

Markus Ralser

List of Publications by Year in descending order

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Version: 2024-02-01

142
papers

13,646
citations

28190

55
h-index

29081

104
g-index

190
all docs

190
docs citations

190
times ranked

21616
citing authors

#	ARTICLE	IF	CITATIONS
1	Increasing the throughput of sensitive proteomics by plexDIA. <i>Nature Biotechnology</i> , 2023, 41, 50-59.	9.4	92
2	Functional profiling of long intergenic non-coding RNAs in fission yeast. <i>ELife</i> , 2022, 11, .	2.8	7
3	A proteomic survival predictor for COVID-19 patients in intensive care. , 2022, 1, e0000007.		28
4	Complement activation induces excessive T cell cytotoxicity in severe COVID-19. <i>Cell</i> , 2022, 185, 493-512.e25.	13.5	122
5	Age-Related Differences in Structure and Function of Nasal Epithelial Cultures From Healthy Children and Elderly People. <i>Frontiers in Immunology</i> , 2022, 13, 822437.	2.2	5
6	Microbial communities form rich extracellular metabolomes that foster metabolic interactions and promote drug tolerance. <i>Nature Microbiology</i> , 2022, 7, 542-555.	5.9	58
7	High-Throughput, High-Precision Colony Phenotyping with Pyphe. <i>Methods in Molecular Biology</i> , 2022, 2477, 381-397.	0.4	6
8	Understudied proteins: opportunities and challenges for functional proteomics. <i>Nature Methods</i> , 2022, 19, 774-779.	9.0	83
9	An open invitation to the Understudied Proteins Initiative. <i>Nature Biotechnology</i> , 2022, 40, 815-817.	9.4	25
10	Human umbilical cord mesenchymal stem cell-derived treatment of severe pulmonary arterial hypertension. , 2022, 1, 568-576.		6
11	A multiplex protein panel assay for severity prediction and outcome prognosis in patients with COVID-19: An observational multi-cohort study. <i>EClinicalMedicine</i> , 2022, 49, 101495.	3.2	17
12	Editorial overview: The metabolic network. <i>Current Opinion in Systems Biology</i> , 2022, , 100432.	1.3	0
13	dia-PASEF data analysis using FragPipe and DIA-NN for deep proteomics of low sample amounts. <i>Nature Communications</i> , 2022, 13, .	5.8	120
14	Ribosome profiling reveals ribosome stalling on tryptophan codons and ribosome queuing upon oxidative stress in fission yeast. <i>Nucleic Acids Research</i> , 2021, 49, 383-399.	6.5	40
15	Amino Acids Whose Intracellular Levels Change Most During Aging Alter Chronological Life Span of Fission Yeast. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2021, 76, 205-210.	1.7	9
16	Ultra-fast proteomics with Scanning SWATH. <i>Nature Biotechnology</i> , 2021, 39, 846-854.	9.4	173
17	Swarm Learning for decentralized and confidential clinical machine learning. <i>Nature</i> , 2021, 594, 265-270.	13.7	375
18	Barcode sequencing and a high-throughput assay for chronological lifespan uncover ageing-associated genes in fission yeast. <i>Microbial Cell</i> , 2021, 8, 146-160.	1.4	19

