

Matthias Selbach

List of Publications by Year in descending order

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Version: 2024-02-01

105
papers

20,610
citations

41339

49
h-index

28296

105
g-index

118
all docs

118
docs citations

118
times ranked

32392
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteome-wide quantitative RNA-interactome capture identifies phosphorylation sites with regulatory potential in RBM20. <i>Molecular Cell</i> , 2022, 82, 2069-2083.e8.	9.7	9
2	MYCN mediates cysteine addiction and sensitizes neuroblastoma to ferroptosis. <i>Nature Cancer</i> , 2022, 3, 471-485.	13.2	73
3	GIMAP6 regulates autophagy, immune competence, and inflammation in mice and humans. <i>Journal of Experimental Medicine</i> , 2022, 219, .	8.5	4
4	HDLBP binds ER-targeted mRNAs by multivalent interactions to promote protein synthesis of transmembrane and secreted proteins. <i>Nature Communications</i> , 2022, 13, 2727.	12.8	9
5	Physiological Functions of Intracellular Protein Degradation. <i>Annual Review of Cell and Developmental Biology</i> , 2022, 38, 241-262.	9.4	6
6	In Vitro Kinase-to-Phosphosite Database (iKiP-DB) Predicts Kinase Activity in Phosphoproteomic Datasets. <i>Journal of Proteome Research</i> , 2022, 21, 1575-1587.	3.7	6
7	Protein Synthesis in the Developing Neocortex at Near-Atomic Resolution Reveals Ebp1-Mediated Neuronal Proteostasis at the 60S Tunnel Exit. <i>Molecular Cell</i> , 2021, 81, 304-322.e16.	9.7	27
8	Alternative lengthening of telomeres in childhood neuroblastoma from genome to proteome. <i>Nature Communications</i> , 2021, 12, 1269.	12.8	46
9	The UBA domain of conjugating enzyme Ubc1/Ube2K facilitates assembly of K48/K63â€ branched ubiquitin chains. <i>EMBO Journal</i> , 2021, 40, e106094.	7.8	25
10	Transcriptomic profiling of SARS-CoV-2 infected human cell lines identifies HSP90 as target for COVID-19 therapy. <i>IScience</i> , 2021, 24, 102151.	4.1	202
11	Snapshots of native pre-50S ribosomes reveal a biogenesis factor network and evolutionary specialization. <i>Molecular Cell</i> , 2021, 81, 1200-1215.e9.	9.7	35
12	Opportunities and Challenges in Global Quantification of RNA-Protein Interaction via UV Cross-Linking. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 669939.	3.5	16
13	Novel LOTUS-domain proteins are organizational hubs that recruit <i>C. elegans</i> Vasa to germ granules. <i>ELife</i> , 2021, 10, .	6.0	11
14	An Introduction to Advanced Targeted Acquisition Methods. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100165.	3.8	52
15	Cargo-specific recruitment in clathrin- and dynamin-independent endocytosis. <i>Nature Cell Biology</i> , 2021, 23, 1073-1084.	10.3	34
16	Neuroblastoma signalling models unveil combination therapies targeting feedback-mediated resistance. <i>PLoS Computational Biology</i> , 2021, 17, e1009515.	3.2	5
17	SARS-CoV-2 infection triggers profibrotic macrophage responses and lung fibrosis. <i>Cell</i> , 2021, 184, 6243-6261.e27.	28.9	277
18	Cross-regulation of viral kinases with cyclin A secures shutoff of host DNA synthesis. <i>Nature Communications</i> , 2020, 11, 4845.	12.8	16

