

# Martin Beck

## List of Publications by Year in descending order

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Version: 2024-02-01

101  
papers

13,153  
citations

26567

56  
h-index

33814

99  
g-index

131  
all docs

131  
docs citations

131  
times ranked

15968  
citing authors

#	ARTICLE	IF	CITATIONS
1	Co-translational assembly orchestrates competing biogenesis pathways. <i>Nature Communications</i> , 2022, 13, 1224.	5.8	25
2	Conserved exchange of paralog proteins during neuronal differentiation. <i>Life Science Alliance</i> , 2022, 5, e202201397.	1.3	0
3	Conformational dynamics of nuclear pores. <i>FASEB Journal</i> , 2022, 36, .	0.2	0
4	AI-based structure prediction empowers integrative structural analysis of human nuclear pores. <i>Science</i> , 2022, 376, .	6.0	136
5	Cone-shaped HIV-1 capsids are transported through intact nuclear pores. <i>Cell</i> , 2021, 184, 1032-1046.e18.	13.5	179
6	Coupling proteomics and metabolomics for the unsupervised identification of proteinâ€™metabolite interactions in <i>Chaetomium thermophilum</i> . <i>PLoS ONE</i> , 2021, 16, e0254429.	1.1	5
7	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.	0.9	37
8	Bioaccumulation of therapeutic drugs by human gut bacteria. <i>Nature</i> , 2021, 597, 533-538.	13.7	159
9	Structural biology in the fight against COVID-19. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 2-7.	3.6	20
10	Profiling cellular diversity in sponges informs animal cell type and nervous system evolution. <i>Science</i> , 2021, 374, 717-723.	6.0	111
11	Nuclear pores dilate and constrict in cellulose. <i>Science</i> , 2021, 374, eabd9776.	6.0	162
12	A modular platform for automated cryo-FIB workflows. <i>eLife</i> , 2021, 10, .	2.8	65
13	Cryo-EM structures of holo condensin reveal a subunit flip-flop mechanism. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 743-751.	3.6	90
14	Spatially resolved analysis of FFPE tissue proteomes by quantitative mass spectrometry. <i>Nature Protocols</i> , 2020, 15, 2956-2979.	5.5	35
15	In-cell architecture of the nuclear pore and snapshots of its turnover. <i>Nature</i> , 2020, 586, 796-800.	13.7	139
16	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.	3.3	21
17	In situ structural analysis of SARS-CoV-2 spike reveals flexibility mediated by three hinges. <i>Science</i> , 2020, 370, 203-208.	6.0	531
18	Quality over quantity: Achieving Better Resolution in Subtomogram Averaging Using Less particles. <i>Microscopy and Microanalysis</i> , 2020, 26, 2514-2514.	0.2	0