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19	A serum proteome signature to predict mortality in severe COVID-19 patients. <i>Life Science Alliance</i> , 2021, 4, e202101099.	1.3	62
20	Temporal omics analysis in Syrian hamsters unravel cellular effector responses to moderate COVID-19. <i>Nature Communications</i> , 2021, 12, 4869.	5.8	68
21	A time-resolved proteomic and prognostic map of COVID-19. <i>Cell Systems</i> , 2021, 12, 780-794.e7.	2.9	125
22	Metabolic decisions in development and disease—a Keystone Symposia report. <i>Annals of the New York Academy of Sciences</i> , 2021, 1506, 55-73.	1.8	6
23	Time-resolved in vivo ubiquitinome profiling by DIA-MS reveals USP7 targets on a proteome-wide scale. <i>Nature Communications</i> , 2021, 12, 5399.	5.8	57
24	Glycolysis: How a 300yr long research journey that started with the desire to improve alcoholic beverages kept revolutionizing biochemistry. <i>Current Opinion in Systems Biology</i> , 2021, 28, 100380.	1.3	8
25	Early IFN- γ signatures and persistent dysfunction are distinguishing features of NK cells in severe COVID-19. <i>Immunity</i> , 2021, 54, 2650-2669.e14.	6.6	145
26	Virus-induced senescence is a driver and therapeutic target in COVID-19. <i>Nature</i> , 2021, 599, 283-289.	13.7	195
27	The evolution of the metabolic network over long timelines. <i>Current Opinion in Systems Biology</i> , 2021, 28, 100402.	1.3	7
28	Recombination and biased segregation of mitochondrial genomes during crossing and meiosis of different strains. <i>MicroPublication Biology</i> , 2021, 2021, .	0.1	0
29	The metabolic growth limitations of petite cells lacking the mitochondrial genome. <i>Nature Metabolism</i> , 2021, 3, 1521-1535.	5.1	29
30	Cysteine and iron accelerate the formation of ribose-5-phosphate, providing insights into the evolutionary origins of the metabolic network structure. <i>PLoS Biology</i> , 2021, 19, e3001468.	2.6	14
31	DIA-NN: neural networks and interference correction enable deep proteome coverage in high throughput. <i>Nature Methods</i> , 2020, 17, 41-44.	9.0	882
32	Longitudinal Multi-omics Analyses Identify Responses of Megakaryocytes, Erythroid Cells, and Plasmablasts as Hallmarks of Severe COVID-19. <i>Immunity</i> , 2020, 53, 1296-1314.e9.	6.6	278
33	Severe COVID-19 Is Marked by a Dysregulated Myeloid Cell Compartment. <i>Cell</i> , 2020, 182, 1419-1440.e23.	13.5	1,162
34	Slow Growth and Increased Spontaneous Mutation Frequency in Respiratory Deficient <i>afp1</i> -Yeast Suppressed by a Dominant Mutation in <i>ATP3</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 4637-4648.	0.8	7
35	Genetic architecture of host proteins involved in SARS-CoV-2 infection. <i>Nature Communications</i> , 2020, 11, 6397.	5.8	71
36	Extraction and Integration of Genetic Networks from Short-Profile Omic Data Sets. <i>Metabolites</i> , 2020, 10, 435.	1.3	6

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37	Marmota marmota. Trends in Genetics, 2020, 36, 383-384.	2.9	1
38	Ultra-High-Throughput Clinical Proteomics Reveals Classifiers of COVID-19 Infection. Cell Systems, 2020, 11, 11-24.e4.	2.9	439
39	Mitochondrial respiration is required to provide amino acids during fermentative proliferation of fission yeast. EMBO Reports, 2020, 21, e50845.	2.0	28
40	Pyruvate kinase variant of fission yeast tunes carbon metabolism, cell regulation, growth and stress resistance. Molecular Systems Biology, 2020, 16, e9270.	3.2	27
41	Pyphe, a python toolbox for assessing microbial growth and cell viability in high-throughput colony screens. ELife, 2020, 9, .	2.8	37
42	Lysine harvesting is an antioxidant strategy and triggers underground polyamine metabolism. Nature, 2019, 572, 249-253.	13.7	99
43	The next decade of metabolism. Nature Metabolism, 2019, 1, 2-4.	5.1	8
44	Reply to "Do sulfate radicals really enable a non-enzymatic Krebs cycle precursor?" TM . Nature Ecology and Evolution, 2019, 3, 139-140.	3.4	5
45	Low catalytic activity is insufficient to induce disease pathology in triosephosphate isomerase deficiency. Journal of Inherited Metabolic Disease, 2019, 42, 839-849.	1.7	13
46	Ice-Age Climate Adaptations Trap the Alpine Marmot in a State of Low Genetic Diversity. Current Biology, 2019, 29, 1712-1720.e7.	1.8	27
47	Evolthon: A community endeavor to evolve lab evolution. PLoS Biology, 2019, 17, e3000182.	2.6	10
48	A mouse model for intellectual disability caused by mutations in the X-linked 2â€²â€™Oâ€™methyltransferase Ftsj1 gene. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2019, 1865, 2083-2093.	1.8	17
49	Self-Establishing Communities: A Yeast Model to Study the Physiological Impact of Metabolic Cooperation in Eukaryotic Cells. Methods in Molecular Biology, 2019, 2049, 263-282.	0.4	6
50	Biochemical principles enabling metabolic cooperativity and phenotypic heterogeneity at the single cell level. Current Opinion in Systems Biology, 2018, 8, 97-108.	1.3	29
51	Cost-effective generation of precise label-free quantitative proteomes in high-throughput by microLC and data-independent acquisition. Scientific Reports, 2018, 8, 4346.	1.6	66
52	Changes of Cell Biochemical States Are Revealed in Protein Homomeric Complex Dynamics. Cell, 2018, 175, 1418-1429.e9.	13.5	36
53	Freeing Yeast from Alcohol Addiction (Just) to Make (It) Fat Instead. Cell, 2018, 174, 1342-1344.	13.5	2
54	Machine Learning Predicts the Yeast Metabolome from the Quantitative Proteome of Kinase Knockouts. Cell Systems, 2018, 7, 269-283.e6.	2.9	80

