molecular Oncology</i> , 2019, 13, 185-201.	4.6	48
39	Metabolic and proteomic signatures of hypoglycaemia in type 2 diabetes. <i>Diabetes, Obesity and Metabolism</i> , 2019, 21, 909-919.	4.4	20
40	Shear stress-induced endothelial adrenomedullin signaling regulates vascular tone and blood pressure. <i>Journal of Clinical Investigation</i> , 2019, 129, 2775-2791.	8.2	129
41	Proteomic profiling of human cancer pseudopodia for the identification of anti-metastatic drug candidates. <i>Scientific Reports</i> , 2018, 8, 5858.	3.3	8
42	Deep molecular phenotypes link complex disorders and physiological insult to CpG methylation. <i>Human Molecular Genetics</i> , 2018, 27, 1106-1121.	2.9	30
43	Proteotranscriptomics Reveal Signaling Networks in the Ovarian Cancer Microenvironment. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 270-289.	3.8	55
44	Loss of the Mia40a oxidoreductase leads to hepato-pancreatic insufficiency in zebrafish. <i>PLoS Genetics</i> , 2018, 14, e1007743.	3.5	10
45	Myh10 deficiency leads to defective extracellular matrix remodeling and pulmonary disease. <i>Nature Communications</i> , 2018, 9, 4600.	12.8	27
46	The CCT chaperonin is a novel regulator of Ca ²⁺ signaling through modulation of Orai1 trafficking. <i>Science Advances</i> , 2018, 4, eaau1935.	10.3	16
47	Genome-wide mapping of plasma protein QTLs identifies putatively causal genes and pathways for cardiovascular disease. <i>Nature Communications</i> , 2018, 9, 3268.	12.8	221
48	MiCEE is a ncRNA-protein complex that mediates epigenetic silencing and nucleolar organization. <i>Nature Genetics</i> , 2018, 50, 990-1001.	21.4	52
49	multi-panel-figure : Simple Assembly of Multiple Plots and Images into a Compound Figure. <i>Journal of Statistical Software</i> , 2018, 84, .	3.7	6
50	Screening for insulin-independent pathways that modulate glucose homeostasis identifies androgen receptor antagonists. <i>ELife</i> , 2018, 7, .	6.0	16
51	Connecting genetic risk to disease end points through the human blood plasma proteome. <i>Nature Communications</i> , 2017, 8, 14357.	12.8	460
52	Using hESCs to Probe the Interaction of the Diabetes-Associated Genes CDKAL1 and MT1E. <i>Cell Reports</i> , 2017, 19, 1512-1521.	6.4	32
53	The arc of Mass Spectrometry Exchange Formats is long, but it bends toward HDF5. <i>Mass Spectrometry Reviews</i> , 2017, 36, 668-673.	5.4	10
54	flippant: An R package for the automated analysis of fluorescence-based scramblase assays. <i>BMC Bioinformatics</i> , 2017, 18, 146.	2.6	0

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55	Complementarity of SOMAscan to LC-MS/MS and RNA-seq for quantitative profiling of human embryonic and mesenchymal stem cells. <i>Journal of Proteomics</i> , 2017, 150, 86-97.	2.4	46
56	MicroRNAs of the miR-290/295 Family Maintain Bivalency in Mouse Embryonic Stem Cells. <i>Stem Cell Reports</i> , 2016, 6, 635-642.	4.8	24
57	An Isogenic Human ESC Platform for Functional Evaluation of Genome-wide-Association-Study-Identified Diabetes Genes and Drug Discovery. <i>Cell Stem Cell</i> , 2016, 19, 326-340.	11.1	98
58	Comprehensive transcriptomic and proteomic characterization of human mesenchymal stem cells reveals source specific cellular markers. <i>Scientific Reports</i> , 2016, 6, 21507.	3.3	101
59	Dimerization deficiency of enigmatic retinitis pigmentosa-linked rhodopsin mutants. <i>Nature Communications</i> , 2016, 7, 12832.	12.8	54
60	readat: An R package for reading and working with SomaLogic ADAT files. <i>BMC Bioinformatics</i> , 2016, 17, 201.	2.6	13
61	SIRT1 Limits Adipocyte Hyperplasia through c-Myc Inhibition. <i>Journal of Biological Chemistry</i> , 2016, 291, 2119-2135.	3.4	33
62	Quantitative Proteomic Approaches in Mouse: Stable Isotope Incorporation by Metabolic (SILAC) or Chemical Labeling (Reductive Dimethylation) Combined with High-Resolution Mass Spectrometry. <i>Current Protocols in Mouse Biology</i> , 2015, 5, 1-20.	1.2	8
