

Michael P Rout

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.

163
papers

15,097
citations

66
h-index

121
g-index

190
ext. papers

16,951
ext. citations

11.6
avg, IF

6.53
L-index

#	Paper	IF	Citations
163	Proteomic elucidation of the targets and primary functions of the picornavirus 2A protease.. <i>Journal of Biological Chemistry</i> , 2022 , 101882	5.4	1
162	Affinity Isolation of Endogenous <i>Saccharomyces Cerevisiae</i> Nuclear Pore Complexes.. <i>Methods in Molecular Biology</i> , 2022 , 2502, 3-34	1.4	0
161	Comprehensive structure and functional adaptations of the yeast nuclear pore complex.. <i>Cell</i> , 2021 ,	56.2	18
160	Highly synergistic combinations of nanobodies that target SARS-CoV-2 and are resistant to escape. <i>ELife</i> , 2021 , 10,	8.9	3
159	Replication and single-cycle delivery of SARS-CoV-2 replicons. <i>Science</i> , 2021 , 374, 1099-1106	33.3	7
158	Nanobody Repertoires for Exposing Vulnerabilities of SARS-CoV-2 2021 ,		4
157	One Ring to Rule them All? Structural and Functional Diversity in the Nuclear Pore Complex. <i>Trends in Biochemical Sciences</i> , 2021 , 46, 595-607	10.3	19
156	Heh2/Man1 may be an evolutionarily conserved sensor of NPC assembly state. <i>Molecular Biology of the Cell</i> , 2021 , 32, 1359-1373	3.5	4
155	Dissecting the Structural Dynamics of the Nuclear Pore Complex. <i>Molecular Cell</i> , 2021 , 81, 153-165.e7	17.6	11
154	Malaria parasites use a soluble RhopH complex for erythrocyte invasion and an integral form for nutrient uptake. <i>ELife</i> , 2021 , 10,	8.9	13
153	Measuring protein turnover and exchange in yeast macromolecular assemblies. <i>STAR Protocols</i> , 2021 , 2, 100800	1.4	0
152	Integrative structure and function of the yeast exocyst complex. <i>Protein Science</i> , 2020 , 29, 1486-1501	6.3	10
151	Crippling life support for SARS-CoV-2 and other viruses through synthetic lethality. <i>Journal of Cell Biology</i> , 2020 , 219,	7.3	9
150	Affinity proteomic dissection of the human nuclear cap-binding complex interactome. <i>Nucleic Acids Research</i> , 2020 , 48, 10456-10469	20.1	7
149	Analysis of Multivalent IDP Interactions: Stoichiometry, Affinity, and Local Concentration Effect Measurements. <i>Methods in Molecular Biology</i> , 2020 , 2141, 463-475	1.4	2
148	Interactions of nuclear transport factors and surface-conjugated FG nucleoporins: Insights and limitations. <i>PLoS ONE</i> , 2019 , 14, e0217897	3.7	4
147	Principles for Integrative Structural Biology Studies. <i>Cell</i> , 2019 , 177, 1384-1403	56.2	108

