

Juri Rappsilber

List of Publications by Year in descending order

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Version: 2024-02-01

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	Complex Portal 2022: new curation frontiers. <i>Nucleic Acids Research</i> , 2022, 50, D578-D586.	6.5	27
2	The IntAct database: efficient access to fine-grained molecular interaction data. <i>Nucleic Acids Research</i> , 2022, 50, D648-D653.	6.5	89
3	Mapping the invisible chromatin transactions of prophase chromosome remodeling. <i>Molecular Cell</i> , 2022, 82, 696-708.e4.	4.5	10
4	Leveraging crosslinking mass spectrometry in structural and cell biology. <i>Structure</i> , 2022, 30, 37-54.	1.6	44
5	Leveraging Parameter Dependencies in High-Field Asymmetric Waveform Ion-Mobility Spectrometry and Size Exclusion Chromatography for Proteome-wide Cross-Linking Mass Spectrometry. <i>Analytical Chemistry</i> , 2022, 94, 4627-4634.	3.2	6
6	Understudied proteins: opportunities and challenges for functional proteomics. <i>Nature Methods</i> , 2022, 19, 774-779.	9.0	83
7	An open invitation to the Understudied Proteins Initiative. <i>Nature Biotechnology</i> , 2022, 40, 815-817.	9.4	25
8	Mpe1 senses the binding of pre-mRNA and controls 3' end processing by CPF. <i>Molecular Cell</i> , 2022, 82, 2490-2504.e12.	4.5	9
9	Improved Peptide Backbone Fragmentation Is the Primary Advantage of MS-Cleavable Crosslinkers. <i>Analytical Chemistry</i> , 2022, 94, 7779-7786.	3.2	15
10	The phospho-docking protein 14-3-3 regulates microtubule-associated proteins in oocytes including the chromosomal passenger Borealin. <i>PLoS Genetics</i> , 2022, 18, e1009995.	1.5	2
11	Mechanistic basis for Sgo1-mediated centromere localization and function of the CPC. <i>Journal of Cell Biology</i> , 2022, 221, .	2.3	5
12	Isolation of Acetylated and Unmodified Protein N-Terminal Peptides by Strong Cation Exchange Chromatographic Separation of TrypN-Digested Peptides. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100003.	2.5	21
13	The Proteomic Landscape of Centromeric Chromatin Reveals an Essential Role for the Ctf19CCAN Complex in Meiotic Kinetochore Assembly. <i>Current Biology</i> , 2021, 31, 283-296.e7.	1.8	14
14	Anatomy of a crosslinker. <i>Current Opinion in Chemical Biology</i> , 2021, 60, 39-46.	2.8	50
15	Multimiomics Analysis Provides Insight into the Laboratory Evolution of <i>Escherichia coli</i> toward the Metabolic Usage of Fluorinated Indoles. <i>ACS Central Science</i> , 2021, 7, 81-92.	5.3	27
16	Integrative structure of a 10-megadalton eukaryotic pyruvate dehydrogenase complex from native cell extracts. <i>Cell Reports</i> , 2021, 34, 108727.	2.9	36
17	Shulin packages axonemal outer dynein arms for ciliary targeting. <i>Science</i> , 2021, 371, 910-916.	6.0	31
18	Cryo-EM reveals the complex architecture of dynactin's shoulder region and pointed end. <i>EMBO Journal</i> , 2021, 40, e106164.	3.5	22

