Michael P Rout

List of Publications by Citations

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	The yeast nuclear pore complex: composition, architecture, and transport mechanism. *Journal of Cell Biology*, **2000**, 148, 635-51	7.3	1207
162	The molecular architecture of the nuclear pore complex. *Nature*, **2007**, 450, 695-701	50.4	830
161	The nuclear pore complex and nuclear transport. *Cold Spring Harbor Perspectives in Biology*, **2010**, 2, a000562	8.2	464
160	Determining the architectures of macromolecular assemblies. *Nature*, **2007**, 450, 683-94	50.4	437
159	The nuclear pore complex: bridging nuclear transport and gene regulation. *Nature Reviews Molecular Cell Biology*, **2010**, 11, 490-501	48.7	382
158	Components of coated vesicles and nuclear pore complexes share a common molecular architecture. *PLoS Biology*, **2004**, 2, e380	9.7	318
157	Three-dimensional architecture of the isolated yeast nuclear pore complex: functional and evolutionary implications. *Molecular Cell*, **1998**, 1, 223-34	17.6	306
156	Virtual gating and nuclear transport: the hole picture. *Trends in Cell Biology*, **2003**, 13, 622-8	18.3	306
155	A distinct nuclear import pathway used by ribosomal proteins. *Cell*, **1997**, 89, 715-25	56.2	301
154	Kap104p: a karyopherin involved in the nuclear transport of messenger RNA binding proteins. *Science*, **1996**, 274, 624-7	33.3	284
153	Integrative structure and functional anatomy of a nuclear pore complex. *Nature*, **2018**, 555, 475-482	50.4	280
152	Induction of autophagy in axonal dystrophy and degeneration. *Journal of Neuroscience*, **2006**, 26, 8057-68	8.6	270
151	Composition and functional characterization of yeast 66S ribosome assembly intermediates. *Molecular Cell*, **2001**, 8, 505-15	17.6	263
150	A robust pipeline for rapid production of versatile nanobody repertoires. *Nature Methods*, **2014**, 11, 1253-60	25.0	253
149	Pores for thought: nuclear pore complex proteins. *Trends in Cell Biology*, **1994**, 4, 357-65	18.3	253
148	Isolation of the yeast nuclear pore complex. *Journal of Cell Biology*, **1993**, 123, 771-83	7.3	244
147	Components of the yeast spindle and spindle pole body. *Journal of Cell Biology*, **1990**, 111, 1913-27	7.3	238

146	A new family of yeast nuclear pore complex proteins. *Journal of Cell Biology*, **1992**, 119, 705-23	7.3	235
145	Simple fold composition and modular architecture of the nuclear pore complex. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 2172-7	11.5	231
144	Artificial nanopores that mimic the transport selectivity of the nuclear pore complex. *Nature*, **2009**, 457, 1023-7	50.4	226
143	The nuclear pore complex as a transport machine. *Journal of Biological Chemistry*, **2001**, 276, 16593-6	5.4	216
142	Comprehensive analysis of diverse ribonucleoprotein complexes. *Nature Methods*, **2007**, 4, 951-6	21.6	212
141	Fluorescent proteins as proteomic probes. *Molecular and Cellular Proteomics*, **2005**, 4, 1933-41	7.6	202
140	Karyopherins and kissing cousins. *Trends in Cell Biology*, **1998**, 8, 184-8	18.3	199
139	Simple rules for passive diffusion through the nuclear pore complex. *Journal of Cell Biology*, **2016**, 215, 57-76	7.3	199
138	Proteins connecting the nuclear pore complex with the nuclear interior. *Journal of Cell Biology*, **1999**, 144, 839-55	7.3	189
137	Evidence for a shared nuclear pore complex architecture that is conserved from the last common eukaryotic ancestor. *Molecular and Cellular Proteomics*, **2009**, 8, 2119-30	7.6	169
136	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. *Journal of Cell Biology*, **1995**, 131, 1133-48	7.3	167
135	The human cap-binding complex is functionally connected to the nuclear RNA exosome. *Nature Structural and Molecular Biology*, **2013**, 20, 1367-76	17.6	157
134	The yeast spindle pole body is assembled around a central crystal of Spc42p. *Cell*, **1997**, 89, 1077-86	56.2	157
133	Human cytomegalovirus protein UL38 inhibits host cell stress responses by antagonizing the tuberous sclerosis protein complex. *Cell Host and Microbe*, **2008**, 3, 253-62	23.4	149
132	Assembly factors Rpf2 and Rrs1 recruit 5S rRNA and ribosomal proteins rpL5 and rpL11 into nascent ribosomes. *Genes and Development*, **2007**, 21, 2580-92	12.6	147
131	Nuclear export dynamics of RNA-protein complexes. *Nature*, **2011**, 475, 333-41	50.4	142
130	Tracking and elucidating alphavirus-host protein interactions. *Journal of Biological Chemistry*, **2006**, 281, 30269-78	5.4	142
129	Nup2p dynamically associates with the distal regions of the yeast nuclear pore complex. *Journal of Cell Biology*, **2001**, 153, 1465-78	7.3	137