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19	mRNAs, proteins and the emerging principles of gene expression control. Nature Reviews Genetics, 2020, 21, 630-644.	16.3	576
20	Murine Cytomegalovirus M25 Proteins Sequester the Tumor Suppressor Protein p53 in Nuclear Accumulations. Journal of Virology, 2020, 94, .	3.4	5
21	Peptide-based Interaction Proteomics. Molecular and Cellular Proteomics, 2020, 19, 1070-1075.	3.8	22
22	Keeping the Proportions of Protein Complex Components in Check. Cell Systems, 2020, 10, 125-132.	6.2	71
23	The human ZC3H3 and RBM26/27 proteins are critical for PAXT-mediated nuclear RNA decay. Nucleic Acids Research, 2020, 48, 2518-2530.	14.5	50
24	Recruitment of Histone Methyltransferase Ehmt1 to Foxp3 TSDR Counteracts Differentiation of Induced Regulatory T Cells. Journal of Molecular Biology, 2019, 431, 3606-3625.	4.2	6
25	Integrated Phosphoproteome and Transcriptome Analysis Reveals Chlamydia-Induced Epithelial-to-Mesenchymal Transition in Host Cells. Cell Reports, 2019, 26, 1286-1302.e8.	6.4	46
26	Autocrine LTA signaling drives NF- κ B and JAK-STAT activity and myeloid gene expression in Hodgkin lymphoma. Blood, 2019, 133, 1489-1494.	1.4	20
27	Purification of cross-linked RNA-protein complexes by phenol-toluol extraction. Nature Communications, 2019, 10, 990.	12.8	168
28	The dynamic proteome of influenza A virus infection identifies M segment splicing as a host range determinant. Nature Communications, 2019, 10, 5518.	12.8	34
29	Picky: a simple online PRM and SRM method designer for targeted proteomics. Nature Methods, 2018, 15, 156-157.	19.0	32
30	Mutations in Disordered Regions Can Cause Disease by Creating Dileucine Motifs. Cell, 2018, 175, 239-253.e17.	28.9	97
31	Phosphorylation of the Ribosomal Protein RPL12/uL11 Affects Translation during Mitosis. Molecular Cell, 2018, 72, 84-98.e9.	9.7	73
32	Kinase-controlled phase transition of membraneless organelles in mitosis. Nature, 2018, 559, 211-216.	27.8	296
33	Maf links Neuregulin1 signaling to cholesterol synthesis in myelinating Schwann cells. Genes and Development, 2018, 32, 645-657.	5.9	22
34	Evolutionary plasticity in the innate immune function of Akirin. PLoS Genetics, 2018, 14, e1007494.	3.5	31
35	Deciphering the Ubiquitin Code. Molecular Cell, 2017, 65, 779-780.	9.7	12
36	Quantitative GTPase Affinity Purification Identifies Rho Family Protein Interaction Partners. Molecular and Cellular Proteomics, 2017, 16, 73-85.	3.8	20

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37	DDX54 regulates transcriptome dynamics during DNA damage response. <i>Genome Research</i> , 2017, 27, 1344-1359.	5.5	46
38	Quantitative Proteomic Approach Identifies Vpr Binding Protein as Novel Host Factor Supporting Influenza A Virus Infections in Human Cells. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 728-742.	3.8	13
39	RNA localization is a key determinant of neurite-enriched proteome. <i>Nature Communications</i> , 2017, 8, 583.	12.8	176
40	Conservation of miRNA-mediated silencing mechanisms across 600 million years of animal evolution. <i>Nucleic Acids Research</i> , 2017, 45, 938-950.	14.5	26
41	In Vivo Interaction Proteomics in <i>Caenorhabditis elegans</i> Embryos Provides New Insights into P Granule Dynamics. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1642-1657.	3.8	29
42	Hypofunctional TrkA Accounts for the Absence of Pain Sensitization in the African Naked Mole-Rat. <i>Cell Reports</i> , 2016, 17, 748-758.	6.4	51
43	Kinetic Analysis of Protein Stability Reveals Age-Dependent Degradation. <i>Cell</i> , 2016, 167, 803-815.e21.	28.9	259
44	Systematic Errors in Peptide and Protein Identification and Quantification by Modified Peptides. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2791-2801.	3.8	65
45	The mRNA-bound proteome of the early fly embryo. <i>Genome Research</i> , 2016, 26, 1000-1009.	5.5	66
46	Bimodal antagonism of PKA signalling by ARHGAP36. <i>Nature Communications</i> , 2016, 7, 12963.	12.8	33
47	Quantitative interaction mapping reveals an extended UBX domain in ASPL that disrupts functional p97 hexamers. <i>Nature Communications</i> , 2016, 7, 13047.	12.8	35
48	Detecting actively translated open reading frames in ribosome profiling data. <i>Nature Methods</i> , 2016, 13, 165-170.	19.0	368
49	Isolation of Human Colon Stem Cells Using Surface Expression of PTK7. <i>Stem Cell Reports</i> , 2015, 5, 979-987.	4.8	52
50	Extensive allele-specific translational regulation in hybrid mice. <i>Molecular Systems Biology</i> , 2015, 11, 825.	7.2	31
51	Quantitative affinity purification mass spectrometry: a versatile technology to study protein-protein interactions. <i>Frontiers in Genetics</i> , 2015, 6, 237.	2.3	55
52	GABA Blocks Pathological but Not Acute TRPV1 Pain Signals. <i>Cell</i> , 2015, 160, 759-770.	28.9	119
53	Quantitative Proteomics Reveals Dynamic Interaction of c-Jun N-terminal Kinase (JNK) with RNA Transport Granule Proteins Splicing Factor Proline- and Glutamine-rich (Sfpq) and Non-POU Domain-containing Octamer-binding Protein (Nono) during Neuronal Differentiation. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 50-65.	3.8	17
54	miR-184 Regulates Pancreatic β -Cell Function According to Glucose Metabolism. <i>Journal of Biological Chemistry</i> , 2015, 290, 20284-20294.	3.4	53