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19	Structural basis for VPS34 kinase activation by Rab1 and Rab5 on membranes. <i>Nature Communications</i> , 2021, 12, 1564.	5.8	50
20	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
21	SUMOylation stabilizes sister kinetochore biorientation to allow timely anaphase. <i>Journal of Cell Biology</i> , 2021, 220, .	2.3	5
22	Retention time prediction using neural networks increases identifications in crosslinking mass spectrometry. <i>Nature Communications</i> , 2021, 12, 3237.	5.8	22
23	RNA pull-down confocal nanoscanning (RP-CONA) detects quercetin as pri-miR-7/HuR interaction inhibitor that decreases $\hat{\iota}$ -synuclein levels. <i>Nucleic Acids Research</i> , 2021, 49, 6456-6473.	6.5	7
24	NANOS2 is a sequence-specific mRNA-binding protein that promotes transcript degradation in spermatogonial stem cells. <i>IScience</i> , 2021, 24, 102762.	1.9	11
25	Reliable identification of protein-protein interactions by crosslinking mass spectrometry. <i>Nature Communications</i> , 2021, 12, 3564.	5.8	69
26	DNAJC9 integrates heat shock molecular chaperones into the histone chaperone network. <i>Molecular Cell</i> , 2021, 81, 2533-2548.e9.	4.5	31
27	Structural insights into Cullin4-RING ubiquitin ligase remodelling by Vpr from simian immunodeficiency viruses. <i>PLoS Pathogens</i> , 2021, 17, e1009775.	2.1	11
28	A systematic analysis of <i>Trypanosoma brucei</i> chromatin factors identifies novel protein interaction networks associated with sites of transcription initiation and termination. <i>Genome Research</i> , 2021, 31, 2138-2154.	2.4	33
29	STING nuclear partners contribute to innate immune signaling responses. <i>IScience</i> , 2021, 24, 103055.	1.9	22
30	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
31	Stress-Induced Translation Inhibition through Rapid Displacement of Scanning Initiation Factors. <i>Molecular Cell</i> , 2020, 80, 470-484.e8.	4.5	58
32	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
33	The C-terminal helix of BubR1 is essential for CENP-E-dependent chromosome alignment. <i>Journal of Cell Science</i> , 2020, 133, .	1.2	24
34	Megadalton-sized Dityrosine Aggregates of $\hat{\iota}$ -Synuclein Retain High Degrees of Structural Disorder and Internal Dynamics. <i>Journal of Molecular Biology</i> , 2020, 432, 166689.	2.0	5
35	TEX15 is an essential executor of MIWI2-directed transposon DNA methylation and silencing. <i>Nature Communications</i> , 2020, 11, 3739.	5.8	44
36	In-cell architecture of an actively transcribing-translating expressome. <i>Science</i> , 2020, 369, 554-557.	6.0	192

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37	A Structure-Based Mechanism for DNA Entry into the Cohesin Ring. <i>Molecular Cell</i> , 2020, 79, 917-933.e9.	4.5	112
38	SPOCD1 is an essential executor of piRNA-directed de novo DNA methylation. <i>Nature</i> , 2020, 584, 635-639.	13.7	96
39	Purified Smc5/6 Complex Exhibits DNA Substrate Recognition and Compaction. <i>Molecular Cell</i> , 2020, 80, 1039-1054.e6.	4.5	51
40	Ultraviolet Photodissociation of Tryptic Peptide Backbones at 213 nm. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 1282-1290.	1.2	8
41	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
42	The domesticated transposase ALP2 mediates formation of a novel Polycomb protein complex by direct interaction with MSI1, a core subunit of Polycomb Repressive Complex 2 (PRC2). <i>PLoS Genetics</i> , 2020, 16, e1008681.	1.5	22
43	Substrate specificity of the TRAMP nuclear surveillance complexes. <i>Nature Communications</i> , 2020, 11, 3122.	5.8	25
44	The <i>Arabidopsis</i> epigenetic regulator ICU11 as an accessory protein of Polycomb Repressive Complex 2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 16660-16666.	3.3	26
45	Proteomics Using Protease Alternatives to Trypsin Benefits from Sequential Digestion with Trypsin. <i>Analytical Chemistry</i> , 2020, 92, 9523-9527.	3.2	50
46	A protocol for studying structural dynamics of proteins by quantitative crosslinking mass spectrometry and data-independent acquisition. <i>Journal of Proteomics</i> , 2020, 218, 103721.	1.2	9
47	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.	3.6	80
48	Hap2-Ino80-facilitated transcription promotes de novo establishment of CENP-A chromatin. <i>Genes and Development</i> , 2020, 34, 226-238.	2.7	18
49	The $\hat{1}$ subunit and NTPase HelD institute a two-pronged mechanism for RNA polymerase recycling. <i>Nature Communications</i> , 2020, 11, 6418.	5.8	32
50	The structure of human thyroglobulin. <i>Nature</i> , 2020, 578, 627-630.	13.7	81
51	Structural basis for centromere maintenance by <i>Drosophila</i> CENP-A chaperone CAL1. <i>EMBO Journal</i> , 2020, 39, e103234.	3.5	29
52	Title is missing!. , 2020, 16, e1008681.		0
53	Title is missing!. , 2020, 16, e1008681.		0
54	Title is missing!. , 2020, 16, e1008681.		0

