Martin Beck

List of Publications by Year in descending order

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	26630	33894
13,153	56	99
citations	h-index	g-index
131	131	15968
docs citations	times ranked	citing authors
	13,153 citations 131 docs citations	13,15356citationsh-index131131docs citations131times ranked

Μαρτινι Βεςκ

#	Article	IF	CITATIONS
1	Co-translational assembly orchestrates competing biogenesis pathways. Nature Communications, 2022, 13, 1224.	12.8	25
2	Conserved exchange of paralog proteins during neuronal differentiation. Life Science Alliance, 2022, 5, e202201397.	2.8	0
3	Conformational dynamics of nuclear pores. FASEB Journal, 2022, 36, .	0.5	0
4	Al-based structure prediction empowers integrative structural analysis of human nuclear pores. Science, 2022, 376, .	12.6	136
5	Cone-shaped HIV-1 capsids are transported through intact nuclear pores. Cell, 2021, 184, 1032-1046.e18.	28.9	179
6	Coupling proteomics and metabolomics for the unsupervised identification of protein–metabolite interactions in Chaetomium thermophilum. PLoS ONE, 2021, 16, e0254429.	2.5	5
7	Three-dimensional superresolution fluorescence microscopy maps the variable molecular architecture of the nuclear pore complex. Molecular Biology of the Cell, 2021, 32, 1523-1533.	2.1	37
8	Bioaccumulation of therapeutic drugs by human gut bacteria. Nature, 2021, 597, 533-538.	27.8	159
9	Structural biology in the fight against COVID-19. Nature Structural and Molecular Biology, 2021, 28, 2-7.	8.2	20
10	Profiling cellular diversity in sponges informs animal cell type and nervous system evolution. Science, 2021, 374, 717-723.	12.6	111
11	Nuclear pores dilate and constrict in cellulo. Science, 2021, 374, eabd9776.	12.6	162
12	A modular platform for automated cryo-FIB workflows. ELife, 2021, 10, .	6.0	65
13	Cryo-EM structures of holo condensin reveal a subunit flip-flop mechanism. Nature Structural and Molecular Biology, 2020, 27, 743-751.	8.2	90
14	Spatially resolved analysis of FFPE tissue proteomes by quantitative mass spectrometry. Nature Protocols, 2020, 15, 2956-2979.	12.0	35
15	In-cell architecture of the nuclear pore and snapshots of its turnover. Nature, 2020, 586, 796-800.	27.8	139
16	Structural impact of K63 ubiquitin on yeast translocating ribosomes under oxidative stress. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 22157-22166.	7.1	21
17	In situ structural analysis of SARS-CoV-2 spike reveals flexibility mediated by three hinges. Science, 2020, 370, 203-208.	12.6	531
18	Quality over quantity: Achieving Better Resolution in Subtomogram Averaging Using Less particles. Microscopy and Microanalysis, 2020, 26, 2514-2514.	0.4	0

