

Juri Rappsilber

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273
papers

25,565
citations

67
h-index

156
g-index

335
ext. papers

30,340
ext. citations

12.1
avg, IF

7.12
L-index

#	Paper	IF	Citations
273	Protocol for micro-purification, enrichment, pre-fractionation and storage of peptides for proteomics using StageTips. <i>Nature Protocols</i> , 2007 , 2, 1896-906	18.8	2539
272	Stop and go extraction tips for matrix-assisted laser desorption/ionization, nanoelectrospray, and LC/MS sample pretreatment in proteomics. <i>Analytical Chemistry</i> , 2003 , 75, 663-70	7.8	1812
271	Exponentially modified protein abundance index (emPAI) for estimation of absolute protein amount in proteomics by the number of sequenced peptides per protein. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 1265-72	7.6	1582
270	UTX and JMJD3 are histone H3K27 demethylases involved in HOX gene regulation and development. <i>Nature</i> , 2007 , 449, 731-4	50.4	975
269	miRNPs: a novel class of ribonucleoproteins containing numerous microRNAs. <i>Genes and Development</i> , 2002 , 16, 720-8	12.6	808
268	TET1 and hydroxymethylcytosine in transcription and DNA methylation fidelity. <i>Nature</i> , 2011 , 473, 343-8	50.4	796
267	Large-scale proteomic analysis of the human spliceosome. <i>Genome Research</i> , 2002 , 12, 1231-45	9.7	691
266	The putative oncogene GASC1 demethylates tri- and dimethylated lysine 9 on histone H3. <i>Nature</i> , 2006 , 442, 307-11	50.4	599
265	A model for transmission of the H3K27me3 epigenetic mark. <i>Nature Cell Biology</i> , 2008 , 10, 1291-300	23.4	558
264	Mass spectrometry and EST-database searching allows characterization of the multi-protein spliceosome complex. <i>Nature Genetics</i> , 1998 , 20, 46-50	36.3	436
263	BoxPlotR: a web tool for generation of box plots. <i>Nature Methods</i> , 2014 , 11, 121-2	21.6	434
262	JARID2 regulates binding of the Polycomb repressive complex 2 to target genes in ES cells. <i>Nature</i> , 2010 , 464, 306-10	50.4	427
261	RBP2 belongs to a family of demethylases, specific for tri- and dimethylated lysine 4 on histone 3. <i>Cell</i> , 2007 , 128, 1063-76	56.2	416
260	Implications for kinetochore-microtubule attachment from the structure of an engineered Ndc80 complex. <i>Cell</i> , 2008 , 133, 427-39	56.2	403
259	Protein abundance profiling of the Escherichia coli cytosol. <i>BMC Genomics</i> , 2008 , 9, 102	4.5	353
258	Architecture of the RNA polymerase II-TFIIF complex revealed by cross-linking and mass spectrometry. <i>EMBO Journal</i> , 2010 , 29, 717-26	13	322
257	The methylosome, a 20S complex containing JBP1 and pICln, produces dimethylarginine-modified Sm proteins. <i>Molecular and Cellular Biology</i> , 2001 , 21, 8289-300	4.8	320

