

# Brian T Chait

## List of Publications by Year in descending order

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136  
papers

20,031  
citations

18482

62  
h-index

11607

135  
g-index

155  
all docs

155  
docs citations

155  
times ranked

22775  
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive structure and functional adaptations of the yeast nuclear pore complex. <i>Cell</i> , 2022, 185, 361-378.e25.	28.9	87
2	Proteomic elucidation of the targets and primary functions of the picornavirus 2A protease. <i>Journal of Biological Chemistry</i> , 2022, 298, 101882.	3.4	10
3	Protection of nascent DNA at stalled replication forks is mediated by phosphorylation of RIF1 intrinsically disordered region. <i>ELife</i> , 2022, 11, .	6.0	11
4	Native Mass Spectrometry-Based Screening for Optimal Sample Preparation in Single-Particle Cryo-EM. <i>Structure</i> , 2021, 29, 186-195.e6.	3.3	19
5	Dissecting the Structural Dynamics of the Nuclear Pore Complex. <i>Molecular Cell</i> , 2021, 81, 153-165.e7.	9.7	31
6	Biochemical reconstitutions reveal principles of human $\hat{\beta}$ -TuRC assembly and function. <i>Journal of Cell Biology</i> , 2021, 220, .	5.2	23
7	Malaria parasites use a soluble RhopH complex for erythrocyte invasion and an integral form for nutrient uptake. <i>ELife</i> , 2021, 10, .	6.0	35
8	Structural basis for transcription complex disruption by the Mfd translocase. <i>ELife</i> , 2021, 10, .	6.0	36
9	Dynamic regulation of TFH selection during the germinal centre reaction. <i>Nature</i> , 2021, 591, 458-463.	27.8	58
10	Structural basis for backtracking by the SARS-CoV-2 replication-transcription complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	76
11	Analysis of the mechanosensor channel functionality of TACAN. <i>ELife</i> , 2021, 10, .	6.0	24
12	Genome-wide gene expression tuning reveals diverse vulnerabilities of <i>M. tuberculosis</i> . <i>Cell</i> , 2021, 184, 4579-4592.e24.	28.9	131
13	Measuring in vivo protein turnover and exchange in yeast macromolecular assemblies. <i>STAR Protocols</i> , 2021, 2, 100800.	1.2	3
14	A Polycomb repressive complex is required for RNAi-mediated heterochromatin formation and dynamic distribution of nuclear bodies. <i>Nucleic Acids Research</i> , 2021, 49, 5407-5425.	14.5	27
15	Highly synergistic combinations of nanobodies that target SARS-CoV-2 and are resistant to escape. <i>ELife</i> , 2021, 10, .	6.0	36
16	Asymmetric Molecular Architecture of the Human $\hat{\beta}$ -Tubulin Ring Complex. <i>Cell</i> , 2020, 180, 165-175.e16.	28.9	111
17	Long-range intramolecular allostery and regulation in the dynein-like AAA protein Mdn1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 18459-18469.	7.1	6
18	Structural Basis for Helicase-Polymerase Coupling in the SARS-CoV-2 Replication-Transcription Complex. <i>Cell</i> , 2020, 182, 1560-1573.e13.	28.9	360