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55	An appeal to magic? The discovery of a non-enzymatic metabolism and its role in the origins of life. <i>Biochemical Journal</i> , 2018, 475, 2577-2592.	1.7	69
56	Computational tools and workflows in metabolomics: An international survey highlights the opportunity for harmonisation through Galaxy. <i>Metabolomics</i> , 2017, 13, 12.	1.4	69
57	THADA Regulates the Organismal Balance between Energy Storage and Heat Production. <i>Developmental Cell</i> , 2017, 41, 72-81.e6.	3.1	51
58	Sulfate radicals enable a non-enzymatic Krebs cycle precursor. <i>Nature Ecology and Evolution</i> , 2017, 1, 83.	3.4	88
59	Yeast Creates a Niche for Symbiotic Lactic Acid Bacteria through Nitrogen Overflow. <i>Cell Systems</i> , 2017, 5, 345-357.e6.	2.9	247
60	Metabolomics in Yeast. <i>Cold Spring Harbor Protocols</i> , 2017, 2017, pdb.top083576.	0.2	6
61	A High-Throughput Method for the Quantitative Determination of Free Amino Acids in <i>Saccharomyces cerevisiae</i> by Hydrophilic Interaction Chromatography-Tandem Mass Spectrometry. <i>Cold Spring Harbor Protocols</i> , 2017, 2017, pdb.prot089094.	0.2	21
62	Designing and interpreting "multi-omic" experiments that may change our understanding of biology. <i>Current Opinion in Systems Biology</i> , 2017, 6, 37-45.	1.3	81
63	Partitioning of One-Carbon Units in Folate and Methionine Metabolism Is Essential for Neural Tube Closure. <i>Cell Reports</i> , 2017, 21, 1795-1808.	2.9	69
64	Nonenzymatic gluconeogenesis-like formation of fructose 1,6-bisphosphate in ice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7403-7407.	3.3	48
65	The self-inhibitory nature of metabolic networks and its alleviation through compartmentalization. <i>Nature Communications</i> , 2017, 8, 16018.	5.8	95
66	Variable repeats in the eukaryotic polyubiquitin gene <i>ubi4</i> modulate proteostasis and stress survival. <i>Nature Communications</i> , 2017, 8, 397.	5.8	22
67	Cell-to-cell heterogeneity emerges as consequence of metabolic cooperation in a synthetic yeast community. <i>Biotechnology Journal</i> , 2016, 11, 1169-1178.	1.8	41
68	Functional Metabolomics Describes the Yeast Biosynthetic Regulome. <i>Cell</i> , 2016, 167, 553-565.e12.	13.5	137
69	The metabolic background is a global player in <i>Saccharomyces</i> gene expression epistasis. <i>Nature Microbiology</i> , 2016, 1, 15030.	5.9	76
70	Analysis of <i>Drosophila melanogaster</i> proteome dynamics during embryonic development by a combination of label-free proteomics approaches. <i>Proteomics</i> , 2016, 16, 2068-2080.	1.3	24
71	Conditional iron and pH-dependent activity of a non-enzymatic glycolysis and pentose phosphate pathway. <i>Science Advances</i> , 2016, 2, e1501235.	4.7	65
72	Unbiased Metabolomic Investigation of Alzheimer's Disease Brain Points to Dysregulation of Mitochondrial Aspartate Metabolism. <i>Journal of Proteome Research</i> , 2016, 15, 608-618.	1.8	107

