

Juri Rappsilber

List of Publications by Year in descending order

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266
papers

33,562
citations

9234

74
h-index

4870

168
g-index

335
all docs

335
docs citations

335
times ranked

42631
citing authors

#	ARTICLE	IF	CITATIONS
1	Protocol for micro-purification, enrichment, pre-fractionation and storage of peptides for proteomics using StageTips. <i>Nature Protocols</i> , 2007, 2, 1896-1906.	5.5	3,693
2	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, 663-670.	3.2	2,337
3	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, 1265-1272.	2.5	1,817
4	UTX and JMJD3 are histone H3K27 demethylases involved in HOX gene regulation and development. <i>Nature</i> , 2007, 449, 731-734.	13.7	1,183
5	miRNPs: a novel class of ribonucleoproteins containing numerous microRNAs. <i>Genes and Development</i> , 2002, 16, 720-728.	2.7	926
6	TET1 and hydroxymethylcytosine in transcription and DNA methylation fidelity. <i>Nature</i> , 2011, 473, 343-348.	13.7	905
7	Large-Scale Proteomic Analysis of the Human Spliceosome. <i>Genome Research</i> , 2002, 12, 1231-1245.	2.4	808
8	The putative oncogene GASC1 demethylates tri- and dimethylated lysine 9 on histone H3. <i>Nature</i> , 2006, 442, 307-311.	13.7	670
9	BoxPlotR: a web tool for generation of box plots. <i>Nature Methods</i> , 2014, 11, 121-122.	9.0	665
10	A model for transmission of the H3K27me3 epigenetic mark. <i>Nature Cell Biology</i> , 2008, 10, 1291-1300.	4.6	656
11	JARID2 regulates binding of the Polycomb repressive complex to target genes in ES cells. <i>Nature</i> , 2010, 464, 306-310.	13.7	499
12	RBP2 Belongs to a Family of Demethylases, Specific for Tri-and Dimethylated Lysine 4 on Histone 3. <i>Cell</i> , 2007, 128, 1063-1076.	13.5	485
13	Implications for Kinetochore-Microtubule Attachment from the Structure of an Engineered Ndc80 Complex. <i>Cell</i> , 2008, 133, 427-439.	13.5	479
14	Mass spectrometry and EST-database searching allows characterization of the multi-protein spliceosome complex. <i>Nature Genetics</i> , 1998, 20, 46-50.	9.4	470
15	Protein abundance profiling of the Escherichia coli cytosol. <i>BMC Genomics</i> , 2008, 9, 102.	1.2	432
16	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, 530-540.	1.3	376
17	The Methylosome, a 20S Complex Containing JBP1 and pICln, Produces Dimethylarginine-Modified Sm Proteins. <i>Molecular and Cellular Biology</i> , 2001, 21, 8289-8300.	1.1	365
18	Architecture of the RNA polymerase II-TFIIF complex revealed by cross-linking and mass spectrometry. <i>EMBO Journal</i> , 2010, 29, 717-726.	3.5	355

