

Michael P Rout

List of Publications by Year in descending order

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165
papers

18,127
citations

12322

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14197

128
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all docs

190
docs citations

190
times ranked

14974
citing authors

#	ARTICLE	IF	CITATIONS
1	Planet Hunters TESS IV: a massive, compact hierarchical triple star system TICÂ470710327. Monthly Notices of the Royal Astronomical Society, 2022, 511, 4710-4723.	1.6	10
2	Comprehensive structure and functional adaptations of the yeast nuclear pore complex. Cell, 2022, 185, 361-378.e25.	13.5	87
3	Proteomic elucidation of the targets and primary functions of the picornavirus 2A protease. Journal of Biological Chemistry, 2022, 298, 101882.	1.6	10
4	Affinity Isolation of Endogenous Saccharomyces Cerevisiae Nuclear Pore Complexes. Methods in Molecular Biology, 2022, 2502, 3-34.	0.4	2
5	Dissecting the Structural Dynamics of the Nuclear Pore Complex. Molecular Cell, 2021, 81, 153-165.e7.	4.5	31
6	Malaria parasites use a soluble RhopH complex for erythrocyte invasion and an integral form for nutrient uptake. ELife, 2021, 10, .	2.8	35
7	One Ring to Rule them All? Structural and Functional Diversity in the Nuclear Pore Complex. Trends in Biochemical Sciences, 2021, 46, 595-607.	3.7	64
8	Heh2/Man1 may be an evolutionarily conserved sensor of NPC assembly state. Molecular Biology of the Cell, 2021, 32, 1359-1373.	0.9	10
9	Measuring in vivo protein turnover and exchange in yeast macromolecular assemblies. STAR Protocols, 2021, 2, 100800.	0.5	3
10	Replication and single-cycle delivery of SARS-CoV-2 replicons. Science, 2021, 374, 1099-1106.	6.0	49
11	Highly synergistic combinations of nanobodies that target SARS-CoV-2 and are resistant to escape. ELife, 2021, 10, .	2.8	36
12	Affinity proteomic dissection of the human nuclear cap-binding complex interactome. Nucleic Acids Research, 2020, 48, 10456-10469.	6.5	18
13	Integrative structure and function of the yeast exocyst complex. Protein Science, 2020, 29, 1486-1501.	3.1	29
14	Analysis of Multivalent IDP Interactions: Stoichiometry, Affinity, and Local Concentration Effect Measurements. Methods in Molecular Biology, 2020, 2141, 463-475.	0.4	3
15	Crippling life support for SARS-CoV-2 and other viruses through synthetic lethality. Journal of Cell Biology, 2020, 219, .	2.3	20
16	Interactions of nuclear transport factors and surface-conjugated FG nucleoporins: Insights and limitations. PLoS ONE, 2019, 14, e0217897.	1.1	9
17	Principles for Integrative Structural Biology Studies. Cell, 2019, 177, 1384-1403.	13.5	201
18	Pore timing: the evolutionary origins of the nucleus and nuclear pore complex. F1000Research, 2019, 8, 369.	0.8	37

