

Bettina Warscheid

List of Publications by Year in descending order

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144
papers

9,076
citations

44069

48
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51608

86
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165
all docs

165
docs citations

165
times ranked

10564
citing authors

#	ARTICLE	IF	CITATIONS
1	Protein labeling by iTRAQ: A new tool for quantitative mass spectrometry in proteome research. <i>Proteomics</i> , 2007, 7, 340-350.	2.2	699
2	Mitochondrial proteins: from biogenesis to functional networks. <i>Nature Reviews Molecular Cell Biology</i> , 2019, 20, 267-284.	37.0	569
3	Dual Role of Mitofilin in Mitochondrial Membrane Organization and Protein Biogenesis. <i>Developmental Cell</i> , 2011, 21, 694-707.	7.0	361
4	Mistargeted mitochondrial proteins activate a proteostatic response in the cytosol. <i>Nature</i> , 2015, 524, 485-488.	27.8	348
5	Definition of a High-Confidence Mitochondrial Proteome at Quantitative Scale. <i>Cell Reports</i> , 2017, 19, 2836-2852.	6.4	346
6	Proteomics Characterization of Mouse Kidney Peroxisomes by Tandem Mass Spectrometry and Protein Correlation Profiling. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 2045-2057.	3.8	210
7	Mitochondrial protein translocation-associated degradation. <i>Nature</i> , 2019, 569, 679-683.	27.8	203
8	Rcf1 Mediates Cytochrome Oxidase Assembly and Respirasome Formation, Revealing Heterogeneity of the Enzyme Complex. <i>Cell Metabolism</i> , 2012, 15, 336-347.	16.2	195
9	Genome-wide Characterization of miR-34a Induced Changes in Protein and mRNA Expression by a Combined Pulsed SILAC and Microarray Analysis. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.010462.	3.8	181
10	MITRAC Links Mitochondrial Protein Translocation to Respiratory-Chain Assembly and Translational Regulation. <i>Cell</i> , 2012, 151, 1528-1541.	28.9	181
11	Quantitative proteomics identifies redox switches for global translation modulation by mitochondrially produced reactive oxygen species. <i>Nature Communications</i> , 2018, 9, 324.	12.8	161
12	Subcellular proteomics. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	21.2	159
13	Mitochondrial Protein Synthesis Adapts to Influx of Nuclear-Encoded Protein. <i>Cell</i> , 2016, 167, 471-483.e10.	28.9	158
14	Composition and Topology of the Endoplasmic Reticulum-Mitochondria Encounter Structure. <i>Journal of Molecular Biology</i> , 2011, 413, 743-750.	4.2	143
15	Dual Function of Sdh3 in the Respiratory Chain and TIM22 Protein Translocase of the Mitochondrial Inner Membrane. <i>Molecular Cell</i> , 2011, 44, 811-818.	9.7	121
16	Mdm38 interacts with ribosomes and is a component of the mitochondrial protein export machinery. <i>Journal of Cell Biology</i> , 2006, 172, 553-564.	5.2	118
17	Members of the E2D (UbcH5) Family Mediate the Ubiquitination of the Conserved Cysteine of Pex5p, the Peroxisomal Import Receptor. <i>Journal of Biological Chemistry</i> , 2008, 283, 14190-14197.	3.4	118
18	Shy1 couples Cox1 translational regulation to cytochrome c oxidase assembly. <i>EMBO Journal</i> , 2007, 26, 4347-4358.	7.8	117