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19	Pre-mRNA splicing and mRNA export linked by direct interactions between UAP56 and Aly. <i>Nature</i> , 2001, 413, 644-647.	13.7	339
20	Microcolumns with self-assembled particle frits for proteomics. <i>Journal of Chromatography A</i> , 2002, 979, 233-239.	1.8	327
21	Rett syndrome mutations abolish the interaction of MeCP2 with the NCoR/SMRT co-repressor. <i>Nature Neuroscience</i> , 2013, 16, 898-902.	7.1	317
22	Nascent chromatin capture proteomics determines chromatin dynamics during DNA replication and identifies unknown fork components. <i>Nature Cell Biology</i> , 2014, 16, 281-291.	4.6	312
23	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, 988-994.	1.8	294
24	The Protein Composition of Mitotic Chromosomes Determined Using Multiclassifier Combinatorial Proteomics. <i>Cell</i> , 2010, 142, 810-821.	13.5	266
25	Phosphodependent Recruitment of Bub1 and Bub3 to Spc7/KNL1 by Mph1 Kinase Maintains the Spindle Checkpoint. <i>Current Biology</i> , 2012, 22, 891-899.	1.8	253
26	xiNET: Cross-link Network Maps With Residue Resolution. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1137-1147.	2.5	242
27	Cross-linking mass spectrometry: methods and applications in structural, molecular and systems biology. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 1000-1008.	3.6	237
28	Exploring the Hidden Human Urinary Proteome via Ligand Library Beads. <i>Journal of Proteome Research</i> , 2005, 4, 1917-1930.	1.8	232
29	eIF4A3 is a novel component of the exon junction complex. <i>Rna</i> , 2004, 10, 200-209.	1.6	215
30	Structural Analysis of Multiprotein Complexes by Cross-linking, Mass Spectrometry, and Database Searching. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 2200-2211.	2.5	214
31	A Functional Interaction between the Survival Motor Neuron Complex and RNA Polymerase II. <i>Journal of Cell Biology</i> , 2001, 152, 75-86.	2.3	213
32	A Generic Strategy To Analyze the Spatial Organization of Multi-Protein Complexes by Cross-Linking and Mass Spectrometry. <i>Analytical Chemistry</i> , 2000, 72, 267-275.	3.2	202
33	A Novel WD Repeat Protein Component of the Methylosome Binds Sm Proteins. <i>Journal of Biological Chemistry</i> , 2002, 277, 8243-8247.	1.6	199
34	Stc1: A Critical Link between RNAi and Chromatin Modification Required for Heterochromatin Integrity. <i>Cell</i> , 2010, 140, 666-677.	13.5	195
35	In-cell architecture of an actively transcribing-translating expressome. <i>Science</i> , 2020, 369, 554-557.	6.0	192
36	The NOT proteins are part of the CCR4 transcriptional complex and affect gene expression both positively and negatively. <i>EMBO Journal</i> , 1998, 17, 1096-1106.	3.5	190

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37	Fission Yeast Scm3: A CENP-A Receptor Required for Integrity of Subkinetochore Chromatin. <i>Molecular Cell</i> , 2009, 33, 299-311.	4.5	187
38	A Functional Link between the Histone Demethylase PHF8 and the Transcription Factor ZNF711 in X-Linked Mental Retardation. <i>Molecular Cell</i> , 2010, 38, 165-178.	4.5	186
39	Bypass of senescence by the polycomb group protein CBX8 through direct binding to the INK4A-ARF locus. <i>EMBO Journal</i> , 2007, 26, 1637-1648.	3.5	175
40	What does it mean to identify a protein in proteomics?. <i>Trends in Biochemical Sciences</i> , 2002, 27, 74-78.	3.7	174
41	Repo-Man Coordinates Chromosomal Reorganization with Nuclear Envelope Reassembly during Mitotic Exit. <i>Developmental Cell</i> , 2011, 21, 328-342.	3.1	172
42	Proteomic Analysis of Human Blood Serum Using Peptide Library Beads. <i>Journal of Proteome Research</i> , 2007, 6, 4055-4062.	1.8	165
43	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , 2015, 23, 1156-1167.	1.6	159
44	Detection of Arginine Dimethylated Peptides by Parallel Precursor Ion Scanning Mass Spectrometry in Positive Ion Mode. <i>Analytical Chemistry</i> , 2003, 75, 3107-3114.	3.2	158
45	Mitotic chromosomes are compacted laterally by KIF4 and condensin and axially by topoisomerase II \pm . <i>Journal of Cell Biology</i> , 2012, 199, 755-770.	2.3	155
46	Multiple molecular architectures of the eye lens chaperone β -crystallin elucidated by a triple hybrid approach. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 20491-20496.	3.3	143
47	REST-Mediated Recruitment of Polycomb Repressor Complexes in Mammalian Cells. <i>PLoS Genetics</i> , 2012, 8, e1002494.	1.5	140
48	Gemin5, a Novel WD Repeat Protein Component of the SMN Complex That Binds Sm Proteins. <i>Journal of Biological Chemistry</i> , 2002, 277, 5631-5636.	1.6	139
49	Quirks of Error Estimation in Cross-Linking/Mass Spectrometry. <i>Analytical Chemistry</i> , 2017, 89, 3829-3833.	3.2	136
50	Tissue-specific control of brain-enriched miR-7 biogenesis. <i>Genes and Development</i> , 2013, 27, 24-38.	2.7	131
51	Spot overlapping in two-dimensional maps: A serious problem ignored for much too long. <i>Proteomics</i> , 2005, 5, 2385-2395.	1.3	130
52	Structural basis of Mcm2-7 replicative helicase loading by ORC-Cdc6 and Cdt1. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 316-324.	3.6	130
53	Purification and characterization of the 1.0 MDa CCR4-NOT complex identifies two novel components of the complex 1 Edited by D. Draper. <i>Journal of Molecular Biology</i> , 2001, 314, 683-694.	2.0	128
54	RNA-binding activity of TRIM25 is mediated by its PRY/SPRY domain and is required for ubiquitination. <i>BMC Biology</i> , 2017, 15, 105.	1.7	125