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19	Affinity proteomic dissection of the human nuclear cap-binding complex interactome. <i>Nucleic Acids Research</i> , 2020, 48, 10456-10469.	14.5	18
20	Stepwise Promoter Melting by Bacterial RNA Polymerase. <i>Molecular Cell</i> , 2020, 78, 275-288.e6.	9.7	88
21	Integrative structure and function of the yeast exocyst complex. <i>Protein Science</i> , 2020, 29, 1486-1501.	7.6	29
22	National Cancer Institute Think-Tank Meeting Report on Proteomic Cartography and Biomarkers at the Single-Cell Level: Interrogation of Premalignant Lesions. <i>Journal of Proteome Research</i> , 2020, 19, 1900-1912.	3.7	8
23	Native Mass Spectrometry Analysis of Affinity-Captured Endogenous Yeast RNA Exosome Complexes. <i>Methods in Molecular Biology</i> , 2020, 2062, 357-382.	0.9	23
24	Embryonic and Fetal Human Hemoglobins: Structures, Oxygen Binding, and Physiological Roles. <i>Sub-Cellular Biochemistry</i> , 2020, 94, 275-296.	2.4	7
25	Crippling life support for SARS-CoV-2 and other viruses through synthetic lethality. <i>Journal of Cell Biology</i> , 2020, 219, .	5.2	20
26	Structural basis of substrate recognition by a polypeptide processing and secretion transporter. <i>ELife</i> , 2020, 9, .	6.0	25
27	Interactions of nuclear transport factors and surface-conjugated FG nucleoporins: Insights and limitations. <i>PLoS ONE</i> , 2019, 14, e0217897.	2.5	9
28	Palaeoproteomics resolves sloth relationships. <i>Nature Ecology and Evolution</i> , 2019, 3, 1121-1130.	7.8	91
29	Mcm10 has potent strand-annealing activity and limits translocase-mediated fork regression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 798-803.	7.1	35
30	Modular assembly of the nucleolar pre-60S ribosomal subunit. <i>Nature</i> , 2018, 556, 126-129.	27.8	127
31	Integrative structure and functional anatomy of a nuclear pore complex. <i>Nature</i> , 2018, 555, 475-482.	27.8	435
32	A Chemical Proteomics Approach to Reveal Direct Protein-Protein Interactions in Living Cells. <i>Cell Chemical Biology</i> , 2018, 25, 110-120.e3.	5.2	62
33	The Chromatin Reader ZMYND8 Regulates Igh Enhancers to Promote Immunoglobulin Class Switch Recombination. <i>Molecular Cell</i> , 2018, 72, 636-649.e8.	9.7	34
34	Architecture of Pol II(G) and molecular mechanism of transcription regulation by Gdown1. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 859-867.	8.2	31
35	Dissection of affinity captured LINE-1 macromolecular complexes. <i>ELife</i> , 2018, 7, .	6.0	63
36	Nuclear ARP2/3 drives DNA break clustering for homology-directed repair. <i>Nature</i> , 2018, 559, 61-66.	27.8	304

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37	Mechanisms of opening and closing of the bacterial replicative helicase. <i>ELife</i> , 2018, 7, .	6.0	16
38	The replication initiator of the cholera pathogen's second chromosome shows structural similarity to plasmid initiators. <i>Nucleic Acids Research</i> , 2017, 45, gkw1288.	14.5	20
39	Gel filtration of dilute human embryonic hemoglobins reveals basis for their increased oxygen binding. <i>Analytical Biochemistry</i> , 2017, 519, 38-41.	2.4	6
40	Functional Plasticity of the AgrC Receptor Histidine Kinase Required for Staphylococcal Virulence. <i>Cell Chemical Biology</i> , 2017, 24, 76-86.	5.2	25
41	Lineage-specific proteins essential for endocytosis in trypanosomes. <i>Journal of Cell Science</i> , 2017, 130, 1379-1392.	2.0	16
42	The complete structure of the small-subunit processome. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 944-953.	8.2	114
43	The Trypanosome Exocyst: A Conserved Structure Revealing a New Role in Endocytosis. <i>PLoS Pathogens</i> , 2017, 13, e1006063.	4.7	27
44	Structural basis of transcription arrest by coliphage HK022 Nun in an Escherichia coli RNA polymerase elongation complex. <i>ELife</i> , 2017, 6, .	6.0	120
45	UtpA and UtpB chaperone nascent pre-ribosomal RNA and U3 snoRNA to initiate eukaryotic ribosome assembly. <i>Nature Communications</i> , 2016, 7, 12090.	12.8	63
46	High-Efficiency Isolation of Nuclear Envelope Protein Complexes from Trypanosomes. <i>Methods in Molecular Biology</i> , 2016, 1411, 67-80.	0.9	31
47	Revealing Higher Order Protein Structure Using Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 952-965.	2.8	51
48	Phosphorylation-Dependent Targeting of <i>Tetrahymena</i> HP1 to Condensed Chromatin. <i>MSphere</i> , 2016, 1, .	2.9	4
49	Structure and Function of the Nuclear Pore Complex Cytoplasmic mRNA Export Platform. <i>Cell</i> , 2016, 167, 1215-1228.e25.	28.9	148
50	Developing genetic tools to exploit <i>Chaetomium thermophilum</i> for biochemical analyses of eukaryotic macromolecular assemblies. <i>Scientific Reports</i> , 2016, 6, 20937.	3.3	43
51	HIV host interactome revealed directly from infected cells. <i>Nature Microbiology</i> , 2016, 1, 16068.	13.3	49
52	Optimizing selection of large animals for antibody production by screening immune response to standard vaccines. <i>Journal of Immunological Methods</i> , 2016, 430, 56-60.	1.4	17
53	A Robust Workflow for Native Mass Spectrometric Analysis of Affinity-Isolated Endogenous Protein Assemblies. <i>Analytical Chemistry</i> , 2016, 88, 2799-2807.	6.5	21
54	Proteomics of HCV virions reveals an essential role for the nucleoporin Nup98 in virus morphogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2484-2489.	7.1	63

