

Matthias Selbach

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

105
papers

15,360
citations

45
h-index

118
g-index

118
ext. papers

18,618
ext. citations

14.1
avg, IF

6.54
L-index

#	Paper	IF	Citations
105	MYCN mediates cysteine addiction and sensitizes neuroblastoma to ferroptosis.. <i>Nature Cancer</i> , 2022 , 3, 471-485	15.4	0
104	HDLBP binds ER-targeted mRNAs by multivalent interactions to promote protein synthesis of transmembrane and secreted proteins.. <i>Nature Communications</i> , 2022 , 13, 2727	17.4	1
103	In Vitro Kinase-to-Phosphosite Database (iKiP-DB) Predicts Kinase Activity in Phosphoproteomic Datasets. <i>Journal of Proteome Research</i> , 2022 , 21, 1575-1587	5.6	0
102	Neuroblastoma signalling models unveil combination therapies targeting feedback-mediated resistance. <i>PLoS Computational Biology</i> , 2021 , 17, e1009515	5	0
101	SARS-CoV-2 infection triggers profibrotic macrophage responses and lung fibrosis.. <i>Cell</i> , 2021 , 184, 6243-6261.e27	35.6	21
100	An Introduction to Advanced Targeted Acquisition Methods. <i>Molecular and Cellular Proteomics</i> , 2021 , 20, 100165	7.6	9
99	Cargo-specific recruitment in clathrin- and dynamin-independent endocytosis. <i>Nature Cell Biology</i> , 2021 , 23, 1073-1084	23.4	10
98	Transcriptomic profiling of SARS-CoV-2 infected human cell lines identifies HSP90 as target for COVID-19 therapy. <i>IScience</i> , 2021 , 24, 102151	6.1	72
97	Snapshots of native pre-50S ribosomes reveal a biogenesis factor network and evolutionary specialization. <i>Molecular Cell</i> , 2021 , 81, 1200-1215.e9	17.6	8
96	Opportunities and Challenges in Global Quantification of RNA-Protein Interaction UV Cross-Linking. <i>Frontiers in Molecular Biosciences</i> , 2021 , 8, 669939	5.6	4
95	Novel LOTUS-domain proteins are organizational hubs that recruit Vasa to germ granules. <i>ELife</i> , 2021 , 10,	8.9	3
94	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	17.6	8
93	Alternative lengthening of telomeres in childhood neuroblastoma from genome to proteome. <i>Nature Communications</i> , 2021 , 12, 1269	17.4	12
92	The UBA domain of conjugating enzyme Ubc1/Ube2K facilitates assembly of K48/K63-branched ubiquitin chains. <i>EMBO Journal</i> , 2021 , 40, e106094	13	7
91	Peptide-based Interaction Proteomics. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 1070-1075	7.6	11
90	Keeping the Proportions of Protein Complex Components in Check. <i>Cell Systems</i> , 2020 , 10, 125-132	10.6	27
89	The human ZC3H3 and RBM26/27 proteins are critical for PAXT-mediated nuclear RNA decay. <i>Nucleic Acids Research</i> , 2020 , 48, 2518-2530	20.1	18

88	Cross-regulation of viral kinases with cyclin A secures shutoff of host DNA synthesis. <i>Nature Communications</i> , 2020 , 11, 4845	17.4	6
87	mRNAs, proteins and the emerging principles of gene expression control. <i>Nature Reviews Genetics</i> , 2020 , 21, 630-644	30.1	157
86	Murine Cytomegalovirus M25 Proteins Sequester the Tumor Suppressor Protein p53 in Nuclear Accumulations. <i>Journal of Virology</i> , 2020 , 94,	6.6	3
85	Integrated Phosphoproteome and Transcriptome Analysis Reveals Chlamydia-Induced Epithelial-to-Mesenchymal Transition in Host Cells. <i>Cell Reports</i> , 2019 , 26, 1286-1302.e8	10.6	26
84	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	2.2	11
83	Purification of cross-linked RNA-protein complexes by phenol-toluol extraction. <i>Nature Communications</i> , 2019 , 10, 990	17.4	94
82	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	6.5	4
81	The dynamic proteome of influenza A virus infection identifies M segment splicing as a host range determinant. <i>Nature Communications</i> , 2019 , 10, 5518	17.4	19
80	Picky: a simple online PRM and SRM method designer for targeted proteomics. <i>Nature Methods</i> , 2018 , 15, 156-157	21.6	25
79	Maf links Neuregulin1 signaling to cholesterol synthesis in myelinating Schwann cells. <i>Genes and Development</i> , 2018 , 32, 645-657	12.6	11
78	Evolutionary plasticity in the innate immune function of Akirin. <i>PLoS Genetics</i> , 2018 , 14, e1007494	6	17
77	Mutations in Disordered Regions Can Cause Disease by Creating Dileucine Motifs. <i>Cell</i> , 2018 , 175, 239-253.e17	53.1	58
76	Phosphorylation of the Ribosomal Protein RPL12/uL11 Affects Translation during Mitosis. <i>Molecular Cell</i> , 2018 , 72, 84-98.e9	17.6	45
75	Kinase-controlled phase transition of membraneless organelles in mitosis. <i>Nature</i> , 2018 , 559, 211-216	50.4	173
74	Deciphering the Ubiquitin Code. <i>Molecular Cell</i> , 2017 , 65, 779-780	17.6	8
73	Quantitative GTPase Affinity Purification Identifies Rho Family Protein Interaction Partners. <i>Molecular and Cellular Proteomics</i> , 2017 , 16, 73-85	7.6	12
72	DDX54 regulates transcriptome dynamics during DNA damage response. <i>Genome Research</i> , 2017 , 27, 1344-1359	9.7	32
71	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	7.6	12