256	The beginning of a beautiful friendship: cross-linking/mass spectrometry and modelling of proteins and multi-protein complexes. <i>Journal of Structural Biology</i> , 2011 , 173, 530-40	3.4	314
255	Pre-mRNA splicing and mRNA export linked by direct interactions between UAP56 and Aly. <i>Nature</i> , 2001 , 413, 644-7	50.4	306
254	Microcolumns with self-assembled particle frits for proteomics. <i>Journal of Chromatography A</i> , 2002 , 979, 233-9	4.5	260
253	Rett syndrome mutations abolish the interaction of MeCP2 with the NCoR/SMRT co-repressor. <i>Nature Neuroscience</i> , 2013 , 16, 898-902	25.5	252
252	Modular stop and go extraction tips with stacked disks for parallel and multidimensional Peptide fractionation in proteomics. <i>Journal of Proteome Research</i> , 2006 , 5, 988-94	5.6	231
251	Nascent chromatin capture proteomics determines chromatin dynamics during DNA replication and identifies unknown fork components. <i>Nature Cell Biology</i> , 2014 , 16, 281-93	23.4	225
250	The protein composition of mitotic chromosomes determined using multiclassifier combinatorial proteomics. <i>Cell</i> , 2010 , 142, 810-21	56.2	217
249	Exploring the hidden human urinary proteome via ligand library beads. <i>Journal of Proteome Research</i> , 2005 , 4, 1917-30	5.6	214
248	Phosphodependent recruitment of Bub1 and Bub3 to Spc7/KNL1 by Mph1 kinase maintains the spindle checkpoint. <i>Current Biology</i> , 2012 , 22, 891-9	6.3	204
247	A functional interaction between the survival motor neuron complex and RNA polymerase II. <i>Journal of Cell Biology</i> , 2001 , 152, 75-85	7.3	198
246	Structural analysis of multiprotein complexes by cross-linking, mass spectrometry, and database searching. <i>Molecular and Cellular Proteomics</i> , 2007 , 6, 2200-11	7.6	185
245	eIF4A3 is a novel component of the exon junction complex. <i>Rna</i> , 2004 , 10, 200-9	5.8	180
244	A generic strategy to analyze the spatial organization of multi-protein complexes by cross-linking and mass spectrometry. <i>Analytical Chemistry</i> , 2000 , 72, 267-75	7.8	178
243	The NOT proteins are part of the CCR4 transcriptional complex and affect gene expression both positively and negatively. <i>EMBO Journal</i> , 1998 , 17, 1096-106	13	169
242	xiNET: cross-link network maps with residue resolution. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 1137-47	7.47	167
241	A novel WD repeat protein component of the methylosome binds Sm proteins. <i>Journal of Biological Chemistry</i> , 2002 , 277, 8243-7	5.4	163
240	A functional link between the histone demethylase PHF8 and the transcription factor ZNF711 in X-linked mental retardation. <i>Molecular Cell</i> , 2010 , 38, 165-78	17.6	162
239	What does it mean to identify a protein in proteomics?. <i>Trends in Biochemical Sciences</i> , 2002 , 27, 74-8	10.3	161

238	Stc1: a critical link between RNAi and chromatin modification required for heterochromatin integrity. <i>Cell</i> , 2010 , 140, 666-77	56.2	160
237	Fission yeast Scm3: A CENP-A receptor required for integrity of subkinetochore chromatin. <i>Molecular Cell</i> , 2009 , 33, 299-311	17.6	159
236	Bypass of senescence by the polycomb group protein CBX8 through direct binding to the INK4A-ARF locus. <i>EMBO Journal</i> , 2007 , 26, 1637-48	13	157
235	Proteomic analysis of human blood serum using peptide library beads. <i>Journal of Proteome Research</i> , 2007 , 6, 4055-62	5.6	149
234	Detection of arginine dimethylated peptides by parallel precursor ion scanning mass spectrometry in positive ion mode. <i>Analytical Chemistry</i> , 2003 , 75, 3107-14	7.8	140
233	Repo-Man coordinates chromosomal reorganization with nuclear envelope reassembly during mitotic exit. <i>Developmental Cell</i> , 2011 , 21, 328-42	10.2	139
232	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , 2015 , 23, 1156-67	5.2	131
231	Spot overlapping in two-dimensional maps: a serious problem ignored for much too long. <i>Proteomics</i> , 2005 , 5, 2385-95	4.8	123
230	Cross-linking mass spectrometry: methods and applications in structural, molecular and systems biology. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 1000-1008	17.6	122
229	Gemin5, a novel WD repeat protein component of the SMN complex that binds Sm proteins. <i>Journal of Biological Chemistry</i> , 2002 , 277, 5631-6	5.4	120
228	Mitotic chromosomes are compacted laterally by KIF4 and condensin and axially by topoisomerase II. <i>Journal of Cell Biology</i> , 2012 , 199, 755-70	7.3	118
227	Multiple molecular architectures of the eye lens chaperone B-crystallin elucidated by a triple hybrid approach. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 20491-6	11.5	118
226	REST-mediated recruitment of polycomb repressor complexes in mammalian cells. <i>PLoS Genetics</i> , 2012 , 8, e1002494	6	116
225	Purification and characterization of the 1.0 MDa CCR4-NOT complex identifies two novel components of the complex. <i>Journal of Molecular Biology</i> , 2001 , 314, 683-94	6.5	113
224	Quantitative cross-linking/mass spectrometry using isotope-labelled cross-linkers. <i>Journal of Proteomics</i> , 2013 , 88, 120-8	3.9	109
223	Tissue-specific control of brain-enriched miR-7 biogenesis. <i>Genes and Development</i> , 2013 , 27, 24-38	12.6	108
222	Purification of native survival of motor neurons complexes and identification of Gemin6 as a novel component. <i>Journal of Biological Chemistry</i> , 2002 , 277, 7540-5	5.4	106
221	Splicing factors facilitate RNAi-directed silencing in fission yeast. <i>Science</i> , 2008 , 322, 602-6	33.3	104