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73	Methionine Metabolism Alters Oxidative Stress Resistance via the Pentose Phosphate Pathway. Antioxidants and Redox Signaling, 2016, 24, 543-547.	2.5	93
74	Saccharomyces cerevisiae single-copy plasmids for auxotrophy compensation, multiple marker selection, and for designing metabolically cooperating communities. F1000Research, 2016, 5, 2351.	0.8	30
75	Metabolic network rewiring of propionate flux compensates vitamin B12 deficiency in C. elegans. ELife, 2016, 5, .	2.8	96
76	The Impact of Non-Enzymatic Reactions and Enzyme Promiscuity on Cellular Metabolism during (Oxidative) Stress Conditions. Biomolecules, 2015, 5, 2101-2122.	1.8	69
77	Self-establishing communities enable cooperative metabolite exchange in a eukaryote. ELife, 2015, 4, .	2.8	81
78	The genomic and phenotypic diversity of Schizosaccharomyces pombe. Nature Genetics, 2015, 47, 235-241.	9.4	174
79	A roadmap for interpreting ¹³ C metabolite labeling patterns from cells. Current Opinion in Biotechnology, 2015, 34, 189-201.	3.3	513
80	A haploproficient interaction of the transaldolase paralogue NQM1 with the transcription factor VHR1 affects stationary phase survival and oxidative stress resistance. BMC Genetics, 2015, 16, 13.	2.7	7
81	Tetrahydrobiopterin and alkylglycerol monooxygenase substantially alter the murine macrophage lipidome. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 2431-2436.	3.3	50
82	Remaining Mysteries of Molecular Biology: The Role of Polyamines in the Cell. Journal of Molecular Biology, 2015, 427, 3389-3406.	2.0	508
83	MitoLoc: A method for the simultaneous quantification of mitochondrial network morphology and membrane potential in single cells. Mitochondrion, 2015, 24, 77-86.	1.6	68
84	Using the canary genome to decipher the evolution of hormone-sensitive gene regulation in seasonal singing birds. Genome Biology, 2015, 16, 19.	3.8	60
85	Regulation of ribosomal DNA amplification by the TOR pathway. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 9674-9679.	3.3	74
86	Metabolic Remodeling in Times of Stress: Who Shoots Faster than His Shadow?. Molecular Cell, 2015, 59, 519-521.	4.5	44
87	The widespread role of non-enzymatic reactions in cellular metabolism. Current Opinion in Biotechnology, 2015, 34, 153-161.	3.3	105
88	Hyperpolarized [² H, ¹³ C]Glucose reports on glycolytic and pentose phosphate pathway activity in EL4 tumors and glycolytic activity in yeast cells. Magnetic Resonance in Medicine, 2015, 74, 1543-1547.	1.9	38
89	The return of metabolism: biochemistry and physiology of the pentose phosphate pathway. Biological Reviews, 2015, 90, 927-963.	4.7	908
90	Inhibition of triosephosphate isomerase by phosphoenolpyruvate in the feedback-regulation of glycolysis. Open Biology, 2014, 4, 130232.	1.5	83