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19	Proteome-Wide Structural Probing of Low-Abundant Protein Interactions by Cross-Linking Mass Spectrometry. Analytical Chemistry, 2020, 92, 4016-4022.	6.5	36
20	Selective autophagy degrades nuclear pore complexes. Nature Cell Biology, 2020, 22, 159-166.	10.3	86
21	Benchmarking tomographic acquisition schemes for high-resolution structural biology. Nature Communications, 2020, 11, 876.	12.8	49
22	The Benefits of Cotranslational Assembly: A Structural Perspective. Trends in Cell Biology, 2019, 29, 791-803.	7.9	62
23	Nuclear Pores Assemble from Nucleoporin Condensates During Oogenesis. Cell, 2019, 179, 671-686.e17.	28.9	87
24	Nucleoporin Nup155 is part of the p53 network in liver cancer. Nature Communications, 2019, 10, 2147.	12.8	29
25	Disentangling Genetic and Environmental Effects on the Proteotypes of Individuals. Cell, 2019, 177, 1308-1318.e10.	28.9	48
26	Structure and Assembly of the Nuclear Pore Complex. Annual Review of Biophysics, 2019, 48, 515-536.	10.0	205
27	Quantitative Proteome Landscape of the NCI-60 Cancer Cell Lines. IScience, 2019, 21, 664-680.	4.1	52
28	An ESCRT-LEM protein surveillance system is poised to directly monitor the nuclear envelope and nuclear transport system. ELife, 2019, 8, .	6.0	92
29	Kernporen-Transport maschinen in der Kernhülle und darüber hinaus. BioSpektrum, 2018, 24, 149-151.	0.0	0
30	Systematic analysis of protein turnover in primary cells. Nature Communications, 2018, 9, 689.	12.8	280
31	Postmitotic nuclear pore assembly proceeds by radial dilation of small membrane openings. Nature Structural and Molecular Biology, 2018, 25, 21-28.	8.2	75
32	Spatial Tissue Proteomics Quantifies Inter- and Intratumor Heterogeneity in Hepatocellular Carcinoma (HCC). Molecular and Cellular Proteomics, 2018, 17, 810-825.	3.8	65
33	Pervasive Protein Thermal Stability Variation during the Cell Cycle. Cell, 2018, 173, 1495-1507.e18.	28.9	183
34	Quantifying compartmentâ€associated variations ofÂprotein abundance in proteomics data. Molecular Systems Biology, 2018, 14, e8131.	7.2	14
35	Nuclear Pore Complex Components in the Malaria Parasite Plasmodium berghei. Scientific Reports, 2018, 8, 11249.	3.3	19
36	From the resolution revolution to evolution: structural insights into the evolutionary relationships between vesicle coats and the nuclear pore. Current Opinion in Structural Biology, 2018, 52, 32-40.	5.7	21

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37	In situ architecture of the algal nuclear pore complex. Nature Communications, 2018, 9, 2361.	12.8	107
38	Architecture of the yeast Elongator complex. EMBO Reports, 2017, 18, 264-279.	4.5	75
39	The nuclear pore complex: understanding its function through structural insight. Nature Reviews Molecular Cell Biology, 2017, 18, 73-89.	37.0	511
40	A short linear motif in scaffold Nup145C connects Y-complex with pre-assembled outer ring Nup82 complex. Nature Communications, 2017, 8, 1107.	12.8	32
41	Structural insights into transcription initiation by yeast RNA polymerase I. EMBO Journal, 2017, 36, 2698-2709.	7.8	58
42	Capturing protein communities by structural proteomics in a thermophilic eukaryote. Molecular Systems Biology, 2017, 13, 936.	7.2	108
43	Proteasomes tether to two distinct sites at the nuclear pore complex. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 13726-13731.	7.1	123
44	Alterations of the nuclear transport system in hepatocellular carcinoma – New basis for therapeutic strategies. Journal of Hepatology, 2017, 67, 1051-1061.	3.7	25
45	Landscape of nuclear transport receptor cargoÂspecificity. Molecular Systems Biology, 2017, 13, 962.	7.2	88
46	Pre-assembled Nuclear Pores Insert into the Nuclear Envelope during Early Development. Cell, 2016, 166, 664-678.	28.9	101
47	Molecular architecture of the inner ring scaffold of the human nuclear pore complex. Science, 2016, 352, 363-365.	12.6	284
48	Automated structure modeling of large protein assemblies using crosslinks as distance restraints. Nature Methods, 2016, 13, 515-520.	19.0	49
49	Cryo-Electron Tomography: Can it Reveal the Molecular Sociology of Cells in Atomic Detail?. Trends in Cell Biology, 2016, 26, 825-837.	7.9	261
50	Structure of the ribosome post-recycling complex probed by chemical cross-linking and mass spectrometry. Nature Communications, 2016, 7, 13248.	12.8	27
51	The endosomal transcriptional regulator RNF11 integrates degradation and transport of EGFR. Journal of Cell Biology, 2016, 215, 543-558.	5.2	51
52	Toward the atomic structure of the nuclear pore complex: when top down meets bottom up. Nature Structural and Molecular Biology, 2016, 23, 624-630.	8.2	74
53	Spatiotemporal variation of mammalian protein complex stoichiometries. Genome Biology, 2016, 17, 47.	8.8	115
54	Structure Determination of the Nuclear Pore Complex with Three-Dimensional Cryo electron Microscopy. Journal of Molecular Biology, 2016, 428, 2001-2010.	4.2	57