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19	Involvement in surface antigen expression by a moonlighting FG-repeat nucleoporin in trypanosomes. <i>Molecular Biology of the Cell</i> , 2018, 29, 1100-1110.	0.9	5
20	Integrative structure and functional anatomy of a nuclear pore complex. <i>Nature</i> , 2018, 555, 475-482.	13.7	435
21	Deciphering the "Fuzzy" Interaction of FG Nucleoporins and Transport Factors Using Small-Angle Neutron Scattering. <i>Structure</i> , 2018, 26, 477-484.e4.	1.6	19
22	Thermodynamic characterization of the multivalent interactions underlying rapid and selective translocation through the nuclear pore complex. <i>Journal of Biological Chemistry</i> , 2018, 293, 4555-4563.	1.6	47
23	Dissection of affinity captured LINE-1 macromolecular complexes. <i>ELife</i> , 2018, 7, .	2.8	63
24	Molecular Architecture of the Major Membrane Ring Component of the Nuclear Pore Complex. <i>Structure</i> , 2017, 25, 434-445.	1.6	61
25	Lineage-specific proteins essential for endocytosis in trypanosomes. <i>Journal of Cell Science</i> , 2017, 130, 1379-1392.	1.2	16
26	The Evolution of Organellar Coat Complexes and Organization of the Eukaryotic Cell. <i>Annual Review of Biochemistry</i> , 2017, 86, 637-657.	5.0	101
27	Comparative interactomics provides evidence for functional specialization of the nuclear pore complex. <i>Nucleus</i> , 2017, 8, 340-352.	0.6	16
28	The nuclear pore complex core scaffold and permeability barrier: variations of a common theme. <i>Current Opinion in Cell Biology</i> , 2017, 46, 110-118.	2.6	38
29	The Trypanosome Exocyst: A Conserved Structure Revealing a New Role in Endocytosis. <i>PLoS Pathogens</i> , 2017, 13, e1006063.	2.1	27
30	Specialising the parasite nucleus: Pores, lamins, chromatin, and diversity. <i>PLoS Pathogens</i> , 2017, 13, e1006170.	2.1	11
31	Interactome Mapping Reveals the Evolutionary History of the Nuclear Pore Complex. <i>PLoS Biology</i> , 2016, 14, e1002365.	2.6	90
32	High-Efficiency Isolation of Nuclear Envelope Protein Complexes from Trypanosomes. <i>Methods in Molecular Biology</i> , 2016, 1411, 67-80.	0.4	31
33	Revealing Higher Order Protein Structure Using Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 952-965.	1.2	51
34	Slide-and-exchange mechanism for rapid and selective transport through the nuclear pore complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E2489-97.	3.3	85
35	Cilia and Nuclear Pore Proteins: Pore No More?. <i>Developmental Cell</i> , 2016, 38, 445-446.	3.1	4
36	Simple rules for passive diffusion through the nuclear pore complex. <i>Journal of Cell Biology</i> , 2016, 215, 57-76.	2.3	337

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37	Optimized Affinity Capture of Yeast Protein Complexes. Cold Spring Harbor Protocols, 2016, 2016, pdb.prot087932.	0.2	10
38	Native Elution of Yeast Protein Complexes Obtained by Affinity Capture. Cold Spring Harbor Protocols, 2016, 2016, pdb.prot087940.	0.2	8
39	Protein Complex Purification by Affinity Capture. Cold Spring Harbor Protocols, 2016, 2016, pdb.top077545.	0.2	16
40	Purification and analysis of endogenous human RNA exosome complexes. Rna, 2016, 22, 1467-1475.	1.6	13
41	Structure and Function of the Nuclear Pore Complex Cytoplasmic mRNA Export Platform. Cell, 2016, 167, 1215-1228.e25.	13.5	148
42	Developing genetic tools to exploit Chaetomium thermophilum for biochemical analyses of eukaryotic macromolecular assemblies. Scientific Reports, 2016, 6, 20937.	1.6	43
43	HIV host interactome revealed directly from infected cells. Nature Microbiology, 2016, 1, 16068.	5.9	49
44	Co-dependence between trypanosome nuclear lamina components in nuclear stability and control of gene expression. Nucleic Acids Research, 2016, 44, 10554-10570.	6.5	23
45	Protein Complex Affinity Capture from Cryomilled Mammalian Cells. Journal of Visualized Experiments, 2016, , .	0.2	23
46	Optimizing selection of large animals for antibody production by screening immune response to standard vaccines. Journal of Immunological Methods, 2016, 430, 56-60.	0.6	17
47	Subunit connectivity, assembly determinants and architecture of the yeast exocyst complex. Nature Structural and Molecular Biology, 2016, 23, 59-66.	3.6	108
48	A Robust Workflow for Native Mass Spectrometric Analysis of Affinity-Isolated Endogenous Protein Assemblies. Analytical Chemistry, 2016, 88, 2799-2807.	3.2	21
49	Characterization of L1-Ribonucleoprotein Particles. Methods in Molecular Biology, 2016, 1400, 311-338.	0.4	19
50	Density Gradient Ultracentrifugation to Isolate Endogenous Protein Complexes after Affinity Capture. Cold Spring Harbor Protocols, 2016, 2016, pdb.prot087957.	0.2	8
51	The interactome challenge. Journal of Cell Biology, 2015, 211, 729-732.	2.3	14
52	Affinity proteomics to study endogenous protein complexes: Pointers, pitfalls, preferences and perspectives. BioTechniques, 2015, 58, 103-119.	0.8	49
53	Altering nuclear pore complex function impacts longevity and mitochondrial function in <i>S. cerevisiae</i> . Journal of Cell Biology, 2015, 208, 729-744.	2.3	55
54	SEA you later alli-GATOR a dynamic regulator of the TORC1 stress response pathway. Journal of Cell Science, 2015, 128, 2219-2228.	1.2	63