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55	Quantitative Interaction Proteomics of Neurodegenerative Disease Proteins. Cell Reports, 2015, 11, 1134-1146.	6.4	88
56	Extensive identification and analysis of conserved small ORFs in animals. Genome Biology, 2015, 16, 179.	8.8	180
57	PI3 Kinase and FOXO1 Transcription Factor Activity Differentially Control B Cells in the Germinal Center Light and Dark Zones. Immunity, 2015, 43, 1075-1086.	14.3	206
58	SILAC for biomarker discovery. Proteomics - Clinical Applications, 2015, 9, 301-306.	1.6	20
59	Alteration of Protein Levels during Influenza Virus H1N1 Infection in Host Cells: A Proteomic Survey of Host and Virus Reveals Differential Dynamics. PLoS ONE, 2014, 9, e94257.	2.5	38
60	Suicidal Autointegration of Sleeping Beauty and piggyBac Transposons in Eukaryotic Cells. PLoS Genetics, 2014, 10, e1004103.	3.5	37
61	Activation of MAPK overrides the termination of myelin growth and replaces Nrg1/ErbB3 signals during Schwann cell development and myelination. Genes and Development, 2014, 28, 290-303.	5.9	76
62	Assessment of Serum Protein Dynamics by Native SILAC Flooding (SILflood). Analytical Chemistry, 2014, 86, 11033-11037.	6.5	13
63	Global characterization of the oocyte-to-embryo transition in <i>C. elegans</i> uncovers a novel mRNA clearance mechanism. EMBO Journal, 2014, 33, 1751-1766.	7.8	68
64	Conservation of mRNA and Protein Expression during Development of <i>C. elegans</i> . Cell Reports, 2014, 6, 565-577.	6.4	98
65	IPG Strip-Based Peptide Fractionation for Shotgun Proteomics. Methods in Molecular Biology, 2014, 1156, 67-77.	0.9	12
66	RNA-binding protein RBM20 represses splicing to orchestrate cardiac pre-mRNA processing. Journal of Clinical Investigation, 2014, 124, 3419-3430.	8.2	176
67	Quantitative Proteomic Analysis of Gene Regulation by miR-34a and miR-34c. PLoS ONE, 2014, 9, e92166.	2.5	25
68	Orchestrated Intron Retention Regulates Normal Granulocyte Differentiation. Cell, 2013, 154, 583-595.	28.9	408
69	Argonaute2 Regulates the Pancreatic β -Cell Secretome. Molecular and Cellular Proteomics, 2013, 12, 1214-1225.	3.8	42
70	Synthesis and degradation jointly determine the responsiveness of the cellular proteome. BioEssays, 2013, 35, 597-601.	2.5	34
71	Proteomic Analysis of Mitotic RNA Polymerase II Reveals Novel Interactors and Association With Proteins Dysfunctional in Disease. Molecular and Cellular Proteomics, 2012, 11, M111.011767.	3.8	13
72	In Vivo Quantitative Proteome Profiling: Planning and Evaluation of SILAC Experiments. Methods in Molecular Biology, 2012, 893, 175-199.	0.9	15