63	Genome-wide identification and functional analysis of Apobec-1-mediated C-to-U RNA editing in mouse small intestine and liver. <i>Genome Biology</i> , 2014, 15, R79.	9.6	87
64	microRNA-mediated regulation of mTOR complex components facilitates discrimination between activation and anergy in CD4 T cells. <i>Journal of Experimental Medicine</i> , 2014, 211, 2281-2295.	8.5	57
65	microRNA-mediated regulation of mTOR complex components facilitates discrimination between activation and anergy in CD4 T cells. <i>Journal of Cell Biology</i> , 2014, 207, 2072-2081.	5.2	0
66	Adaptation of a Commonly Used, Chemically Defined Medium for Human Embryonic Stem Cells to Stable Isotope Labeling with Amino Acids in Cell Culture. <i>Journal of Proteome Research</i> , 2013, 12, 3233-3245.	3.7	10
67	A SILAC-based Approach Identifies Substrates of Caspase-dependent Cleavage upon TRAIL-induced Apoptosis. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1436-1450.	3.8	27
68	Quantitative proteomics approach towards the identification of yeast endoplasmic reticulum flippase. <i>Journal of Proteome Research</i> , 2013, 12, 3233-3245.		0
69	A Framework for Intelligent Data Acquisition and Real-Time Database Searching for Shotgun Proteomics. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.013185.	3.8	50
70	MicroRNA Regulation of Cbx7 Mediates a Switch of Polycomb Orthologs during ESC Differentiation. <i>Cell Stem Cell</i> , 2012, 10, 33-46.	11.1	191
71	Assessment of ultrasonic-assisted enzymatic digestion of complex protein mixtures by high-resolution mass spectrometry. <i>Qatar Foundation Annual Research Forum Proceedings</i> , 2012, , BMP110.	0.0	0
72	Chromatin-Remodeling Components of the BAF Complex Facilitate Reprogramming. <i>Cell</i> , 2010, 141, 943-955.	28.9	357

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73	UBXD7 Binds Multiple Ubiquitin Ligases and Implicates p97 in HIF1 α Turnover. <i>Cell</i> , 2008, 134, 804-816.	28.9	277
74	Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC) and Proteome Quantitation of Mouse Embryonic Stem Cells to a Depth of 5,111 Proteins. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 672-683.	3.8	261
75	Quantitative Profiling of Ubiquitylated Proteins Reveals Proteasome Substrates and the Substrate Repertoire Influenced by the Rpn10 Receptor Pathway. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1885-1895.	3.8	90
76	Labeling, detection and identification of newly synthesized proteomes with bioorthogonal non-canonical amino-acid tagging. <i>Nature Protocols</i> , 2007, 2, 532-540.	12.0	291
77	Selective identification of newly synthesized proteins in mammalian cells using bioorthogonal noncanonical amino acid tagging (BONCAT). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 9482-9487.	7.1	716
78	Analysis of Polyubiquitin Conjugates Reveals That the Rpn10 Substrate Receptor Contributes to the Turnover of Multiple Proteasome Targets. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 741-751.	3.8	89
79	The WD40 protein Caf4p is a component of the mitochondrial fission machinery and recruits Dnm1p to mitochondria. <i>Journal of Cell Biology</i> , 2005, 170, 237-248.	5.2	246
80	Applicability of Tandem Affinity Purification MudPIT to Pathway Proteomics in Yeast. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 226-237.	3.8	130
81	MS1, MS2, and SQT—three unified, compact, and easily parsed file formats for the storage of shotgun proteomic spectra and identifications. <i>Rapid Communications in Mass Spectrometry</i> , 2004, 18, 2162-2168.	1.5	350
82	Multiubiquitin Chain Receptors Define a Layer of Substrate Selectivity in the Ubiquitin-Proteasome System. <i>Cell</i> , 2004, 118, 99-110.	28.9	410
83	The 2.2 Å... Crystal Structure of Hsp33. <i>Structure</i> , 2001, 9, 367-375.	3.3	54
84	Activation of the Redox-Regulated Molecular Chaperone Hsp33—A Two-Step Mechanism. <i>Structure</i> , 2001, 9, 377-387.	3.3	142