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55	Title is missing!. , 2020, 16, e1008681.		0
56	The depolymerase activity of MCAK shows graded response to Aurora B kinase phosphorylation through allosteric regulation. <i>Journal of Cell Science</i> , 2019, 132, .	1.2	22
57	Reconstitution of Microtubule Nucleation In Vitro Reveals Novel Roles for Mzt1. <i>Current Biology</i> , 2019, 29, 2199-2207.e10.	1.8	22
58	Lamin A molecular compression and sliding as mechanisms behind nucleoskeleton elasticity. <i>Nature Communications</i> , 2019, 10, 3056.	5.8	41
59	Assessment of chemical crosslink-assisted protein structure modeling in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1283-1297.	1.5	27
60	An integrated workflow for crosslinking mass spectrometry. <i>Molecular Systems Biology</i> , 2019, 15, e8994.	3.2	120
61	Posttranscriptional Regulation of 14q32 MicroRNAs by the CIRBP and HADHB during Vascular Regeneration after Ischemia. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 14, 329-338.	2.3	24
62	The molecular basis of monopolin recruitment to the kinetochore. <i>Chromosoma</i> , 2019, 128, 331-354.	1.0	17
63	Quantitative Photo-crosslinking Mass Spectrometry Revealing Protein Structure Response to Environmental Changes. <i>Analytical Chemistry</i> , 2019, 91, 9041-9048.	3.2	21
64	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
65	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019, 91, 6953-6961.	3.2	100
66	Reductional Meiosis I Chromosome Segregation Is Established by Coordination of Key Meiotic Kinases. <i>Developmental Cell</i> , 2019, 49, 526-541.e5.	3.1	29
67	A folded conformation of MukBEF and cohesin. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 227-236.	3.6	121
68	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
69	Fission Yeast NDR/LATS Kinase Orb6 Regulates Exocytosis via Phosphorylation of the Exocyst Complex. <i>Cell Reports</i> , 2019, 26, 1654-1667.e7.	2.9	27
70	Sequential Digestion with Trypsin and Elastase in Cross-Linking Mass Spectrometry. <i>Analytical Chemistry</i> , 2019, 91, 4472-4478.	3.2	26
71	Borealin nucleosome interaction secures chromosome association of the chromosomal passenger complex. <i>Journal of Cell Biology</i> , 2019, 218, 3912-3925.	2.3	34
72	The structure and oxidation of the eye lens chaperone γ -crystallin. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 1141-1150.	3.6	42

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73	Structure of the Fanconi anaemia monoubiquitin ligase complex. <i>Nature</i> , 2019, 575, 234-237.	13.7	80
74	Co-regulation map of the human proteome enables identification of protein functions. <i>Nature Biotechnology</i> , 2019, 37, 1361-1371.	9.4	106
75	A Primer on Data Analytics in Functional Genomics: How to Move from Data to Insight?. <i>Trends in Biochemical Sciences</i> , 2019, 44, 21-32.	3.7	16
76	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
77	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
78	Data-independent Acquisition Improves Quantitative Cross-linking Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 786-795.	2.5	31
79	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
80	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
81	Noncovalently Associated Peptides Observed during Liquid Chromatography-Mass Spectrometry and Their Effect on Cross-Link Analyses. <i>Analytical Chemistry</i> , 2019, 91, 2678-2685.	3.2	19
82	The kinetochore module Okp1 ^{CENPâ€œQ} /Ame1 ^{CENPâ€œU} is a reader for Nâ€œterminal modifications on the centromeric histone Cse4 ^{CENPâ€œA} . <i>EMBO Journal</i> , 2019, 38, .	3.5	34
83	Quantitative Proteomics of the Mitotic Chromosome Scaffold Reveals the Association of BAZ1B with Chromosomal Axes*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 169-181.	2.5	18
84	Molecular interactions between Hel2 and RNA supporting ribosome-associated quality control. <i>Nature Communications</i> , 2019, 10, 563.	5.8	32
85	Defects in Signal Recognition Particle (SRP) Components Reveal an Essential and Non-Redundant Role for Granule Biogenesis and Differentiation of Neutrophil Granulocytes. <i>Blood</i> , 2019, 134, 216-216.	0.6	1
86	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
87	Protein Tertiary Structure by Crosslinking/Mass Spectrometry. <i>Trends in Biochemical Sciences</i> , 2018, 43, 157-169.	3.7	77
88	Genes Important for <i>Schizosaccharomyces pombe</i> Meiosis Identified Through a Functional Genomics Screen. <i>Genetics</i> , 2018, 208, 589-603.	1.2	23
89	Small angle Xâ€œray scattering and crossâ€œlinking for data assisted protein structure prediction in CASP 12 with prospects for improved accuracy. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 202-214.	1.5	23
90	Peptide Retention in Hydrophilic Strong Anion Exchange Chromatography Is Driven by Charged and Aromatic Residues. <i>Analytical Chemistry</i> , 2018, 90, 4635-4640.	3.2	13

