

Martin Beck

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.

108
papers

9,325
citations

49
h-index

96
g-index

131
ext. papers

11,633
ext. citations

17.4
avg, IF

6.32
L-index

#	Paper	IF	Citations
108	Co-translational assembly orchestrates competing biogenesis pathways.. <i>Nature Communications</i> , 2022 , 13, 1224	17.4	2
107	Nuclear pores dilate and constrict in cellulose. <i>Science</i> , 2021 , 374, eabd9776	33.3	32
106	A modular platform for automated cryo-FIB workflows.. <i>ELife</i> , 2021 , 10,	8.9	8
105	Profiling cellular diversity in sponges informs animal cell type and nervous system evolution. <i>Science</i> , 2021 , 374, 717-723	33.3	15
104	Coupling proteomics and metabolomics for the unsupervised identification of protein-metabolite interactions in <i>Chaetomium thermophilum</i> . <i>PLoS ONE</i> , 2021 , 16, e0254429	3.7	3
103	Cone-shaped HIV-1 capsids are transported through intact nuclear pores. <i>Cell</i> , 2021 , 184, 1032-1046.e1856.2		61
102	Three-dimensional superresolution fluorescence microscopy maps the variable molecular architecture of the nuclear pore complex. <i>Molecular Biology of the Cell</i> , 2021 , 32, 1523-1533	3.5	7
101	Bioaccumulation of therapeutic drugs by human gut bacteria. <i>Nature</i> , 2021 , 597, 533-538	50.4	29
100	Quality over quantity: Achieving Better Resolution in Subtomogram Averaging Using Less particles. <i>Microscopy and Microanalysis</i> , 2020 , 26, 2514-2514	0.5	
99	Proteome-Wide Structural Probing of Low-Abundant Protein Interactions by Cross-Linking Mass Spectrometry. <i>Analytical Chemistry</i> , 2020 , 92, 4016-4022	7.8	20
98	Selective autophagy degrades nuclear pore complexes. <i>Nature Cell Biology</i> , 2020 , 22, 159-166	23.4	48
97	Benchmarking tomographic acquisition schemes for high-resolution structural biology. <i>Nature Communications</i> , 2020 , 11, 876	17.4	18
96	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
95	Spatially resolved analysis of FFPE tissue proteomes by quantitative mass spectrometry. <i>Nature Protocols</i> , 2020 , 15, 2956-2979	18.8	10
94	In-cell architecture of the nuclear pore and snapshots of its turnover. <i>Nature</i> , 2020 , 586, 796-800	50.4	71
93	Structural impact of K63 ubiquitin on yeast translocating ribosomes under oxidative stress. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 22157-22166	11.5	7
92	In situ structural analysis of SARS-CoV-2 spike reveals flexibility mediated by three hinges. <i>Science</i> , 2020 , 370, 203-208	33.3	287