146	Pore timing: the evolutionary origins of the nucleus and nuclear pore complex. <i>F1000Research</i> , 2019 , 8,	3.6	24
145	Involvement in surface antigen expression by a moonlighting FG-repeat nucleoporin in trypanosomes. <i>Molecular Biology of the Cell</i> , 2018 , 29, 1100-1110	3.5	3
144	Integrative structure and functional anatomy of a nuclear pore complex. <i>Nature</i> , 2018 , 555, 475-482	50.4	280
143	Deciphering the "Fuzzy" Interaction of FG Nucleoporins and Transport Factors Using Small-Angle Neutron Scattering. <i>Structure</i> , 2018 , 26, 477-484.e4	5.2	8
142	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	5.4	32
141	Dissection of affinity captured LINE-1 macromolecular complexes. <i>ELife</i> , 2018 , 7,	8.9	38
140	Molecular Architecture of the Major Membrane Ring Component of the Nuclear Pore Complex. <i>Structure</i> , 2017 , 25, 434-445	5.2	31
139	Lineage-specific proteins essential for endocytosis in trypanosomes. <i>Journal of Cell Science</i> , 2017 , 130, 1379-1392	5.3	11
138	The Evolution of Organellar Coat Complexes and Organization of the Eukaryotic Cell. <i>Annual Review of Biochemistry</i> , 2017 , 86, 637-657	29.1	65
137	Comparative interactomics provides evidence for functional specialization of the nuclear pore complex. <i>Nucleus</i> , 2017 , 8, 340-352	3.9	11
136	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	9	26
135	The Trypanosome Exocyst: A Conserved Structure Revealing a New Role in Endocytosis. <i>PLoS Pathogens</i> , 2017 , 13, e1006063	7.6	19
134	Specialising the parasite nucleus: Pores, lamins, chromatin, and diversity. <i>PLoS Pathogens</i> , 2017 , 13, e1006670	7	7
133	Protein Complex Purification by Affinity Capture. <i>Cold Spring Harbor Protocols</i> , 2016 , 2016,	1.2	13
132	Purification and analysis of endogenous human RNA exosome complexes. <i>Rna</i> , 2016 , 22, 1467-75	5.8	11
131	Structure and Function of the Nuclear Pore Complex Cytoplasmic mRNA Export Platform. <i>Cell</i> , 2016 , 167, 1215-1228.e25	56.2	110
130	Developing genetic tools to exploit <i>Chaetomium thermophilum</i> for biochemical analyses of eukaryotic macromolecular assemblies. <i>Scientific Reports</i> , 2016 , 6, 20937	4.9	29
129	HIV-host interactome revealed directly from infected cells. <i>Nature Microbiology</i> , 2016 , 1, 16068	26.6	33

128	Co-dependence between trypanosome nuclear lamina components in nuclear stability and control of gene expression. <i>Nucleic Acids Research</i> , 2016 , 44, 10554-10570	20.1	13
127	Protein Complex Affinity Capture from Cryomilled Mammalian Cells. <i>Journal of Visualized Experiments</i> , 2016 ,	1.6	16
126	Optimizing selection of large animals for antibody production by screening immune response to standard vaccines. <i>Journal of Immunological Methods</i> , 2016 , 430, 56-60	2.5	11
125	Subunit connectivity, assembly determinants and architecture of the yeast exocyst complex. <i>Nature Structural and Molecular Biology</i> , 2016 , 23, 59-66	17.6	76
124	A Robust Workflow for Native Mass Spectrometric Analysis of Affinity-Isolated Endogenous Protein Assemblies. <i>Analytical Chemistry</i> , 2016 , 88, 2799-807	7.8	19
123	Characterization of L1-Ribonucleoprotein Particles. <i>Methods in Molecular Biology</i> , 2016 , 1400, 311-38	1.4	13
122	Density Gradient Ultracentrifugation to Isolate Endogenous Protein Complexes after Affinity Capture. <i>Cold Spring Harbor Protocols</i> , 2016 , 2016,	1.2	7
121	Interactome Mapping Reveals the Evolutionary History of the Nuclear Pore Complex. <i>PLoS Biology</i> , 2016 , 14, e1002365	9.7	64
120	High-Efficiency Isolation of Nuclear Envelope Protein Complexes from Trypanosomes. <i>Methods in Molecular Biology</i> , 2016 , 1411, 67-80	1.4	19
119	Revealing Higher Order Protein Structure Using Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2016 , 27, 952-65	3.5	45
118	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	11.5	63
117	Cilia and Nuclear Pore Proteins: Pore No More?. <i>Developmental Cell</i> , 2016 , 38, 445-6	10.2	3
116	Simple rules for passive diffusion through the nuclear pore complex. <i>Journal of Cell Biology</i> , 2016 , 215, 57-76	7.3	199
115	Optimized Affinity Capture of Yeast Protein Complexes. <i>Cold Spring Harbor Protocols</i> , 2016 , 2016,	1.2	9
114	Native Elution of Yeast Protein Complexes Obtained by Affinity Capture. <i>Cold Spring Harbor Protocols</i> , 2016 , 2016,	1.2	8
113	Engineered high-affinity nanobodies recognizing staphylococcal Protein A and suitable for native isolation of protein complexes. <i>Analytical Biochemistry</i> , 2015 , 477, 92-4	3.1	9
112	Rapid, optimized interactomic screening. <i>Nature Methods</i> , 2015 , 12, 553-60	21.6	53
111	A strategy for dissecting the architectures of native macromolecular assemblies. <i>Nature Methods</i> , 2015 , 12, 1135-8	21.6	94