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19	Proteome-Wide Structural Probing of Low-Abundant Protein Interactions by Cross-Linking Mass Spectrometry. <i>Analytical Chemistry</i> , 2020, 92, 4016-4022.	3.2	36
20	Selective autophagy degrades nuclear pore complexes. <i>Nature Cell Biology</i> , 2020, 22, 159-166.	4.6	86
21	Benchmarking tomographic acquisition schemes for high-resolution structural biology. <i>Nature Communications</i> , 2020, 11, 876.	5.8	49
22	The Benefits of Cotranslational Assembly: A Structural Perspective. <i>Trends in Cell Biology</i> , 2019, 29, 791-803.	3.6	62
23	Nuclear Pores Assemble from Nucleoporin Condensates During Oogenesis. <i>Cell</i> , 2019, 179, 671-686.e17.	13.5	87
24	Nucleoporin Nup155 is part of the p53 network in liver cancer. <i>Nature Communications</i> , 2019, 10, 2147.	5.8	29
25	Disentangling Genetic and Environmental Effects on the Proteotypes of Individuals. <i>Cell</i> , 2019, 177, 1308-1318.e10.	13.5	48
26	Structure and Assembly of the Nuclear Pore Complex. <i>Annual Review of Biophysics</i> , 2019, 48, 515-536.	4.5	205
27	Quantitative Proteome Landscape of the NCI-60 Cancer Cell Lines. <i>IScience</i> , 2019, 21, 664-680.	1.9	52
28	An ESCRT-LEM protein surveillance system is poised to directly monitor the nuclear envelope and nuclear transport system. <i>ELife</i> , 2019, 8, .	2.8	92
29	Kernporen-Transport maschinen in der KernhÄ¼lle und darÄ¼ber hinaus. <i>BioSpektrum</i> , 2018, 24, 149-151.	0.0	0
30	Systematic analysis of protein turnover in primary cells. <i>Nature Communications</i> , 2018, 9, 689.	5.8	280
31	Postmitotic nuclear pore assembly proceeds by radial dilation of small membrane openings. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 21-28.	3.6	75
32	Spatial Tissue Proteomics Quantifies Inter- and Intratumor Heterogeneity in Hepatocellular Carcinoma (HCC). <i>Molecular and Cellular Proteomics</i> , 2018, 17, 810-825.	2.5	65
33	Pervasive Protein Thermal Stability Variation during the Cell Cycle. <i>Cell</i> , 2018, 173, 1495-1507.e18.	13.5	183
34	Quantifying compartment-associated variations of protein abundance in proteomics data. <i>Molecular Systems Biology</i> , 2018, 14, e8131.	3.2	14
35	Nuclear Pore Complex Components in the Malaria Parasite <i>Plasmodium berghei</i> . <i>Scientific Reports</i> , 2018, 8, 11249.	1.6	19
36	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.	2.6	21

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37	In situ architecture of the algal nuclear pore complex. <i>Nature Communications</i> , 2018, 9, 2361.	5.8	107
38	Architecture of the yeast Elongator complex. <i>EMBO Reports</i> , 2017, 18, 264-279.	2.0	75
39	The nuclear pore complex: understanding its function through structural insight. <i>Nature Reviews Molecular Cell Biology</i> , 2017, 18, 73-89.	16.1	511
40	A short linear motif in scaffold Nup145C connects Y-complex with pre-assembled outer ring Nup82 complex. <i>Nature Communications</i> , 2017, 8, 1107.	5.8	32
41	Structural insights into transcription initiation by yeast RNA polymerase I. <i>EMBO Journal</i> , 2017, 36, 2698-2709.	3.5	58
42	Capturing protein communities by structural proteomics in a thermophilic eukaryote. <i>Molecular Systems Biology</i> , 2017, 13, 936.	3.2	108
43	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.	3.3	123
44	Alterations of the nuclear transport system in hepatocellular carcinoma – New basis for therapeutic strategies. <i>Journal of Hepatology</i> , 2017, 67, 1051-1061.	1.8	25
45	Landscape of nuclear transport receptor cargo specificity. <i>Molecular Systems Biology</i> , 2017, 13, 962.	3.2	88
46	Pre-assembled Nuclear Pores Insert into the Nuclear Envelope during Early Development. <i>Cell</i> , 2016, 166, 664-678.	13.5	101
47	Molecular architecture of the inner ring scaffold of the human nuclear pore complex. <i>Science</i> , 2016, 352, 363-365.	6.0	284
48	Automated structure modeling of large protein assemblies using crosslinks as distance restraints. <i>Nature Methods</i> , 2016, 13, 515-520.	9.0	49
49	Cryo-Electron Tomography: Can it Reveal the Molecular Sociology of Cells in Atomic Detail?. <i>Trends in Cell Biology</i> , 2016, 26, 825-837.	3.6	261
50	Structure of the ribosome post-recycling complex probed by chemical cross-linking and mass spectrometry. <i>Nature Communications</i> , 2016, 7, 13248.	5.8	27
51	The endosomal transcriptional regulator RNF11 integrates degradation and transport of EGFR. <i>Journal of Cell Biology</i> , 2016, 215, 543-558.	2.3	51
52	Toward the atomic structure of the nuclear pore complex: when top down meets bottom up. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 624-630.	3.6	74
53	Spatiotemporal variation of mammalian protein complex stoichiometries. <i>Genome Biology</i> , 2016, 17, 47.	3.8	115
54	Structure Determination of the Nuclear Pore Complex with Three-Dimensional Cryo electron Microscopy. <i>Journal of Molecular Biology</i> , 2016, 428, 2001-2010.	2.0	57

