Juergen Cox

List of Publications by Citations

153 papers	44,960 citations	76 h-index	162 g-index
162 ext. papers	58,844 ext. citations	12.6 avg, IF	7.94 L-index

#	Paper	IF	Citations
153	MaxQuant enables high peptide identification rates, individualized p.p.b.-range mass accuracies and proteome-wide protein quantification. *Nature Biotechnology*, **2008**, 26, 1367-72	44.5	9012
152	The PRIDE database and related tools and resources in 2019: improving support for quantification data. *Nucleic Acids Research*, **2019**, 47, D442-D450	20.1	3856
151	Andromeda: a peptide search engine integrated into the MaxQuant environment. *Journal of Proteome Research*, **2011**, 10, 1794-805	5.6	3402
150	The Perseus computational platform for comprehensive analysis of (prote)omics data. *Nature Methods*, **2016**, 13, 731-40	21.6	3257
149	Accurate proteome-wide label-free quantification by delayed normalization and maximal peptide ratio extraction, termed MaxLFQ. *Molecular and Cellular Proteomics*, **2014**, 13, 2513-26	7.6	2578
148	The MaxQuant computational platform for mass spectrometry-based shotgun proteomics. *Nature Protocols*, **2016**, 11, 2301-2319	18.8	1656
147	Quantitative phosphoproteomics reveals widespread full phosphorylation site occupancy during mitosis. *Science Signaling*, **2010**, 3, ra3	8.8	1106
146	A human interactome in three quantitative dimensions organized by stoichiometries and abundances. *Cell*, **2015**, 163, 712-23	56.2	788
145	Comprehensive mass-spectrometry-based proteome quantification of haploid versus diploid yeast. *Nature*, **2008**, 455, 1251-4	50.4	745
144	Deep proteome and transcriptome mapping of a human cancer cell line. *Molecular Systems Biology*, **2011**, 7, 548	12.2	723
143	A proteome-wide, quantitative survey of in vivo ubiquitylation sites reveals widespread regulatory roles. *Molecular and Cellular Proteomics*, **2011**, 10, M111.013284	7.6	644
142	A practical guide to the MaxQuant computational platform for SILAC-based quantitative proteomics. *Nature Protocols*, **2009**, 4, 698-705	18.8	637
141	Ultradeep human phosphoproteome reveals a distinct regulatory nature of Tyr and Ser/Thr-based signaling. *Cell Reports*, **2014**, 8, 1583-94	10.6	616
140	Mass spectrometry-based proteomics using Q Exactive, a high-performance benchtop quadrupole Orbitrap mass spectrometer. *Molecular and Cellular Proteomics*, **2011**, 10, M111.011015	7.6	614
139	Comparative proteomic analysis of eleven common cell lines reveals ubiquitous but varying expression of most proteins. *Molecular and Cellular Proteomics*, **2012**, 11, M111.014050	7.6	566
138	Quantitative, high-resolution proteomics for data-driven systems biology. *Annual Review of Biochemistry*, **2011**, 80, 273-99	29.1	550
137	More than 100,000 detectable peptide species elute in single shotgun proteomics runs but the majority is inaccessible to data-dependent LC-MS/MS. *Journal of Proteome Research*, **2011**, 10, 1785-93	5.6	486