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91	Phosphorylation of SOS1 on tyrosine 1196 promotes its RAC GEF activity and contributes to BCR-ABL leukemogenesis. <i>Leukemia</i> , 2018, 32, 820-827.	3.3	22
92	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
93	False discovery rate estimation and heterobifunctional cross-linkers. <i>PLoS ONE</i> , 2018, 13, e0196672.	1.1	14
94	Protein Dynamics in Solution by Quantitative Crosslinking/Mass Spectrometry. <i>Trends in Biochemical Sciences</i> , 2018, 43, 908-920.	3.7	44
95	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
96	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
97	Heterologous Biosynthesis, Modifications and Structural Characterization of Ruminococcin-A, a Lanthipeptide From the Gut Bacterium <i>Ruminococcus gnavus</i> E1, in <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1688.	1.5	24
98	Exportin Crm1 is repurposed as a docking protein to generate microtubule organizing centers at the nuclear pore. <i>ELife</i> , 2018, 7, .	2.8	15
99	JAMI: a Java library for molecular interactions and data interoperability. <i>BMC Bioinformatics</i> , 2018, 19, 133.	1.2	6
100	xiSPEC: web-based visualization, analysis and sharing of proteomics data. <i>Nucleic Acids Research</i> , 2018, 46, W473-W478.	6.5	38
101	Epigenetic Variability Confounds Transcriptome but Not Proteome Profiling for Coexpression-based Gene Function Prediction. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2082-2090.	2.5	9
102	Repo-Man/PP1 regulates heterochromatin formation in interphase. <i>Nature Communications</i> , 2017, 8, 14048.	5.8	46
103	Nano Random Forests to mine protein complexes and their relationships in quantitative proteomics data. <i>Molecular Biology of the Cell</i> , 2017, 28, 673-680.	0.9	12
104	Quirks of Error Estimation in Cross-Linking/Mass Spectrometry. <i>Analytical Chemistry</i> , 2017, 89, 3829-3833.	3.2	136
105	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
106	Optimizing the Parameters Governing the Fragmentation of Cross-Linked Peptides in a Tribid Mass Spectrometer. <i>Analytical Chemistry</i> , 2017, 89, 5311-5318.	3.2	58
107	Complementary Benzophenone Cross-Linking/Mass Spectrometry Photochemistry. <i>Analytical Chemistry</i> , 2017, 89, 5319-5324.	3.2	22
108	Transposon-driven transcription is a conserved feature of vertebrate spermatogenesis and transcript evolution. <i>EMBO Reports</i> , 2017, 18, 1231-1247.	2.0	34

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109	Pervasive coexpression of spatially proximal genes is buffered at the protein level. <i>Molecular Systems Biology</i> , 2017, 13, 937.	3.2	90
110	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.	2.3	29
111	Capturing protein communities by structural proteomics in a thermophilic eukaryote. <i>Molecular Systems Biology</i> , 2017, 13, 936.	3.2	108
112	Cross-linking mass spectrometry identifies new interfaces of Augmin required to localise the $\hat{1}^3$ -Tubulin Ring Complex to the mitotic spindle. <i>Biology Open</i> , 2017, 6, 654-663.	0.6	25
113	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
114	Cdc14 phosphatase directs centrosome re-duplication at the meiosis I to meiosis II transition in budding yeast. <i>Wellcome Open Research</i> , 2017, 2, 2.	0.9	20
115	RNA polymerase II stalling at pre-mRNA splice sites is enforced by ubiquitination of the catalytic subunit. <i>ELife</i> , 2017, 6, .	2.8	16
116	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
117	ComplexViewer: visualization of curated macromolecular complexes. <i>Bioinformatics</i> , 2017, 33, 3673-3675.	1.8	10
118	Architecture of TAF11/TAF13/TBP complex suggests novel regulation properties of general transcription factor TFIID. <i>ELife</i> , 2017, 6, .	2.8	29
119	Mps1Mph1 Kinase Phosphorylates Mad3 to Inhibit Cdc20Sp1-APC/C and Maintain Spindle Checkpoint Arrests. <i>PLoS Genetics</i> , 2016, 12, e1005834.	1.5	10
120	Endogenous Mouse Dicer Is an Exclusively Cytoplasmic Protein. <i>PLoS Genetics</i> , 2016, 12, e1006095.	1.5	27
121	Blind testing of cross-linking/mass spectrometry hybrid methods in CASP11. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 152-163.	1.5	27
122	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
123	Pre-40S ribosome biogenesis factor Tsr1 is an inactive structural mimic of translational GTPases. <i>Nature Communications</i> , 2016, 7, 11789.	5.8	40
124	Repression of RNA polymerase by the archaeo-viral regulator ORF145/RIP. <i>Nature Communications</i> , 2016, 7, 13595.	5.8	20
125	A central cavity within the holo-translocon suggests a mechanism for membrane protein insertion. <i>Scientific Reports</i> , 2016, 6, 38399.	1.6	54
126	Multiclassifier combinatorial proteomics of organelle shadows at the example of mitochondria in chromatin data. <i>Proteomics</i> , 2016, 16, 393-401.	1.3	12