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19	Coupling of Mitochondrial Import and Export Translocases by Receptor-Mediated Supercomplex Formation. <i>Cell</i> , 2013, 154, 596-608.	28.9	115
20	A systems study reveals concurrent activation of AMPK and mTOR by amino acids. <i>Nature Communications</i> , 2016, 7, 13254.	12.8	113
21	Quantitative high-confidence human mitochondrial proteome and its dynamics in cellular context. <i>Cell Metabolism</i> , 2021, 33, 2464-2483.e18.	16.2	113
22	Role of MINOS in Mitochondrial Membrane Architecture: Cristae Morphology and Outer Membrane Interactions Differentially Depend on Mitofilin Domains. <i>Journal of Molecular Biology</i> , 2012, 422, 183-191.	4.2	112
23	Vps39 Interacts with Tom40 to Establish One of Two Functionally Distinct Vacuole-Mitochondria Contact Sites. <i>Developmental Cell</i> , 2018, 45, 621-636.e7.	7.0	109
24	Role of mitochondrial inner membrane organizing system in protein biogenesis of the mitochondrial outer membrane. <i>Molecular Biology of the Cell</i> , 2012, 23, 3948-3956.	2.1	108
25	Mitochondrial Preprotein Translocase of Trypanosomatids Has a Bacterial Origin. <i>Current Biology</i> , 2011, 21, 1738-1743.	3.9	104
26	Coa3 and Cox14 are essential for negative feedback regulation of <i>COX1</i> translation in mitochondria. <i>Journal of Cell Biology</i> , 2010, 191, 141-154.	5.2	99
27	Ubp15p, a Ubiquitin Hydrolase Associated with the Peroxisomal Export Machinery. <i>Journal of Biological Chemistry</i> , 2011, 286, 28223-28234.	3.4	98
28	Tmem16b is Specifically Expressed in the Cilia of Olfactory Sensory Neurons. <i>Chemical Senses</i> , 2010, 35, 239-245.	2.0	94
29	The Proteome of Human Liver Peroxisomes: Identification of Five New Peroxisomal Constituents by a Label-Free Quantitative Proteomics Survey. <i>PLoS ONE</i> , 2013, 8, e57395.	2.5	89
30	COA6 is a mitochondrial complex IV assembly factor critical for biogenesis of mtDNA-encoded COX2. <i>Human Molecular Genetics</i> , 2015, 24, 5404-5415.	2.9	89
31	Mitochondrial Outer Membrane Proteome of <i>Trypanosoma brucei</i> Reveals Novel Factors Required to Maintain Mitochondrial Morphology. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 515-528.	3.8	88
32	YidC Occupies the Lateral Gate of the SecYEG Translocon and Is Sequentially Displaced by a Nascent Membrane Protein. <i>Journal of Biological Chemistry</i> , 2013, 288, 16295-16307.	3.4	88
33	Charting organellar importomes by quantitative mass spectrometry. <i>Nature Communications</i> , 2017, 8, 15272.	12.8	80
34	Mgr2 promotes coupling of the mitochondrial presequence translocase to partner complexes. <i>Journal of Cell Biology</i> , 2012, 197, 595-604.	5.2	79
35	Promiscuous targeting of polytopic membrane proteins to SecYEG or YidC by the <i>Escherichia coli</i> signal recognition particle. <i>Molecular Biology of the Cell</i> , 2012, 23, 464-479.	2.1	79
36	A Combined Approach of Quantitative Interaction Proteomics and Live-cell Imaging Reveals a Regulatory Role for Endoplasmic Reticulum (ER) Reticulon Homology Proteins in Peroxisome Biogenesis. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2408-2425.	3.8	79