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55	Engineered high-affinity nanobodies recognizing staphylococcal Protein A and suitable for native isolation of protein complexes. <i>Analytical Biochemistry</i> , 2015, 477, 92-94.	1.1	16
56	Rapid, optimized interactomic screening. <i>Nature Methods</i> , 2015, 12, 553-560.	9.0	68
57	A strategy for dissecting the architectures of native macromolecular assemblies. <i>Nature Methods</i> , 2015, 12, 1135-1138.	9.0	113
58	The molecular mechanism of nuclear transport revealed by atomic-scale measurements. <i>ELife</i> , 2015, 4, .	2.8	130
59	Touching from a distance. <i>Nucleus</i> , 2014, 5, 304-310.	0.6	6
60	NPC Mimics. <i>Methods in Cell Biology</i> , 2014, 122, 379-393.	0.5	4
61	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, 2927-2943.	2.5	152
62	Enriching the Pore: Splendid Complexity from Humble Origins. <i>Traffic</i> , 2014, 15, 141-156.	1.3	40
63	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, 2911-2926.	2.5	67
64	Molecular Architecture and Function of the SEA Complex, a Modulator of the TORC1 Pathway. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2855-2870.	2.5	64
65	Cancer and the Nuclear Pore Complex. <i>Advances in Experimental Medicine and Biology</i> , 2014, 773, 285-307.	0.8	101
66	A robust pipeline for rapid production of versatile nanobody repertoires. <i>Nature Methods</i> , 2014, 11, 1253-1260.	9.0	391
67	Nuclear pore complex evolution: a trypanosome Mlp analogue functions in chromosomal segregation but lacks transcriptional barrier activity. <i>Molecular Biology of the Cell</i> , 2014, 25, 1421-1436.	0.9	26
68	Editorial overview: Cell nucleus: The nucleus: a dynamic organelle. <i>Current Opinion in Cell Biology</i> , 2014, 28, iv-vii.	2.6	2
69	Affinity Proteomics Reveals Human Host Factors Implicated in Discrete Stages of LINE-1 Retrotransposition. <i>Cell</i> , 2013, 155, 1034-1048.	13.5	190
70	The human cap-binding complex is functionally connected to the nuclear RNA exosome. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1367-1376.	3.6	199
71	Structure, Dynamics, Evolution, and Function of a Major Scaffold Component in the Nuclear Pore Complex. <i>Structure</i> , 2013, 21, 560-571.	1.6	53
72	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, 3920-3938.	0.9	100

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73	Supervillin binding to myosin II and synergism with anillin are required for cytokinesis. <i>Molecular Biology of the Cell</i> , 2013, 24, 3603-3619.	0.9	32
74	Improved Native Isolation of Endogenous Protein A-Tagged Protein Complexes. <i>BioTechniques</i> , 2013, 54, 213-216.	0.8	10
75	Telomeres, tethers and trypanosomes. <i>Nucleus</i> , 2012, 3, 478-486.	0.6	20
76	Nucleocytoplasmic Transport: A Role for Nonspecific Competition in Karyopherin-Nucleoporin Interactions. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 31-46.	2.5	56
77	Proteomics on the rims: insights into the biology of the nuclear envelope and flagellar pocket of trypanosomes. <i>Parasitology</i> , 2012, 139, 1158-1167.	0.7	11
78	Structure–function mapping of a heptameric module in the nuclear pore complex. <i>Journal of Cell Biology</i> , 2012, 196, 419-434.	2.3	110
79	Ciliary and Nuclear Transport: Different Places, Similar Routes?. <i>Developmental Cell</i> , 2012, 22, 693-694.	3.1	15
80	The Yeast Nuclear Pore Complex and Transport Through It. <i>Genetics</i> , 2012, 190, 855-883.	1.2	126
81	NUP-1 Is a Large Coiled-Coil Nucleoskeletal Protein in Trypanosomes with Lamin-Like Functions. <i>PLoS Biology</i> , 2012, 10, e1001287.	2.6	105
82	Improved methodology for the affinity isolation of human protein complexes expressed at near endogenous levels. <i>BioTechniques</i> , 2012, 0, 1-6.	0.8	48
83	Atomic structure of the nuclear pore complex targeting domain of a Nup116 homologue from the yeast, <i>Candida glabrata</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2110-2116.	1.5	7
84	A jumbo problem: mapping the structure and functions of the nuclear pore complex. <i>Current Opinion in Cell Biology</i> , 2012, 24, 92-99.	2.6	46
85	High-throughput, single-step purification of affinity-tagged protein complexes. <i>FASEB Journal</i> , 2012, 26, .	0.2	0
86	A 3D Physical Model of Karyopherin-2. <i>FASEB Journal</i> , 2012, 26, lb268.	0.2	0
87	Nuclear export dynamics of RNA–protein complexes. <i>Nature</i> , 2011, 475, 333-341.	13.7	162
88	Structure of the C-terminal domain of <i>Saccharomyces cerevisiae</i> Nup133, a component of the nuclear pore complex. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1672-1677.	1.5	16
89	A Conserved Coatmer-related Complex Containing Sec13 and Seh1 Dynamically Associates With the Vacuole in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.006478.	2.5	115
90	A Cell Cycle Phosphoproteome of the Yeast Centrosome. <i>Science</i> , 2011, 332, 1557-1561.	6.0	88

