

Juri Rappsilber

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/478043/juri-rappsilber-publications-by-year.pdf>

Version: 2024-04-24

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Mapping the invisible chromatin transactions of prophase chromosome remodeling.. <i>Molecular Cell</i> , 2022 ,	17.6	1
272	Understudied proteins: opportunities and challenges for functional proteomics.. <i>Nature Methods</i> , 2022 ,	21.6	6
271	An open invitation to the Understudied Proteins Initiative.. <i>Nature Biotechnology</i> , 2022 ,	44.5	2
270	Leveraging crosslinking mass spectrometry in structural and cell biology.. <i>Structure</i> , 2021 ,	5.2	4
269	Complex Portal 2022: new curation frontiers. <i>Nucleic Acids Research</i> , 2021 ,	20.1	4
268	The IntAct database: efficient access to fine-grained molecular interaction data. <i>Nucleic Acids Research</i> , 2021 ,	20.1	15
267	Cryo-EM reveals the complex architecture of dynactin's shoulder region and pointed end. <i>EMBO Journal</i> , 2021 , 40, e106164	13	5
266	Structural basis for VPS34 kinase activation by Rab1 and Rab5 on membranes. <i>Nature Communications</i> , 2021 , 12, 1564	17.4	8
265	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	17.6	17
264	SUMOylation stabilizes sister kinetochore biorientation to allow timely anaphase. <i>Journal of Cell Biology</i> , 2021 , 220,	7.3	1
263	Retention time prediction using neural networks increases identifications in crosslinking mass spectrometry. <i>Nature Communications</i> , 2021 , 12, 3237	17.4	3
262	RNA pull-down confocal nanoscanning (RP-CONA) detects quercetin as pri-miR-7/HuR interaction inhibitor that decreases Eynuclein levels. <i>Nucleic Acids Research</i> , 2021 , 49, 6456-6473	20.1	0
261	NANOS2 is a sequence-specific mRNA-binding protein that promotes transcript degradation in spermatogonial stem cells. <i>IScience</i> , 2021 , 24, 102762	6.1	2
260	Reliable identification of protein-protein interactions by crosslinking mass spectrometry. <i>Nature Communications</i> , 2021 , 12, 3564	17.4	15
259	DNAJC9 integrates heat shock molecular chaperones into the histone chaperone network. <i>Molecular Cell</i> , 2021 , 81, 2533-2548.e9	17.6	6
258	The Proteomic Landscape of Centromeric Chromatin Reveals an Essential Role for the Ctf19 Complex in Meiotic Kinetochore Assembly. <i>Current Biology</i> , 2021 , 31, 283-296.e7	6.3	4
257	Anatomy of a crosslinker. <i>Current Opinion in Chemical Biology</i> , 2021 , 60, 39-46	9.7	18

256	Multimomics Analysis Provides Insight into the Laboratory Evolution of toward the Metabolic Usage of Fluorinated Indoles. <i>ACS Central Science</i> , 2021 , 7, 81-92	16.8	8
255	Integrative structure of a 10-megadalton eukaryotic pyruvate dehydrogenase complex from native cell extracts. <i>Cell Reports</i> , 2021 , 34, 108727	10.6	10
254	Shulin packages axonemal outer dynein arms for ciliary targeting. <i>Science</i> , 2021 , 371, 910-916	33.3	11
253	Structural insights into Cullin4-RING ubiquitin ligase remodelling by Vpr from simian immunodeficiency viruses. <i>PLoS Pathogens</i> , 2021 , 17, e1009775	7.6	3
252	A systematic analysis of chromatin factors identifies novel protein interaction networks associated with sites of transcription initiation and termination. <i>Genome Research</i> , 2021 , 31, 2138-2154	9.7	7
251	STING nuclear partners contribute to innate immune signaling responses. <i>iScience</i> , 2021 , 24, 103055	6.1	6
250	Purified Smc5/6 Complex Exhibits DNA Substrate Recognition and Compaction. <i>Molecular Cell</i> , 2020 , 80, 1039-1054.e6	17.6	17
249	Ultraviolet Photodissociation of Tryptic Peptide Backbones at 213 nm. <i>Journal of the American Society for Mass Spectrometry</i> , 2020 , 31, 1282-1290	3.5	3
248	Microtubule Nucleation Properties of Single Human β uRCs Explained by Their Cryo-EM Structure. <i>Developmental Cell</i> , 2020 , 53, 603-617.e8	10.2	49
247	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	6	11
246	Substrate specificity of the TRAMP nuclear surveillance complexes. <i>Nature Communications</i> , 2020 , 11, 3122	17.4	10
245	The 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	11.5	15
244	Proteomics Using Protease Alternatives to Trypsin Benefits from Sequential Digestion with Trypsin. <i>Analytical Chemistry</i> , 2020 , 92, 9523-9527	7.8	16
243	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	3.9	5
242	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
241	Hap2-Ino80-facilitated transcription promotes de novo establishment of CENP-A chromatin. <i>Genes and Development</i> , 2020 , 34, 226-238	12.6	6
240	Structural basis for centromere maintenance by Drosophila CENP-A chaperone CAL1. <i>EMBO Journal</i> , 2020 , 39, e103234	13	13
239	The β subunit and NTPase HelD institute a two-pronged mechanism for RNA polymerase recycling. <i>Nature Communications</i> , 2020 , 11, 6418	17.4	14