91	Nucleoporin Nup155 is part of the p53 network in liver cancer. <i>Nature Communications</i> , 2019 , 10, 2147	17.4	15
90	Disentangling Genetic and Environmental Effects on the Proteotypes of Individuals. <i>Cell</i> , 2019 , 177, 1308-1318.e10	13.1	10
89	Structure and Assembly of the Nuclear Pore Complex. <i>Annual Review of Biophysics</i> , 2019 , 48, 515-536	21.1	102
88	The Benefits of Cotranslational Assembly: A Structural Perspective. <i>Trends in Cell Biology</i> , 2019 , 29, 791-803	8.3	28
87	Nuclear Pores Assemble from Nucleoporin Condensates During Oogenesis. <i>Cell</i> , 2019 , 179, 671-686.e17	56.2	40
86	An ESCRT-LEM protein surveillance system is poised to directly monitor the nuclear envelope and nuclear transport system. <i>ELife</i> , 2019 , 8,	8.9	60
85	Quantitative Proteome Landscape of the NCI-60 Cancer Cell Lines. <i>Science</i> , 2019 , 21, 664-680	6.1	21
84	Kernporen-Transport maschinen in der Kernhülle und darüber hinaus. <i>BioSpektrum</i> , 2018 , 24, 149-151	0.1	
83	Systematic analysis of protein turnover in primary cells. <i>Nature Communications</i> , 2018 , 9, 689	17.4	145
82	Postmitotic nuclear pore assembly proceeds by radial dilation of small membrane openings. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 21-28	17.6	53
81	Spatial Tissue Proteomics Quantifies Inter- and Intratumor Heterogeneity in Hepatocellular Carcinoma (HCC). <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 810-825	7.6	41
80	Pervasive Protein Thermal Stability Variation during the Cell Cycle. <i>Cell</i> , 2018 , 173, 1495-1507.e18	56.2	109
79	Nuclear Pore Complex Components in the Malaria Parasite Plasmodium berghei. <i>Scientific Reports</i> , 2018 , 8, 11249	4.9	9
78	From the resolution revolution to evolution: structural insights into the evolutionary relationships between vesicle coats and the nuclear pore. <i>Current Opinion in Structural Biology</i> , 2018 , 52, 32-40	8.1	14
77	In situ architecture of the algal nuclear pore complex. <i>Nature Communications</i> , 2018 , 9, 2361	17.4	76
76	Quantifying compartment-associated variations of protein abundance in proteomics data. <i>Molecular Systems Biology</i> , 2018 , 14, e8131	12.2	10
75	Architecture of the yeast Elongator complex. <i>EMBO Reports</i> , 2017 , 18, 264-279	6.5	53
74	The nuclear pore complex: understanding its function through structural insight. <i>Nature Reviews Molecular Cell Biology</i> , 2017 , 18, 73-89	48.7	345

73	A short linear motif in scaffold Nup145C connects Y-complex with pre-assembled outer ring Nup82 complex. <i>Nature Communications</i> , 2017 , 8, 1107	17.4	23
72	Structural insights into transcription initiation by yeast RNA polymerase I. <i>EMBO Journal</i> , 2017 , 36, 2698-2709	13.7	45
71	Capturing protein communities by structural proteomics in a thermophilic eukaryote. <i>Molecular Systems Biology</i> , 2017 , 13, 936	12.2	79
70	Proteasomes tether to two distinct sites at the nuclear pore complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 13726-13731	11.5	79
69	Alterations of the nuclear transport system in hepatocellular carcinoma - New basis for therapeutic strategies. <i>Journal of Hepatology</i> , 2017 , 67, 1051-1061	13.4	18
68	Landscape of nuclear transport receptor cargo specificity. <i>Molecular Systems Biology</i> , 2017 , 13, 962	12.2	51
67	Structure of the ribosome post-recycling complex probed by chemical cross-linking and mass spectrometry. <i>Nature Communications</i> , 2016 , 7, 13248	17.4	22
66	The endosomal transcriptional regulator RNF11 integrates degradation and transport of EGFR. <i>Journal of Cell Biology</i> , 2016 , 215, 543-558	7.3	29
65	Toward the atomic structure of the nuclear pore complex: when top down meets bottom up. <i>Nature Structural and Molecular Biology</i> , 2016 , 23, 624-30	17.6	59
64	Spatiotemporal variation of mammalian protein complex stoichiometries. <i>Genome Biology</i> , 2016 , 17, 47	18.3	71
63	Structure Determination of the Nuclear Pore Complex with Three-Dimensional Cryo electron Microscopy. <i>Journal of Molecular Biology</i> , 2016 , 428, 2001-10	6.5	42
62	Influenza Polymerase Can Adopt an Alternative Configuration Involving a Radical Repacking of PB2 Domains. <i>Molecular Cell</i> , 2016 , 61, 125-37	17.6	92
61	The Combination of X-Ray Crystallography and Cryo-Electron Microscopy Provides Insight into the Overall Architecture of the Dodecameric Rvb1/Rvb2 Complex. <i>PLoS ONE</i> , 2016 , 11, e0146457	3.7	11
60	Nuclear pore assembly proceeds by an inside-out extrusion of the nuclear envelope. <i>ELife</i> , 2016 , 5,	8.9	107
59	Pre-assembled Nuclear Pores Insert into the Nuclear Envelope during Early Development. <i>Cell</i> , 2016 , 166, 664-678	56.2	67
58	Molecular architecture of the inner ring scaffold of the human nuclear pore complex. <i>Science</i> , 2016 , 352, 363-5	33.3	216
57	Automated structure modeling of large protein assemblies using crosslinks as distance restraints. <i>Nature Methods</i> , 2016 , 13, 515-20	21.6	44
56	Cryo-Electron Tomography: Can it Reveal the Molecular Sociology of Cells in Atomic Detail?. <i>Trends in Cell Biology</i> , 2016 , 26, 825-837	18.3	189