220	Arginine methylation of Aubergine mediates Tudor binding and germ plasm localization. <i>Rna</i> , 2010 , 16, 70-8	5.8	95
219	Quirks of Error Estimation in Cross-Linking/Mass Spectrometry. <i>Analytical Chemistry</i> , 2017 , 89, 3829-3833	3.8	89
218	Identification and characterization of Gemin7, a novel component of the survival of motor neuron complex. <i>Journal of Biological Chemistry</i> , 2002 , 277, 31957-62	5.4	88
217	Structural basis of Mcm2-7 replicative helicase loading by ORC-Cdc6 and Cdt1. <i>Nature Structural and Molecular Biology</i> , 2017 , 24, 316-324	17.6	86
216	In-cell architecture of an actively transcribing-translating expressome. <i>Science</i> , 2020 , 369, 554-557	33.3	82
215	RNA-binding activity of TRIM25 is mediated by its PRY/SPRY domain and is required for ubiquitination. <i>BMC Biology</i> , 2017 , 15, 105	7.3	80
214	Capturing protein communities by structural proteomics in a thermophilic eukaryote. <i>Molecular Systems Biology</i> , 2017 , 13, 936	12.2	79
213	A novel in vitro metabolomics approach for neurotoxicity testing, proof of principle for methyl mercury chloride and caffeine. <i>NeuroToxicology</i> , 2008 , 29, 1-12	4.4	77
212	Gemin8 is a novel component of the survival motor neuron complex and functions in small nuclear ribonucleoprotein assembly. <i>Journal of Biological Chemistry</i> , 2006 , 281, 8126-34	5.4	77
211	A folded conformation of MukBEF and cohesin. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 227-236	17.6	75
210	A yeast exosome cofactor, Mpp6, functions in RNA surveillance and in the degradation of noncoding RNA transcripts. <i>Molecular and Cellular Biology</i> , 2008 , 28, 5446-57	4.8	75
209	Structure of hibernating ribosomes studied by cryoelectron tomography in vitro and in situ. <i>Journal of Cell Biology</i> , 2010 , 190, 613-21	7.3	73
208	Cohesin-dependent association of scc2/4 with the centromere initiates pericentromeric cohesion establishment. <i>Current Biology</i> , 2013 , 23, 599-606	6.3	71
207	Arginine methylation of vasa protein is conserved across phyla. <i>Journal of Biological Chemistry</i> , 2010 , 285, 8148-54	5.4	67
206	Defining the RNA interactome by total RNA-associated protein purification. <i>Molecular Systems Biology</i> , 2019 , 15, e8689	12.2	66
205	Structural basis for microtubule recognition by the human kinetochore Ska complex. <i>Nature Communications</i> , 2014 , 5, 2964	17.4	66
204	Serum Albumin Domain Structures in Human Blood Serum by Mass Spectrometry and Computational Biology. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 1105-16	7.6	63
203	Trim25 Is an RNA-Specific Activator of Lin28a/TuT4-Mediated Uridylation. <i>Cell Reports</i> , 2014 , 9, 1265-72	10.6	62