110	The interactome challenge. <i>Journal of Cell Biology</i> , 2015 , 211, 729-32	7.3	11
109	Affinity proteomics to study endogenous protein complexes: pointers, pitfalls, preferences and perspectives. <i>BioTechniques</i> , 2015 , 58, 103-19	2.5	39
108	Altering nuclear pore complex function impacts longevity and mitochondrial function in <i>S. cerevisiae</i> . <i>Journal of Cell Biology</i> , 2015 , 208, 729-44	7.3	43
107	SEA you later alli-GATOR--a dynamic regulator of the TORC1 stress response pathway. <i>Journal of Cell Science</i> , 2015 , 128, 2219-28	5.3	37
106	The molecular mechanism of nuclear transport revealed by atomic-scale measurements. <i>ELife</i> , 2015 , 4,	8.9	93
105	A robust pipeline for rapid production of versatile nanobody repertoires. <i>Nature Methods</i> , 2014 , 11, 1253-60	6.0	253
104	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, 1421-36	3.5	19
103	Touching from a distance. <i>Nucleus</i> , 2014 , 5, 304-10	3.9	5
102	NPC mimics: probing the mechanism of nucleocytoplasmic transport. <i>Methods in Cell Biology</i> , 2014 , 122, 379-93	1.8	1
101	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, 2927-43	7.6	122
100	Enriching the pore: splendid complexity from humble origins. <i>Traffic</i> , 2014 , 15, 141-56	5.7	34
99	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, 2911-26	7.6	54
98	Molecular architecture and function of the SEA complex, a modulator of the TORC1 pathway. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 2855-70	7.6	52
97	Cancer and the nuclear pore complex. <i>Advances in Experimental Medicine and Biology</i> , 2014 , 773, 285-307	3.6	74
96	Affinity proteomics reveals human host factors implicated in discrete stages of LINE-1 retrotransposition. <i>Cell</i> , 2013 , 155, 1034-48	56.2	133
95	The human cap-binding complex is functionally connected to the nuclear RNA exosome. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 1367-76	17.6	157
94	Structure, dynamics, evolution, and function of a major scaffold component in the nuclear pore complex. <i>Structure</i> , 2013 , 21, 560-71	5.2	48
93	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, 3920-38	3.5	80