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55	Purification of Native Survival of Motor Neurons Complexes and Identification of Gemin6 as a Novel Component. <i>Journal of Biological Chemistry</i> , 2002, 277, 7540-7545.	1.6	121
56	Quantitative cross-linking/mass spectrometry using isotope-labelled cross-linkers. <i>Journal of Proteomics</i> , 2013, 88, 120-128.	1.2	121
57	A folded conformation of MukBEF and cohesin. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 227-236.	3.6	121
58	An integrated workflow for crosslinking mass spectrometry. <i>Molecular Systems Biology</i> , 2019, 15, e8994.	3.2	120
59	Defining the <sc>RNA</sc> interactome by total <sc>RNA</sc> associated protein purification. <i>Molecular Systems Biology</i> , 2019, 15, e8689.	3.2	114
60	Splicing Factors Facilitate RNAi-Directed Silencing in Fission Yeast. <i>Science</i> , 2008, 322, 602-606.	6.0	113
61	Arginine methylation of Aubergine mediates Tudor binding and germ plasm localization. <i>Rna</i> , 2010, 16, 70-78.	1.6	113
62	A Structure-Based Mechanism for DNA Entry into the Cohesin Ring. <i>Molecular Cell</i> , 2020, 79, 917-933.e9.	4.5	112
63	C9a/GLP Complex Maintains Imprinted DNA Methylation in Embryonic Stem Cells. <i>Cell Reports</i> , 2016, 15, 77-85.	2.9	111
64	Gain-of-function DNMT3A mutations cause microcephalic dwarfism and hypermethylation of Polycomb-regulated regions. <i>Nature Genetics</i> , 2019, 51, 96-105.	9.4	110
65	Identification and Characterization of Gemin7, a Novel Component of the Survival of Motor Neuron Complex. <i>Journal of Biological Chemistry</i> , 2002, 277, 31957-31962.	1.6	109
66	Capturing protein communities by structural proteomics in a thermophilic eukaryote. <i>Molecular Systems Biology</i> , 2017, 13, 936.	3.2	108
67	Co-regulation map of the human proteome enables identification of protein functions. <i>Nature Biotechnology</i> , 2019, 37, 1361-1371.	9.4	106
68	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019, 91, 6953-6961.	3.2	100
69	Microtubule Nucleation Properties of Single Human $\hat{1}^3$ TuRCs Explained by Their Cryo-EM Structure. <i>Developmental Cell</i> , 2020, 53, 603-617.e8.	3.1	99
70	SPOCD1 is an essential executor of piRNA-directed de novo DNA methylation. <i>Nature</i> , 2020, 584, 635-639.	13.7	96
71	Cohesin-Dependent Association of Scc2/4 with the Centromere Initiates Pericentromeric Cohesion Establishment. <i>Current Biology</i> , 2013, 23, 599-606.	1.8	92
72	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, 8126-8134.	1.6	91