202	When less can yield more - Computational preprocessing of MS/MS spectra for peptide identification. <i>Proteomics</i> , 2009 , 9, 4978-84	4.8	62
201	Rio1 mediates ATP-dependent final maturation of 40S ribosomal subunits. <i>Nucleic Acids Research</i> , 2014 , 42, 12189-99	20.1	61
200	Unrip is a component of SMN complexes active in snRNP assembly. <i>FEBS Letters</i> , 2005 , 579, 2348-54	3.8	61
199	A Single α -Helix Drives Extensive Remodeling of the Proteasome Lid and Completion of Regulatory Particle Assembly. <i>Cell</i> , 2015 , 163, 432-44	56.2	60
198	Co-regulation map of the human proteome enables identification of protein functions. <i>Nature Biotechnology</i> , 2019 , 37, 1361-1371	44.5	60
197	Gain-of-function DNMT3A mutations cause microcephalic dwarfism and hypermethylation of Polycomb-regulated regions. <i>Nature Genetics</i> , 2019 , 51, 96-105	36.3	60
196	SCF(Cyclin F)-dependent degradation of CDC6 suppresses DNA re-replication. <i>Nature Communications</i> , 2016 , 7, 10530	17.4	59
195	A genetic engineering solution to the "arginine conversion problem" in stable isotope labeling by amino acids in cell culture (SILAC). <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 1567-77	7.6	59
194	Model for stathmin/OP18 binding to tubulin. <i>EMBO Journal</i> , 2000 , 19, 213-22	13	59
193	G9a/GLP Complex Maintains Imprinted DNA Methylation in Embryonic Stem Cells. <i>Cell Reports</i> , 2016 , 15, 77-85	10.6	59
192	An integrated workflow for crosslinking mass spectrometry. <i>Molecular Systems Biology</i> , 2019 , 15, e8994	12.2	58
191	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019 , 91, 6953-6961	7.8	57
190	Cytoplasmic TAF2-TAF8-TAF10 complex provides evidence for nuclear holo-TFIID assembly from preformed submodules. <i>Nature Communications</i> , 2015 , 6, 6011	17.4	57
189	Sister kinetochores are mechanically fused during meiosis I in yeast. <i>Science</i> , 2014 , 346, 248-51	33.3	56
188	A Study into the Collision-induced Dissociation (CID) Behavior of Cross-Linked Peptides. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 1094-104	7.6	55
187	Protein Tertiary Structure by Crosslinking/Mass Spectrometry. <i>Trends in Biochemical Sciences</i> , 2018 , 43, 157-169	10.3	54
186	Chromatin enrichment for proteomics. <i>Nature Protocols</i> , 2014 , 9, 2090-9	18.8	53
185	Pervasive coexpression of spatially proximal genes is buffered at the protein level. <i>Molecular Systems Biology</i> , 2017 , 13, 937	12.2	52