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91	A novel coatomer-related SEA complex dynamically associates with the vacuole in yeast and is implicated in the response to nitrogen starvation. <i>Autophagy</i> , 2011, 7, 1392-1393.	4.3	20
92	On a benderâ€”BARs, ESCRTs, COPs, and finally getting your coat. <i>Journal of Cell Biology</i> , 2011, 193, 963-972.	2.3	88
93	The Mechanism of Nucleocytoplasmic Transport through the Nuclear Pore Complex. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2010, 75, 567-584.	2.0	45
94	Structures of the autoproteolytic domain from the <i>Saccharomyces cerevisiae</i> nuclear pore complex component, Nup145. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 1992-1998.	1.5	13
95	The nuclear pore complex: bridging nuclear transport and gene regulation. <i>Nature Reviews Molecular Cell Biology</i> , 2010, 11, 490-501.	16.1	473
96	Human Cytomegalovirus pUL83 Stimulates Activity of the Viral Immediate-Early Promoter through Its Interaction with the Cellular IFI16 Protein. <i>Journal of Virology</i> , 2010, 84, 7803-7814.	1.5	143
97	The Nuclear Pore Complex and Nuclear Transport. <i>Cold Spring Harbor Perspectives in Biology</i> , 2010, 2, a000562-a000562.	2.3	569
98	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, 6720-6732.	1.5	101
99	Human Cytomegalovirus UL29/28 Protein Interacts with Components of the NuRD Complex Which Promote Accumulation of Immediate-Early RNA. <i>PLoS Pathogens</i> , 2010, 6, e1000965.	2.1	65
100	Enhancement of Transport Selectivity through Nano-Channels by Non-Specific Competition. <i>PLoS Computational Biology</i> , 2010, 6, e1000804.	1.5	57
101	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, 2119-2130.	2.5	200
102	Cell structure and dynamics. <i>Current Opinion in Cell Biology</i> , 2009, 21, 1-3.	2.6	41
103	Nuclear pore complex biogenesis. <i>Current Opinion in Cell Biology</i> , 2009, 21, 603-612.	2.6	58
104	Artificial nanopores that mimic the transport selectivity of the nuclear pore complex. <i>Nature</i> , 2009, 457, 1023-1027.	13.7	264
105	Rrp17p Is a Eukaryotic Exonuclease Required for 5' End Processing of Pre-60S Ribosomal RNA. <i>Molecular Cell</i> , 2009, 36, 768-781.	4.5	83
106	Integrative Structure Determination of Protein Assemblies by Satisfaction of Spatial Restraints. <i>Computational Biology</i> , 2008, , 99-114.	0.1	6
107	Human Cytomegalovirus Protein UL38 Inhibits Host Cell Stress Responses by Antagonizing the Tuberous Sclerosis Protein Complex. <i>Cell Host and Microbe</i> , 2008, 3, 253-262.	5.1	175
108	Rapid Isolation and Identification of Bacteriophage T4-Encoded Modifications of <i>Escherichia coli</i> RNA Polymerase: A Generic Method to Study Bacteriophage/Host Interactions. <i>Journal of Proteome Research</i> , 2008, 7, 1244-1250.	1.8	14

