

Matthias Selbach

List of Publications by Year in descending order

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Version: 2024-02-01

105
papers

20,610
citations

47409

49
h-index

32181

105
g-index

118
all docs

118
docs citations

118
times ranked

35899
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.	4.5	9
2	MYCN mediates cysteine addiction and sensitizes neuroblastoma to ferroptosis. <i>Nature Cancer</i> , 2022, 3, 471-485.	5.7	73
3	GIMAP6 regulates autophagy, immune competence, and inflammation in mice and humans. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	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.	5.8	9
5	Physiological Functions of Intracellular Protein Degradation. <i>Annual Review of Cell and Developmental Biology</i> , 2022, 38, 241-262.	4.0	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.	1.8	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.	4.5	27
8	Alternative lengthening of telomeres in childhood neuroblastoma from genome to proteome. <i>Nature Communications</i> , 2021, 12, 1269.	5.8	46
9	The UBA domain of conjugating enzyme Ubc1/Ube2K facilitates assembly of K48/K63-branched ubiquitin chains. <i>EMBO Journal</i> , 2021, 40, e106094.	3.5	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.	1.9	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.	4.5	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.	1.6	16
13	Novel LOTUS-domain proteins are organizational hubs that recruit <i>C. elegans</i> Vasa to germ granules. <i>ELife</i> , 2021, 10, .	2.8	11
14	An Introduction to Advanced Targeted Acquisition Methods. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100165.	2.5	52
15	Cargo-specific recruitment in clathrin- and dynamin-independent endocytosis. <i>Nature Cell Biology</i> , 2021, 23, 1073-1084.	4.6	34
16	Neuroblastoma signalling models unveil combination therapies targeting feedback-mediated resistance. <i>PLoS Computational Biology</i> , 2021, 17, e1009515.	1.5	5
17	SARS-CoV-2 infection triggers profibrotic macrophage responses and lung fibrosis. <i>Cell</i> , 2021, 184, 6243-6261.e27.	13.5	277
18	Cross-regulation of viral kinases with cyclin A secures shutoff of host DNA synthesis. <i>Nature Communications</i> , 2020, 11, 4845.	5.8	16

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19	mRNAs, proteins and the emerging principles of gene expression control. <i>Nature Reviews Genetics</i> , 2020, 21, 630-644.	7.7	576
20	Murine Cytomegalovirus M25 Proteins Sequester the Tumor Suppressor Protein p53 in Nuclear Accumulations. <i>Journal of Virology</i> , 2020, 94, .	1.5	5
21	Peptide-based Interaction Proteomics. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1070-1075.	2.5	22
22	Keeping the Proportions of Protein Complex Components in Check. <i>Cell Systems</i> , 2020, 10, 125-132.	2.9	71
23	The human ZC3H3 and RBM26/27 proteins are critical for PAXT-mediated nuclear RNA decay. <i>Nucleic Acids Research</i> , 2020, 48, 2518-2530.	6.5	50
24	Recruitment of Histone Methyltransferase Ehmt1 to Foxp3 TSDR Counteracts Differentiation of Induced Regulatory T Cells. <i>Journal of Molecular Biology</i> , 2019, 431, 3606-3625.	2.0	6
25	Integrated Phosphoproteome and Transcriptome Analysis Reveals Chlamydia-Induced Epithelial-to-Mesenchymal Transition in Host Cells. <i>Cell Reports</i> , 2019, 26, 1286-1302.e8.	2.9	46
26	Autocrine LTA signaling drives NF- κ B and JAK-STAT activity and myeloid gene expression in Hodgkin lymphoma. <i>Blood</i> , 2019, 133, 1489-1494.	0.6	20
27	Purification of cross-linked RNA-protein complexes by phenol-toluol extraction. <i>Nature Communications</i> , 2019, 10, 990.	5.8	168
28	The dynamic proteome of influenza A virus infection identifies M segment splicing as a host range determinant. <i>Nature Communications</i> , 2019, 10, 5518.	5.8	34
29	Picky: a simple online PRM and SRM method designer for targeted proteomics. <i>Nature Methods</i> , 2018, 15, 156-157.	9.0	32
30	Mutations in Disordered Regions Can Cause Disease by Creating Dileucine Motifs. <i>Cell</i> , 2018, 175, 239-253.e17.	13.5	97
31	Phosphorylation of the Ribosomal Protein RPL12/uL11 Affects Translation during Mitosis. <i>Molecular Cell</i> , 2018, 72, 84-98.e9.	4.5	73
32	Kinase-controlled phase transition of membraneless organelles in mitosis. <i>Nature</i> , 2018, 559, 211-216.	13.7	296
33	Maf links Neuregulin1 signaling to cholesterol synthesis in myelinating Schwann cells. <i>Genes and Development</i> , 2018, 32, 645-657.	2.7	22
34	Evolutionary plasticity in the innate immune function of Akirin. <i>PLoS Genetics</i> , 2018, 14, e1007494.	1.5	31
35	Deciphering the Ubiquitin Code. <i>Molecular Cell</i> , 2017, 65, 779-780.	4.5	12
36	Quantitative GTPase Affinity Purification Identifies Rho Family Protein Interaction Partners. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 73-85.	2.5	20