136	Quantitative proteomics reveals subset-specific viral recognition in dendritic cells. *Immunity*, **2010**, 32, 279-89	32.3	435
135	Super-SILAC mix for quantitative proteomics of human tumor tissue. *Nature Methods*, **2010**, 7, 383-5	21.6	431
134	1D and 2D annotation enrichment: a statistical method integrating quantitative proteomics with complementary high-throughput data. *BMC Bioinformatics*, **2012**, 13 Suppl 16, S12	3.6	393
133	Direct identification of clinically relevant neoepitopes presented on native human melanoma tissue by mass spectrometry. *Nature Communications*, **2016**, 7, 13404	17.4	386
132	PHOSIDA (phosphorylation site database): management, structural and evolutionary investigation, and prediction of phosphosites. *Genome Biology*, **2007**, 8, R250	18.3	376
131	System-wide changes to SUMO modifications in response to heat shock. *Science Signaling*, **2009**, 2, ra24	8.8	367
130	Is proteomics the new genomics?. *Cell*, **2007**, 130, 395-8	56.2	350
129	Quantitative proteomics combined with BAC TransgeneOmics reveals in vivo protein interactions. *Journal of Cell Biology*, **2010**, 189, 739-54	7.3	341
128	A "proteomic ruler" for protein copy number and concentration estimation without spike-in standards. *Molecular and Cellular Proteomics*, **2014**, 13, 3497-506	7.6	324
127	System-wide perturbation analysis with nearly complete coverage of the yeast proteome by single-shot ultra HPLC runs on a bench top Orbitrap. *Molecular and Cellular Proteomics*, **2012**, 11, M111.013722	7.6	313
126	The coming age of complete, accurate, and ubiquitous proteomes. *Molecular Cell*, **2013**, 49, 583-90	17.6	294
125	Global, quantitative and dynamic mapping of protein subcellular localization. *ELife*, **2016**, 5,	8.9	282
124	Online Parallel Accumulation-Serial Fragmentation (PASEF) with a Novel Trapped Ion Mobility Mass Spectrometer. *Molecular and Cellular Proteomics*, **2018**, 17, 2534-2545	7.6	280
123	Defining the transcriptome and proteome in three functionally different human cell lines. *Molecular Systems Biology*, **2010**, 6, 450	12.2	269
122	Global analysis of genome, transcriptome and proteome reveals the response to aneuploidy in human cells. *Molecular Systems Biology*, **2012**, 8, 608	12.2	266
121	Deep and highly sensitive proteome coverage by LC-MS/MS without prefractionation. *Molecular and Cellular Proteomics*, **2011**, 10, M110.003699	7.6	264
120	In-vivo quantitative proteomics reveals a key contribution of post-transcriptional mechanisms to the circadian regulation of liver metabolism. *PLoS Genetics*, **2014**, 10, e1004047	6	260
119	Ultra high resolution linear ion trap Orbitrap mass spectrometer (Orbitrap Elite) facilitates top down LC MS/MS and versatile peptide fragmentation modes. *Molecular and Cellular Proteomics*, **2012**, 11, O111.013698	7.6	255

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118	Mislocalized activation of oncogenic RTKs switches downstream signaling outcomes. *Molecular Cell*, **2009**, 36, 326-39	17.6	245
117	Stable isotope labeling by amino acids in cell culture (SILAC) and proteome quantitation of mouse embryonic stem cells to a depth of 5,111 proteins. *Molecular and Cellular Proteomics*, **2008**, 7, 672-83	7.6	242
116	Iodoacetamide-induced artifact mimics ubiquitination in mass spectrometry. *Nature Methods*, **2008**, 5, 459-60	21.6	237
115	Use of stable isotope labeling by amino acids in cell culture as a spike-in standard in quantitative proteomics. *Nature Protocols*, **2011**, 6, 147-57	18.8	232
114	MSQuant, an open source platform for mass spectrometry-based quantitative proteomics. *Journal of Proteome Research*, **2010**, 9, 393-403	5.6	225
113	Perseus: A Bioinformatics Platform for Integrative Analysis of Proteomics Data in Cancer Research. *Methods in Molecular Biology*, **2018**, 1711, 133-148	1.4	200
112	BoxCar acquisition method enables single-shot proteomics at a depth of 10,000 proteins in 100 minutes. *Nature Methods*, **2018**, 15, 440-448	21.6	198
111	Proteomics on an Orbitrap benchtop mass spectrometer using all-ion fragmentation. *Molecular and Cellular Proteomics*, **2010**, 9, 2252-61	7.6	189
110	Acetylation site specificities of lysine deacetylase inhibitors in human cells. *Nature Biotechnology*, **2015**, 33, 415-23	44.5	186
109	The nucleolus functions as a phase-separated protein quality control compartment. *Science*, **2019**, 365, 342-347	33.3	185
108	Proteomic maps of breast cancer subtypes. *Nature Communications*, **2016**, 7, 10259	17.4	178
107	Initial quantitative proteomic map of 28 mouse tissues using the SILAC mouse. *Molecular and Cellular Proteomics*, **2013**, 12, 1709-22	7.6	166
106	Deep proteomics of mouse skeletal muscle enables quantitation of protein isoforms, metabolic pathways, and transcription factors. *Molecular and Cellular Proteomics*, **2015**, 14, 841-53	7.6	162
105	Visualization of LC-MS/MS proteomics data in MaxQuant. *Proteomics*, **2015**, 15, 1453-6	4.8	143
104	Thermalization of quantum fields from time-reversal invariant evolution equations. *Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics*, **2001**, 517, 369-374	4.2	143
103	Feasibility of large-scale phosphoproteomics with higher energy collisional dissociation fragmentation. *Journal of Proteome Research*, **2010**, 9, 6786-94	5.6	139
102	Super-SILAC allows classification of diffuse large B-cell lymphoma subtypes by their protein expression profiles. *Molecular and Cellular Proteomics*, **2012**, 11, 77-89	7.6	135
101	A large synthetic peptide and phosphopeptide reference library for mass spectrometry-based proteomics. *Nature Biotechnology*, **2013**, 31, 557-64	44.5	132