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55	Influenza Polymerase Can Adopt an Alternative Configuration Involving a Radical Repacking of PB2 Domains. <i>Molecular Cell</i> , 2016, 61, 125-137.	4.5	123
56	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.	1.1	14
57	Nuclear pore assembly proceeds by an inside-out extrusion of the nuclear envelope. <i>ELife</i> , 2016, 5, .	2.8	143
58	Characterization and quantification of proteins secreted by single human embryos prior to implantation. <i>EMBO Molecular Medicine</i> , 2015, 7, 1465-1479.	3.3	36
59	Towards understanding nuclear pore complex architecture and dynamics in the age of integrative structural analysis. <i>Current Opinion in Cell Biology</i> , 2015, 34, 31-38.	2.6	66
60	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, 177-183.	1.3	156
61	Structural basis for assembly and function of the Nup82 complex in the nuclear pore scaffold. <i>Journal of Cell Biology</i> , 2015, 208, 283-297.	2.3	64
62	Histone Deacetylase Inhibitors (HDACi) Cause the Selective Depletion of Bromodomain Containing Proteins (BCPs). <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1350-1360.	2.5	23
63	A structure of the COPI coat and the role of coat proteins in membrane vesicle assembly. <i>Science</i> , 2015, 349, 195-198.	6.0	159
64	Integrated Transcriptome and Proteome Analyses Reveal Organ-Specific Proteome Deterioration in Old Rats. <i>Cell Systems</i> , 2015, 1, 224-237.	2.9	176
65	In situ structural analysis of the human nuclear pore complex. <i>Nature</i> , 2015, 526, 140-143.	13.7	361
66	Architecture of TFIIC and its role in RNA polymerase III pre-initiation complex assembly. <i>Nature Communications</i> , 2015, 6, 7387.	5.8	57
67	Symportin 1 chaperones 5S RNP assembly during ribosome biogenesis by occupying an essential rRNA-binding site. <i>Nature Communications</i> , 2015, 6, 6510.	5.8	51
68	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, 7600-7611.	6.5	51
69	Toward understanding the structure of the vertebrate nuclear pore complex. <i>Nucleus</i> , 2014, 5, 119-123.	0.6	10
70	The Use of Targeted Proteomics to Determine the Stoichiometry of Large Macromolecular Assemblies. <i>Methods in Cell Biology</i> , 2014, 122, 117-146.	0.5	22
71	An integrated approach for genome annotation of the eukaryotic thermophile <i>Chaetomium thermophilum</i> . <i>Nucleic Acids Research</i> , 2014, 42, 13525-13533.	6.5	55
72	Prosurvival function of the cellular apoptosis susceptibility/importin- $\beta$ 1 transport cycle is repressed by p53 in liver cancer. <i>Hepatology</i> , 2014, 60, 884-895.	3.6	29