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37	DDX54 regulates transcriptome dynamics during DNA damage response. <i>Genome Research</i> , 2017, 27, 1344-1359.	2.4	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.	2.5	13
39	RNA localization is a key determinant of neurite-enriched proteome. <i>Nature Communications</i> , 2017, 8, 583.	5.8	176
40	Conservation of miRNA-mediated silencing mechanisms across 600 million years of animal evolution. <i>Nucleic Acids Research</i> , 2017, 45, 938-950.	6.5	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.	2.5	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.	2.9	51
43	Kinetic Analysis of Protein Stability Reveals Age-Dependent Degradation. <i>Cell</i> , 2016, 167, 803-815.e21.	13.5	259
44	Systematic Errors in Peptide and Protein Identification and Quantification by Modified Peptides. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2791-2801.	2.5	65
45	The mRNA-bound proteome of the early fly embryo. <i>Genome Research</i> , 2016, 26, 1000-1009.	2.4	66
46	Bimodal antagonism of PKA signalling by ARHGAP36. <i>Nature Communications</i> , 2016, 7, 12963.	5.8	33
47	Quantitative interaction mapping reveals an extended UBX domain in ASPL that disrupts functional p97 hexamers. <i>Nature Communications</i> , 2016, 7, 13047.	5.8	35
48	Detecting actively translated open reading frames in ribosome profiling data. <i>Nature Methods</i> , 2016, 13, 165-170.	9.0	368
49	Isolation of Human Colon Stem Cells Using Surface Expression of PTK7. <i>Stem Cell Reports</i> , 2015, 5, 979-987.	2.3	52
50	Extensive allele-specific translational regulation in hybrid mice. <i>Molecular Systems Biology</i> , 2015, 11, 825.	3.2	31
51	Quantitative affinity purification mass spectrometry: a versatile technology to study protein-protein interactions. <i>Frontiers in Genetics</i> , 2015, 6, 237.	1.1	55
52	GABA Blocks Pathological but Not Acute TRPV1 Pain Signals. <i>Cell</i> , 2015, 160, 759-770.	13.5	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.	2.5	17
54	miR-184 Regulates Pancreatic β -Cell Function According to Glucose Metabolism. <i>Journal of Biological Chemistry</i> , 2015, 290, 20284-20294.	1.6	53