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37	PEX14 is required for microtubule-based peroxisome motility in human cells. <i>Journal of Cell Science</i> , 2011, 124, 1759-1768.	2.0	71
38	Mitochondrial protein import receptors in Kinetoplastids reveal convergent evolution over large phylogenetic distances. <i>Nature Communications</i> , 2015, 6, 6646.	12.8	68
39	Recruitment of Cytosolic J-Proteins by TOM Receptors Promotes Mitochondrial Protein Biogenesis. <i>Cell Reports</i> , 2018, 25, 2036-2043.e5.	6.4	68
40	The Bacterial SRP Receptor, SecA and the Ribosome Use Overlapping Binding Sites on the SecY Translocon. <i>Traffic</i> , 2011, 12, 563-578.	2.7	64
41	PLK1 (polo like kinase 1) inhibits MTOR complex 1 and promotes autophagy. <i>Autophagy</i> , 2017, 13, 486-505.	9.1	63
42	Assembly of β -barrel proteins in the mitochondrial outer membrane. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2015, 1853, 74-88.	4.1	62
43	A bacterial toxin catalyzing tyrosine glycosylation of Rho and deamidation of Gq and Gi proteins. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1273-1280.	8.2	61
44	Mitochondrial OXA Translocase Plays a Major Role in Biogenesis of Inner-Membrane Proteins. <i>Cell Metabolism</i> , 2016, 23, 901-908.	16.2	60
45	Identification of Core Components and Transient Interactors of the Peroxisomal Importomer by Dual-Track Stable Isotope Labeling with Amino Acids in Cell Culture Analysis. <i>Journal of Proteome Research</i> , 2012, 11, 2567-2580.	3.7	59
46	p53-Regulated Networks of Protein, mRNA, miRNA, and lncRNA Expression Revealed by Integrated Pulsed Stable Isotope Labeling With Amino Acids in Cell Culture (pSILAC) and Next Generation Sequencing (NGS) Analyses. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2609-2629.	3.8	59
47	Mitochondrial Heat Shock Protein (Hsp) 70 and Hsp10 Cooperate in the Formation of Hsp60 Complexes. <i>Journal of Biological Chemistry</i> , 2015, 290, 11611-11622.	3.4	59
48	The interaction network of the YidC insertase with the SecYEG translocon, SRP and the SRP receptor FtsY. <i>Scientific Reports</i> , 2018, 8, 578.	3.3	55
49	Peroxisomal Targeting of PTS2 Pre-Import Complexes in the Yeast <i>Saccharomyces cerevisiae</i> . <i>Traffic</i> , 2009, 10, 451-460.	2.7	54
50	MITRAC7 Acts as a COX1-Specific Chaperone and Reveals a Checkpoint during Cytochrome c Oxidase Assembly. <i>Cell Reports</i> , 2015, 12, 1644-1655.	6.4	52
51	Mic10, a Core Subunit of the Mitochondrial Contact Site and Cristae Organizing System, Interacts with the Dimeric F ₁ F ₀ -ATP Synthase. <i>Journal of Molecular Biology</i> , 2017, 429, 1162-1170.	4.2	51
52	Role of membrane contact sites in protein import into mitochondria. <i>Protein Science</i> , 2015, 24, 277-297.	7.6	50
53	Trypanosomal TAC40 constitutes a novel subclass of mitochondrial β -barrel proteins specialized in mitochondrial genome inheritance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 7624-7629.	7.1	47
54	The Diverged Trypanosome MICOS Complex as a Hub for Mitochondrial Cristae Shaping and Protein Import. <i>Current Biology</i> , 2018, 28, 3393-3407.e5.	3.9	47