238	The structure of human thyroglobulin. <i>Nature</i> , 2020 , 578, 627-630	50.4	36
237	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
236	Stress-Induced Translation Inhibition through Rapid Displacement of Scanning Initiation Factors. <i>Molecular Cell</i> , 2020 , 80, 470-484.e8	17.6	15
235	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
234	The C-terminal helix of BubR1 is essential for CENP-E-dependent chromosome alignment. <i>Journal of Cell Science</i> , 2020 , 133,	5.3	11
233	Megadalton-sized Dityrosine Aggregates of β Synuclein Retain High Degrees of Structural Disorder and Internal Dynamics. <i>Journal of Molecular Biology</i> , 2020 , 432, 166689	6.5	3
232	TEX15 is an essential executor of MIWI2-directed transposon DNA methylation and silencing. <i>Nature Communications</i> , 2020 , 11, 3739	17.4	20
231	In-cell architecture of an actively transcribing-translating expressome. <i>Science</i> , 2020 , 369, 554-557	33.3	82
230	A Structure-Based Mechanism for DNA Entry into the Cohesin Ring. <i>Molecular Cell</i> , 2020 , 79, 917-933.e9	17.6	48
229	SPOCD1 is an essential executor of piRNA-directed de novo DNA methylation. <i>Nature</i> , 2020 , 584, 635-639	30.4	38
228	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> , 2020 , 20, 100003	7.6	7
227	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) 2020 , 16, e1008681		
226	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) 2020 , 16, e1008681		
225	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) 2020 , 16, e1008681		
224	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) 2020 , 16, e1008681		
223	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	10.7	13
222	The molecular basis of monopolin recruitment to the kinetochore. <i>Chromosoma</i> , 2019 , 128, 331-354	2.8	12
221	Quantitative Photo-crosslinking Mass Spectrometry Revealing Protein Structure Response to Environmental Changes. <i>Analytical Chemistry</i> , 2019 , 91, 9041-9048	7.8	11

220	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
219	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019 , 91, 6953-6961	7.8	57
218	Reductional Meiosis I Chromosome Segregation Is Established by Coordination of Key Meiotic Kinases. <i>Developmental Cell</i> , 2019 , 49, 526-541.e5	10.2	16
217	A folded conformation of MukBEF and cohesin. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 227-236	16.6	75
216	Defining the RNA interactome by total RNA-associated protein purification. <i>Molecular Systems Biology</i> , 2019 , 15, e8689	12.2	66
215	Fission Yeast NDR/LATS Kinase Orb6 Regulates Exocytosis via Phosphorylation of the Exocyst Complex. <i>Cell Reports</i> , 2019 , 26, 1654-1667.e7	10.6	15
214	Reconstitution of Microtubule Nucleation In Vitro Reveals Novel Roles for Mzt1. <i>Current Biology</i> , 2019 , 29, 2199-2207.e10	6.3	11
213	Lamin A molecular compression and sliding as mechanisms behind nucleoskeleton elasticity. <i>Nature Communications</i> , 2019 , 10, 3056	17.4	27
212	Assessment of chemical-crosslink-assisted protein structure modeling in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 1283-1297	4.2	18
211	An integrated workflow for crosslinking mass spectrometry. <i>Molecular Systems Biology</i> , 2019 , 15, e8994	12.2	58
210	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	2.2	
209	Molecular interactions between Hel2 and RNA supporting ribosome-associated quality control. <i>Nature Communications</i> , 2019 , 10, 563	17.4	16
208	Sequential Digestion with Trypsin and Elastase in Cross-Linking Mass Spectrometry. <i>Analytical Chemistry</i> , 2019 , 91, 4472-4478	7.8	14
207	Borealin-nucleosome interaction secures chromosome association of the chromosomal passenger complex. <i>Journal of Cell Biology</i> , 2019 , 218, 3912-3925	7.3	15
206	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
205	Structure of the Fanconi anaemia monoubiquitin ligase complex. <i>Nature</i> , 2019 , 575, 234-237	50.4	46
204	Co-regulation map of the human proteome enables identification of protein functions. <i>Nature Biotechnology</i> , 2019 , 37, 1361-1371	44.5	60
203	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	10.3	11