100	Guidelines for Genome-Scale Analysis of Biological Rhythms. *Journal of Biological Rhythms*, **2017**, 32, 380-393	3.2	127
99	The ubiquitin-proteasome system is a key component of the SUMO-2/3 cycle. *Molecular and Cellular Proteomics*, **2008**, 7, 2107-22	7.6	124
98	Ultra-deep and quantitative saliva proteome reveals dynamics of the oral microbiome. *Genome Medicine*, **2016**, 8, 44	14.4	122
97	Proteomics strategy for quantitative protein interaction profiling in cell extracts. *Nature Methods*, **2009**, 6, 741-4	21.6	121
96	Solid tumor proteome and phosphoproteome analysis by high resolution mass spectrometry. *Journal of Proteome Research*, **2008**, 7, 5314-26	5.6	119
95	High-quality MS/MS spectrum prediction for data-dependent and data-independent acquisition data analysis. *Nature Methods*, **2019**, 16, 519-525	21.6	116
94	The Impact II, a Very High-Resolution Quadrupole Time-of-Flight Instrument (QTOF) for Deep Shotgun Proteomics. *Molecular and Cellular Proteomics*, **2015**, 14, 2014-29	7.6	116
93	DNA repair. Proteomics reveals dynamic assembly of repair complexes during bypass of DNA cross-links. *Science*, **2015**, 348, 1253671	33.3	116
92	Analysis of high accuracy, quantitative proteomics data in the MaxQB database. *Molecular and Cellular Proteomics*, **2012**, 11, M111.014068	7.6	116
91	Proteomic portrait of human breast cancer progression identifies novel prognostic markers. *Cancer Research*, **2012**, 72, 2428-39	10.1	107
90	Cell-type-resolved quantitative proteomics of murine liver. *Cell Metabolism*, **2014**, 20, 1076-87	24.6	106
89	Software lock mass by two-dimensional minimization of peptide mass errors. *Journal of the American Society for Mass Spectrometry*, **2011**, 22, 1373-80	3.5	103
88	High-accuracy identification and bioinformatic analysis of in vivo protein phosphorylation sites in yeast. *Proteomics*, **2009**, 9, 4642-52	4.8	103
87	The Proteome of Primary Prostate Cancer. *European Urology*, **2016**, 69, 942-52	10.2	97
86	Proteomic changes resulting from gene copy number variations in cancer cells. *PLoS Genetics*, **2010**, 6, e1001090	6	97
85	The mzTab data exchange format: communicating mass-spectrometry-based proteomics and metabolomics experimental results to a wider audience. *Molecular and Cellular Proteomics*, **2014**, 13, 2765-75	7.6	96
84	The ER membrane protein complex interacts cotranslationally to enable biogenesis of multipass membrane proteins. *ELife*, **2018**, 7,	8.9	92
83	Combined use of RNAi and quantitative proteomics to study gene function in Drosophila. *Molecular Cell*, **2008**, 31, 762-72	17.6	87