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73	The mRNA-Bound Proteome and Its Global Occupancy Profile on Protein-Coding Transcripts. <i>Molecular Cell</i> , 2012, 46, 674-690.	9.7	1,077
74	In Vivo Conditions to Identify Prkci Phosphorylation Targets Using the Analog-Sensitive Kinase Method in Zebrafish. <i>PLoS ONE</i> , 2012, 7, e40000.	2.5	10
75	Transcriptome-wide Analysis of Regulatory Interactions of the RNA-Binding Protein HuR. <i>Molecular Cell</i> , 2011, 43, 340-352.	9.7	640
76	Analyzing protein-protein interactions by quantitative mass spectrometry. <i>Methods</i> , 2011, 54, 387-395.	3.8	60
77	Iron regulatory protein-1 and -2: transcriptome-wide definition of binding mRNAs and shaping of the cellular proteome by iron regulatory proteins. <i>Blood</i> , 2011, 118, e168-e179.	1.4	108
78	Global quantification of mammalian gene expression control. <i>Nature</i> , 2011, 473, 337-342.	27.8	5,498
79	Whole Cell Proteome Regulation by MicroRNAs Captured in a Pulsed SILAC Mass Spectrometry Approach. <i>Methods in Molecular Biology</i> , 2011, 725, 315-331.	0.9	12
80	The Versatility of <i>Helicobacter pylori</i> CagA Effector Protein Functions: The Master Key Hypothesis. <i>Helicobacter</i> , 2010, 15, 163-176.	3.5	202
81	Quantitative Proteomics Reveals Subset-Specific Viral Recognition in Dendritic Cells. <i>Immunity</i> , 2010, 32, 279-289.	14.3	544
82	The SILAC Fly Allows for Accurate Protein Quantification in Vivo. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2173-2183.	3.8	150
83	The tyrosine phosphatase Shp2 (PTPN11) directs Neuregulin-1/ErbB signaling throughout Schwann cell development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 16704-16709.	7.1	100
84	Quantitative proteomics: a tool to assess cell differentiation. <i>Current Opinion in Cell Biology</i> , 2009, 21, 761-766.	5.4	23
85	Global analysis of cellular protein translation by pulsed SILAC. <i>Proteomics</i> , 2009, 9, 205-209.	2.2	314
86	A practical guide to the MaxQuant computational platform for SILAC-based quantitative proteomics. <i>Nature Protocols</i> , 2009, 4, 698-705.	12.0	769
87	Host Cell Interactome of Tyrosine-Phosphorylated Bacterial Proteins. <i>Cell Host and Microbe</i> , 2009, 5, 397-403.	11.0	175
88	Novel insights into proteomic technologies and their clinical perspective. <i>Genome Medicine</i> , 2009, 1, 53.	8.2	1
89	Phosphorylation of tyrosine 972 of the <i>Helicobacter pylori</i> CagA protein is essential for induction of a scattering phenotype in gastric epithelial cells. <i>Molecular Microbiology</i> , 2008, 42, 631-644.	2.5	211
90	Complex kinase requirements for <i>Chlamydia trachomatis</i> Tarp phosphorylation. <i>FEMS Microbiology Letters</i> , 2008, 289, 233-240.	1.8	44

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91	Widespread changes in protein synthesis induced by microRNAs. <i>Nature</i> , 2008, 455, 58-63.	27.8	3,120
92	Role of type IV secretion in <i>Helicobacter pylori</i> pathogenesis. <i>Cellular Microbiology</i> , 2008, 10, 1573-1581.	2.1	227
93	The <i>Helicobacter pylori</i> CagA protein disrupts matrix adhesion of gastric epithelial cells by dephosphorylation of vinculin. <i>Cellular Microbiology</i> , 2007, 9, 1148-1161.	2.1	80
94	Protein interaction screening by quantitative immunoprecipitation combined with knockdown (QUICK). <i>Nature Methods</i> , 2006, 3, 981-983.	19.0	239
95	Robust <i>Salmonella</i> metabolism limits possibilities for new antimicrobials. <i>Nature</i> , 2006, 440, 303-307.	27.8	327
96	Subproteomes of soluble and structure-bound <i>Helicobacter pylori</i> proteins analyzed by two-dimensional gel electrophoresis and mass spectrometry. <i>Proteomics</i> , 2005, 5, 1331-1345.	2.2	79
97	Analysis of Cell Type-Specific Responses Mediated by the Type IV Secretion System of <i>Helicobacter pylori</i> . <i>Infection and Immunity</i> , 2005, 73, 4643-4652.	2.2	33
98	Cortactin: an Achilles' heel of the actin cytoskeleton targeted by pathogens. <i>Trends in Microbiology</i> , 2005, 13, 181-189.	7.7	97
99	Tyrosine-phosphorylated bacterial effector proteins: the enemies within. <i>Trends in Microbiology</i> , 2005, 13, 476-484.	7.7	80
100	<i>Helicobacter pylori</i> Induces AGS Cell Motility and Elongation via Independent Signaling Pathways. <i>Infection and Immunity</i> , 2004, 72, 3646-3649.	2.2	67
101	The <i>Helicobacter pylori</i> CagA protein induces tyrosine dephosphorylation of ezrin. <i>Proteomics</i> , 2004, 4, 2961-2968.	2.2	79
102	The <i>Helicobacter pylori</i> CagA protein induces cortactin dephosphorylation and actin rearrangement by c-Src inactivation. <i>EMBO Journal</i> , 2003, 22, 515-528.	7.8	212
103	Functional Analysis of the <i>Helicobacter pylori</i> cag Pathogenicity Island Reveals Both VirD4-CagA-Dependent and VirD4-CagA-Independent Mechanisms. <i>Infection and Immunity</i> , 2002, 70, 665-671.	2.2	140
104	Src Is the Kinase of the <i>Helicobacter pylori</i> CagA Protein in Vitro and in Vivo. <i>Journal of Biological Chemistry</i> , 2002, 277, 6775-6778.	3.4	374
105	cag + <i>Helicobacter pylori</i> Induces Homotypic Aggregation of Macrophage-Like Cells by Up-Regulation and Recruitment of Intracellular Adhesion Molecule 1 to the Cell Surface. <i>Infection and Immunity</i> , 2002, 70, 4687-4691.	2.2	27