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55	Mitochondrial inner membrane protease promotes assembly of presequence translocase by removing a carboxy-terminal targeting sequence. <i>Nature Communications</i> , 2013, 4, 2853.	12.8	45
56	The Membrane Proteome of Sensory Cilia to the Depth of Olfactory Receptors. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1828-1843.	3.8	45
57	Expanding the archaeellum regulatory network - the eukaryotic protein kinases ArnC and ArnD influence motility of <i>Sulfolobus acidocaldarius</i> . <i>MicrobiologyOpen</i> , 2017, 6, e00414.	3.0	45
58	A complex of Cox4 and mitochondrial Hsp70 plays an important role in the assembly of the cytochrome <i>c</i> oxidase. <i>Molecular Biology of the Cell</i> , 2013, 24, 2609-2619.	2.1	44
59	The BTG2-PRMT1 module limits pre-B cell expansion by regulating the CDK4-Cyclin-D3 complex. <i>Nature Immunology</i> , 2017, 18, 911-920.	14.5	44
60	Ribosome binding induces repositioning of the signal recognition particle receptor on the translocon. <i>Journal of Cell Biology</i> , 2015, 211, 91-104.	5.2	43
61	Regulation of peroxisome dynamics by phosphorylation. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2016, 1863, 1027-1037.	4.1	41
62	The non-canonical mitochondrial inner membrane presequence translocase of trypanosomatids contains two essential rhomboid-like proteins. <i>Nature Communications</i> , 2016, 7, 13707.	12.8	40
63	Identification of new channels by systematic analysis of the mitochondrial outer membrane. <i>Journal of Cell Biology</i> , 2017, 216, 3485-3495.	5.2	40
64	New dimensions in the study of protein complexes using quantitative mass spectrometry. <i>FEBS Letters</i> , 2009, 583, 1674-1683.	2.8	38
65	Comparison of Alternative MS/MS and Bioinformatics Approaches for Confident Phosphorylation Site Localization. <i>Journal of Proteome Research</i> , 2014, 13, 1128-1137.	3.7	37
66	Cox17 Protein Is an Auxiliary Factor Involved in the Control of the Mitochondrial Contact Site and Cristae Organizing System. <i>Journal of Biological Chemistry</i> , 2015, 290, 15304-15312.	3.4	36
67	Outer membrane protein functions as integrator of protein import and DNA inheritance in mitochondria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4467-75.	7.1	36
68	Myofibrillar Z-discs Are a Protein Phosphorylation Hot Spot with Protein Kinase C (PKC ζ) Modulating Protein Dynamics. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 346-367.	3.8	36
69	The <i>INA</i> complex facilitates assembly of the peripheral stalk of the mitochondrial F ₁ F _o -ATP synthase. <i>EMBO Journal</i> , 2014, 33, 1624-1638.	7.8	33
70	Noncompetitive binding of PpiD and YidC to the SecYEG translocon expands the global view on the SecYEG interactome in <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2019, 294, 19167-19183.	3.4	33
71	A Universally Conserved ATPase Regulates the Oxidative Stress Response in <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2012, 287, 43585-43598.	3.4	30
72	RhoA Regulates Peroxisome Association to Microtubules and the Actin Cytoskeleton. <i>PLoS ONE</i> , 2010, 5, e13886.	2.5	30