184	Chemical Evolution of a Bacterial Proteome. <i>Angewandte Chemie - International Edition</i> , 2015 , 54, 10030-46.4	46.4	52
183	Kicking against the PRCs - A Domesticated Transposase Antagonises Silencing Mediated by Polycomb Group Proteins and Is an Accessory Component of Polycomb Repressive Complex 2. <i>PLoS Genetics</i> , 2015 , 11, e1005660	6	52
182	Complement Evasion Mediated by Enhancement of Captured Factor H: Implications for Protection of Self-Surfaces from Complement. <i>Journal of Immunology</i> , 2015 , 195, 4986-98	5.3	51
181	The histone lysine demethylase JMJD3/KDM6B is recruited to p53 bound promoters and enhancer elements in a p53 dependent manner. <i>PLoS ONE</i> , 2014 , 9, e96545	3.7	51
180	Molecular and genetic analysis of condensin function in vertebrate cells. <i>Molecular Biology of the Cell</i> , 2008 , 19, 3070-9	3.5	50
179	Experiences and perspectives of MALDI MS and MS/MS in proteomic research. <i>International Journal of Mass Spectrometry</i> , 2003 , 226, 223-237	1.9	50
178	Microtubule Nucleation Properties of Single Human γ uRCs Explained by Their Cryo-EM Structure. <i>Developmental Cell</i> , 2020 , 53, 603-617.e8	10.2	49
177	Shugoshin biases chromosomes for biorientation through condensin recruitment to the pericentromere. <i>ELife</i> , 2014 , 3, e01374	8.9	49
176	FANCD2-FANCI is a clamp stabilized on DNA by monoubiquitination of FANCD2 during DNA repair. <i>Nature Structural and Molecular Biology</i> , 2020 , 27, 240-248	17.6	48
175	Genetic code expansion for multiprotein complex engineering. <i>Nature Methods</i> , 2016 , 13, 997-1000	21.6	48
174	A Structure-Based Mechanism for DNA Entry into the Cohesin Ring. <i>Molecular Cell</i> , 2020 , 79, 917-933.e9	17.6	48
173	Direct interaction of actin filaments with F-BAR protein pacsin2. <i>EMBO Reports</i> , 2014 , 15, 1154-62	6.5	47
172	Cryo-EM structures of holo condensin reveal a subunit flip-flop mechanism. <i>Nature Structural and Molecular Biology</i> , 2020 , 27, 743-751	17.6	47
171	Optimizing the Parameters Governing the Fragmentation of Cross-Linked Peptides in a Tribrid Mass Spectrometer. <i>Analytical Chemistry</i> , 2017 , 89, 5311-5318	7.8	46
170	Structure of Complement C3(H2O) Revealed By Quantitative Cross-Linking/Mass Spectrometry And Modeling. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 2730-43	7.6	46
169	Rrp5 binding at multiple sites coordinates pre-rRNA processing and assembly. <i>Molecular Cell</i> , 2013 , 52, 707-19	17.6	46
168	Dynamics of ribosomal protein S1 on a bacterial ribosome with cross-linking and mass spectrometry. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 1965-76	7.6	46
167	Drosophila Syncrip binds the gurken mRNA localisation signal and regulates localised transcripts during axis specification. <i>Biology Open</i> , 2012 , 1, 488-97	2.2	46

166	Nop9 is an RNA binding protein present in pre-40S ribosomes and required for 18S rRNA synthesis in yeast. <i>Rna</i> , 2007 , 13, 2165-74	5.8	46
165	Structure of the Fanconi anaemia monoubiquitin ligase complex. <i>Nature</i> , 2019 , 575, 234-237	50.4	46
164	Loss of 5-methylcytosine alters the biogenesis of vault-derived small RNAs to coordinate epidermal differentiation. <i>Nature Communications</i> , 2019 , 10, 2550	17.4	43
163	Cyclin F suppresses B-Myb activity to promote cell cycle checkpoint control. <i>Nature Communications</i> , 2015 , 6, 5800	17.4	43
162	Lin28a regulates neuronal differentiation and controls miR-9 production. <i>Nature Communications</i> , 2014 , 5, 3687	17.4	43
161	Three-dimensional topology of the SMC2/SMC4 subcomplex from chicken condensin I revealed by cross-linking and molecular modelling. <i>Open Biology</i> , 2015 , 5, 150005	7	42
160	Proteomics of a fuzzy organelle: interphase chromatin. <i>EMBO Journal</i> , 2014 , 33, 648-64	13	41
159	CENP-A confers a reduction in height on octameric nucleosomes. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 763-5	17.6	40
158	Pom1 regulates the assembly of Cdr2-Mid1 cortical nodes for robust spatial control of cytokinesis. <i>Journal of Cell Biology</i> , 2014 , 206, 61-77	7.3	39
157	Proteomic profiling of PrP27-30-enriched preparations extracted from the brain of hamsters with experimental scrapie. <i>Proteomics</i> , 2009 , 9, 3802-14	4.8	38
156	SPOCD1 is an essential executor of piRNA-directed de novo DNA methylation. <i>Nature</i> , 2020 , 584, 635-639	50.4	38
155	A central cavity within the holo-translocon suggests a mechanism for membrane protein insertion. <i>Scientific Reports</i> , 2016 , 6, 38399	4.9	38
154	The mzIdentML Data Standard Version 1.2, Supporting Advances in Proteome Informatics. <i>Molecular and Cellular Proteomics</i> , 2017 , 16, 1275-1285	7.6	37
153	Improved results in proteomics by use of local and peptide-class specific false discovery rates. <i>BMC Bioinformatics</i> , 2009 , 10, 179	3.6	37
152	Prdm5 regulates collagen gene transcription by association with RNA polymerase II in developing bone. <i>PLoS Genetics</i> , 2012 , 8, e1002711	6	37
151	SPF30 is an essential human splicing factor required for assembly of the U4/U5/U6 tri-small nuclear ribonucleoprotein into the spliceosome. <i>Journal of Biological Chemistry</i> , 2001 , 276, 31142-50	5.4	36
150	The structure of human thyroglobulin. <i>Nature</i> , 2020 , 578, 627-630	50.4	36
149	Quantitative cross-linking/mass spectrometry to elucidate structural changes in proteins and their complexes. <i>Nature Protocols</i> , 2019 , 14, 171-201	18.8	34

