

Brian T Chait

List of Publications by Year in Descending Order

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

138
papers

16,374
citations

58
h-index

127
g-index

154
ext. papers

18,541
ext. citations

14.5
avg, IF

6.44
L-index

#	Paper	IF	Citations
138	Proteomic elucidation of the targets and primary functions of the picornavirus 2A protease.. <i>Journal of Biological Chemistry</i> , 2022 , 101882	5.4	1
137	Comprehensive structure and functional adaptations of the yeast nuclear pore complex.. <i>Cell</i> , 2021 ,	56.2	18
136	Highly synergistic combinations of nanobodies that target SARS-CoV-2 and are resistant to escape. <i>ELife</i> , 2021 , 10,	8.9	3
135	Structural basis for backtracking by the SARS-CoV-2 replication-transcription complex 2021 ,		8
134	Nanobody Repertoires for Exposing Vulnerabilities of SARS-CoV-2 2021 ,		4
133	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,	11.5	29
132	Native Mass Spectrometry-Based Screening for Optimal Sample Preparation in Single-Particle Cryo-EM. <i>Structure</i> , 2021 , 29, 186-195.e6	5.2	10
131	Dissecting the Structural Dynamics of the Nuclear Pore Complex. <i>Molecular Cell</i> , 2021 , 81, 153-165.e7	17.6	11
130	Biochemical reconstitutions reveal principles of human β TuRC assembly and function. <i>Journal of Cell Biology</i> , 2021 , 220,	7.3	9
129	Malaria parasites use a soluble RhopH complex for erythrocyte invasion and an integral form for nutrient uptake. <i>ELife</i> , 2021 , 10,	8.9	13
128	Structural basis for transcription complex disruption by the Mfd translocase. <i>ELife</i> , 2021 , 10,	8.9	14
127	Dynamic regulation of T selection during the germinal centre reaction. <i>Nature</i> , 2021 , 591, 458-463	50.4	19
126	Analysis of the mechanosensor channel functionality of TACAN. <i>ELife</i> , 2021 , 10,	8.9	7
125	Genome-wide gene expression tuning reveals diverse vulnerabilities of M. <i>tuberculosis</i> . <i>Cell</i> , 2021 , 184, 4579-4592.e24	56.2	27
124	Measuring protein turnover and exchange in yeast macromolecular assemblies. <i>STAR Protocols</i> , 2021 , 2, 100800	1.4	0
123	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	20.1	6
122	Stepwise Promoter Melting by Bacterial RNA Polymerase. <i>Molecular Cell</i> , 2020 , 78, 275-288.e6	17.6	43

121	Integrative structure and function of the yeast exocyst complex. <i>Protein Science</i> , 2020 , 29, 1486-1501	6.3	10
120	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	5.6	4
119	Structural basis of substrate recognition by a polypeptide processing and secretion transporter. <i>ELife</i> , 2020 , 9,	8.9	17
118	Native Mass Spectrometry Analysis of Affinity-Captured Endogenous Yeast RNA Exosome Complexes. <i>Methods in Molecular Biology</i> , 2020 , 2062, 357-382	1.4	11
117	Embryonic and Fetal Human Hemoglobins: Structures, Oxygen Binding, and Physiological Roles. <i>Sub-Cellular Biochemistry</i> , 2020 , 94, 275-296	5.5	3
116	Crippling life support for SARS-CoV-2 and other viruses through synthetic lethality. <i>Journal of Cell Biology</i> , 2020 , 219,	7.3	9
115	Structural basis for helicase-polymerase coupling in the SARS-CoV-2 replication-transcription complex 2020 ,		5
114	Asymmetric Molecular Architecture of the Human β Tubulin Ring Complex. <i>Cell</i> , 2020 , 180, 165-175.e16	56.2	56
113	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	11.5	2
112	Structural Basis for Helicase-Polymerase Coupling in the SARS-CoV-2 Replication-Transcription Complex. <i>Cell</i> , 2020 , 182, 1560-1573.e13	56.2	191
111	Affinity proteomic dissection of the human nuclear cap-binding complex interactome. <i>Nucleic Acids Research</i> , 2020 , 48, 10456-10469	20.1	7
110	Interactions of nuclear transport factors and surface-conjugated FG nucleoporins: Insights and limitations. <i>PLoS ONE</i> , 2019 , 14, e0217897	3.7	4
109	Palaeoproteomics resolves sloth relationships. <i>Nature Ecology and Evolution</i> , 2019 , 3, 1121-1130	12.3	47
108	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	11.5	22
107	Modular assembly of the nucleolar pre-60S ribosomal subunit. <i>Nature</i> , 2018 , 556, 126-129	50.4	65
106	Integrative structure and functional anatomy of a nuclear pore complex. <i>Nature</i> , 2018 , 555, 475-482	50.4	280
105	Nuclear ARP2/3 drives DNA break clustering for homology-directed repair. <i>Nature</i> , 2018 , 559, 61-66	50.4	164
104	Mechanisms of opening and closing of the bacterial replicative helicase. <i>ELife</i> , 2018 , 7,	8.9	9