202	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
201	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
200	Data-independent Acquisition Improves Quantitative Cross-linking Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 786-795	7.6	20
199	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
198	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
197	Noncovalently Associated Peptides Observed during Liquid Chromatography-Mass Spectrometry and Their Effect on Cross-Link Analyses. <i>Analytical Chemistry</i> , 2019 , 91, 2678-2685	7.8	11
196	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
195	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	7.6	8
194	The depolymerase activity of MCAK shows a graded response to Aurora B kinase phosphorylation through allosteric regulation. <i>Journal of Cell Science</i> , 2019 , 132,	5.3	11
193	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
192	Protein Tertiary Structure by Crosslinking/Mass Spectrometry. <i>Trends in Biochemical Sciences</i> , 2018 , 43, 157-169	10.3	54
191	Genes Important for Meiosis Identified Through a Functional Genomics Screen. <i>Genetics</i> , 2018 , 208, 589-603	4.03	13
190	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
189	Peptide Retention in Hydrophilic Strong Anion Exchange Chromatography Is Driven by Charged and Aromatic Residues. <i>Analytical Chemistry</i> , 2018 , 90, 4635-4640	7.8	6
188	Phosphorylation of SOS1 on tyrosine 1196 promotes its RAC GEF activity and contributes to BCR-ABL leukemogenesis. <i>Leukemia</i> , 2018 , 32, 820-827	10.7	14
187	Exportin Crm1 is repurposed as a docking protein to generate microtubule organizing centers at the nuclear pore. <i>ELife</i> , 2018 , 7,	8.9	10
186	JAMI: a Java library for molecular interactions and data interoperability. <i>BMC Bioinformatics</i> , 2018 , 19, 133	3.6	5
185	xiSPEC: web-based visualization, analysis and sharing of proteomics data. <i>Nucleic Acids Research</i> , 2018 , 46, W473-W478	20.1	25

184	Epigenetic Variability Confounds Transcriptome but Not Proteome Profiling for Coexpression-based Gene Function Prediction. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 2082-2090	7.6	5
183	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
182	False discovery rate estimation and heterobifunctional cross-linkers. <i>PLoS ONE</i> , 2018 , 13, e0196672	3.7	7
181	Protein Dynamics in Solution by Quantitative Crosslinking/Mass Spectrometry. <i>Trends in Biochemical Sciences</i> , 2018 , 43, 908-920	10.3	34
180	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
179	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
178	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
177	Repo-Man/PP1 regulates heterochromatin formation in interphase. <i>Nature Communications</i> , 2017 , 8, 14048	17.4	32
176	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	3.5	9
175	Quirks of Error Estimation in Cross-Linking/Mass Spectrometry. <i>Analytical Chemistry</i> , 2017 , 89, 3829-3833	7.8	89
174	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
173	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
172	Complementary Benzophenone Cross-Linking/Mass Spectrometry Photochemistry. <i>Analytical Chemistry</i> , 2017 , 89, 5319-5324	7.8	16
171	Transposon-driven transcription is a conserved feature of vertebrate spermatogenesis and transcript evolution. <i>EMBO Reports</i> , 2017 , 18, 1231-1247	6.5	26
170	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
169	ComplexViewer: visualization of curated macromolecular complexes. <i>Bioinformatics</i> , 2017 , 33, 3673-3675	5.2	8
168	Pervasive coexpression of spatially proximal genes is buffered at the protein level. <i>Molecular Systems Biology</i> , 2017 , 13, 937	12.2	52
167	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