92	Supervillin binding to myosin II and synergism with anillin are required for cytokinesis. <i>Molecular Biology of the Cell</i> , 2013 , 24, 3603-19	3.5	19
91	Improved native isolation of endogenous Protein A-tagged protein complexes. <i>BioTechniques</i> , 2013 , 54, 213-6	2.5	10
90	Ciliary and nuclear transport: different places, similar routes?. <i>Developmental Cell</i> , 2012 , 22, 693-4	10.2	15
89	The yeast nuclear pore complex and transport through it. <i>Genetics</i> , 2012 , 190, 855-83	4	109
88	NUP-1 Is a large coiled-coil nucleoskeletal protein in trypanosomes with lamin-like functions. <i>PLoS Biology</i> , 2012 , 10, e1001287	9.7	86
87	Improved methodology for the affinity isolation of human protein complexes expressed at near endogenous levels. <i>BioTechniques</i> , 2012 , 1-6	2.5	36
86	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, 2110-6	4.2	6
85	A jumbo problem: mapping the structure and functions of the nuclear pore complex. <i>Current Opinion in Cell Biology</i> , 2012 , 24, 92-9	9	42
84	Telomeres, tethers and trypanosomes. <i>Nucleus</i> , 2012 , 3, 478-86	3.9	19
83	Nucleocytoplasmic transport: a role for nonspecific competition in karyopherin-nucleoporin interactions. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 31-46	7.6	46
82	Proteomics on the rims: insights into the biology of the nuclear envelope and flagellar pocket of trypanosomes. <i>Parasitology</i> , 2012 , 139, 1158-67	2.7	10
81	Structure-function mapping of a heptameric module in the nuclear pore complex. <i>Journal of Cell Biology</i> , 2012 , 196, 419-34	7.3	95
80	A 3D Physical Model of Karyopherin- β . <i>FASEB Journal</i> , 2012 , 26, lb268	0.9	
79	Nuclear export dynamics of RNA-protein complexes. <i>Nature</i> , 2011 , 475, 333-41	50.4	142
78	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, 1672-7	4.2	16
77	A conserved coatamer-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	7.6	95
76	A cell cycle phosphoproteome of the yeast centrosome. <i>Science</i> , 2011 , 332, 1557-61	33.3	80
75	A novel coatamer-related SEA complex dynamically associates with the vacuole in yeast and is implicated in the response to nitrogen starvation. <i>Autophagy</i> , 2011 , 7, 1392-3	10.2	14

74	Evolution: On a bender--BARs, ESCRTs, COPs, and finally getting your coat. <i>Journal of Cell Biology</i> , 2011 , 193, 963-72	7.3	78
73	The nuclear pore complex: bridging nuclear transport and gene regulation. <i>Nature Reviews Molecular Cell Biology</i> , 2010 , 11, 490-501	48.7	382
72	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, 7803-14	6.6	127
71	The nuclear pore complex and nuclear transport. <i>Cold Spring Harbor Perspectives in Biology</i> , 2010 , 2, a000562	15.6	464
70	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, 6720-32	6.6	81
69	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	7.6	58
68	Enhancement of transport selectivity through nano-channels by non-specific competition. <i>PLoS Computational Biology</i> , 2010 , 6, e1000804	5	46
67	The mechanism of nucleocytoplasmic transport through the nuclear pore complex. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2010 , 75, 567-84	3.9	34
66	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, 1992-8	4.2	9
65	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, 2119-30	7.6	169
64	Nuclear pore complex biogenesis. <i>Current Opinion in Cell Biology</i> , 2009 , 21, 603-12	9	53
63	Artificial nanopores that mimic the transport selectivity of the nuclear pore complex. <i>Nature</i> , 2009 , 457, 1023-7	50.4	226
62	Rrp17p is a eukaryotic exonuclease required for 5'end processing of Pre-60S ribosomal RNA. <i>Molecular Cell</i> , 2009 , 36, 768-81	17.6	64
61	Integrative Structure Determination of Protein Assemblies by Satisfaction of Spatial Restraints. <i>Computational Biology</i> , 2008 , 99-114	0.7	6
60	Human cytomegalovirus protein UL38 inhibits host cell stress responses by antagonizing the tuberous sclerosis protein complex. <i>Cell Host and Microbe</i> , 2008 , 3, 253-62	23.4	149
59	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, 1244-50	5.6	14
58	The peroxisome: a production in four acts. <i>Journal of Cell Biology</i> , 2008 , 181, 185-7	7.3	2
57	High-yield isolation and subcellular proteomic characterization of nuclear and subnuclear structures from trypanosomes. <i>Methods in Molecular Biology</i> , 2008 , 463, 77-92	1.4	19