148	Protein Dynamics in Solution by Quantitative Crosslinking/Mass Spectrometry. <i>Trends in Biochemical Sciences</i> , 2018 , 43, 908-920	10.3	34
147	Whole-proteome genetic analysis of dependencies in assembly of a vertebrate kinetochore. <i>Journal of Cell Biology</i> , 2015 , 211, 1141-56	7.3	33
146	Repo-Man/PP1 regulates heterochromatin formation in interphase. <i>Nature Communications</i> , 2017 , 8, 14048	17.4	32
145	Kinase activity of fission yeast Mph1 is required for Mad2 and Mad3 to stably bind the anaphase promoting complex. <i>Current Biology</i> , 2012 , 22, 296-301	6.3	31
144	Building mitotic chromosomes. <i>Current Opinion in Cell Biology</i> , 2011 , 23, 114-21	9	31
143	Pre-40S ribosome biogenesis factor Tsr1 is an inactive structural mimic of translational GTPases. <i>Nature Communications</i> , 2016 , 7, 11789	17.4	29
142	Tumor suppressor ASXL1 is essential for the activation of INK4B expression in response to oncogene activity and anti-proliferative signals. <i>Cell Research</i> , 2015 , 25, 1205-18	24.7	28
141	Eic1 links Mis18 with the CCAN/Mis6/Ctf19 complex to promote CENP-A assembly. <i>Open Biology</i> , 2014 , 4, 140043	7	28
140	Mechanism for Aar2p function as a U5 snRNP assembly factor. <i>Genes and Development</i> , 2011 , 25, 1601-12	2.6	28
139	In Situ Structural Restraints from Cross-Linking Mass Spectrometry in Human Mitochondria. <i>Journal of Proteome Research</i> , 2020 , 19, 327-336	5.6	28
138	On the Reproducibility of Label-Free Quantitative Cross-Linking/Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2018 , 29, 405-412	3.5	27
137	Lamin A molecular compression and sliding as mechanisms behind nucleoskeleton elasticity. <i>Nature Communications</i> , 2019 , 10, 3056	17.4	27
136	Comprehensive identification of proteins binding to RNA G-quadruplex motifs in the 5' UTR of tumor-associated mRNAs. <i>Biochimie</i> , 2018 , 144, 169-184	4.6	27
135	Transposon-driven transcription is a conserved feature of vertebrate spermatogenesis and transcript evolution. <i>EMBO Reports</i> , 2017 , 18, 1231-1247	6.5	26
134	The mitosis and neurodevelopment proteins NDE1 and NDEL1 form dimers, tetramers, and polymers with a folded back structure in solution. <i>Journal of Biological Chemistry</i> , 2012 , 287, 32381-93	5.4	26
133	Labile sulfogroup allows differentiation of sulfotyrosine and phosphotyrosine in peptides. <i>Journal of Mass Spectrometry</i> , 2001 , 36, 832-3	2.2	26
132	Quantitative Cross-linking/Mass Spectrometry Using Isotope-labeled Cross-linkers and MaxQuant. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 2769-78	7.6	26
131	Optimized Fragmentation Regime for Diazirine Photo-Cross-Linked Peptides. <i>Analytical Chemistry</i> , 2016 , 88, 8239-47	7.8	26