166	Capturing protein communities by structural proteomics in a thermophilic eukaryote. <i>Molecular Systems Biology</i> , 2017 , 13, 936	12.2	79
165	Cross-linking mass spectrometry identifies new interfaces of Augmin required to localise the β -tubulin ring complex to the mitotic spindle. <i>Biology Open</i> , 2017 , 6, 654-663	2.2	13
164	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
163	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	4.8	13
162	RNA polymerase II stalling at pre-mRNA splice sites is enforced by ubiquitination of the catalytic subunit. <i>ELife</i> , 2017 , 6,	8.9	11
161	Architecture of TAF11/TAF13/TBP complex suggests novel regulation properties of general transcription factor TFIID. <i>ELife</i> , 2017 , 6,	8.9	19
160	Genetic code expansion for multiprotein complex engineering. <i>Nature Methods</i> , 2016 , 13, 997-1000	21.6	48
159	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
158	SCF(Cyclin F)-dependent degradation of CDC6 suppresses DNA re-replication. <i>Nature Communications</i> , 2016 , 7, 10530	17.4	59
157	Blind Evaluation of Hybrid Protein Structure Analysis Methods based on Cross-Linking. <i>Trends in Biochemical Sciences</i> , 2016 , 41, 564-567	10.3	17
156	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
155	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	7	17
154	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
153	Molecular architecture of the Dam1 complex-microtubule interaction. <i>Open Biology</i> , 2016 , 6,	7	17
152	Blind testing cross-linking/mass spectrometry under the auspices of the 11 critical assessment of methods of protein structure prediction (CASP11). <i>Wellcome Open Research</i> , 2016 , 1, 24	4.8	12
151	Quantitative cross-linking/mass spectrometry reveals subtle protein conformational changes. <i>Wellcome Open Research</i> , 2016 , 1, 5	4.8	22
150	Mps1Mph1 Kinase Phosphorylates Mad3 to Inhibit Cdc20Slp1-APC/C and Maintain Spindle Checkpoint Arrests. <i>PLoS Genetics</i> , 2016 , 12, e1005834	6	7
149	Endogenous Mouse Dicer Is an Exclusively Cytoplasmic Protein. <i>PLoS Genetics</i> , 2016 , 12, e1006095	6	20

148	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
147	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
146	Pre-40S ribosome biogenesis factor Tsr1 is an inactive structural mimic of translational GTPases. <i>Nature Communications</i> , 2016 , 7, 11789	17.4	29
145	Repression of RNA polymerase by the archaeo-viral regulator ORF145/RIP. <i>Nature Communications</i> , 2016 , 7, 13595	17.4	16
144	A central cavity within the holo-translocon suggests a mechanism for membrane protein insertion. <i>Scientific Reports</i> , 2016 , 6, 38399	4.9	38
143	Multiclassifier combinatorial proteomics of organelle shadows at the example of mitochondria in chromatin data. <i>Proteomics</i> , 2016 , 16, 393-401	4.8	9
142	G9a/GLP Complex Maintains Imprinted DNA Methylation in Embryonic Stem Cells. <i>Cell Reports</i> , 2016 , 15, 77-85	10.6	59
141	Compositional Dynamics: Defining the Fuzzy Cell. <i>Trends in Cell Biology</i> , 2016 , 26, 800-803	18.3	4
140	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
139	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, 2802-18	7.6	16
138	Optimized Fragmentation Regime for Diazirine Photo-Cross-Linked Peptides. <i>Analytical Chemistry</i> , 2016 , 88, 8239-47	7.8	26
137	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , 2015 , 23, 1156-67	5.2	131
136	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
135	Mto2 multisite phosphorylation inactivates non-spindle microtubule nucleation complexes during mitosis. <i>Nature Communications</i> , 2015 , 6, 7929	17.4	20
134	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
133	A Single Helix Drives Extensive Remodeling of the Proteasome Lid and Completion of Regulatory Particle Assembly. <i>Cell</i> , 2015 , 163, 432-44	56.2	60
132	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
131	Chemical Evolution of a Bacterial Proteome. <i>Angewandte Chemie - International Edition</i> , 2015 , 54, 10030-46.4	46.4	52

