Andre Hoelz

List of Publications by Year
in descending order

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47 papers	4,125 citations	126907 33 h-index	233421 45 g-index
54 all docs	54 docs citations	54 times ranked	4947 citing authors

#	Article	IF	Citations
1	Architecture of the linker-scaffold in the nuclear pore. Science, 2022, 376, .	12.6	51
2	Forced entry into the nucleus. Nature Cell Biology, 2022, 24, 810-812.	10.3	1
3	Architecture of the cytoplasmic face of the nuclear pore. Science, 2022, 376, .	12.6	65
4	Nucleoporin Condensates Drive Nuclear Pore Complex Assembly in Oocytes. Trends in Biochemical Sciences, 2020, 45, 278-280.	7.5	5
5	The Structure of the Nuclear Pore Complex (An Update). Annual Review of Biochemistry, 2019, 88, 725-783.	11.1	302
6	GÃ¼nter Blobel (1936â€“2018). Nature Cell Biology, 2018, 20, 364-364.	10.3	0
7	Structural and functional analysis of mRNA export regulation by the nuclear pore complex. Nature Communications, 2018, 9, 2319.	12.8	52
8	A new MR-SAD algorithm for the automatic building of protein models from low-resolution X-ray data and a poor starting model. IUCrJ, 2018, 5, 166-171.	2.2	33
9	Molecular basis for protection of ribosomal protein L4 from cellular degradation. Nature Communications, 2017, 8, 14354.	12.8	29
10	Histone-binding of DPF2 mediates its repressive role in myeloid differentiation. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 6016-6021.	7.1	23
11	Architecture of the symmetric core of the nuclear pore. Science, 2016, 352, aaf1015.	12.6	223
12	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
13	A conserved quality-control pathway that mediates degradation of unassembled ribosomal proteins. ELife, 2016, 5, .	6.0	147
14	Architecture of the nuclear pore complex coat. Science, 2015, 347, 1148-1152.	12.6	104
15	Coordinated Ribosomal L4 Protein Assembly into the Pre-Ribosome Is Regulated by Its Eukaryote-Specific Extension. Molecular Cell, 2015, 58, 854-862.	9.7	69
16	Architecture of the fungal nuclear pore inner ring complex. Science, 2015, 350, 56-64.	12.6	125
17	Evidence for an evolutionary relationship between the large adaptor nucleoporin Nup192 and karyopherins. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2530-2535.	7.1	44
18	Structural and Functional Analysis of Human SIRT1. Journal of Molecular Biology, 2014, 426, 526-541.	4.2	122

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19	Structural and Functional Characterization of the Î±-Tubulin Acetyltransferase MEC-17. Journal of Molecular Biology, 2014, 426, 2605-2616.	4.2	23
20	Structural and Functional Analysis of the C-Terminal Domain of Nup358/RanBP2. Journal of Molecular Biology, 2013, 425, 1318-1329.	4.2	54
21	Molecular Basis for the Anchoring of Proto-Oncoprotein Nup98 to the Cytoplasmic Face of the Nuclear Pore Complex. Journal of Molecular Biology, 2012, 419, 330-346.	4.2	30
22	Crystal Structure of the N-Terminal Domain of Nup358/RanBP2. Journal of Molecular Biology, 2012, 423, 752-765.	4.2	34
23	Structure of an Enclosed Dimer Formed by the Drosophila Period Protein. Journal of Molecular Biology, 2011, 413, 561-572.	4.2	19
24	The Structure of the Nuclear Pore Complex. Annual Review of Biochemistry, 2011, 80, 613-643.	11.1	461
25	Rae1: A new clue for nucleoporin leukemias. Cell Cycle, 2011, 10, 2059-2058.	2.6	0
26	Structural and functional analysis of an essential nucleoporin heterotrimer on the cytoplasmic face of the nuclear pore complex. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 16571-16576.	7.1	59
27	Crystal structure of Î±-COP in complex with Ïµ-COP provides insight into the architecture of the COPI vesicular coat. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 11271-11276.	7.1	45
28	Structural and functional analysis of the interaction between the nucleoporin Nup98 and the mRNA export factor Rae1. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10406-10411.	7.1	99
29	Characterization of the membrane-coating Nup84 complex. Nucleus, 2010, 1, 150-157.	2.2	9
30	Characterization of the membrane-coating Nup84 complex: Paradigm for the nuclear pore complex structure. Nucleus, 2010, 1, 150-157.	2.2	9
31	Structural and functional analysis of the interaction between the nucleoporin Nup214 and the DEAD-box helicase Ddx19. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3089-3094.	7.1	88
32	Structural and functional analysis of Nup120 suggests ring formation of the Nup84 complex. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 14281-14286.	7.1	74
33	Structure of a trimeric nucleoporin complex reveals alternate oligomerization states. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 17693-17698.	7.1	57
34	Nuclear transport comes full circle. Nature Structural and Molecular Biology, 2009, 16, 457-459.	8.2	9
35	A Fence-like Coat for the Nuclear Pore Membrane. Molecular Cell, 2008, 32, 815-826.	9.7	117
36	Molecular basis for the autoregulation of the protein acetyl transferase Rtt109. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 12236-12241.	7.1	55

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37	Crystal structure of the N-terminal domain of the human protooncogene Nup214/CAN. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 1783-1788.	7.1	57
38	Structure of Nup58/45 Suggests Flexible Nuclear Pore Diameter by Intermolecular Sliding. Science, 2007, 315, 1729-1732.	12.6	106
39	Architecture of a Coat for the Nuclear Pore Membrane. Cell, 2007, 131, 1313-1326.	28.9	124
40	Crystal Structure of the SH3 Domain of Î²PIX in Complex with a High Affinity Peptide from PAK2. Journal of Molecular Biology, 2006, 358, 509-522.	4.2	45
41	A Dimeric Kinase Assembly Underlying Autophosphorylation in the p21 Activated Kinases. Journal of Molecular Biology, 2006, 361, 312-326.	4.2	82
42	Oligomerization states of the association domain and the holoenyzme of Ca2+/CaM kinase II. FEBS Journal, 2006, 273, 682-694.	4.7	92
43	Crystal structure and mechanism of human lysine-specific demethylase-1. Nature Structural and Molecular Biology, 2006, 13, 626-632.	8.2	237
44	Popping out of the nucleus. Nature, 2004, 432, 815-816.	27.8	45
45	Structural Evidence for Feedback Activation by RasÂ·GTP of the Ras-Specific Nucleotide Exchange Factor SOS. Cell, 2003, 112, 685-695.	28.9	390
46	Crystal Structure of a Tetradecameric Assembly of the Association Domain of Ca2+/Calmodulin-Dependent Kinase II. Molecular Cell, 2003, 11, 1241-1251.	9.7	164
47	Gene structures and properties of enzymes of the plasmid-encoded nicotine catabolism of Arthrobacter nicotinovorans 1 1Edited by J. Karn. Journal of Molecular Biology, 1998, 284, 1323-1339.	4.2	55