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55	Affinity proteomics to study endogenous protein complexes: Pointers, pitfalls, preferences and perspectives. <i>BioTechniques</i> , 2015, 58, 103-119.	1.8	49
56	Assembly and Molecular Architecture of the Phosphoinositide 3-Kinase p85 $\beta$ Homodimer. <i>Journal of Biological Chemistry</i> , 2015, 290, 30390-30405.	3.4	25
57	Architecture of a Host-Parasite Interface: Complex Targeting Mechanisms Revealed Through Proteomics. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1911-1926.	3.8	45
58	Beclin 1-Vps34 complex architecture: Understanding the nuts and bolts of therapeutic targets. <i>Frontiers in Biology</i> , 2015, 10, 398-426.	0.7	48
59	Rapid, optimized interactomic screening. <i>Nature Methods</i> , 2015, 12, 553-560.	19.0	68
60	A strategy for dissecting the architectures of native macromolecular assemblies. <i>Nature Methods</i> , 2015, 12, 1135-1138.	19.0	113
61	The architecture of a eukaryotic replisome. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 976-982.	8.2	161
62	$^{125}$ I-Lactoglobulin detected in human milk forms noncovalent complexes with maltooligosaccharides as revealed by chip-nanoelectrospray high-resolution tandem mass spectrometry. <i>Amino Acids</i> , 2015, 47, 2399-2407.	2.7	1
63	Chemical proteomics reveals a $^{125}$ I-H2AX-53BP1 interaction in the DNA damage response. <i>Nature Chemical Biology</i> , 2015, 11, 807-814.	8.0	96
64	NPC Mimics. <i>Methods in Cell Biology</i> , 2014, 122, 379-393.	1.1	4
65	Structural Characterization by Cross-linking Reveals the Detailed Architecture of a Coatamer-related Heptameric Module from the Nuclear Pore Complex. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2927-2943.	3.8	152
66	Reconstitution of active human core Mediator complex reveals a critical role of the MED14 subunit. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 1028-1034.	8.2	109
67	Integrative Structure-Function Mapping of the Nucleoporin Nup133 Suggests a Conserved Mechanism for Membrane Anchoring of the Nuclear Pore Complex. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2911-2926.	3.8	67
68	Molecular Architecture and Function of the SEA Complex, a Modulator of the TORC1 Pathway. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2855-2870.	3.8	64
69	Nrbf2 Protein Suppresses Autophagy by Modulating Atg14L Protein-containing Beclin 1-Vps34 Complex Architecture and Reducing Intracellular Phosphatidylinositol-3 Phosphate Levels. <i>Journal of Biological Chemistry</i> , 2014, 289, 26021-26037.	3.4	60
70	Method for identifying phosphorylated substrates of specific cyclin/cyclin-dependent kinase complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11323-11328.	7.1	28
71	A Pipeline for Determining Protein-Protein Interactions and Proximities in the Cellular Milieu. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2824-2835.	3.8	45
72	A robust pipeline for rapid production of versatile nanobody repertoires. <i>Nature Methods</i> , 2014, 11, 1253-1260.	19.0	391