103	A Chemical Proteomics Approach to Reveal Direct Protein-Protein Interactions in Living Cells. <i>Cell Chemical Biology</i> , 2018 , 25, 110-120.e3	8.2	41
102	The Chromatin Reader ZMYND8 Regulates Igh Enhancers to Promote Immunoglobulin Class Switch Recombination. <i>Molecular Cell</i> , 2018 , 72, 636-649.e8	17.6	15
101	Architecture of Pol II(G) and molecular mechanism of transcription regulation by Gdown1. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 859-867	17.6	16
100	Dissection of affinity captured LINE-1 macromolecular complexes. <i>ELife</i> , 2018 , 7,	8.9	38
99	Gel filtration of dilute human embryonic hemoglobins reveals basis for their increased oxygen binding. <i>Analytical Biochemistry</i> , 2017 , 519, 38-41	3.1	6
98	Functional Plasticity of the AgrC Receptor Histidine Kinase Required for Staphylococcal Virulence. <i>Cell Chemical Biology</i> , 2017 , 24, 76-86	8.2	18
97	Lineage-specific proteins essential for endocytosis in trypanosomes. <i>Journal of Cell Science</i> , 2017 , 130, 1379-1392	5.3	11
96	The complete structure of the small-subunit processome. <i>Nature Structural and Molecular Biology</i> , 2017 , 24, 944-953	17.6	76
95	The Trypanosome Exocyst: A Conserved Structure Revealing a New Role in Endocytosis. <i>PLoS Pathogens</i> , 2017 , 13, e1006063	7.6	19
94	Structural basis of transcription arrest by coliphage HK022 Nun in an RNA polymerase elongation complex. <i>ELife</i> , 2017 , 6,	8.9	70
93	The replication initiator of the cholera pathogen's second chromosome shows structural similarity to plasmid initiators. <i>Nucleic Acids Research</i> , 2017 , 45, 3724-3737	20.1	13
92	Structure and Function of the Nuclear Pore Complex Cytoplasmic mRNA Export Platform. <i>Cell</i> , 2016 , 167, 1215-1228.e25	56.2	110
91	Developing genetic tools to exploit <i>Chaetomium thermophilum</i> for biochemical analyses of eukaryotic macromolecular assemblies. <i>Scientific Reports</i> , 2016 , 6, 20937	4.9	29
90	HIV-host interactome revealed directly from infected cells. <i>Nature Microbiology</i> , 2016 , 1, 16068	26.6	33
89	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	2.5	11
88	A Robust Workflow for Native Mass Spectrometric Analysis of Affinity-Isolated Endogenous Protein Assemblies. <i>Analytical Chemistry</i> , 2016 , 88, 2799-807	7.8	19
87	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, 2484-9	11.5	52
86	UtpA and UtpB chaperone nascent pre-ribosomal RNA and U3 snoRNA to initiate eukaryotic ribosome assembly. <i>Nature Communications</i> , 2016 , 7, 12090	17.4	43