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55	Influenza Polymerase Can Adopt an Alternative Configuration Involving a Radical Repacking of PB2 Domains. Molecular Cell, 2016, 61, 125-137.	9.7	123
56	The Combination of X-Ray Crystallography and Cryo-Electron Microscopy Provides Insight into the Overall Architecture of the Dodecameric Rvb1/Rvb2 Complex. PLoS ONE, 2016, 11, e0146457.	2.5	14
57	Nuclear pore assembly proceeds by an inside-out extrusion of the nuclear envelope. ELife, 2016, 5, .	6.0	143
58	Characterization and quantification of proteins secreted by single human embryos prior to implantation. EMBO Molecular Medicine, 2015, 7, 1465-1479.	6.9	36
59	Towards understanding nuclear pore complex architecture and dynamics in the age of integrative structural analysis. Current Opinion in Cell Biology, 2015, 34, 31-38.	5.4	66
60	Xlink Analyzer: Software for analysis and visualization of cross-linking data in the context of three-dimensional structures. Journal of Structural Biology, 2015, 189, 177-183.	2.8	156
61	Structural basis for assembly and function of the Nup82 complex in the nuclear pore scaffold. Journal of Cell Biology, 2015, 208, 283-297.	5.2	64
62	Histone Deacetylase Inhibitors (HDACi) Cause the Selective Depletion of Bromodomain Containing Proteins (BCPs). Molecular and Cellular Proteomics, 2015, 14, 1350-1360.	3.8	23
63	A structure of the COPI coat and the role of coat proteins in membrane vesicle assembly. Science, 2015, 349, 195-198.	12.6	159
64	Integrated Transcriptome and Proteome Analyses Reveal Organ-Specific Proteome Deterioration in Old Rats. Cell Systems, 2015, 1, 224-237.	6.2	176
65	In situ structural analysis of the human nuclear pore complex. Nature, 2015, 526, 140-143.	27.8	361
66	Architecture of TFIIIC and its role in RNA polymerase III pre-initiation complex assembly. Nature Communications, 2015, 6, 7387.	12.8	57
67	Symportin 1 chaperones 5S RNP assembly during ribosome biogenesis by occupying an essential rRNA-binding site. Nature Communications, 2015, 6, 6510.	12.8	51
68	A network of SMG-8, SMG-9 and SMG-1 C-terminal insertion domain regulates UPF1 substrate recruitment and phosphorylation. Nucleic Acids Research, 2015, 43, 7600-7611.	14.5	51
69	Toward understanding the structure of the vertebrate nuclear pore complex. Nucleus, 2014, 5, 119-123.	2.2	10
70	The Use of Targeted Proteomics to Determine the Stoichiometry of Large Macromolecular Assemblies. Methods in Cell Biology, 2014, 122, 117-146.	1.1	22
71	An integrated approach for genome annotation of the eukaryotic thermophile Chaetomium thermophilum. Nucleic Acids Research, 2014, 42, 13525-13533.	14.5	55
72	Prosurvival function of the cellular apoptosis susceptibility/importin-α1 transport cycle is repressed by p53 in liver cancer. Hepatology, 2014, 60, 884-895.	7.3	29