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127	A Focus on Chromatin Proteomics. <i>Proteomics</i> , 2016, 16, 379-380.	1.3	1
128	G9a/GLP Complex Maintains Imprinted DNA Methylation in Embryonic Stem Cells. <i>Cell Reports</i> , 2016, 15, 77-85.	2.9	111
129	Compositional Dynamics: Defining the Fuzzy Cell. <i>Trends in Cell Biology</i> , 2016, 26, 800-803.	3.6	4
130	Quantitative Cross-linking/Mass Spectrometry Using Isotope-labeled Cross-linkers and MaxQuant. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2769-2778.	2.5	28
131	Proteomics Analysis with a Nano Random Forest Approach Reveals Novel Functional Interactions Regulated by SMC Complexes on Mitotic Chromosomes. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2802-2818.	2.5	20
132	Optimized Fragmentation Regime for Diazirine Photo-Cross-Linked Peptides. <i>Analytical Chemistry</i> , 2016, 88, 8239-8247.	3.2	34
133	Genetic code expansion for multiprotein complex engineering. <i>Nature Methods</i> , 2016, 13, 997-1000.	9.0	63
134	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
135	SCFCyclin F-dependent degradation of CDC6 suppresses DNA re-replication. <i>Nature Communications</i> , 2016, 7, 10530.	5.8	81
136	Blind Evaluation of Hybrid Protein Structure Analysis Methods based on Cross-Linking. <i>Trends in Biochemical Sciences</i> , 2016, 41, 564-567.	3.7	21
137	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
138	Auxin/AID versus conventional knockouts: distinguishing the roles of CENP-T/W in mitotic kinetochore assembly and stability. <i>Open Biology</i> , 2016, 6, 150230.	1.5	21
139	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
140	Molecular architecture of the Dam1 complex's microtubule interaction. <i>Open Biology</i> , 2016, 6, 150237.	1.5	26
141	Blind testing cross-linking/mass spectrometry under the auspices of the 11th critical assessment of methods of protein structure prediction (CASP11). <i>Wellcome Open Research</i> , 2016, 1, 24.	0.9	12
142	Quantitative cross-linking/mass spectrometry reveals subtle protein conformational changes. <i>Wellcome Open Research</i> , 2016, 1, 5.	0.9	30
143	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
144	Chemical Evolution of a Bacterial Proteome. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 10030-10034.	7.2	71

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145	Deletion of Genes Encoding Arginase Improves Use of ϵ -Heavy-Isotope-Labeled Arginine for Mass Spectrometry in Fission Yeast. <i>PLoS ONE</i> , 2015, 10, e0129548.	1.1	5
146	xiNET: Cross-link Network Maps With Residue Resolution. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1137-1147.	2.5	242
147	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
148	Cyclin F suppresses B-Myb activity to promote cell cycle checkpoint control. <i>Nature Communications</i> , 2015, 6, 5800.	5.8	57
149	Cytoplasmic TAF2-TAF8-TAF10 complex provides evidence for nuclear holo-TFIID assembly from preformed submodules. <i>Nature Communications</i> , 2015, 6, 6011.	5.8	77
150	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , 2015, 23, 1156-1167.	1.6	159
151	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
152	Mto2 multisite phosphorylation inactivates non-spindle microtubule nucleation complexes during mitosis. <i>Nature Communications</i> , 2015, 6, 7929.	5.8	27
153	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
154	A Single α Helix Drives Extensive Remodeling of the Proteasome Lid and Completion of Regulatory Particle Assembly. <i>Cell</i> , 2015, 163, 432-444.	13.5	73
155	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.	1.5	68
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