85	High-Efficiency Isolation of Nuclear Envelope Protein Complexes from Trypanosomes. <i>Methods in Molecular Biology</i> , 2016 , 1411, 67-80	1.4	19
84	Revealing Higher Order Protein Structure Using Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2016 , 27, 952-65	3.5	45
83	Phosphorylation-Dependent Targeting of Tetrahymena HP1 to Condensed Chromatin. <i>MSphere</i> , 2016 , 1,	5	2
82	Rapid, optimized interactomic screening. <i>Nature Methods</i> , 2015 , 12, 553-60	21.6	53
81	A strategy for dissecting the architectures of native macromolecular assemblies. <i>Nature Methods</i> , 2015 , 12, 1135-8	21.6	94
80	The architecture of a eukaryotic replisome. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 976-82	17.6	127
79	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, 2399-407	3.5	1
78	Chemical proteomics reveals a H2AX-53BP1 interaction in the DNA damage response. <i>Nature Chemical Biology</i> , 2015 , 11, 807-14	11.7	66
77	Affinity proteomics to study endogenous protein complexes: pointers, pitfalls, preferences and perspectives. <i>BioTechniques</i> , 2015 , 58, 103-19	2.5	39
76	Assembly and Molecular Architecture of the Phosphoinositide 3-Kinase p85 Homodimer. <i>Journal of Biological Chemistry</i> , 2015 , 290, 30390-405	5.4	17
75	Architecture of a Host-Parasite Interface: Complex Targeting Mechanisms Revealed Through Proteomics. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 1911-26	7.6	34
74	BECLIN 1-VPS34 COMPLEX ARCHITECTURE: UNDERSTANDING THE NUTS AND BOLTS OF THERAPEUTIC TARGETS. <i>Frontiers in Biology</i> , 2015 , 10, 398-426		40
73	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	5.4	53
72	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, 11323-8	11.5	19
71	A pipeline for determining protein-protein interactions and proximities in the cellular milieu. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 2824-35	7.6	33
70	A robust pipeline for rapid production of versatile nanobody repertoires. <i>Nature Methods</i> , 2014 , 11, 1253-60		253
69	NPC mimics: probing the mechanism of nucleocytoplasmic transport. <i>Methods in Cell Biology</i> , 2014 , 122, 379-93	1.8	1
68	Structural characterization by cross-linking reveals the detailed architecture of a coatomer-related heptameric module from the nuclear pore complex. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 2927-43	7.6	122

67	Reconstitution of active human core Mediator complex reveals a critical role of the MED14 subunit. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 1028-34	17.6	78
66	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, 2911-26	7.6	54
65	Molecular architecture and function of the SEA complex, a modulator of the TORC1 pathway. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 2855-70	7.6	52
64	Affinity proteomics reveals human host factors implicated in discrete stages of LINE-1 retrotransposition. <i>Cell</i> , 2013 , 155, 1034-48	56.2	133
63	Activation of DSB processing requires phosphorylation of CtIP by ATR. <i>Molecular Cell</i> , 2013 , 49, 657-67	17.6	95
62	Rif1 prevents resection of DNA breaks and promotes immunoglobulin class switching. <i>Science</i> , 2013 , 339, 711-5	33.3	304
61	Examining post-translational modification-mediated protein-protein interactions using a chemical proteomics approach. <i>Protein Science</i> , 2013 , 22, 287-95	6.3	27
60	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, 3920-38	3.5	80
59	Transcriptional regulation by Pol II(G) involving mediator and competitive interactions of Gdown1 and TFIIF with Pol II. <i>Molecular Cell</i> , 2012 , 45, 51-63	17.6	58
58	Improved methodology for the affinity isolation of human protein complexes expressed at near endogenous levels. <i>BioTechniques</i> , 2012 , 1-6	2.5	36
57	Proteomics on the rims: insights into the biology of the nuclear envelope and flagellar pocket of trypanosomes. <i>Parasitology</i> , 2012 , 139, 1158-67	2.7	10
56	Structure-function mapping of a heptameric module in the nuclear pore complex. <i>Journal of Cell Biology</i> , 2012 , 196, 419-34	7.3	95
55	Conjugation of magnetic beads for immunopurification of protein complexes. <i>Cold Spring Harbor Protocols</i> , 2011 , 2011, pdb.prot5610	1.2	33
54	Mass spectrometry in the postgenomic era. <i>Annual Review of Biochemistry</i> , 2011 , 80, 239-46	29.1	52
53	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	1.9	4
52	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	5.4	48
51	Global analysis of Cdc14 phosphatase reveals diverse roles in mitotic processes. <i>Journal of Biological Chemistry</i> , 2011 , 286, 5434-45	5.4	55
50	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, 6720-32	6.6	81