130	Deletion of Genes Encoding Arginase Improves Use of "Heavy" Isotope-Labeled Arginine for Mass Spectrometry in Fission Yeast. <i>PLoS ONE</i> , 2015 , 10, e0129548	3.7	5
129	xiNET: cross-link network maps with residue resolution. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 1137-47	167	
128	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
127	Cyclin F suppresses B-Myb activity to promote cell cycle checkpoint control. <i>Nature Communications</i> , 2015 , 6, 5800	17.4	43
126	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
125	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
124	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
123	Direct interaction of actin filaments with F-BAR protein pacsin2. <i>EMBO Reports</i> , 2014 , 15, 1154-62	6.5	47
122	Chromatin enrichment for proteomics. <i>Nature Protocols</i> , 2014 , 9, 2090-9	18.8	53
121	Sister kinetochores are mechanically fused during meiosis I in yeast. <i>Science</i> , 2014 , 346, 248-51	33.3	56
120	Eic1 links Mis18 with the CCAN/Mis6/Ctf19 complex to promote CENP-A assembly. <i>Open Biology</i> , 2014 , 4, 140043	7	28
119	Lin28a regulates neuronal differentiation and controls miR-9 production. <i>Nature Communications</i> , 2014 , 5, 3687	17.4	43
118	A systematic genetic screen identifies new factors influencing centromeric heterochromatin integrity in fission yeast. <i>Genome Biology</i> , 2014 , 15, 481	18.3	18
117	BoxPlotR: a web tool for generation of box plots. <i>Nature Methods</i> , 2014 , 11, 121-2	21.6	434
116	Proteomics of a fuzzy organelle: interphase chromatin. <i>EMBO Journal</i> , 2014 , 33, 648-64	13	41
115	Supraspliceosomes at defined functional states portray the pre-assembled nature of the pre-mRNA processing machine in the cell nucleus. <i>International Journal of Molecular Sciences</i> , 2014 , 15, 11637-64	6.3	14
114	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
113	Rio1 mediates ATP-dependent final maturation of 40S ribosomal subunits. <i>Nucleic Acids Research</i> , 2014 , 42, 12189-99	20.1	61

112	Structural basis for microtubule recognition by the human kinetochore Ska complex. <i>Nature Communications</i> , 2014 , 5, 2964	17.4	66
111	Trim25 Is an RNA-Specific Activator of Lin28a/TuT4-Mediated Uridylation. <i>Cell Reports</i> , 2014 , 9, 1265-72	10.6	62
110	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
109	Shugoshin biases chromosomes for biorientation through condensin recruitment to the pericentromere. <i>ELife</i> , 2014 , 3, e01374	8.9	49
108	Rrp5 binding at multiple sites coordinates pre-rRNA processing and assembly. <i>Molecular Cell</i> , 2013 , 52, 707-19	17.6	46
107	Cohesin-dependent association of scc2/4 with the centromere initiates pericentromeric cohesion establishment. <i>Current Biology</i> , 2013 , 23, 599-606	6.3	71
106	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
105	Quantitative cross-linking/mass spectrometry using isotope-labelled cross-linkers. <i>Journal of Proteomics</i> , 2013 , 88, 120-8	3.9	109
104	CENP-A confers a reduction in height on octameric nucleosomes. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 763-5	17.6	40
103	Cell cycle regulation of microtubule interactomes: multi-layered regulation is critical for the interphase/mitosis transition. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 3135-47	7.6	18
102	Multiple RNA interactions position Mrd1 at the site of the small subunit pseudoknot within the 90S pre-ribosome. <i>Nucleic Acids Research</i> , 2013 , 41, 1178-90	20.1	18
101	Tissue-specific control of brain-enriched miR-7 biogenesis. <i>Genes and Development</i> , 2013 , 27, 24-38	12.6	108
100	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
99	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
98	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
97	Prdm5 regulates collagen gene transcription by association with RNA polymerase II in developing bone. <i>PLoS Genetics</i> , 2012 , 8, e1002711	6	37
96	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
95	REST-mediated recruitment of polycomb repressor complexes in mammalian cells. <i>PLoS Genetics</i> , 2012 , 8, e1002494	6	116