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82	A systematic investigation into the nature of tryptic HCD spectra. *Journal of Proteome Research*, **2012**, 11, 5479-91	5.6	85
81	Computational Methods for Understanding Mass Spectrometry-Based Shotgun Proteomics Data. *Annual Review of Biomedical Data Science*, **2018**, 1, 207-234	5.6	82
80	Sleep-wake cycles drive daily dynamics of synaptic phosphorylation. *Science*, **2019**, 366,	33.3	82
79	In vivo SILAC-based proteomics reveals phosphoproteome changes during mouse skin carcinogenesis. *Cell Reports*, **2013**, 3, 552-66	10.6	82
78	Quantitative proteomics reveals that Hsp90 inhibition preferentially targets kinases and the DNA damage response. *Molecular and Cellular Proteomics*, **2012**, 11, M111.014654	7.6	77
77	Analysis of the mouse liver proteome using advanced mass spectrometry. *Journal of Proteome Research*, **2007**, 6, 2963-72	5.6	75
76	Lysine acetylome profiling uncovers novel histone deacetylase substrate proteins in. *Molecular Systems Biology*, **2017**, 13, 949	12.2	74
75	Spatiotemporal Proteomic Profiling of Huntington's Disease Inclusions Reveals Widespread Loss of Protein Function. *Cell Reports*, **2017**, 21, 2291-2303	10.6	71
74	Organellar Proteomics and Phospho-Proteomics Reveal Subcellular Reorganization in Diet-Induced Hepatic Steatosis. *Developmental Cell*, **2018**, 47, 205-221.e7	10.2	70
73	A Mass Spectrometry-Based Approach for Mapping Protein Subcellular Localization Reveals the Spatial Proteome of Mouse Primary Neurons. *Cell Reports*, **2017**, 20, 2706-2718	10.6	68
72	MaxQuant for in-depth analysis of large SILAC datasets. *Methods in Molecular Biology*, **2014**, 1188, 351-64	4.4	66
71	Will my protein crystallize? A sequence-based predictor. *Proteins: Structure, Function and Bioinformatics*, **2006**, 62, 343-55	4.2	65
70	N-linked glycosylation enrichment for in-depth cell surface proteomics of diffuse large B-cell lymphoma subtypes. *Molecular and Cellular Proteomics*, **2014**, 13, 240-51	7.6	64
69	Machine Learning-based Classification of Diffuse Large B-cell Lymphoma Patients by Their Protein Expression Profiles. *Molecular and Cellular Proteomics*, **2015**, 14, 2947-60	7.6	58
68	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. *Analytical Chemistry*, **2019**, 91, 6953-6961	7.8	57
67	EASI-tag enables accurate multiplexed and interference-free MS2-based proteome quantification. *Nature Methods*, **2018**, 15, 527-530	21.6	55
66	Computational principles of determining and improving mass precision and accuracy for proteome measurements in an Orbitrap. *Journal of the American Society for Mass Spectrometry*, **2009**, 20, 1477-85	3.5	55
65	Defining the Adult Neural Stem Cell Niche Proteome Identifies Key Regulators of Adult Neurogenesis. *Cell Stem Cell*, **2020**, 26, 277-293.e8	18	54

64	MaxQuant.Live Enables Global Targeting of More Than 25,000 Peptides. *Molecular and Cellular Proteomics*, **2019**, 18, 982-994	7.6	54
63	Glucose-regulated and drug-perturbed phosphoproteome reveals molecular mechanisms controlling insulin secretion. *Nature Communications*, **2016**, 7, 13250	17.4	53
62	Expert system for computer-assisted annotation of MS/MS spectra. *Molecular and Cellular Proteomics*, **2012**, 11, 1500-9	7.6	53
61	Predicting post-translational lysine acetylation using support vector machines. *Bioinformatics*, **2010**, 26, 1666-8	7.2	52
60	Solution of the complex action problem in the Potts model for dense QCD. *Nuclear Physics B*, **2001**, 602, 61-86	2.8	50
59	MaxQuant Software for Ion Mobility Enhanced Shotgun Proteomics. *Molecular and Cellular Proteomics*, **2020**, 19, 1058-1069	7.6	49
58	Phosphorylation variation during the cell cycle scales with structural propensities of proteins. *PLoS Computational Biology*, **2013**, 9, e1002842	5	48
57	Secretome Analysis of Lipid-Induced Insulin Resistance in Skeletal Muscle Cells by a Combined Experimental and Bioinformatics Workflow. *Journal of Proteome Research*, **2015**, 14, 4885-95	5.6	47
56	The dental proteome of Homo antecessor. *Nature*, **2020**, 580, 235-238	50.4	47
55	Ancient Biomolecules and Evolutionary Inference. *Annual Review of Biochemistry*, **2018**, 87, 1029-1060	29.1	47
54	Securin is not required for chromosomal stability in human cells. *PLoS Biology*, **2005**, 3, e416	9.7	45
53	The Proteome of Prostate Cancer Bone Metastasis Reveals Heterogeneity with Prognostic Implications. *Clinical Cancer Research*, **2018**, 24, 5433-5444	12.9	44
52	Enamel proteome shows that Gigantopithecus was an early diverging pongine. *Nature*, **2019**, 576, 262-265	50.4	41
51	IKAP: A heuristic framework for inference of kinase activities from Phosphoproteomics data. *Bioinformatics*, **2016**, 32, 424-31	7.2	40
50	A framework for intelligent data acquisition and real-time database searching for shotgun proteomics. *Molecular and Cellular Proteomics*, **2012**, 11, M111.013185	7.6	40
49	Systematic Detection of Amino Acid Substitutions in Proteomes Reveals Mechanistic Basis of Ribosome Errors and Selection for Translation Fidelity. *Molecular Cell*, **2019**, 75, 427-441.e5	17.6	36
48	A Network Module for the Perseus Software for Computational Proteomics Facilitates Proteome Interaction Graph Analysis. *Journal of Proteome Research*, **2019**, 18, 2052-2064	5.6	32
47	Comparison of SILAC and mTRAQ quantification for phosphoproteomics on a quadrupole orbitrap mass spectrometer. *Journal of Proteome Research*, **2013**, 12, 4089-100	5.6	28