49	Escherichia coli 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, 18832-7	11.5	75
48	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, 2119-30	7.6	169
47	Proteomic studies of a single CNS synapse type: the parallel fiber/purkinje cell synapse. <i>PLoS Biology</i> , 2009 , 7, e83	9.7	54
46	Distinct regulation of autophagic activity by Atg14L and Rubicon associated with Beclin 1-phosphatidylinositol-3-kinase complex. <i>Nature Cell Biology</i> , 2009 , 11, 468-76	23.4	725
45	Rrp17p is a eukaryotic exonuclease required for 5' end processing of Pre-60S ribosomal RNA. <i>Molecular Cell</i> , 2009 , 36, 768-81	17.6	64
44	Human cytomegalovirus protein UL38 inhibits host cell stress responses by antagonizing the tuberous sclerosis protein complex. <i>Cell Host and Microbe</i> , 2008 , 3, 253-62	23.4	149
43	Rapid isolation and identification of bacteriophage T4-encoded modifications of Escherichia coli RNA polymerase: a generic method to study bacteriophage/host interactions. <i>Journal of Proteome Research</i> , 2008 , 7, 1244-50	5.6	14
42	Efficient identification of phosphorylation by mass spectrometric phosphopeptide fingerprinting. <i>Analytical Chemistry</i> , 2008 , 80, 2419-25	7.8	13
41	Affinity isolation and I-DIRT mass spectrometric analysis of the Escherichia coli O157:H7 Sakai RNA polymerase complex. <i>Journal of Bacteriology</i> , 2008 , 190, 1284-9	3.5	17
40	A novel high-capacity ion trap-quadrupole tandem mass spectrometer. <i>International Journal of Mass Spectrometry</i> , 2007 , 268, 93-105	1.9	5
39	Comprehensive analysis of diverse ribonucleoprotein complexes. <i>Nature Methods</i> , 2007 , 4, 951-6	21.6	212
38	Determining the architectures of macromolecular assemblies. <i>Nature</i> , 2007 , 450, 683-94	50.4	437
37	The molecular architecture of the nuclear pore complex. <i>Nature</i> , 2007 , 450, 695-701	50.4	830
36	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, 2172-7	11.5	231
35	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	17.6	255
34	Chemistry. Mass spectrometry: bottom-up or top-down?. <i>Science</i> , 2006 , 314, 65-6	33.3	314
33	I-DIRT, a general method for distinguishing between specific and nonspecific protein interactions. <i>Journal of Proteome Research</i> , 2005 , 4, 1752-6	5.6	119
32	A method for the rapid and efficient elution of native affinity-purified protein A tagged complexes. <i>Journal of Proteome Research</i> , 2005 , 4, 2250-6	5.6	16