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73	Redox Proteomics Uncovers Peroxynitrite-sensitive Proteins That Help <i>Escherichia coli</i> to Overcome Nitrosative Stress. <i>Journal of Biological Chemistry</i> , 2013, 288, 19698-19714.	3.4	29
74	Localization of Rab proteins to peroxisomes: A proteomics and immunofluorescence study. <i>FEBS Letters</i> , 2013, 587, 328-338.	2.8	29
75	Pex17p-dependent assembly of Pex14p/Dyn2p-subcomplexes of the peroxisomal protein import machinery. <i>European Journal of Cell Biology</i> , 2016, 95, 585-597.	3.6	29
76	Defining the Substrate Spectrum of the TIM22 Complex Identifies Pyruvate Carrier Subunits as Unconventional Cargos. <i>Current Biology</i> , 2020, 30, 1119-1127.e5.	3.9	29
77	Structural Insights into Ca ²⁺ -Calmodulin Regulation of Plectin 1a-Integrin β ²⁴ Interaction in Hemidesmosomes. <i>Structure</i> , 2015, 23, 558-570.	3.3	28
78	<i>Saccharomyces cerevisiae</i> cells lacking Pex3 contain membrane vesicles that harbor a subset of peroxisomal membrane proteins. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2017, 1864, 1656-1667.	4.1	28
79	A combinatorial native MS and LC-MS/MS approach reveals high intrinsic phosphorylation of human Tau but minimal levels of other key modifications. <i>Journal of Biological Chemistry</i> , 2020, 295, 18213-18225.	3.4	28
80	COA6 Facilitates Cytochrome c Oxidase Biogenesis as Thiol-reductase for Copper Metallochaperones in Mitochondria. <i>Journal of Molecular Biology</i> , 2020, 432, 2067-2079.	4.2	28
81	Maintaining proteostasis under mechanical stress. <i>EMBO Reports</i> , 2021, 22, e52507.	4.5	28
82	Structural Insights into Cargo Recognition by the Yeast PTS1 Receptor. <i>Journal of Biological Chemistry</i> , 2015, 290, 26610-26626.	3.4	27
83	An essential novel component of the noncanonical mitochondrial outer membrane protein import system of trypanosomatids. <i>Molecular Biology of the Cell</i> , 2012, 23, 3420-3428.	2.1	26
84	The Mitochondrial ADP/ATP Carrier Associates with the Inner Membrane Presequence Translocase in a Stoichiometric Manner. <i>Journal of Biological Chemistry</i> , 2014, 289, 27352-27362.	3.4	26
85	Phytoene Desaturase from <i>Oryza sativa</i> : Oligomeric Assembly, Membrane Association and Preliminary 3D-Analysis. <i>PLoS ONE</i> , 2015, 10, e0131717.	2.5	26
86	Defining the Mammalian Peroxisomal Proteome. <i>Sub-Cellular Biochemistry</i> , 2018, 89, 47-66.	2.4	26
87	Quantitative phosphoproteomics reveals the protein tyrosine kinase Pyk2 as a central effector of olfactory receptor signaling in prostate cancer cells. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 632-640.	2.3	25
88	Xlmass: A New Approach toward the Identification of Cross-Linked Peptides. <i>Analytical Chemistry</i> , 2016, 88, 9949-9957.	6.5	25
89	The Hsp70 homolog Ssb and the 14-3-3 protein Bmh1 jointly regulate transcription of glucose repressed genes in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2016, 44, 5629-5645.	14.5	25
90	The mitochondrial TMEM177 associates with COX20 during COX2 biogenesis. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2018, 1865, 323-333.	4.1	25

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91	Phosphoproteomics identifies dual-site phosphorylation in an extended basophilic motif regulating FILIP1-mediated degradation of filamin-C. <i>Communications Biology</i> , 2020, 3, 253.	4.4	25
92	INA complex liaises the F1Fo-ATP synthase membrane motor modules. <i>Nature Communications</i> , 2017, 8, 1237.	12.8	24
93	Regulating peroxisome-ER contacts via the ACBD5-VAPB tether by FFAT motif phosphorylation and GSK3 β . <i>Journal of Cell Biology</i> , 2022, 221, .	5.2	24
94	Mitochondrial translation factors of <i>Trypanosoma brucei</i> elongation factor Tu has a unique subdomain that is essential for its function. <i>Molecular Microbiology</i> , 2013, 90, 744-755.	2.5	23
95	Redox Activation of the Universally Conserved ATPase YchF by Thioredoxin 1. <i>Antioxidants and Redox Signaling</i> , 2016, 24, 141-156.	5.4	23
96	Phospho-ubiquitin-PARK2 complex as a marker for mitophagy defects. <i>Autophagy</i> , 2017, 13, 201-211.	9.1	23
97	A trypanosomal orthologue of an intermembrane space chaperone has a non-canonical function in biogenesis of the single mitochondrial inner membrane protein translocase. <i>PLoS Pathogens</i> , 2017, 13, e1006550.	4.7	23
98	Biogenesis of the mitochondrial DNA inheritance machinery in the mitochondrial outer membrane of <i>Trypanosoma brucei</i> . <i>PLoS Pathogens</i> , 2017, 13, e1006808.	4.7	23
99	Comparative profiling of the peroxisomal proteome of wildtype and Pex7 knockout mice by quantitative mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2012, 312, 30-40.	1.5	21
100	Homologue replacement in the import motor of the mitochondrial inner membrane of trypanosomes. <i>ELife</i> , 2020, 9, .	6.0	21
101	New Insight into Stimulus-Induced Plasticity of the Olfactory Epithelium in <i>Mus musculus</i> by Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2008, 7, 1594-1605.	3.7	20
102	Pex14p Phosphorylation Modulates Import of Citrate Synthase 2 Into Peroxisomes in <i>Saccharomyces cerevisiae</i> . <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 549451.	3.7	20
103	Towards the molecular architecture of the peroxisomal receptor docking complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 33216-33224.	7.1	20
104	Ribosome-Associated Mba1 Escorts Cox2 from Insertion Machinery to Maturing Assembly Intermediates. <i>Molecular and Cellular Biology</i> , 2016, 36, 2782-2793.	2.3	19
105	tRNAs and proteins use the same import channel for translocation across the mitochondrial outer membrane of trypanosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E7679-E7687.	7.1	19
106	Membrane localization of acetylated CNK1 mediates a positive feedback on RAF/ERK signaling. <i>Science Advances</i> , 2017, 3, e1700475.	10.3	19
107	SILAC for the Study of Mammalian Cell Lines and Yeast Protein Complexes. <i>Methods in Molecular Biology</i> , 2012, 893, 201-221.	0.9	18
108	Functional Proteomics Identifies Acinus L as a Direct Insulin- and Amino Acid-Dependent Mammalian Target of Rapamycin Complex 1 (mTORC1) Substrate. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2042-2055.	3.8	18