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109	The peroxisome: a production in four acts. <i>Journal of Cell Biology</i> , 2008, 181, 185-187.	2.3	2
110	High-Yield Isolation and Subcellular Proteomic Characterization of Nuclear and Subnuclear Structures from Trypanosomes. <i>Methods in Molecular Biology</i> , 2008, 463, 77-92.	0.4	21
111	Assembly factors Rpf2 and Rrs1 recruit 5S rRNA and ribosomal proteins rpL5 and rpL11 into nascent ribosomes. <i>Genes and Development</i> , 2007, 21, 2580-2592.	2.7	175
112	Efficiency, Selectivity, and Robustness of Nucleocytoplasmic Transport. <i>PLoS Computational Biology</i> , 2007, 3, e125.	1.5	95
113	Yeast Rrp14p is required for ribosomal subunit synthesis and for correct positioning of the mitotic spindle during mitosis. <i>Nucleic Acids Research</i> , 2007, 35, 1354-1366.	6.5	39
114	Comprehensive analysis of diverse ribonucleoprotein complexes. <i>Nature Methods</i> , 2007, 4, 951-956.	9.0	253
115	Determining the architectures of macromolecular assemblies. <i>Nature</i> , 2007, 450, 683-694.	13.7	499
116	The molecular architecture of the nuclear pore complex. <i>Nature</i> , 2007, 450, 695-701.	13.7	947
117	Studying nuclear protein import in yeast. <i>Methods</i> , 2006, 39, 291-308.	1.9	13
118	Protease Accessibility Laddering: A Proteomic Tool for Probing Protein Structure. <i>Structure</i> , 2006, 14, 653-660.	1.6	30
119	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, 2172-2177.	3.3	243
120	Induction of Autophagy in Axonal Dystrophy and Degeneration. <i>Journal of Neuroscience</i> , 2006, 26, 8057-8068.	1.7	298
121	Simple kinetic relationships and nonspecific competition govern nuclear import rates in vivo. <i>Journal of Cell Biology</i> , 2006, 175, 579-593.	2.3	135
122	Tracking and Elucidating Alphavirus-Host Protein Interactions. <i>Journal of Biological Chemistry</i> , 2006, 281, 30269-30278.	1.6	164
123	Proteomic and genomic characterization of chromatin complexes at a boundary. <i>Journal of Cell Biology</i> , 2005, 169, 35-47.	2.3	130
124	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, 225-235.	2.3	81
125	Fluorescent Proteins as Proteomic Probes. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1933-1941.	2.5	225
126	I-DIRT, A General Method for Distinguishing between Specific and Nonspecific Protein Interactions. <i>Journal of Proteome Research</i> , 2005, 4, 1752-1756.	1.8	134

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127	A Method for the Rapid and Efficient Elution of Native Affinity-Purified Protein A Tagged Complexes. <i>Journal of Proteome Research</i> , 2005, 4, 2250-2256.	1.8	16
128	Characterization of Karyopherin Cargoes Reveals Unique Mechanisms of Kap121p-Mediated Nuclear Import. <i>Molecular and Cellular Biology</i> , 2004, 24, 8487-8503.	1.1	46
129	Components of Coated Vesicles and Nuclear Pore Complexes Share a Common Molecular Architecture. <i>PLoS Biology</i> , 2004, 2, e380.	2.6	357
130	Robbing from the pore. <i>Nature Cell Biology</i> , 2004, 6, 177-179.	4.6	3
131	Targeted Proteomic Study of the Cyclin-Cdk Module. <i>Molecular Cell</i> , 2004, 14, 699-711.	4.5	110
132	Virtual gating and nuclear transport: the hole picture. <i>Trends in Cell Biology</i> , 2003, 13, 622-628.	3.6	347
133	Genetic and Biochemical Evaluation of the Importance of Cdc6 in Regulating Mitotic Exit. <i>Molecular Biology of the Cell</i> , 2003, 14, 4592-4604.	0.9	47
134	Kap121p-Mediated Nuclear Import Is Required for Mating and Cellular Differentiation in Yeast. <i>Molecular and Cellular Biology</i> , 2002, 22, 2544-2555.	1.1	43
135	Isolation of nuclear envelope from <i>Saccharomyces cerevisiae</i> . <i>Methods in Enzymology</i> , 2002, 351, 394-408.	0.4	10
136	A Tense Time for the Nuclear Envelope. <i>Cell</i> , 2002, 108, 301-304.	13.5	17
137	Cleave to Leave. <i>Molecular Cell</i> , 2002, 10, 221-223.	4.5	2
138	The Structure and Composition of the Yeast NPC. <i>Results and Problems in Cell Differentiation</i> , 2002, 35, 1-23.	0.2	6
139	Composition and Functional Characterization of Yeast 66S Ribosome Assembly Intermediates. <i>Molecular Cell</i> , 2001, 8, 505-515.	4.5	280
140	Isolation and Characterization of Subnuclear Compartments from <i>Trypanosoma brucei</i> . <i>Journal of Biological Chemistry</i> , 2001, 276, 38261-38271.	1.6	64
141	The Nuclear Pore Complex as a Transport Machine. <i>Journal of Biological Chemistry</i> , 2001, 276, 16593-16596.	1.6	240
142	Nup2p Dynamically Associates with the Distal Regions of the Yeast Nuclear Pore Complex. <i>Journal of Cell Biology</i> , 2001, 153, 1465-1478.	2.3	149
143	The Road to Ribosomes. <i>Journal of Cell Biology</i> , 2000, 151, F23-F26.	2.3	39
144	The Yeast Nuclear Pore Complex. <i>Journal of Cell Biology</i> , 2000, 148, 635-652.	2.3	1,329