70	RNA localization is a key determinant of neurite-enriched proteome. <i>Nature Communications</i> , 2017 , 8, 583	17.4	118
69	Conservation of miRNA-mediated silencing mechanisms across 600 million years of animal evolution. <i>Nucleic Acids Research</i> , 2017 , 45, 938-950	20.1	15
68	The mRNA-bound proteome of the early fly embryo. <i>Genome Research</i> , 2016 , 26, 1000-9	9.7	54
67	Bimodal antagonism of PKA signalling by ARHGAP36. <i>Nature Communications</i> , 2016 , 7, 12963	17.4	25
66	Quantitative interaction mapping reveals an extended UBX domain in ASPL that disrupts functional p97 hexamers. <i>Nature Communications</i> , 2016 , 7, 13047	17.4	15
65	Detecting actively translated open reading frames in ribosome profiling data. <i>Nature Methods</i> , 2016 , 13, 165-70	21.6	225
64	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, 1642-57	7.6	21
63	Hypofunctional TrkA Accounts for the Absence of Pain Sensitization in the African Naked Mole-Rat. <i>Cell Reports</i> , 2016 , 17, 748-758	10.6	33
62	Kinetic Analysis of Protein Stability Reveals Age-Dependent Degradation. <i>Cell</i> , 2016 , 167, 803-815.e21	56.2	166
61	Systematic Errors in Peptide and Protein Identification and Quantification by Modified Peptides. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 2791-801	7.6	42
60	miR-184 Regulates Pancreatic β Cell Function According to Glucose Metabolism. <i>Journal of Biological Chemistry</i> , 2015 , 290, 20284-94	5.4	44
59	Quantitative interaction proteomics of neurodegenerative disease proteins. <i>Cell Reports</i> , 2015 , 11, 1134-1146	11.6	62
58	Extensive identification and analysis of conserved small ORFs in animals. <i>Genome Biology</i> , 2015 , 16, 179	18.3	117
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, 1075-86	32.3	155
56	SILAC for biomarker discovery. <i>Proteomics - Clinical Applications</i> , 2015 , 9, 301-6	3.1	17
55	Isolation of Human Colon Stem Cells Using Surface Expression of PTK7. <i>Stem Cell Reports</i> , 2015 , 5, 979-987		47
54	Extensive allele-specific translational regulation in hybrid mice. <i>Molecular Systems Biology</i> , 2015 , 11, 825	12.2	25
53	Quantitative affinity purification mass spectrometry: a versatile technology to study protein-protein interactions. <i>Frontiers in Genetics</i> , 2015 , 6, 237	4.5	40

52	GABA blocks pathological but not acute TRPV1 pain signals. <i>Cell</i> , 2015 , 160, 759-770	56.2	92
51	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	7.6	14
50	Global characterization of the oocyte-to-embryo transition in <i>Caenorhabditis elegans</i> uncovers a novel mRNA clearance mechanism. <i>EMBO Journal</i> , 2014 , 33, 1751-66	13	52
49	Conservation of mRNA and protein expression during development of <i>C. elegans</i> . <i>Cell Reports</i> , 2014 , 6, 565-77	10.6	64
48	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	3.7	29
47	Suicidal autointegration of sleeping beauty and piggyBac transposons in eukaryotic cells. <i>PLoS Genetics</i> , 2014 , 10, e1004103	6	27
46	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	12.6	65
45	Assessment of serum protein dynamics by native SILAC flooding (SILflood). <i>Analytical Chemistry</i> , 2014 , 86, 11033-7	7.8	9
44	RNA-binding protein RBM20 represses splicing to orchestrate cardiac pre-mRNA processing. <i>Journal of Clinical Investigation</i> , 2014 , 124, 3419-30	15.9	129
43	Quantitative proteomic analysis of gene regulation by miR-34a and miR-34c. <i>PLoS ONE</i> , 2014 , 9, e92166	3.7	20
42	IPG strip-based peptide fractionation for shotgun proteomics. <i>Methods in Molecular Biology</i> , 2014 , 1156, 67-77	1.4	8
41	Orchestrated intron retention regulates normal granulocyte differentiation. <i>Cell</i> , 2013 , 154, 583-95	56.2	290
40	Argonaute2 regulates the pancreatic β cell secretome. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 1214-25	7.5	32
39	Synthesis and degradation jointly determine the responsiveness of the cellular proteome. <i>BioEssays</i> , 2013 , 35, 597-601	4.1	24
38	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	7.6	9
37	In vivo quantitative proteome profiling: planning and evaluation of SILAC experiments. <i>Methods in Molecular Biology</i> , 2012 , 893, 175-99	1.4	14
36	The mRNA-bound proteome and its global occupancy profile on protein-coding transcripts. <i>Molecular Cell</i> , 2012 , 46, 674-90	17.6	833
35	In vivo conditions to identify Prkci phosphorylation targets using the analog-sensitive kinase method in zebrafish. <i>PLoS ONE</i> , 2012 , 7, e40000	3.7	9