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73	Affinity Proteomics Reveals Human Host Factors Implicated in Discrete Stages of LINE-1 Retrotransposition. <i>Cell</i> , 2013, 155, 1034-1048.	28.9	190
74	Activation of DSB Processing Requires Phosphorylation of CtIP by ATR. <i>Molecular Cell</i> , 2013, 49, 657-667.	9.7	112
75	Rif1 Prevents Resection of DNA Breaks and Promotes Immunoglobulin Class Switching. <i>Science</i> , 2013, 339, 711-715.	12.6	356
76	Examining post-translational modification-mediated protein-protein interactions using a chemical proteomics approach. <i>Protein Science</i> , 2013, 22, 287-295.	7.6	33
77	The nuclear basket proteins Mlp1p and Mlp2p are part of a dynamic interactome including Esc1p and the proteasome. <i>Molecular Biology of the Cell</i> , 2013, 24, 3920-3938.	2.1	100
78	Proteomics on the rims: insights into the biology of the nuclear envelope and flagellar pocket of trypanosomes. <i>Parasitology</i> , 2012, 139, 1158-1167.	1.5	11
79	Structure-function mapping of a heptameric module in the nuclear pore complex. <i>Journal of Cell Biology</i> , 2012, 196, 419-434.	5.2	110
80	Transcriptional Regulation by Pol II(G) Involving Mediator and Competitive Interactions of Gdown1 and TFIIIF with Pol II. <i>Molecular Cell</i> , 2012, 45, 51-63.	9.7	68
81	Improved methodology for the affinity isolation of human protein complexes expressed at near endogenous levels. <i>BioTechniques</i> , 2012, 0, 1-6.	1.8	48
82	High-Throughput, Single-Step Purification of Affinity-Tagged Protein Complexes. <i>FASEB Journal</i> , 2012, 26, .	0.5	0
83	Protein Arginine Methyltransferase Prmt5-Mep50 Methylates Histones H2A and H4 and the Histone Chaperone Nucleoplasmin in <i>Xenopus laevis</i> Eggs. <i>Journal of Biological Chemistry</i> , 2011, 286, 42221-42231.	3.4	49
84	Conjugation of Magnetic Beads for Immunopurification of Protein Complexes. <i>Cold Spring Harbor Protocols</i> , 2011, 2011, pdb.prot5610.	0.3	45
85	Mass Spectrometry in the Postgenomic Era. <i>Annual Review of Biochemistry</i> , 2011, 80, 239-246.	11.1	59
86	High-capacity ion trap coupled to a time-of-flight mass spectrometer for comprehensive linked scans with no scanning losses. <i>International Journal of Mass Spectrometry</i> , 2011, 301, 211-219.	1.5	5
87	Global Analysis of Cdc14 Phosphatase Reveals Diverse Roles in Mitotic Processes. <i>Journal of Biological Chemistry</i> , 2011, 286, 5434-5445.	3.4	64
88	Host Factors Associated with the Sindbis Virus RNA-Dependent RNA Polymerase: Role for G3BP1 and G3BP2 in Virus Replication. <i>Journal of Virology</i> , 2010, 84, 6720-6732.	3.4	101
89	<i>Escherichia coli</i> condensin MukB stimulates topoisomerase IV activity by a direct physical interaction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 18832-18837.	7.1	93
90	Evidence for a Shared Nuclear Pore Complex Architecture That Is Conserved from the Last Common Eukaryotic Ancestor. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2119-2130.	3.8	200