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73	Rio1 mediates ATP-dependent final maturation of 40S ribosomal subunits. <i>Nucleic Acids Research</i> , 2014, 42, 12189-12199.	6.5	90
74	Pervasive coexpression of spatially proximal genes is buffered at the protein level. <i>Molecular Systems Biology</i> , 2017, 13, 937.	3.2	90
75	Cryo-EM structures of holo condensin reveal a subunit flip-flop mechanism. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 743-751.	3.6	90
76	The IntAct database: efficient access to fine-grained molecular interaction data. <i>Nucleic Acids Research</i> , 2022, 50, D648-D653.	6.5	89
77	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.	1.4	87
78	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, 5446-5457.	1.1	84
79	Structural basis for microtubule recognition by the human kinetochore Ska complex. <i>Nature Communications</i> , 2014, 5, 2964.	5.8	84
80	Serum Albumin Domain Structures in Human Blood Serum by Mass Spectrometry and Computational Biology. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1105-1116.	2.5	84
81	Self-made frits for nanoscale columns in proteomics. <i>Proteomics</i> , 2005, 5, 3847-3850.	1.3	83
82	Structure of hibernating ribosomes studied by cryoelectron tomography in vitro and in situ. <i>Journal of Cell Biology</i> , 2010, 190, 613-621.	2.3	83
83	Arginine Methylation of Vasa Protein Is Conserved across Phyla. <i>Journal of Biological Chemistry</i> , 2010, 285, 8148-8154.	1.6	83
84	Understudied proteins: opportunities and challenges for functional proteomics. <i>Nature Methods</i> , 2022, 19, 774-779.	9.0	83
85	SCFCyclin F-dependent degradation of CDC6 suppresses DNA re-replication. <i>Nature Communications</i> , 2016, 7, 10530.	5.8	81
86	Loss of 5-methylcytosine alters the biogenesis of vault-derived small RNAs to coordinate epidermal differentiation. <i>Nature Communications</i> , 2019, 10, 2550.	5.8	81
87	The structure of human thyroglobulin. <i>Nature</i> , 2020, 578, 627-630.	13.7	81
88	Trim25 Is an RNA-Specific Activator of Lin28a/TuT4-Mediated Uridylation. <i>Cell Reports</i> , 2014, 9, 1265-1272.	2.9	80
89	Structure of the Fanconi anaemia monoubiquitin ligase complex. <i>Nature</i> , 2019, 575, 234-237.	13.7	80
90	FANCD2 is a clamp stabilized on DNA by monoubiquitination of FANCD2 during DNA repair. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 240-248.	3.6	80

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91	Chromatin enrichment for proteomics. <i>Nature Protocols</i> , 2014, 9, 2090-2099.	5.5	78
92	A Study into the Collision-induced Dissociation (CID) Behavior of Cross-Linked Peptides. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1094-1104.	2.5	78
93	Cytoplasmic TAF2â€“TAF8â€“TAF10 complex provides evidence for nuclear holoâ€“TFIID assembly from preformed submodules. <i>Nature Communications</i> , 2015, 6, 6011.	5.8	77
94	Protein Tertiary Structure by Crosslinking/Mass Spectrometry. <i>Trends in Biochemical Sciences</i> , 2018, 43, 157-169.	3.7	77
95	Shugoshin biases chromosomes for biorientation through condensin recruitment to the pericentromere. <i>ELife</i> , 2014, 3, e01374.	2.8	74
96	When less can yield more â€“ Computational preprocessing of MS/MS spectra for peptide identification. <i>Proteomics</i> , 2009, 9, 4978-4984.	1.3	73
97	A Single Î± Helix Drives Extensive Remodeling of the Proteasome Lid and Completion of Regulatory Particle Assembly. <i>Cell</i> , 2015, 163, 432-444.	13.5	73
98	Chemical Evolution of a Bacterial Proteome. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 10030-10034.	7.2	71
99	Reliable identification of protein-protein interactions by crosslinking mass spectrometry. <i>Nature Communications</i> , 2021, 12, 3564.	5.8	69
100	Unrip is a component of SMN complexes active in snRNP assembly. <i>FEBS Letters</i> , 2005, 579, 2348-2354.	1.3	68
101	Sister kinetochores are mechanically fused during meiosis I in yeast. <i>Science</i> , 2014, 346, 248-251.	6.0	68
102	Kicking against the PRCs â€“ 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.	1.5	68
103	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.	1.1	67
104	A Genetic Engineering Solution to the â€œArginine Conversion Problemâ€“in Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC). <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1567-1577.	2.5	66
105	Rrp5 Binding at Multiple Sites Coordinates Pre-rRNA Processing and Assembly. <i>Molecular Cell</i> , 2013, 52, 707-719.	4.5	65
106	Genetic code expansion for multiprotein complex engineering. <i>Nature Methods</i> , 2016, 13, 997-1000.	9.0	63
107	Model for stathmin/OP18 binding to tubulin. <i>EMBO Journal</i> , 2000, 19, 213-222.	3.5	62
108	Structure of Complement C3(H2O) Revealed By Quantitative Cross-Linking/Mass Spectrometry And Modeling. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2730-2743.	2.5	59