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55	Quantitative Interaction Proteomics of Neurodegenerative Disease Proteins. <i>Cell Reports</i> , 2015, 11, 1134-1146.	2.9	88
56	Extensive identification and analysis of conserved small ORFs in animals. <i>Genome Biology</i> , 2015, 16, 179.	3.8	180
57	PI3 Kinase and FOXO1 Transcription Factor Activity Differentially Control B Cells in the Germinal Center Light and Dark Zones. <i>Immunity</i> , 2015, 43, 1075-1086.	6.6	206
58	SILAC for biomarker discovery. <i>Proteomics - Clinical Applications</i> , 2015, 9, 301-306.	0.8	20
59	Alteration of Protein Levels during Influenza Virus H1N1 Infection in Host Cells: A Proteomic Survey of Host and Virus Reveals Differential Dynamics. <i>PLoS ONE</i> , 2014, 9, e94257.	1.1	38
60	Suicidal Autointegration of Sleeping Beauty and piggyBac Transposons in Eukaryotic Cells. <i>PLoS Genetics</i> , 2014, 10, e1004103.	1.5	37
61	Activation of MAPK overrides the termination of myelin growth and replaces Nrg1/ErbB3 signals during Schwann cell development and myelination. <i>Genes and Development</i> , 2014, 28, 290-303.	2.7	76
62	Assessment of Serum Protein Dynamics by Native SILAC Flooding (SILflood). <i>Analytical Chemistry</i> , 2014, 86, 11033-11037.	3.2	13
63	Global characterization of the oocyte to embryo transition in <i>C. elegans</i> uncovers a novel mRNA clearance mechanism. <i>EMBO Journal</i> , 2014, 33, 1751-1766.	3.5	68
64	Conservation of mRNA and Protein Expression during Development of <i>C. elegans</i> . <i>Cell Reports</i> , 2014, 6, 565-577.	2.9	98
65	IPG Strip-Based Peptide Fractionation for Shotgun Proteomics. <i>Methods in Molecular Biology</i> , 2014, 1156, 67-77.	0.4	12
66	RNA-binding protein RBM20 represses splicing to orchestrate cardiac pre-mRNA processing. <i>Journal of Clinical Investigation</i> , 2014, 124, 3419-3430.	3.9	176
67	Quantitative Proteomic Analysis of Gene Regulation by miR-34a and miR-34c. <i>PLoS ONE</i> , 2014, 9, e92166.	1.1	25
68	Orchestrated Intron Retention Regulates Normal Granulocyte Differentiation. <i>Cell</i> , 2013, 154, 583-595.	13.5	408
69	Argonaute2 Regulates the Pancreatic β -Cell Secretome. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1214-1225.	2.5	42
70	Synthesis and degradation jointly determine the responsiveness of the cellular proteome. <i>BioEssays</i> , 2013, 35, 597-601.	1.2	34
71	Proteomic Analysis of Mitotic RNA Polymerase II Reveals Novel Interactors and Association With Proteins Dysfunctional in Disease. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.011767.	2.5	13
72	In Vivo Quantitative Proteome Profiling: Planning and Evaluation of SILAC Experiments. <i>Methods in Molecular Biology</i> , 2012, 893, 175-199.	0.4	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.	4.5	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.	1.1	10
75	Transcriptome-wide Analysis of Regulatory Interactions of the RNA-Binding Protein HuR. <i>Molecular Cell</i> , 2011, 43, 340-352.	4.5	640
76	Analyzing protein-protein interactions by quantitative mass spectrometry. <i>Methods</i> , 2011, 54, 387-395.	1.9	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.	0.6	108
78	Global quantification of mammalian gene expression control. <i>Nature</i> , 2011, 473, 337-342.	13.7	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.	0.4	12
80	The Versatility of <i>Helicobacter pylori</i> CagA Effector Protein Functions: The Master Key Hypothesis. <i>Helicobacter</i> , 2010, 15, 163-176.	1.6	202
81	Quantitative Proteomics Reveals Subset-Specific Viral Recognition in Dendritic Cells. <i>Immunity</i> , 2010, 32, 279-289.	6.6	544
82	The SILAC Fly Allows for Accurate Protein Quantification in Vivo. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2173-2183.	2.5	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.	3.3	100
84	Quantitative proteomics: a tool to assess cell differentiation. <i>Current Opinion in Cell Biology</i> , 2009, 21, 761-766.	2.6	23
85	Global analysis of cellular protein translation by pulsed SILAC. <i>Proteomics</i> , 2009, 9, 205-209.	1.3	314
86	A practical guide to the MaxQuant computational platform for SILAC-based quantitative proteomics. <i>Nature Protocols</i> , 2009, 4, 698-705.	5.5	769
87	Host Cell Interactome of Tyrosine-Phosphorylated Bacterial Proteins. <i>Cell Host and Microbe</i> , 2009, 5, 397-403.	5.1	175
88	Novel insights into proteomic technologies and their clinical perspective. <i>Genome Medicine</i> , 2009, 1, 53.	3.6	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.	1.2	211
90	Complex kinase requirements for <i>Chlamydia trachomatis</i> Tarp phosphorylation. <i>FEMS Microbiology Letters</i> , 2008, 289, 233-240.	0.7	44

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91	Widespread changes in protein synthesis induced by microRNAs. <i>Nature</i> , 2008, 455, 58-63.	13.7	3,120
92	Role of type IV secretion in <i>Helicobacter pylori</i> pathogenesis. <i>Cellular Microbiology</i> , 2008, 10, 1573-1581.	1.1	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.	1.1	80
94	Protein interaction screening by quantitative immunoprecipitation combined with knockdown (QUICK). <i>Nature Methods</i> , 2006, 3, 981-983.	9.0	239
95	Robust <i>Salmonella</i> metabolism limits possibilities for new antimicrobials. <i>Nature</i> , 2006, 440, 303-307.	13.7	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.	1.3	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.	1.0	33
98	Cortactin: an Achilles' heel of the actin cytoskeleton targeted by pathogens. <i>Trends in Microbiology</i> , 2005, 13, 181-189.	3.5	97
99	Tyrosine-phosphorylated bacterial effector proteins: the enemies within. <i>Trends in Microbiology</i> , 2005, 13, 476-484.	3.5	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.	1.0	67
101	The <i>Helicobacter pylori</i> CagA protein induces tyrosine dephosphorylation of ezrin. <i>Proteomics</i> , 2004, 4, 2961-2968.	1.3	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.	3.5	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.	1.0	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.	1.6	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.	1.0	27