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73	Association of condensin with chromosomes depends on DNA binding by its HEAT-repeat subunits. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 560-568.	3.6	100
74	Cellular Disposal of miR23b by RAB27-Dependent Exosome Release Is Linked to Acquisition of Metastatic Properties. <i>Cancer Research</i> , 2014, 74, 5758-5771.	0.4	237
75	Integrated Structural Analysis of the Human Nuclear Pore Complex Scaffold. <i>Cell</i> , 2013, 155, 1233-1243.	13.5	321
76	Fourier ring correlation as a resolution criterion for super-resolution microscopy. <i>Journal of Structural Biology</i> , 2013, 183, 363-367.	1.3	269
77	Cell type-specific nuclear pores: a case in point for context-dependent stoichiometry of molecular machines. <i>Molecular Systems Biology</i> , 2013, 9, 648.	3.2	277
78	Facilitated aggregation of FG nucleoporins under molecular crowding conditions. <i>EMBO Reports</i> , 2013, 14, 178-183.	2.0	78
79	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, 1672-1682.	1.6	48
80	Structural Probing of a Protein Phosphatase 2A Network by Chemical Cross-Linking and Mass Spectrometry. <i>Science</i> , 2012, 337, 1348-1352.	6.0	357
81	High-throughput subtomogram alignment and classification by Fourier space constrained fast volumetric matching. <i>Journal of Structural Biology</i> , 2012, 178, 152-164.	1.3	52
82	False discovery rate estimation for cross-linked peptides identified by mass spectrometry. <i>Nature Methods</i> , 2012, 9, 901-903.	9.0	273
83	Absolute quantification of microbial proteomes at different states by directed mass spectrometry. <i>Molecular Systems Biology</i> , 2011, 7, 510.	3.2	91
84	Exploring the spatial and temporal organization of a cell's proteome. <i>Journal of Structural Biology</i> , 2011, 173, 483-496.	1.3	36
85	mProphet: automated data processing and statistical validation for large-scale SRM experiments. <i>Nature Methods</i> , 2011, 8, 430-435.	9.0	481
86	Comprehensive proteomics. <i>Current Opinion in Biotechnology</i> , 2011, 22, 3-8.	3.3	79
87	Template-free detection of macromolecular complexes in cryo electron tomograms. <i>Bioinformatics</i> , 2011, 27, i69-i76.	1.8	37
88	The quantitative proteome of a human cell line. <i>Molecular Systems Biology</i> , 2011, 7, 549.	3.2	691
89	Probing Native Protein Structures by Chemical Cross-linking, Mass Spectrometry, and Bioinformatics. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1634-1649.	2.5	407
90	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, 20992-20997.	3.3	130

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91	Visual Proteomics. <i>Methods in Enzymology</i> , 2010, 483, 215-243.	0.4	68
92	Architecture and Molecular Mechanism of PAN, the Archaeal Proteasome Regulatory ATPase. <i>Journal of Biological Chemistry</i> , 2009, 284, 22952-22960.	1.6	14
93	Proteome-wide cellular protein concentrations of the human pathogen <i>Leptospira interrogans</i> . <i>Nature</i> , 2009, 460, 762-765.	13.7	402
94	Visual proteomics of the human pathogen <i>Leptospira interrogans</i> . <i>Nature Methods</i> , 2009, 6, 817-823.	9.0	142
95	Identification of cross-linked peptides from large sequence databases. <i>Nature Methods</i> , 2008, 5, 315-318.	9.0	379
96	Structural and functional insights into nucleocytoplasmic transport. <i>Histology and Histopathology</i> , 2008, 23, 1025-33.	0.5	12
97	Snapshots of nuclear pore complexes in action captured by cryo-electron tomography. <i>Nature</i> , 2007, 449, 611-615.	13.7	330
98	Organization of Actin Networks in Intact Filopodia. <i>Current Biology</i> , 2007, 17, 79-84.	1.8	151
99	Luminal particles within cellular microtubules. <i>Journal of Cell Biology</i> , 2006, 174, 759-765.	2.3	111
100	Nuclear Pore Complex Structure and Dynamics Revealed by Cryoelectron Tomography. <i>Science</i> , 2004, 306, 1387-1390.	6.0	451
101	Exploring the Inner Space of Cells by Cryoelectron-Tomography. <i>Microscopy and Microanalysis</i> , 2004, 10, 152-153.	0.2	1