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109	Identification of Cell Cycle Dependent Interaction Partners of the Septins by Quantitative Mass Spectrometry. <i>PLoS ONE</i> , 2016, 11, e0148340.	2.5	18
110	Order from disorder in the sarcomere: FATZ forms a fuzzy but tight complex and phase-separated condensates with β -actinin. <i>Science Advances</i> , 2021, 7, .	10.3	15
111	Defining the interactome of the human mitochondrial ribosome identifies SMIM4 and TMEM223 as respiratory chain assembly factors. <i>ELife</i> , 2021, 10, .	6.0	15
112	Identification of Novel STAT6-Regulated Proteins in Mouse B Cells by Comparative Transcriptome and Proteome Analysis. <i>Journal of Immunology</i> , 2017, 198, 3737-3745.	0.8	14
113	Evolutionary divergent PEX3 is essential for glycosome biogenesis and survival of trypanosomatid parasites. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2019, 1866, 118520.	4.1	14
114	The highly diverged trypanosomal MICOS complex is organized in a nonessential integral membrane and an essential peripheral module. <i>Molecular Microbiology</i> , 2019, 112, 1731-1743.	2.5	14
115	The Universally Conserved ATPase YchF Regulates Translation of Leaderless mRNA in Response to Stress Conditions. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 643696.	3.5	14
116	Optogenetic clustering of CNK1 reveals mechanistic insights in RAF and AKT signalling controlling cell fate decisions. <i>Scientific Reports</i> , 2016, 6, 38155.	3.3	13
117	The deubiquitination of the PTS1-import receptor Pex5p is required for peroxisomal matrix protein import. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2019, 1866, 199-213.	4.1	13
118	Determinism and contingencies shaped the evolution of mitochondrial protein import. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, e2017774118.	7.1	13
119	DIMA: Data-Driven Selection of an Imputation Algorithm. <i>Journal of Proteome Research</i> , 2021, 20, 3489-3496.	3.7	13
120	Complete Native Stable Isotope Labeling by Amino Acids of <i>Saccharomyces cerevisiae</i> for Global Proteomic Analysis. <i>Analytical Chemistry</i> , 2018, 90, 10501-10509.	6.5	12
121	DNA Repair Protein APE1 Degrades Dysfunctional Abasic mRNA in Mitochondria Affecting Oxidative Phosphorylation. <i>Journal of Molecular Biology</i> , 2021, 433, 167125.	4.2	12
122	Light-Controlled Affinity Purification of Protein Complexes Exemplified by the Resting ZAP70 Interactome. <i>Frontiers in Immunology</i> , 2019, 10, 226.	4.8	11
123	Molecular basis of F-actin regulation and sarcomere assembly via myotilin. <i>PLoS Biology</i> , 2021, 19, e3001148.	5.6	9
124	Characterization of a highly diverged mitochondrial ATP synthase Fo subunit in <i>Trypanosoma brucei</i> . <i>Journal of Biological Chemistry</i> , 2022, 298, 101829.	3.4	9
125	Structural features of the TatC membrane protein that determine docking and insertion of a twin-arginine signal peptide. <i>Journal of Biological Chemistry</i> , 2017, 292, 21320-21329.	3.4	8
126	Cullin 3 Is Crucial for Pro-B Cell Proliferation, Interacts with CD22, and Controls CD22 Internalization on B Cells. <i>Journal of Immunology</i> , 2020, 204, 3360-3374.	0.8	8