34	Transcriptome-wide analysis of regulatory interactions of the RNA-binding protein HuR. <i>Molecular Cell</i> , 2011 , 43, 340-52	17.6	513
33	Analyzing protein-protein interactions by quantitative mass spectrometry. <i>Methods</i> , 2011 , 54, 387-95	4.6	51
32	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, e168-79	2.2	84
31	Global quantification of mammalian gene expression control. <i>Nature</i> , 2011 , 473, 337-42	50.4	4063
30	Quantitative Analyse der Proteomdynamik. <i>BioSpektrum</i> , 2011 , 17, 756-759	0.1	
29	Whole cell proteome regulation by microRNAs captured in a pulsed SILAC mass spectrometry approach. <i>Methods in Molecular Biology</i> , 2011 , 725, 315-31	1.4	11
28	The SILAC fly allows for accurate protein quantification in vivo. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 2173-83	7.6	138
27	The versatility of <i>Helicobacter pylori</i> CagA effector protein functions: The master key hypothesis. <i>Helicobacter</i> , 2010 , 15, 163-76	4.9	180
26	Quantitative proteomics reveals subset-specific viral recognition in dendritic cells. <i>Immunity</i> , 2010 , 32, 279-89	32.3	435
25	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, 16704-9	11.5	85
24	Quantitative proteomics: a tool to assess cell differentiation. <i>Current Opinion in Cell Biology</i> , 2009 , 21, 761-6	9	21
23	Global analysis of cellular protein translation by pulsed SILAC. <i>Proteomics</i> , 2009 , 9, 205-9	4.8	265
22	A practical guide to the MaxQuant computational platform for SILAC-based quantitative proteomics. <i>Nature Protocols</i> , 2009 , 4, 698-705	18.8	637
21	Host cell interactome of tyrosine-phosphorylated bacterial proteins. <i>Cell Host and Microbe</i> , 2009 , 5, 397-403	19.4	149
20	Novel insights into proteomic technologies and their clinical perspective. <i>Genome Medicine</i> , 2009 , 1, 53	14.4	1
19	Widespread changes in protein synthesis induced by microRNAs. <i>Nature</i> , 2008 , 455, 58-63	50.4	2766
18	Role of type IV secretion in <i>Helicobacter pylori</i> pathogenesis. <i>Cellular Microbiology</i> , 2008 , 10, 1573-81	3.9	204
17	Complex kinase requirements for <i>Chlamydia trachomatis</i> Tarp phosphorylation. <i>FEMS Microbiology Letters</i> , 2008 , 289, 233-40	2.9	40

16	The <i>Helicobacter pylori</i> CagA protein disrupts matrix adhesion of gastric epithelial cells by dephosphorylation of vinculin. <i>Cellular Microbiology</i> , 2007 , 9, 1148-61	3.9	73
15	Protein interaction screening by quantitative immunoprecipitation combined with knockdown (QUICK). <i>Nature Methods</i> , 2006 , 3, 981-3	21.6	214
14	Robust <i>Salmonella</i> metabolism limits possibilities for new antimicrobials. <i>Nature</i> , 2006 , 440, 303-7	50.4	287
13	Cortactin: an Achilles' heel of the actin cytoskeleton targeted by pathogens. <i>Trends in Microbiology</i> , 2005 , 13, 181-9	12.4	90
12	Tyrosine-phosphorylated bacterial effector proteins: the enemies within. <i>Trends in Microbiology</i> , 2005 , 13, 476-84	12.4	77
11	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, 1331-45	4.8	72
10	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, 4643-52	3.7	31
9	<i>Helicobacter pylori</i> induces AGS cell motility and elongation via independent signaling pathways. <i>Infection and Immunity</i> , 2004 , 72, 3646-9	3.7	62
8	The <i>Helicobacter pylori</i> CagA protein induces tyrosine dephosphorylation of ezrin. <i>Proteomics</i> , 2004 , 4, 2961-8	4.8	74
7	The <i>Helicobacter pylori</i> CagA protein induces cortactin dephosphorylation and actin rearrangement by c-Src inactivation. <i>EMBO Journal</i> , 2003 , 22, 515-28	13	189
6	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, 4687-91	3.7	26
5	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, 665-71	3.7	131
4	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, 6775-8	5.4	333
3	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> , 2001 , 42, 631-44	4.1	187
2	The architecture of protein synthesis in the developing neocortex at near-atomic resolution reveals Ebp1-mediated neuronal proteostasis at the 60S tunnel exit		1
1	The dynamic proteome of influenza A virus infection identifies M segment splicing as a host range determinant		