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145	Pore relations: nuclear pore complexes and nucleocytoplasmic exchange. <i>Essays in Biochemistry</i> , 2000, 36, 75-88.	2.1	23
146	Proteins Connecting the Nuclear Pore Complex with the Nuclear Interior. <i>Journal of Cell Biology</i> , 1999, 144, 839-855.	2.3	210
147	TAPping into transport. <i>Nature Cell Biology</i> , 1999, 1, E31-E33.	4.6	9
148	Karyopherins and kissing cousins. <i>Trends in Cell Biology</i> , 1998, 8, 184-188.	3.6	212
149	Three-Dimensional Architecture of the Isolated Yeast Nuclear Pore Complex: Functional and Evolutionary Implications. <i>Molecular Cell</i> , 1998, 1, 223-234.	4.5	331
150	<i>Saccharomyces cerevisiae</i> Ndc1p Is a Shared Component of Nuclear Pore Complexes and Spindle Pole Bodies. <i>Journal of Cell Biology</i> , 1998, 143, 1789-1800.	2.3	134
151	A Distinct Nuclear Import Pathway Used by Ribosomal Proteins. <i>Cell</i> , 1997, 89, 715-725.	13.5	315
152	The Yeast Spindle Pole Body Is Assembled around a Central Crystal of Spc42p. <i>Cell</i> , 1997, 89, 1077-1086.	13.5	183
153	Kap104p: A Karyopherin Involved in the Nuclear Transport of Messenger RNA Binding Proteins. <i>Science</i> , 1996, 274, 624-627.	6.0	300
154	The yeast nucleoporin Nup188p interacts genetically and physically with the core structures of the nuclear pore complex.. <i>Journal of Cell Biology</i> , 1996, 133, 1153-1162.	2.3	91
155	Disruption of the nucleoporin gene NUP133 results in clustering of nuclear pore complexes.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 1187-1191.	3.3	84
156	Nup120p: a yeast nucleoporin required for NPC distribution and mRNA transport.. <i>Journal of Cell Biology</i> , 1995, 131, 1659-1675.	2.3	141
157	Two novel related yeast nucleoporins Nup170p and Nup157p: complementation with the vertebrate homologue Nup155p and functional interactions with the yeast nuclear pore-membrane protein Pom152p.. <i>Journal of Cell Biology</i> , 1995, 131, 1133-1148.	2.3	175
158	The Essential Yeast Nucleoporin NUP159 Is Located on the Cytoplasmic Side of the Nuclear Pore Complex and Serves in Karyopherin-mediated Binding of Transport Substrate. <i>Journal of Biological Chemistry</i> , 1995, 270, 19017-19021.	1.6	131
159	Isolation and characterization of nuclear envelopes from the yeast <i>Saccharomyces</i> .. <i>Journal of Cell Biology</i> , 1995, 131, 19-31.	2.3	72
160	POM152 is an integral protein of the pore membrane domain of the yeast nuclear envelope.. <i>Journal of Cell Biology</i> , 1994, 125, 31-42.	2.3	139
161	Pores for thought: nuclear pore complex proteins. <i>Trends in Cell Biology</i> , 1994, 4, 357-365.	3.6	276
162	Isolation of the yeast nuclear pore complex.. <i>Journal of Cell Biology</i> , 1993, 123, 771-783.	2.3	262

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163	A new family of yeast nuclear pore complex proteins.. Journal of Cell Biology, 1992, 119, 705-723.	2.3	256
164	Yeast Spindle Pole Body Components. Cold Spring Harbor Symposia on Quantitative Biology, 1991, 56, 687-692.	2.0	27
165	Components of the yeast spindle and spindle pole body.. Journal of Cell Biology, 1990, 111, 1913-1927.	2.3	266