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109	<i>Drosophila</i> Syncrip binds the <i>gurken</i> mRNA localisation signal and regulates localised transcripts during axis specification. <i>Biology Open</i> , 2012, 1, 488-497.	0.6	58
110	Proteomics of a fuzzy organelle: interphase chromatin. <i>EMBO Journal</i> , 2014, 33, 648-664.	3.5	58
111	Complement Evasion Mediated by Enhancement of Captured Factor H: Implications for Protection of Self-Surfaces from Complement. <i>Journal of Immunology</i> , 2015, 195, 4986-4998.	0.4	58
112	Optimizing the Parameters Governing the Fragmentation of Cross-Linked Peptides in a Tribrid Mass Spectrometer. <i>Analytical Chemistry</i> , 2017, 89, 5311-5318.	3.2	58
113	Stress-Induced Translation Inhibition through Rapid Displacement of Scanning Initiation Factors. <i>Molecular Cell</i> , 2020, 80, 470-484.e8.	4.5	58
114	Lin28a regulates neuronal differentiation and controls miR-9 production. <i>Nature Communications</i> , 2014, 5, 3687.	5.8	57
115	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.	2.3	57
116	Cyclin F suppresses B-Myb activity to promote cell cycle checkpoint control. <i>Nature Communications</i> , 2015, 6, 5800.	5.8	57
117	Proteome dynamics at broken replication forks reveal a distinct ATM-directed repair response suppressing DNA double-strand break ubiquitination. <i>Molecular Cell</i> , 2021, 81, 1084-1099.e6.	4.5	57
118	Direct interaction of actin filaments with F-BAR protein pacsin2. <i>EMBO Reports</i> , 2014, 15, 1154-1162.	2.0	56
119	Nop9 is an RNA binding protein present in pre-40S ribosomes and required for 18S rRNA synthesis in yeast. <i>Rna</i> , 2007, 13, 2165-2174.	1.6	55
120	Dynamics of Ribosomal Protein S1 on a Bacterial Ribosome with Cross-Linking and Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1965-1976.	2.5	55
121	The mzIdentML Data Standard Version 1.2, Supporting Advances in Proteome Informatics. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1275-1285.	2.5	55
122	Experiences and perspectives of MALDI MS and MS/MS in proteomic research. <i>International Journal of Mass Spectrometry</i> , 2003, 226, 223-237.	0.7	54
123	Improved results in proteomics by use of local and peptide-class specific false discovery rates. <i>BMC Bioinformatics</i> , 2009, 10, 179.	1.2	54
124	A central cavity within the holo-translocon suggests a mechanism for membrane protein insertion. <i>Scientific Reports</i> , 2016, 6, 38399.	1.6	54
125	Molecular and Genetic Analysis of Condensin Function in Vertebrate Cells. <i>Molecular Biology of the Cell</i> , 2008, 19, 3070-3079.	0.9	53
126	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.	2.5	52