31	The nuclear pore complex-associated protein, Mlp2p, binds to the yeast spindle pole body and promotes its efficient assembly. <i>Journal of Cell Biology</i> , 2005 , 170, 225-35	7.3	68
30	Fluorescent proteins as proteomic probes. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 1933-41	7.6	202
29	POT1-interacting protein PIP1: a telomere length regulator that recruits POT1 to the TIN2/TRF1 complex. <i>Genes and Development</i> , 2004 , 18, 1649-54	12.6	318
28	TIN2 binds TRF1 and TRF2 simultaneously and stabilizes the TRF2 complex on telomeres. <i>Journal of Biological Chemistry</i> , 2004 , 279, 47264-71	5.4	229
27	Components of coated vesicles and nuclear pore complexes share a common molecular architecture. <i>PLoS Biology</i> , 2004 , 2, e380	9.7	318
26	Analysis of protein phosphorylation by hypothesis-driven multiple-stage mass spectrometry. <i>Analytical Chemistry</i> , 2004 , 76, 4472-83	7.8	66
25	Targeted proteomic study of the cyclin-Cdk module. <i>Molecular Cell</i> , 2004 , 14, 699-711	17.6	100
24	A modular cross-linking approach for exploring protein interactions. <i>Journal of the American Chemical Society</i> , 2003 , 125, 2416-25	16.4	172
23	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, 2795-800	11.5	98
22	X-ray structure of a CLC chloride channel at 3.0 Å reveals the molecular basis of anion selectivity. <i>Nature</i> , 2002 , 415, 287-94	50.4	1364
21	Mass spectrometry as a tool for protein crystallography. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2001 , 30, 67-85		59
20	Nup2p dynamically associates with the distal regions of the yeast nuclear pore complex. <i>Journal of Cell Biology</i> , 2001 , 153, 1465-78	7.3	137
19	Automatic identification of proteins with a MALDI-quadrupole ion trap mass spectrometer. <i>Analytical Chemistry</i> , 2001 , 73, 5066-77	7.8	135
18	A robust, detergent-friendly method for mass spectrometric analysis of integral membrane proteins. <i>Analytical Chemistry</i> , 2000 , 72, 5655-8	7.8	149
17	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	3.5	114
16	The yeast nuclear pore complex: composition, architecture, and transport mechanism. <i>Journal of Cell Biology</i> , 2000 , 148, 635-51	7.3	1207
15	Immunoglobulin motif DNA recognition and heterodimerization of the PEBP2/CBF Runt domain. <i>Nature Structural Biology</i> , 1999 , 6, 615-9		86
14	Modulation of GT-1 DNA-binding activity by calcium-dependent phosphorylation. <i>Plant Molecular Biology</i> , 1999 , 40, 373-86	4.6	33

13	Structural conservation in prokaryotic and eukaryotic potassium channels. <i>Science</i> , 1998 , 280, 106-9	33.3	371
12	Identification and characterization of posttranslational modifications of proteins by MALDI ion trap mass spectrometry. <i>Analytical Chemistry</i> , 1997 , 69, 4002-9	7.8	164
11	Influence of matrix solution conditions on the MALDI-MS analysis of peptides and proteins. <i>Analytical Chemistry</i> , 1996 , 68, 31-7	7.8	485
10	Structural similarity between TAFs and the heterotetrameric core of the histone octamer. <i>Nature</i> , 1996 , 380, 316-22	50.4	232
9	Human leptin characterization. <i>Nature</i> , 1996 , 382, 589	50.4	72
8	Probing the solution structure of the DNA-binding protein Max by a combination of proteolysis and mass spectrometry. <i>Protein Science</i> , 1995 , 4, 1088-99	6.3	139
7	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, 677-86	6.3	46
6	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, 1267-75	6.3	55
5	Mass spectrometry--a useful tool for the protein X-ray crystallographer and NMR spectroscopist. <i>Structure</i> , 1994 , 2, 465-7	5.2	25
4	Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry of Biopolymers. <i>Analytical Chemistry</i> , 1991 , 63, 1193A-1203A	7.8	1220
3	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	16.4	396
2	Probing conformational changes in proteins by mass spectrometry. <i>Journal of the American Chemical Society</i> , 1990 , 112, 9012-9013	16.4	551
1	Modular assembly of the nucleolar large subunit processome		1