94	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
93	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
92	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
91	Repo-Man coordinates chromosomal reorganization with nuclear envelope reassembly during mitotic exit. <i>Developmental Cell</i> , 2011 , 21, 328-42	10.2	139
90	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
89	TET1 and hydroxymethylcytosine in transcription and DNA methylation fidelity. <i>Nature</i> , 2011 , 473, 343-8	50.4	796
88	Building mitotic chromosomes. <i>Current Opinion in Cell Biology</i> , 2011 , 23, 114-21	9	31
87	Mechanism for Aar2p function as a U5 snRNP assembly factor. <i>Genes and Development</i> , 2011 , 25, 1601-12	2.6	28
86	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
85	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
84	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
83	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
82	Arginine methylation of Aubergine mediates Tudor binding and germ plasm localization. <i>Rna</i> , 2010 , 16, 70-8	5.8	95
81	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
80	Arginine methylation of vasa protein is conserved across phyla. <i>Journal of Biological Chemistry</i> , 2010 , 285, 8148-54	5.4	67
79	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
78	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
77	Stc1: a critical link between RNAi and chromatin modification required for heterochromatin integrity. <i>Cell</i> , 2010 , 140, 666-77	56.2	160

76	The protein composition of mitotic chromosomes determined using multiclassifier combinatorial proteomics. <i>Cell</i> , 2010 , 142, 810-21	56.2	217
75	Proteomics of isolated mitotic chromosomes identifies the kinetochore protein Ska3/Rama1. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2010 , 75, 433-8	3.9	11
74	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
73	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
72	When less can yield more - Computational preprocessing of MS/MS spectra for peptide identification. <i>Proteomics</i> , 2009 , 9, 4978-84	4.8	62
71	Fission yeast Scm3: A CENP-A receptor required for integrity of subkinetochore chromatin. <i>Molecular Cell</i> , 2009 , 33, 299-311	17.6	159
70	A model for transmission of the H3K27me3 epigenetic mark. <i>Nature Cell Biology</i> , 2008 , 10, 1291-300	23.4	558
69	Protein abundance profiling of the Escherichia coli cytosol. <i>BMC Genomics</i> , 2008 , 9, 102	4.5	353
68	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
67	Implications for kinetochore-microtubule attachment from the structure of an engineered Ndc80 complex. <i>Cell</i> , 2008 , 133, 427-39	56.2	403
66	Splicing factors facilitate RNAi-directed silencing in fission yeast. <i>Science</i> , 2008 , 322, 602-6	33.3	104
65	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
64	Molecular and genetic analysis of condensin function in vertebrate cells. <i>Molecular Biology of the Cell</i> , 2008 , 19, 3070-9	3.5	50
63	Proteomic analysis of human blood serum using peptide library beads. <i>Journal of Proteome Research</i> , 2007 , 6, 4055-62	5.6	149
62	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
61	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
60	UTX and JMJD3 are histone H3K27 demethylases involved in HOX gene regulation and development. <i>Nature</i> , 2007 , 449, 731-4	50.4	975
59	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

58	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
57	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
56	Analysis of the topology of protein complexes using cross-linking and mass spectrometry. <i>Cold Spring Harbor Protocols</i> , 2007 , 2007, pdb.prot4594	1.2	7
55	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
54	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
53	The putative oncogene GASC1 demethylates tri- and dimethylated lysine 9 on histone H3. <i>Nature</i> , 2006 , 442, 307-11	50.4	599
52	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
51	Exploring the hidden human urinary proteome via ligand library beads. <i>Journal of Proteome Research</i> , 2005 , 4, 1917-30	5.6	214
50	Peptide identification using vectors of small fragment ions. <i>Journal of Proteome Research</i> , 2005 , 4, 1006-16	1.6	2
49	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
48	Unrip is a component of SMN complexes active in snRNP assembly. <i>FEBS Letters</i> , 2005 , 579, 2348-54	3.8	61
47	Sequence tag scanning: a new explorative strategy for recognition of unexpected protein alterations by nanoelectrospray ionization-tandem mass spectrometry. <i>Proteomics</i> , 2005 , 5, 667-74	4.8	6
46	Spot overlapping in two-dimensional maps: a serious problem ignored for much too long. <i>Proteomics</i> , 2005 , 5, 2385-95	4.8	123
45	eIF4A3 is a novel component of the exon junction complex. <i>Rna</i> , 2004 , 10, 200-9	5.8	180
44	Naturstoffanalytik unter der Lupe. <i>Nachrichten Aus Der Chemie</i> , 2003 , 51, 727-728	0.1	
43	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
42	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
41	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