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127	SILAC Labeling of Yeast for the Study of Membrane Protein Complexes. <i>Methods in Molecular Biology</i> , 2014, 1188, 23-46.	0.9	8
128	MaxQuant and MSstats in Galaxy Enable Reproducible Cloud-Based Analysis of Quantitative Proteomics Experiments for Everyone. <i>Journal of Proteome Research</i> , 2022, 21, 1558-1565.	3.7	8
129	Response to Zarsky et al.. <i>Current Biology</i> , 2012, 22, R481-R482.	3.9	7
130	Differential tyrosine phosphorylation controls the function of CNK1 as a molecular switch in signal transduction. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2015, 1853, 2847-2855.	4.1	7
131	Mistargeting of aggregation prone mitochondrial proteins activates a nucleus-mediated posttranscriptional quality control pathway in trypanosomes. <i>Nature Communications</i> , 2022, 13, .	12.8	7
132	AKT-dependent phosphorylation of the SAM domain induces oligomerization and activation of the scaffold protein CNK1. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2017, 1864, 89-100.	4.1	6
133	Quantitative proteomics identifies the universally conserved ATPase Ola1p as a positive regulator of heat shock response in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2021, 297, 101050.	3.4	6
134	Identification of MicroRNA Targets by Pulsed SILAC. <i>Methods in Molecular Biology</i> , 2014, 1188, 327-349.	0.9	5
135	p166 links membrane and intramitochondrial modules of the trypanosomal tripartite attachment complex. <i>PLoS Pathogens</i> , 2022, 18, e1010207.	4.7	5
136	The endoplasmic reticulum membrane protein complex localizes to the mitochondrial - endoplasmic reticulum interface and its subunits modulate phospholipid biosynthesis in <i>Trypanosoma brucei</i> . <i>PLoS Pathogens</i> , 2022, 18, e1009717.	4.7	4
137	Study of Peroxisomal Protein Phosphorylation by Functional Proteomics. <i>Methods in Molecular Biology</i> , 2017, 1595, 267-289.	0.9	3
138	Surface-exposed domains of TatB involved in the structural and functional assembly of the Tat translocase in <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2019, 294, 13902-13914.	3.4	3
139	Using Pull Down Strategies to Analyze the Interactome of Peroxisomal Membrane Proteins in Human Cells. <i>Sub-Cellular Biochemistry</i> , 2018, 89, 261-285.	2.4	2
140	Quantitative proteomics identifies PTP1B as modulator of B cell antigen receptor signaling. <i>Life Science Alliance</i> , 2021, 4, e202101084.	2.8	2
141	The Proteomics Toolbox Applied to Peroxisomes. , 2014, , 275-301.		1
142	2nSILAC for Quantitative of Prototrophic Bakerâ€™s Yeast. <i>Methods in Molecular Biology</i> , 2021, 2228, 253-270.	0.9	0
143	Structure of $\hat{\pm}$ -actinin-2/FATZ-1 fuzzy complex and implications in Z-disk formation via phase separation. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2019, 75, e143-e143.	0.1	0
144	Structure of the $\hat{\pm}$ -actinin actin-binding domain/F-actin complex. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2019, 75, e145-e145.	0.1	0