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91	A gatekeeper helix determines the substrate specificity of Sjögrenâ€“Larsson Syndrome enzyme fatty aldehyde dehydrogenase. <i>Nature Communications</i> , 2014, 5, 4439.	5.8	55
92	Nonâ€“enzymatic glycolysis and pentose phosphate pathwayâ€“like reactions in a plausible <sc>A</sc> rchean ocean. <i>Molecular Systems Biology</i> , 2014, 10, 725.	3.2	182
93	HIF1<i>±</i> Modulates Cell Fate Reprogramming Through Early Glycolytic Shift and Upregulation of PDK1â€“3 and PKM2. <i>Stem Cells</i> , 2014, 32, 364-376.	1.4	226
94	Mitochondria in ageing: there is metabolism beyond the ROS. <i>FEMS Yeast Research</i> , 2014, 14, 198-212.	1.1	71
95	Cytosine DNA Methylation Is Found in <i>Drosophila melanogaster</i> but Absent in <i>Saccharomyces cerevisiae</i>, <i>Schizosaccharomyces pombe</i>, and Other Yeast Species. <i>Analytical Chemistry</i> , 2014, 86, 3697-3702.	3.2	225
96	The RNA world and the origin of metabolic enzymes. <i>Biochemical Society Transactions</i> , 2014, 42, 985-988.	1.6	30
97	Tpo1â€“mediated spermine and spermidine export controls cell cycle delay and times antioxidant protein expression during the oxidative stress response. <i>EMBO Reports</i> , 2013, 14, 1113-1119.	2.0	52
98	Oxidative stress and neurodegeneration: the yeast model system. <i>Frontiers in Bioscience - Landmark</i> , 2013, 18, 1174.	3.0	16
99	The beauty of being (label)-free: sample preparation methods for SWATH-MS and next-generation targeted proteomics. <i>F1000Research</i> , 2013, 2, 272.	0.8	57
100	Mild hemolytic anemia, progressive neuromotor retardation and fatal outcome: a disorder of glycolysis, triose- phosphate isomerase deficiency. <i>Turkish Journal of Pediatrics</i> , 2013, 55, 198-202.	0.3	8
101	Functional Analysis of Centrosomal Kinase Substrates in <i>Drosophila melanogaster</i> Reveals a New Function of the Nuclear Envelope Component Otefin in Cell Cycle Progression. <i>Molecular and Cellular Biology</i> , 2012, 32, 3554-3569.	1.1	12
102	The<i>Saccharomyces cerevisiae</i> W303-K6001 cross-platform genome sequence: insights into ancestry and physiology of a laboratory mutt. <i>Open Biology</i> , 2012, 2, 120093.	1.5	87
103	A prototrophic deletion mutant collection for yeast metabolomics and systems biology. <i>Nature Biotechnology</i> , 2012, 30, 1176-1178.	9.4	107
104	Histaminylation of glutamine residues is a novel posttranslational modification implicated in Gâ€“protein signaling. <i>FEBS Letters</i> , 2012, 586, 3819-3824.	1.3	29
105	Sirtuins as Regulators of the Yeast Metabolic Network. <i>Frontiers in Pharmacology</i> , 2012, 3, 32.	1.6	16
106	Warburg effect and translocation-induced genomic instability: two yeast models for cancer cells. <i>Frontiers in Oncology</i> , 2012, 2, 212.	1.3	21
107	Pyruvate kinase is a dosage-dependent regulator of cellular amino acid homeostasis. <i>Oncotarget</i> , 2012, 3, 1356-1369.	0.8	25
108	Sacrifice for survival. <i>Nature</i> , 2011, 480, 190-191.	13.7	35

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109	The Role of Mitochondria in the Aging Processes of Yeast. <i>Sub-Cellular Biochemistry</i> , 2011, 57, 55-78.	1.0	43
110	Pyruvate Kinase Triggers a Metabolic Feedback Loop that Controls Redox Metabolism in Respiring Cells. <i>Cell Metabolism</i> , 2011, 14, 415-427.	7.2	185
111	ATM Is a Redox Sensor Linking Genome Stability and Carbon Metabolism. <i>Science Signaling</i> , 2011, 4, pe17.	1.6	52
112	Monitoring protein expression in whole-cell extracts by targeted label- and standard-free LC-MS/MS. <i>Nature Protocols</i> , 2011, 6, 859-869.	5.5	52
113	The Pentose Phosphate Pathway Is a Metabolic Redox Sensor and Regulates Transcription During the Antioxidant Response. <i>Antioxidants and Redox Signaling</i> , 2011, 15, 311-324.	2.5	135
114	Human Induced Pluripotent Stem Cells Harbor Homoplasmic and Heteroplasmic Mitochondrial DNA Mutations While Maintaining Human Embryonic Stem Cell-like Metabolic Reprogramming. <i>Stem Cells</i> , 2011, 29, 1338-1348.	1.4	124
115	The KRAB-containing zinc-finger transcriptional regulator ZBRK1 activates SCA2 gene transcription through direct interaction with its gene product, ataxin-2. <i>Human Molecular Genetics</i> , 2011, 20, 104-114.	1.4	36
116	No evidence for a shift in pyruvate kinase PKM1 to PKM2 expression during tumorigenesis. <i>Oncotarget</i> , 2011, 2, 393-400.	0.8	216
117	The difference between rare and exceptionally rare: molecular characterization of ribose 5-phosphate isomerase deficiency. <i>Journal of Molecular Medicine</i> , 2010, 88, 931-939.	1.7	23
118	Regulatory crosstalk of the metabolic network. <i>Trends in Biochemical Sciences</i> , 2010, 35, 220-227.	3.7	94
119	A new dominant peroxiredoxin allele identified by whole-genome re-sequencing of random mutagenized yeast causes oxidant-resistance and premature aging. <i>Aging</i> , 2010, 2, 475-486.	1.4	29
120	Interfering with Glycolysis Causes Sir2-Dependent Hyper-Recombination of <i>Saccharomyces cerevisiae</i> Plasmids. <i>PLoS ONE</i> , 2009, 4, e5376.	1.1	8
121	Metabolic reconfiguration precedes transcriptional regulation in the antioxidant response. <i>Nature Biotechnology</i> , 2009, 27, 604-605.	9.4	127
122	Building a new bridge between metabolism, free radicals and longevity. <i>Aging</i> , 2009, 1, 836-838.	1.4	7
123	Surviving in the cold: yeast mutants with extended hibernating lifespan are oxidant sensitive. <i>Aging</i> , 2009, 1, 957-960.	1.4	16
124	Sequencing and genotypic analysis of the triosephosphate isomerase (TPI1) locus in a large sample of long-lived Germans. <i>BMC Genetics</i> , 2008, 9, 38.	2.7	11
125	Reductive stress on life span extension in <i>C. elegans</i> . <i>BMC Research Notes</i> , 2008, 1, 19.	0.6	18
126	A catabolic block does not sufficiently explain how 2-deoxy-glucose inhibits cell growth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 17807-17811.	3.3	143