46	High performance computational analysis of large-scale proteome data sets to assess incremental contribution to coverage of the human genome. *Journal of Proteome Research*, **2013**, 12, 2858-68	5.6	26
45	A novel chromatographic method allows on-line reanalysis of the proteome. *Molecular and Cellular Proteomics*, **2008**, 7, 1452-9	7.6	26
44	How much peptide sequence information is contained in ion trap tandem mass spectra?. *Journal of the American Society for Mass Spectrometry*, **2008**, 19, 1813-20	3.5	26
43	Quantitative Cross-linking/Mass Spectrometry Using Isotope-labeled Cross-linkers and MaxQuant. *Molecular and Cellular Proteomics*, **2016**, 15, 2769-78	7.6	26
42	An integrated phosphoproteomics work flow reveals extensive network regulation in early lysophosphatidic acid signaling. *Molecular and Cellular Proteomics*, **2010**, 9, 1047-62	7.6	25
41	Meron-cluster simulation of a chiral phase transition with staggered fermions. *Nuclear Physics B*, **2000**, 576, 481-500	2.8	25
40	MaxQuant goes Linux. *Nature Methods*, **2018**, 15, 401	21.6	24
39	MaxDIA enables library-based and library-free data-independent acquisition proteomics. *Nature Biotechnology*, **2021**,	44.5	24
38	Multiplexed proteome analysis with neutron-encoded stable isotope labeling in cells and mice. *Nature Protocols*, **2018**, 13, 293-306	18.8	22
37	Gauge-ball spectrum of the four-dimensional pure U(1) gauge theory. *Nuclear Physics B*, **1997**, 499, 371-408		21
36	PhosphoSiteAnalyzer: a bioinformatic platform for deciphering phospho proteomes using kinase predictions retrieved from NetworKIN. *Journal of Proteome Research*, **2012**, 11, 3480-6	5.6	17
35	Computational proteomics pitfalls and challenges: HavanaBioinfo 2012 workshop report. *Journal of Proteomics*, **2013**, 87, 134-8	3.9	17
34	Isobaric Matching between Runs and Novel PSM-Level Normalization in MaxQuant Strongly Improve Reporter Ion-Based Quantification. *Journal of Proteome Research*, **2020**, 19, 3945-3954	5.6	16
33	Role for ribosome-associated quality control in sampling proteins for MHC class I-mediated antigen presentation. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 4099-4108	11.5	15
32	Proteomic Analysis of Cellular Systems **2013**, 3-25		13
31	Meron-cluster algorithms and chiral-symmetry breaking in a (2+1)D staggered fermion model. *Nuclear Physics B*, **2000**, 583, 331-346	2.8	13
30	Predicting experimental properties of proteins from sequence by machine learning techniques. *Current Protein and Peptide Science*, **2007**, 8, 121-33	2.8	12
29	Correction to Feasibility of Large-Scale Phosphoproteomics with Higher Energy Collisional Dissociation Fragmentation. *Journal of Proteome Research*, **2012**, 11, 3506-3508	5.6	10