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127	In Situ Structural Restraints from Cross-Linking Mass Spectrometry in Human Mitochondria. <i>Journal of Proteome Research</i> , 2020, 19, 327-336.	1.8	52
128	Purified Smc5/6 Complex Exhibits DNA Substrate Recognition and Compaction. <i>Molecular Cell</i> , 2020, 80, 1039-1054.e6.	4.5	51
129	Proteomics Using Protease Alternatives to Trypsin Benefits from Sequential Digestion with Trypsin. <i>Analytical Chemistry</i> , 2020, 92, 9523-9527.	3.2	50
130	Anatomy of a crosslinker. <i>Current Opinion in Chemical Biology</i> , 2021, 60, 39-46.	2.8	50
131	Structural basis for VPS34 kinase activation by Rab1 and Rab5 on membranes. <i>Nature Communications</i> , 2021, 12, 1564.	5.8	50
132	Quantitative cross-linking/mass spectrometry to elucidate structural changes in proteins and their complexes. <i>Nature Protocols</i> , 2019, 14, 171-201.	5.5	49
133	Prdm5 Regulates Collagen Gene Transcription by Association with RNA Polymerase II in Developing Bone. <i>PLoS Genetics</i> , 2012, 8, e1002711.	1.5	48
134	A programmed wave of uridylation-primed mRNA degradation is essential for meiotic progression and mammalian spermatogenesis. <i>Cell Research</i> , 2019, 29, 221-232.	5.7	48
135	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.	1.5	46
136	Repo-Man/PP1 regulates heterochromatin formation in interphase. <i>Nature Communications</i> , 2017, 8, 14048.	5.8	46
137	Protein Dynamics in Solution by Quantitative Crosslinking/Mass Spectrometry. <i>Trends in Biochemical Sciences</i> , 2018, 43, 908-920.	3.7	44
138	TEX15 is an essential executor of MIWI2-directed transposon DNA methylation and silencing. <i>Nature Communications</i> , 2020, 11, 3739.	5.8	44
139	Leveraging crosslinking mass spectrometry in structural and cell biology. <i>Structure</i> , 2022, 30, 37-54.	1.6	44
140	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, 31142-31150.	1.6	43
141	Proteomic profiling of PrP27 ⁺ -enriched preparations extracted from the brain of hamsters with experimental scrapie. <i>Proteomics</i> , 2009, 9, 3802-3814.	1.3	43
142	CENP-A confers a reduction in height on octameric nucleosomes. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 763-765.	3.6	43
143	Whole-proteome genetic analysis of dependencies in assembly of a vertebrate kinetochore. <i>Journal of Cell Biology</i> , 2015, 211, 1141-1156.	2.3	42
144	The structure and oxidation of the eye lens chaperone α -crystallin. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 1141-1150.	3.6	42

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145	Eic1 links Mis18 with the CCAN/Mis6/Ctf19 complex to promote CENP-A assembly. <i>Open Biology</i> , 2014, 4, 140043.	1.5	41
146	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, 1205-1218.	5.7	41
147	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.	1.3	41
148	Lamin A molecular compression and sliding as mechanisms behind nucleoskeleton elasticity. <i>Nature Communications</i> , 2019, 10, 3056.	5.8	41
149	Building mitotic chromosomes. <i>Current Opinion in Cell Biology</i> , 2011, 23, 114-121.	2.6	40
150	Pre-40S ribosome biogenesis factor Tsr1 is an inactive structural mimic of translational GTPases. <i>Nature Communications</i> , 2016, 7, 11789.	5.8	40
151	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.	1.2	39
152	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, 32381-32393.	1.6	38
153	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.	1.8	38
154	xiSPEC: web-based visualization, analysis and sharing of proteomics data. <i>Nucleic Acids Research</i> , 2018, 46, W473-W478.	6.5	38
155	Ska3 Ensures Timely Mitotic Progression by Interacting Directly With Microtubules and Ska1 Microtubule Binding Domain. <i>Scientific Reports</i> , 2016, 6, 34042.	1.6	36
156	In-Search Assignment of Monoisotopic Peaks Improves the Identification of Cross-Linked Peptides. <i>Journal of Proteome Research</i> , 2018, 17, 3923-3931.	1.8	36
157	Integrative structure of a 10-megadalton eukaryotic pyruvate dehydrogenase complex from native cell extracts. <i>Cell Reports</i> , 2021, 34, 108727.	2.9	36
158	Mechanism for Aar2p function as a U5 snRNP assembly factor. <i>Genes and Development</i> , 2011, 25, 1601-1612.	2.7	35
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