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127	Ataxin-2 Interacts with the DEAD/H-Box RNA Helicase DDX6 and Interferes with P-Bodies and Stress Granules. <i>Molecular Biology of the Cell</i> , 2007, 18, 1385-1396.	0.9	301
128	Dynamic rerouting of the carbohydrate flux is key to counteracting oxidative stress. <i>Journal of Biology</i> , 2007, 6, 10.	2.7	492
129	An efficient and economic enhancer mix for PCR. <i>Biochemical and Biophysical Research Communications</i> , 2006, 347, 747-751.	1.0	177
130	Triose Phosphate Isomerase Deficiency Is Caused by Altered Dimerizationâ€“Not Catalytic Inactivityâ€“of the Mutant Enzymes. <i>PLoS ONE</i> , 2006, 1, e30.	1.1	70
131	Generation of a yeast two-hybrid strain suitable for competitive protein binding analysis. <i>BioTechniques</i> , 2005, 39, 165-168.	0.8	10
132	Ataxin-2 and huntingtin interact with endophilin-A complexes to function in plastin-associated pathways. <i>Human Molecular Genetics</i> , 2005, 14, 2893-2909.	1.4	93
133	An Integrative Approach to Gain Insights into the Cellular Function of Human Ataxin-2. <i>Journal of Molecular Biology</i> , 2005, 346, 203-214.	2.0	132
134	Quantification of <i>Saccharomyces cerevisiae</i> pentose-phosphate pathway intermediates by LC-MS/MS. <i>Protocol Exchange</i> , 0, , .	0.3	4
135	The beauty of being (label)-free: sample preparation methods for SWATH-MS and next-generation targeted proteomics. <i>F1000Research</i> , 0, 2, 272.	0.8	46
136	Primordial Krebs-cycle-like non-enzymatic reactions detected by mass spectrometry and nuclear magnetic resonance. <i>Wellcome Open Research</i> , 0, 2, 52.	0.9	3
137	¹ H-NMR as implemented in several origin of life studies artificially implies the absence of metabolism-like non-enzymatic reactions by being signal-suppressed. <i>Wellcome Open Research</i> , 0, 2, 52.	0.9	6
138	Functional association of the polyglutamine proteins ataxin-2 and huntingtin. , 0, 2005, .		0
139	Combining SELEX and reverse yeast-2-hybrid system. , 0, 2005, .		0
140	The Response to Past Climate Perturbations Explains Extremely Low Genetic Diversity in the Genome of an Abundant Ice-Age Remnant, the Alpine Marmot. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
141	From its origins to the modern metabolic network. <i>Endocrine Abstracts</i> , 0, , .	0.0	0
142	Optimization of Microflow LC Coupled with Scanning SWATH and Its Application in Hepatocellular Carcinoma Tissues. <i>Journal of Proteome Research</i> , 0, , .	1.8	5