56	Comprehensive analysis of diverse ribonucleoprotein complexes. <i>Nature Methods</i> , 2007 , 4, 951-6	21.6	212
55	Determining the architectures of macromolecular assemblies. <i>Nature</i> , 2007 , 450, 683-94	50.4	437
54	The molecular architecture of the nuclear pore complex. <i>Nature</i> , 2007 , 450, 695-701	50.4	830
53	Assembly factors Rpf2 and Rrs1 recruit 5S rRNA and ribosomal proteins rpL5 and rpL11 into nascent ribosomes. <i>Genes and Development</i> , 2007 , 21, 2580-92	12.6	147
52	Efficiency, selectivity, and robustness of nucleocytoplasmic transport. <i>PLoS Computational Biology</i> , 2007 , 3, e125	5	82
51	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, 1354-66	20.1	34
50	Protease accessibility laddering: a proteomic tool for probing protein structure. <i>Structure</i> , 2006 , 14, 653-60	30	
49	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, 2172-7	11.5	231
48	Induction of autophagy in axonal dystrophy and degeneration. <i>Journal of Neuroscience</i> , 2006 , 26, 8057-68	6	270
47	Simple kinetic relationships and nonspecific competition govern nuclear import rates in vivo. <i>Journal of Cell Biology</i> , 2006 , 175, 579-93	7.3	112
46	Tracking and elucidating alphavirus-host protein interactions. <i>Journal of Biological Chemistry</i> , 2006 , 281, 30269-78	5.4	142
45	Studying nuclear protein import in yeast. <i>Methods</i> , 2006 , 39, 291-308	4.6	10
44	I-DIRT, a general method for distinguishing between specific and nonspecific protein interactions. <i>Journal of Proteome Research</i> , 2005 , 4, 1752-6	5.6	119
43	A method for the rapid and efficient elution of native affinity-purified protein A tagged complexes. <i>Journal of Proteome Research</i> , 2005 , 4, 2250-6	5.6	16
42	Proteomic and genomic characterization of chromatin complexes at a boundary. <i>Journal of Cell Biology</i> , 2005 , 169, 35-47	7.3	117
41	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, 225-35	7.3	68
40	Fluorescent proteins as proteomic probes. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 1933-41	7.6	202
39	Characterization of Karyopherin Cargoes Reveals Unique Mechanisms of Kap121p-Mediated Nuclear Import. <i>Molecular and Cellular Biology</i> , 2004 , 24, 10099-10099	4.8	78