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91	Proteomic Studies of a Single CNS Synapse Type: The Parallel Fiber/Purkinje Cell Synapse. <i>PLoS Biology</i> , 2009, 7, e1000083.	5.6	59
92	Distinct regulation of autophagic activity by Atg14L and Rubicon associated with Beclin 1â€™phosphatidylinositol-3-kinase complex. <i>Nature Cell Biology</i> , 2009, 11, 468-476.	10.3	845
93	Rrp17p Is a Eukaryotic Exonuclease Required for 5â€™ End Processing of Pre-60S Ribosomal RNA. <i>Molecular Cell</i> , 2009, 36, 768-781.	9.7	83
94	Human Cytomegalovirus Protein UL38 Inhibits Host Cell Stress Responses by Antagonizing the Tuberous Sclerosis Protein Complex. <i>Cell Host and Microbe</i> , 2008, 3, 253-262.	11.0	175
95	Rapid Isolation and Identification of Bacteriophage T4-Encoded Modifications of <i>Escherichia coli</i> RNA Polymerase: A Generic Method to Study Bacteriophage/Host Interactions. <i>Journal of Proteome Research</i> , 2008, 7, 1244-1250.	3.7	14
96	Efficient Identification of Phosphorylation by Mass Spectrometric Phosphopeptide Fingerprinting. <i>Analytical Chemistry</i> , 2008, 80, 2419-2425.	6.5	15
97	Affinity Isolation and I-DIRT Mass Spectrometric Analysis of the <i>Escherichia coli</i> O157:H7 Sakai RNA Polymerase Complex. <i>Journal of Bacteriology</i> , 2008, 190, 1284-1289.	2.2	17
98	A novel high-capacity ion trap-quadrupole tandem mass spectrometer. <i>International Journal of Mass Spectrometry</i> , 2007, 268, 93-105.	1.5	6
99	Comprehensive analysis of diverse ribonucleoprotein complexes. <i>Nature Methods</i> , 2007, 4, 951-956.	19.0	253
100	Determining the architectures of macromolecular assemblies. <i>Nature</i> , 2007, 450, 683-694.	27.8	499
101	The molecular architecture of the nuclear pore complex. <i>Nature</i> , 2007, 450, 695-701.	27.8	947
102	Yng1 PHD Finger Binding to H3 Trimethylated at K4 Promotes NuA3 HAT Activity at K14 of H3 and Transcription at a Subset of Targeted ORFs. <i>Molecular Cell</i> , 2006, 24, 785-796.	9.7	283
103	Mass Spectrometry: Bottom-Up or Top-Down?. <i>Science</i> , 2006, 314, 65-66.	12.6	354
104	Simple fold composition and modular architecture of the nuclear pore complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 2172-2177.	7.1	243
105	The nuclear pore complexâ€™associated protein, Mlp2p, binds to the yeast spindle pole body and promotes its efficient assembly. <i>Journal of Cell Biology</i> , 2005, 170, 225-235.	5.2	81
106	Fluorescent Proteins as Proteomic Probes. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1933-1941.	3.8	225
107	I-DIRT, A General Method for Distinguishing between Specific and Nonspecific Protein Interactions. <i>Journal of Proteome Research</i> , 2005, 4, 1752-1756.	3.7	134
108	A Method for the Rapid and Efficient Elution of Native Affinity-Purified Protein A Tagged Complexes. <i>Journal of Proteome Research</i> , 2005, 4, 2250-2256.	3.7	16