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73	Association of condensin with chromosomes depends on DNA binding by its HEAT-repeat subunits. Nature Structural and Molecular Biology, 2014, 21, 560-568.	8.2	100
74	Cellular Disposal of miR23b by RAB27-Dependent Exosome Release Is Linked to Acquisition of Metastatic Properties. Cancer Research, 2014, 74, 5758-5771.	0.9	237
75	Integrated Structural Analysis of the Human Nuclear Pore Complex Scaffold. Cell, 2013, 155, 1233-1243.	28.9	321
76	Fourier ring correlation as a resolution criterion for super-resolution microscopy. Journal of Structural Biology, 2013, 183, 363-367.	2.8	269
77	Cell typeâ€specific nuclear pores: a case in point for contextâ€dependent stoichiometry of molecular machines. Molecular Systems Biology, 2013, 9, 648.	7.2	277
78	Facilitated aggregation of FG nucleoporins under molecular crowding conditions. EMBO Reports, 2013, 14, 178-183.	4.5	78
79	Protein Interfaces of the Conserved Nup84 Complex from Chaetomium thermophilum Shown by Crosslinking Mass Spectrometry and Electron Microscopy. Structure, 2013, 21, 1672-1682.	3.3	48
80	Structural Probing of a Protein Phosphatase 2A Network by Chemical Cross-Linking and Mass Spectrometry. Science, 2012, 337, 1348-1352.	12.6	357
81	High-throughput subtomogram alignment and classification by Fourier space constrained fast volumetric matching. Journal of Structural Biology, 2012, 178, 152-164.	2.8	52
82	False discovery rate estimation for cross-linked peptides identified by mass spectrometry. Nature Methods, 2012, 9, 901-903.	19.0	273
83	Absolute quantification of microbial proteomes at different states by directed mass spectrometry. Molecular Systems Biology, 2011, 7, 510.	7.2	91
84	Exploring the spatial and temporal organization of a cell's proteome. Journal of Structural Biology, 2011, 173, 483-496.	2.8	36
85	mProphet: automated data processing and statistical validation for large-scale SRM experiments. Nature Methods, 2011, 8, 430-435.	19.0	481
86	Comprehensive proteomics. Current Opinion in Biotechnology, 2011, 22, 3-8.	6.6	79
87	Template-free detection of macromolecular complexes in cryo electron tomograms. Bioinformatics, 2011, 27, i69-i76.	4.1	37
88	The quantitative proteome of a human cell line. Molecular Systems Biology, 2011, 7, 549.	7.2	691
89	Probing Native Protein Structures by Chemical Cross-linking, Mass Spectrometry, and Bioinformatics. Molecular and Cellular Proteomics, 2010, 9, 1634-1649.	3.8	407
90	Structure of the 26S proteasome from <i>Schizosaccharomyces pombe</i> at subnanometer resolution. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 20992-20997.	7.1	130

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91	Visual Proteomics. Methods in Enzymology, 2010, 483, 215-243.	1.0	68
92	Architecture and Molecular Mechanism of PAN, the Archaeal Proteasome Regulatory ATPase. Journal of Biological Chemistry, 2009, 284, 22952-22960.	3.4	14
93	Proteome-wide cellular protein concentrations of the human pathogen Leptospira interrogans. Nature, 2009, 460, 762-765.	27.8	402
94	Visual proteomics of the human pathogen Leptospira interrogans. Nature Methods, 2009, 6, 817-823.	19.0	142
95	Identification of cross-linked peptides from large sequence databases. Nature Methods, 2008, 5, 315-318.	19.0	379
96	Structural and functional insights into nucleocytoplasmic transport. Histology and Histopathology, 2008, 23, 1025-33.	0.7	12
97	Snapshots of nuclear pore complexes in action captured by cryo-electron tomography. Nature, 2007, 449, 611-615.	27.8	330
98	Organization of Actin Networks in Intact Filopodia. Current Biology, 2007, 17, 79-84.	3.9	151
99	Luminal particles within cellular microtubules. Journal of Cell Biology, 2006, 174, 759-765.	5.2	111
100	Nuclear Pore Complex Structure and Dynamics Revealed by Cryoelectron Tomography. Science, 2004, 306, 1387-1390.	12.6	451
101	Exploring the Inner Space of Cells by Cryoelectron-Tomography. Microscopy and Microanalysis, 2004,	0.4	1

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