130	Ska3 Ensures Timely Mitotic Progression by Interacting Directly With Microtubules and Ska1 Microtubule Binding Domain. <i>Scientific Reports</i> , 2016 , 6, 34042	4.9	25
129	xiSPEC: web-based visualization, analysis and sharing of proteomics data. <i>Nucleic Acids Research</i> , 2018 , 46, W473-W478	20.1	25
128	Silencing mediated by the <i>Schizosaccharomyces pombe</i> HIRA complex is dependent upon the Hpc2-like protein, Hip4. <i>PLoS ONE</i> , 2010 , 5, e13488	3.7	25
127	A programmed wave of uridylation-primed mRNA degradation is essential for meiotic progression and mammalian spermatogenesis. <i>Cell Research</i> , 2019 , 29, 221-232	24.7	24
126	In-Search Assignment of Monoisotopic Peaks Improves the Identification of Cross-Linked Peptides. <i>Journal of Proteome Research</i> , 2018 , 17, 3923-3931	5.6	24
125	Proteomic analysis of pancreatic ductal carcinoma cells after combined treatment with gemcitabine and trichostatin A. <i>Journal of Proteome Research</i> , 2005 , 4, 1909-16	5.6	23
124	Blind testing of cross-linking/mass spectrometry hybrid methods in CASP11. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016 , 84 Suppl 1, 152-63	4.2	23
123	Proteome Analysis of Human Neutrophil Granulocytes From Patients With Monogenic Disease Using Data-independent Acquisition. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 760-772	7.6	23
122	Raf1 Is a DCAF for the Rik1 DDB1-like protein and has separable roles in siRNA generation and chromatin modification. <i>PLoS Genetics</i> , 2012 , 8, e1002499	6	22
121	Quantitative cross-linking/mass spectrometry reveals subtle protein conformational changes. <i>Wellcome Open Research</i> , 2016 , 1, 5	4.8	22
120	14-3-3 regulation of Ncd reveals a new mechanism for targeting proteins to the spindle in oocytes. <i>Journal of Cell Biology</i> , 2017 , 216, 3029-3039	7.3	21
119	The structure and oxidation of the eye lens chaperone α -crystallin. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 1141-1150	17.6	21
118	The kinetochore module Okp1/Ame1 is a reader for N-terminal modifications on the centromeric histone Cse4. <i>EMBO Journal</i> , 2019 , 38,	13	21
117	Mto2 multisite phosphorylation inactivates non-spindle microtubule nucleation complexes during mitosis. <i>Nature Communications</i> , 2015 , 6, 7929	17.4	20
116	Small angle X-ray scattering and cross-linking for data assisted protein structure prediction in CASP 12 with prospects for improved accuracy. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018 , 86 Suppl 1, 202-214	4.2	20
115	TEX15 is an essential executor of MIWI2-directed transposon DNA methylation and silencing. <i>Nature Communications</i> , 2020 , 11, 3739	17.4	20
114	Endogenous Mouse Dicer Is an Exclusively Cytoplasmic Protein. <i>PLoS Genetics</i> , 2016 , 12, e1006095	6	20
113	Data-independent Acquisition Improves Quantitative Cross-linking Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 786-795	7.6	20

112	Architecture of TAF11/TAF13/TBP complex suggests novel regulation properties of general transcription factor TFIID. <i>ELife</i> , 2017 , 6,	8.9	19
111	Heterologous Biosynthesis, Modifications and Structural Characterization of Ruminococcin-A, a Lanthipeptide From the Gut Bacterium E1, in. <i>Frontiers in Microbiology</i> , 2018 , 9, 1688	5.7	19
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