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109	POT1-interacting protein PIP1: a telomere length regulator that recruits POT1 to the TIN2/TRF1 complex. <i>Genes and Development</i> , 2004, 18, 1649-1654.	5.9	383
110	TIN2 Binds TRF1 and TRF2 Simultaneously and Stabilizes the TRF2 Complex on Telomeres. <i>Journal of Biological Chemistry</i> , 2004, 279, 47264-47271.	3.4	275
111	Components of Coated Vesicles and Nuclear Pore Complexes Share a Common Molecular Architecture. <i>PLoS Biology</i> , 2004, 2, e380.	5.6	357
112	Analysis of Protein Phosphorylation by Hypothesis-Driven Multiple-Stage Mass Spectrometry. <i>Analytical Chemistry</i> , 2004, 76, 4472-4483.	6.5	72
113	Targeted Proteomic Study of the Cyclin-Cdk Module. <i>Molecular Cell</i> , 2004, 14, 699-711.	9.7	110
114	A Modular Cross-Linking Approach for Exploring Protein Interactions. <i>Journal of the American Chemical Society</i> , 2003, 125, 2416-2425.	13.7	189
115	Detection of secreted peptides by using hypothesis-driven multistage mass spectrometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 2795-2800.	7.1	108
116	X-ray structure of a CIC chloride channel at 3.0 Å... reveals the molecular basis of anion selectivity. <i>Nature</i> , 2002, 415, 287-294.	27.8	1,529
117	Automatic Identification of Proteins with a MALDI-Quadrupole Ion Trap Mass Spectrometer. <i>Analytical Chemistry</i> , 2001, 73, 5066-5077.	6.5	144
118	Mass Spectrometry as a Tool for Protein Crystallography. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2001, 30, 67-85.	18.3	62
119	Nup2p Dynamically Associates with the Distal Regions of the Yeast Nuclear Pore Complex. <i>Journal of Cell Biology</i> , 2001, 153, 1465-1478.	5.2	149
120	A Robust, Detergent-Friendly Method for Mass Spectrometric Analysis of Integral Membrane Proteins. <i>Analytical Chemistry</i> , 2000, 72, 5655-5658.	6.5	164
121	Rapidly switchable matrix-assisted laser desorption/ionization and electrospray quadrupole-time-of-flight mass spectrometry for protein identification. <i>Journal of the American Society for Mass Spectrometry</i> , 2000, 11, 493-504.	2.8	119
122	The Yeast Nuclear Pore Complex. <i>Journal of Cell Biology</i> , 2000, 148, 635-652.	5.2	1,329
123	Immunoglobulin motif DNA recognition and heterodimerization of the PEBP2/CBF Runt domain. <i>Nature Structural Biology</i> , 1999, 6, 615-619.	9.7	97
124	Modulation of GT-1 DNA-binding activity by calcium-dependent phosphorylation. <i>Plant Molecular Biology</i> , 1999, 40, 373-386.	3.9	42
125	Structural Conservation in Prokaryotic and Eukaryotic Potassium Channels. <i>Science</i> , 1998, 280, 106-109.	12.6	404
126	Identification and Characterization of Posttranslational Modifications of Proteins by MALDI Ion Trap Mass Spectrometry. <i>Analytical Chemistry</i> , 1997, 69, 4002-4009.	6.5	175



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127	Influence of Matrix Solution Conditions on the MALDI-MS Analysis of Peptides and Proteins. <i>Analytical Chemistry</i> , 1996, 68, 31-37.	6.5	520
128	Structural similarity between TAFs and the heterotetrameric core of the histone octamer. <i>Nature</i> , 1996, 380, 316-322.	27.8	251
129	Human leptin characterization. <i>Nature</i> , 1996, 382, 589-589.	27.8	88
130	Probing the solution structure of the DNA-binding protein Max by a combination of proteolysis and mass spectrometry. <i>Protein Science</i> , 1995, 4, 1088-1099.	7.6	149
131	Matrix-assisted laser desorption mass spectrometric peptide mapping of proteins separated by two-dimensional gel electrophoresis: Determination of phosphorylation in synapsin I. <i>Protein Science</i> , 1994, 3, 677-686.	7.6	53
132	Two-step selective formation of three disulfide bridges in the synthesis of the C-terminal epidermal growth factor-like domain in human blood coagulation factor IX. <i>Protein Science</i> , 1994, 3, 1267-1275.	7.6	57
133	Mass spectrometry – a useful tool for the protein X-ray crystallographer and NMR spectroscopist. <i>Structure</i> , 1994, 2, 465-467.	3.3	29
134	Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry of Biopolymers. <i>Analytical Chemistry</i> , 1991, 63, 1193A-1203A.	6.5	1,326
135	Observation of the heme-globin complex in native myoglobin by electrospray-ionization mass spectrometry. <i>Journal of the American Chemical Society</i> , 1991, 113, 8534-8535.	13.7	451
136	Probing conformational changes in proteins by mass spectrometry. <i>Journal of the American Chemical Society</i> , 1990, 112, 9012-9013.	13.7	607