38	Characterization of karyopherin cargoes reveals unique mechanisms of Kap121p-mediated nuclear import. <i>Molecular and Cellular Biology</i> , 2004 , 24, 8487-503	4.8	46
37	Components of coated vesicles and nuclear pore complexes share a common molecular architecture. <i>PLoS Biology</i> , 2004 , 2, e380	9.7	318
36	Targeted proteomic study of the cyclin-Cdk module. <i>Molecular Cell</i> , 2004 , 14, 699-711	17.6	100
35	Genetic and biochemical evaluation of the importance of Cdc6 in regulating mitotic exit. <i>Molecular Biology of the Cell</i> , 2003 , 14, 4592-604	3.5	42
34	Virtual gating and nuclear transport: the hole picture. <i>Trends in Cell Biology</i> , 2003 , 13, 622-8	18.3	306
33	Kap121p-mediated nuclear import is required for mating and cellular differentiation in yeast. <i>Molecular and Cellular Biology</i> , 2002 , 22, 2544-55	4.8	41
32	Isolation of nuclear envelope from <i>Saccharomyces cerevisiae</i> . <i>Methods in Enzymology</i> , 2002 , 351, 394-408	8.7	10
31	A tense time for the nuclear envelope. <i>Cell</i> , 2002 , 108, 301-4	56.2	13
30	Cleave to leave: structural insights into the dynamic organization of the nuclear pore complex. <i>Molecular Cell</i> , 2002 , 10, 221-3	17.6	2
29	The structure and composition of the yeast NPC. <i>Results and Problems in Cell Differentiation</i> , 2002 , 35, 1-23	1.4	2
28	Isolation and characterization of subnuclear compartments from <i>Trypanosoma brucei</i> . Identification of a major repetitive nuclear lamina component. <i>Journal of Biological Chemistry</i> , 2001 , 276, 38261-71	5.4	60
27	The nuclear pore complex as a transport machine. <i>Journal of Biological Chemistry</i> , 2001 , 276, 16593-6	5.4	216
26	Nup2p dynamically associates with the distal regions of the yeast nuclear pore complex. <i>Journal of Cell Biology</i> , 2001 , 153, 1465-78	7.3	137
25	Composition and functional characterization of yeast 66S ribosome assembly intermediates. <i>Molecular Cell</i> , 2001 , 8, 505-15	17.6	263
24	The road to ribosomes. Filling potholes in the export pathway. <i>Journal of Cell Biology</i> , 2000 , 151, F23-6	7.3	30
23	The yeast nuclear pore complex: composition, architecture, and transport mechanism. <i>Journal of Cell Biology</i> , 2000 , 148, 635-51	7.3	1207
22	Pore relations: nuclear pore complexes and nucleocytoplasmic exchange. <i>Essays in Biochemistry</i> , 2000 , 36, 75-88	7.6	22
21	Proteins connecting the nuclear pore complex with the nuclear interior. <i>Journal of Cell Biology</i> , 1999 , 144, 839-55	7.3	189

20	Karyopherins and kissing cousins. <i>Trends in Cell Biology</i> , 1998 , 8, 184-8	18.3	199
19	Three-dimensional architecture of the isolated yeast nuclear pore complex: functional and evolutionary implications. <i>Molecular Cell</i> , 1998 , 1, 223-34	17.6	306
18	<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, 1789-800	7.3	117
17	A distinct nuclear import pathway used by ribosomal proteins. <i>Cell</i> , 1997 , 89, 715-25	56.2	301
16	The yeast spindle pole body is assembled around a central crystal of Spc42p. <i>Cell</i> , 1997 , 89, 1077-86	56.2	157
15	Kap104p: a karyopherin involved in the nuclear transport of messenger RNA binding proteins. <i>Science</i> , 1996 , 274, 624-7	33.3	284
14	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, 1153-62	7.3	86
13	Nup120p: a yeast nucleoporin required for NPC distribution and mRNA transport. <i>Journal of Cell Biology</i> , 1995 , 131, 1659-75	7.3	127
12	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, 1133-48	7.3	167
11	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, 19017-21	5.4	119
10	Isolation and characterization of nuclear envelopes from the yeast <i>Saccharomyces</i> . <i>Journal of Cell Biology</i> , 1995 , 131, 19-31	7.3	67
9	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, 1187-91	11.5	78
8	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	7.3	125
7	Pores for thought: nuclear pore complex proteins. <i>Trends in Cell Biology</i> , 1994 , 4, 357-65	18.3	253
6	Isolation of the yeast nuclear pore complex. <i>Journal of Cell Biology</i> , 1993 , 123, 771-83	7.3	244
5	A new family of yeast nuclear pore complex proteins. <i>Journal of Cell Biology</i> , 1992 , 119, 705-23	7.3	235
4	Yeast spindle pole body components. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 1991 , 56, 687-92	3.9	23
3	Components of the yeast spindle and spindle pole body. <i>Journal of Cell Biology</i> , 1990 , 111, 1913-27	7.3	238

2	Rapid isolation of functionally intact nuclei from the yeast <i>Saccharomyces</i>	4
1	Heh2/Man1 may be an evolutionarily conserved sensor of NPC assembly state	1