55	Histone Deacetylase Inhibitors (HDACi) Cause the Selective Depletion of Bromodomain Containing Proteins (BCPs). <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 1350-60	7.6	19
54	VESICULAR TRANSPORT. A structure of the COPI coat and the role of coat proteins in membrane vesicle assembly. <i>Science</i> , 2015 , 349, 195-8	33.3	116
53	Integrated Transcriptome and Proteome Analyses Reveal Organ-Specific Proteome Deterioration in Old Rats. <i>Cell Systems</i> , 2015 , 1, 224-37	10.6	120
52	In situ structural analysis of the human nuclear pore complex. <i>Nature</i> , 2015 , 526, 140-143	50.4	267
51	Architecture of TFIIC and its role in RNA polymerase III pre-initiation complex assembly. <i>Nature Communications</i> , 2015 , 6, 7387	17.4	40
50	Symportin 1 chaperones 5S RNP assembly during ribosome biogenesis by occupying an essential rRNA-binding site. <i>Nature Communications</i> , 2015 , 6, 6510	17.4	37
49	A network of SMG-8, SMG-9 and SMG-1 C-terminal insertion domain regulates UPF1 substrate recruitment and phosphorylation. <i>Nucleic Acids Research</i> , 2015 , 43, 7600-11	20.1	35
48	Characterization and quantification of proteins secreted by single human embryos prior to implantation. <i>EMBO Molecular Medicine</i> , 2015 , 7, 1465-79	12	33
47	Towards understanding nuclear pore complex architecture and dynamics in the age of integrative structural analysis. <i>Current Opinion in Cell Biology</i> , 2015 , 34, 31-8	9	56
46	Xlink Analyzer: software for analysis and visualization of cross-linking data in the context of three-dimensional structures. <i>Journal of Structural Biology</i> , 2015 , 189, 177-83	3.4	104
45	Structural basis for assembly and function of the Nup82 complex in the nuclear pore scaffold. <i>Journal of Cell Biology</i> , 2015 , 208, 283-97	7.3	52
44	Prosurvival function of the cellular apoptosis susceptibility/importin- β transport cycle is repressed by p53 in liver cancer. <i>Hepatology</i> , 2014 , 60, 884-95	11.2	25
43	Association of condensin with chromosomes depends on DNA binding by its HEAT-repeat subunits. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 560-8	17.6	86
42	Cellular disposal of miR23b by RAB27-dependent exosome release is linked to acquisition of metastatic properties. <i>Cancer Research</i> , 2014 , 74, 5758-71	10.1	195
41	Toward understanding the structure of the vertebrate nuclear pore complex. <i>Nucleus</i> , 2014 , 5, 119-23	3.9	9
40	The use of targeted proteomics to determine the stoichiometry of large macromolecular assemblies. <i>Methods in Cell Biology</i> , 2014 , 122, 117-46	1.8	21
39	An integrated approach for genome annotation of the eukaryotic thermophile <i>Chaetomium thermophilum</i> . <i>Nucleic Acids Research</i> , 2014 , 42, 13525-33	20.1	40
38	Integrated structural analysis of the human nuclear pore complex scaffold. <i>Cell</i> , 2013 , 155, 1233-43	56.2	273