28	Meron-cluster approach to systems of strongly correlated electrons. *Nuclear Physics B*, **2003**, 673, 405-436	3.8	9
27	Homology-driven assembly of NOn-redundant protEin sequence sets (NOmESS) for mass spectrometry. *Bioinformatics*, **2016**, 32, 1417-9	7.2	8
26	Facing challenges in Proteomics today and in the coming decade: Report of Roundtable Discussions at the 4th EuPA Scientific Meeting, Portugal, Estoril 2010. *Journal of Proteomics*, **2011**, 75, 4-17	3.9	8
25	Nanoelectrospray peptide mapping revisited: Composite survey spectra allow high dynamic range protein characterization without LCMS on an orbitrap mass spectrometer. *International Journal of Mass Spectrometry*, **2007**, 268, 158-167	1.9	8
24	What computational non-targeted mass spectrometry-based metabolomics can gain from shotgun proteomics. *Current Opinion in Biotechnology*, **2017**, 43, 141-146	11.4	7
23	Online parallel accumulation serial fragmentation (PASEF) with a novel trapped ion mobility mass spectrometer		7
22	MaxQuant software for ion mobility enhanced shotgun proteomics		7
21	Strongly coupled compact lattice QED with staggered fermions. *Nuclear Physics B*, **1998**, 532, 315-336	2.8	6
20	Scaling of gauge balls and static potential in the confinement phase of the pure U(1) lattice gauge theory. *Nuclear Physics, Section B, Proceedings Supplements*, **1998**, 63, 691-693		5
19	Properties of the non-Gaussian fixed point in 4D compact U(1) lattice gauge theory. *Nuclear Physics, Section B, Proceedings Supplements*, **1997**, 53, 696-698		4
18	Universality of the gauge-ball spectrum of the four-dimensional pure U (1) gauge theory. *Nuclear Physics B*, **1999**, 545, 607-619	2.8	4
17	Systematic detection of amino acid substitutions in proteome reveals a mechanistic basis of ribosome errors		4
16	Expanding the Perseus Software for Omics Data Analysis With Custom Plugins. *Current Protocols in Bioinformatics*, **2020**, 71, e105	24.2	4
15	Deubiquitinating enzymes and the proteasome regulate preferential sets of ubiquitin substrates.. *Nature Communications*, **2022**, 13, 2736	17.4	4
14	Author response: Global, quantitative and dynamic mapping of protein subcellular localization **2016**,		3
13	Study of the order of the phase transition in pure U(1) gauge theory with Villain action. *Nuclear Physics, Section B, Proceedings Supplements*, **1999**, 73, 712-714		2
12	Isobaric matching between runs and novel PSM-level normalization in MaxQuant strongly improve reporter ion-based quantification		2
11	Meron-Cluster Solution of Fermion and Other Sign Problems. *Nuclear Physics, Section B, Proceedings Supplements*, **2000**, 83-84, 777-791		2

10	Quantitative cross-linking/mass spectrometry using isotope-labeled cross-linkers and MaxQuant		2
9	EASI-tag enables accurate multiplexed and interference-free MS2-based proteome quantification		2
8	MaxQuant.Live enables global targeting of more than 25,000 peptides		2
7	Redirected nuclear glutamate dehydrogenase supplies Tet3 with ꞵ-ketoglutarate in neurons. *Nature Communications*, **2021**, 12, 4100	17.4	1
6	Accurate and automated high-coverage identification of chemically cross-linked peptides with MaxLynx		1
5	Benchmarking differential expression, imputation and quantification methods for proteomics data.. *Briefings in Bioinformatics*, **2022**,	13.4	1
4	Tracing back variations in archaeal ESCRT-based cell division to protein domain architectures.. *PLoS ONE*, **2022**, 17, e0266395	3.7	0
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2	Generation and Validation of a Reference System for Toxicogenomics DNA Microarray Experiments **2005**, 185-200		
1	Perseus plugin "Metis" for metabolic-pathway-centered quantitative multi-omics data analysis for static and time-series experimental designs.. *Cell Reports Methods*, **2022**, 2, 100198		