40	Multi-Protein Complexes Studied by Mass Spectrometry. <i>Scientific World Journal, The</i> , 2002 , 2, 91-92	2.2	1
39	What does it mean to identify a protein in proteomics?. <i>Trends in Biochemical Sciences</i> , 2002 , 27, 74-8	10.3	161
38	Microcolumns with self-assembled particle frits for proteomics. <i>Journal of Chromatography A</i> , 2002 , 979, 233-9	4.5	260
37	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
36	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
35	miRNPs: a novel class of ribonucleoproteins containing numerous microRNAs. <i>Genes and Development</i> , 2002 , 16, 720-8	12.6	808
34	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
33	Large-scale proteomic analysis of the human spliceosome. <i>Genome Research</i> , 2002 , 12, 1231-45	9.7	691
32	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
31	Biochemie und Molekulargenetik 2001. <i>Nachrichten Aus Der Chemie</i> , 2002 , 50, 312-326	0.1	
30	Is mass spectrometry ready for proteome-wide protein expression analysis?. <i>Genome Biology</i> , 2002 , 3, COMMENT2008	18.3	12
29	Labile sulfogroup allows differentiation of sulfotyrosine and phosphotyrosine in peptides. <i>Journal of Mass Spectrometry</i> , 2001 , 36, 832-3	2.2	26
28	Pre-mRNA splicing and mRNA export linked by direct interactions between UAP56 and Aly. <i>Nature</i> , 2001 , 413, 644-7	50.4	306
27	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
26	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
25	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
24	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
23	Model for stathmin/OP18 binding to tubulin. <i>EMBO Journal</i> , 2000 , 19, 213-22	13	59

22	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
21	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
20	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
19	Cdc14 phosphatase directs centrosome re-duplication at the meiosis I to meiosis II transition in budding yeast. <i>Wellcome Open Research</i> , 2, 2	4.8	8
18	The C-terminal helix of BubR1 is essential for CENP-E-dependent chromosome alignment		3
17	A folded conformation of MukBEF and Cohesin		2
16	A generic solution for quantifying cross-linked peptides using software Skyline. <i>Protocol Exchange</i> ,		6
15	Quantitative cross-linking/mass spectrometry using isotope-labeled cross-linkers and MaxQuant		2
14	In-cell architecture of an actively transcribing-translating expressome		9
13	A Structure-Based Mechanism for DNA Entry into the Cohesin Ring		5
12	Stress-induced translation inhibition through rapid displacement of scanning initiation factors		2
11	Reliable identification of protein-protein interactions by crosslinking mass spectrometry		3
10	Cryo-EM reveals the complex architecture of dynactin's shoulder and pointed end		2
9	In-Search Assignment of Monoisotopic Peaks Improves the Identification of Cross-Linked Peptides		2
8	An integrated workflow for crosslinking mass spectrometry		7
7	Cross-linking/Mass Spectrometry: A Community-Wide, Comparative Study Towards Establishing Best Practice Guidelines		4
6	xiView: A common platform for the downstream analysis of Crosslinking Mass Spectrometry data		18
5	Quantitative Cross-Linking/Mass Spectrometry Reveals Subtle Protein Conformational Changes		4

- | | | |
|---|--|---|
| 4 | Structure of complement C3(H2O) revealed by quantitative cross-linking/mass spectrometry and modeling | 1 |
| 3 | A systematic analysis of <i>Trypanosoma brucei</i> chromatin factors identifies novel protein interaction networks associated with sites of transcription initiation and termination | 2 |
| 2 | Molecular Basis for CPC-Sgo1 Interaction: Implications for Centromere Localisation and Function of the CPC | 2 |
| 1 | Mpe1 senses the polyadenylation signal in pre-mRNA to control cleavage and polyadenylation | 3 |