37	Fourier ring correlation as a resolution criterion for super-resolution microscopy. <i>Journal of Structural Biology</i> , 2013 , 183, 363-367	3.4	167
36	Cell type-specific nuclear pores: a case in point for context-dependent stoichiometry of molecular machines. <i>Molecular Systems Biology</i> , 2013 , 9, 648	12.2	219
35	Facilitated aggregation of FG nucleoporins under molecular crowding conditions. <i>EMBO Reports</i> , 2013 , 14, 178-83	6.5	49
34	Protein interfaces of the conserved Nup84 complex from <i>Chaetomium thermophilum</i> shown by crosslinking mass spectrometry and electron microscopy. <i>Structure</i> , 2013 , 21, 1672-82	5.2	41
33	Structural probing of a protein phosphatase 2A network by chemical cross-linking and mass spectrometry. <i>Science</i> , 2012 , 337, 1348-52	33.3	323
32	High-throughput subtomogram alignment and classification by Fourier space constrained fast volumetric matching. <i>Journal of Structural Biology</i> , 2012 , 178, 152-64	3.4	42
31	False discovery rate estimation for cross-linked peptides identified by mass spectrometry. <i>Nature Methods</i> , 2012 , 9, 901-3	21.6	219
30	Absolute quantification of microbial proteomes at different states by directed mass spectrometry. <i>Molecular Systems Biology</i> , 2011 , 7, 510	12.2	80
29	Exploring the spatial and temporal organization of a cell's proteome. <i>Journal of Structural Biology</i> , 2011 , 173, 483-96	3.4	31
28	mProphet: automated data processing and statistical validation for large-scale SRM experiments. <i>Nature Methods</i> , 2011 , 8, 430-5	21.6	357
27	Comprehensive proteomics. <i>Current Opinion in Biotechnology</i> , 2011 , 22, 3-8	11.4	72
26	Template-free detection of macromolecular complexes in cryo electron tomograms. <i>Bioinformatics</i> , 2011 , 27, i69-76	7.2	25
25	The quantitative proteome of a human cell line. <i>Molecular Systems Biology</i> , 2011 , 7, 549	12.2	586
24	Probing native protein structures by chemical cross-linking, mass spectrometry, and bioinformatics. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 1634-49	7.6	367
23	Structure of the 26S proteasome from <i>Schizosaccharomyces pombe</i> at subnanometer resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 20992-7	11.5	124
22	Visual proteomics. <i>Methods in Enzymology</i> , 2010 , 483, 215-43	1.7	57
21	Architecture and molecular mechanism of PAN, the archaeal proteasome regulatory ATPase. <i>Journal of Biological Chemistry</i> , 2009 , 284, 22952-60	5.4	13
20	Proteome-wide cellular protein concentrations of the human pathogen <i>Leptospira interrogans</i> . <i>Nature</i> , 2009 , 460, 762-5	50.4	349

19	Visual proteomics of the human pathogen <i>Leptospira interrogans</i> . <i>Nature Methods</i> , 2009 , 6, 817-23	21.6	128
18	Identification of cross-linked peptides from large sequence databases. <i>Nature Methods</i> , 2008 , 5, 315-8	21.6	323
17	Structural and functional insights into nucleocytoplasmic transport. <i>Histology and Histopathology</i> , 2008 , 23, 1025-33	1.4	11
16	Snapshots of nuclear pore complexes in action captured by cryo-electron tomography. <i>Nature</i> , 2007 , 449, 611-5	50.4	302
15	Organization of actin networks in intact filopodia. <i>Current Biology</i> , 2007 , 17, 79-84	6.3	127
14	Luminal particles within cellular microtubules. <i>Journal of Cell Biology</i> , 2006 , 174, 759-65	7.3	95
13	Nuclear pore complex structure and dynamics revealed by cryoelectron tomography. <i>Science</i> , 2004 , 306, 1387-90	33.3	408
12	Exploring the Inner Space of Cells by Cryoelectron-Tomography. <i>Microscopy and Microanalysis</i> , 2004 , 10, 152-153	0.5	1
11	In situ architecture of the algal nuclear pore complex		1
10	Benchmarking tomographic acquisition schemes for high-resolution structural biology		1
9	Artificial intelligence reveals nuclear pore complexity		7
8	In cell architecture of the nuclear pore complex and snapshots of its turnover		4
7	In situ structural analysis of SARS-CoV-2 spike reveals flexibility mediated by three hinges		19
6	Cone-shaped HIV-1 capsids are transported through intact nuclear pores		6
5	Nuclear pores constrict upon energy depletion		14
4	3D super-resolution fluorescence microscopy maps the variable molecular architecture of the Nuclear Pore Complex		1
3	Rapid proteotyping reveals cancer biology and drug response determinants in the NCI-60 cells		3
2	A Modular Platform for Streamlining Automated Cryo-FIB Workflows		2

1 Co-translational assembly counteracts promiscuous interactions

1