128	Affinity proteomics reveals human host factors implicated in discrete stages of LINE-1 retrotransposition. *Cell*, **2013**, 155, 1034-48	56.2	133
127	Human cytomegalovirus pUL83 stimulates activity of the viral immediate-early promoter through its interaction with the cellular IFI16 protein. *Journal of Virology*, **2010**, 84, 7803-14	6.6	127
126	Nup120p: a yeast nucleoporin required for NPC distribution and mRNA transport. *Journal of Cell Biology*, **1995**, 131, 1659-75	7.3	127
125	POM152 is an integral protein of the pore membrane domain of the yeast nuclear envelope. *Journal of Cell Biology*, **1994**, 125, 31-42	7.3	125
124	Structural characterization by cross-linking reveals the detailed architecture of a coatomer-related heptameric module from the nuclear pore complex. *Molecular and Cellular Proteomics*, **2014**, 13, 2927-43	7.6	122
123	I-DIRT, a general method for distinguishing between specific and nonspecific protein interactions. *Journal of Proteome Research*, **2005**, 4, 1752-6	5.6	119
122	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. *Journal of Biological Chemistry*, **1995**, 270, 19017-21	5.4	119
121	Proteomic and genomic characterization of chromatin complexes at a boundary. *Journal of Cell Biology*, **2005**, 169, 35-47	7.3	117
120	Saccharomyces cerevisiae Ndc1p is a shared component of nuclear pore complexes and spindle pole bodies. *Journal of Cell Biology*, **1998**, 143, 1789-800	7.3	117
119	Simple kinetic relationships and nonspecific competition govern nuclear import rates in vivo. *Journal of Cell Biology*, **2006**, 175, 579-93	7.3	112
118	Structure and Function of the Nuclear Pore Complex Cytoplasmic mRNA Export Platform. *Cell*, **2016**, 167, 1215-1228.e25	56.2	110
117	The yeast nuclear pore complex and transport through it. *Genetics*, **2012**, 190, 855-83	4	109
116	Principles for Integrative Structural Biology Studies. *Cell*, **2019**, 177, 1384-1403	56.2	108
115	Targeted proteomic study of the cyclin-Cdk module. *Molecular Cell*, **2004**, 14, 699-711	17.6	100
114	A conserved coatomer-related complex containing Sec13 and Seh1 dynamically associates with the vacuole in Saccharomyces cerevisiae. *Molecular and Cellular Proteomics*, **2011**, 10, M110.006478	7.6	95
113	Structure-function mapping of a heptameric module in the nuclear pore complex. *Journal of Cell Biology*, **2012**, 196, 419-34	7.3	95
112	A strategy for dissecting the architectures of native macromolecular assemblies. *Nature Methods*, **2015**, 12, 1135-8	21.6	94
111	The molecular mechanism of nuclear transport revealed by atomic-scale measurements. *ELife*, **2015** , 4,	8.9	93

110	NUP-1 Is a large coiled-coil nucleoskeletal protein in trypanosomes with lamin-like functions. *PLoS Biology*, **2012**, 10, e1001287	9.7	86
109	The yeast nucleoporin Nup188p interacts genetically and physically with the core structures of the nuclear pore complex. *Journal of Cell Biology*, **1996**, 133, 1153-62	7.3	86
108	Efficiency, selectivity, and robustness of nucleocytoplasmic transport. *PLoS Computational Biology*, **2007**, 3, e125	5	82
107	Host factors associated with the Sindbis virus RNA-dependent RNA polymerase: role for G3BP1 and G3BP2 in virus replication. *Journal of Virology*, **2010**, 84, 6720-32	6.6	81
106	The nuclear basket proteins Mlp1p and Mlp2p are part of a dynamic interactome including Esc1p and the proteasome. *Molecular Biology of the Cell*, **2013**, 24, 3920-38	3.5	80
105	A cell cycle phosphoproteome of the yeast centrosome. *Science*, **2011**, 332, 1557-61	33.3	80
104	Evolution: On a bender--BARs, ESCRTs, COPs, and finally getting your coat. *Journal of Cell Biology*, **2011**, 193, 963-72	7.3	78
103	Characterization of Karyopherin Cargoes Reveals Unique Mechanisms of Kap121p-Mediated Nuclear Import. *Molecular and Cellular Biology*, **2004**, 24, 10099-10099	4.8	78
102	Disruption of the nucleoporin gene NUP133 results in clustering of nuclear pore complexes. *Proceedings of the National Academy of Sciences of the United States of America*, **1995**, 92, 1187-91	11.5	78
101	Subunit connectivity, assembly determinants and architecture of the yeast exocyst complex. *Nature Structural and Molecular Biology*, **2016**, 23, 59-66	17.6	76
100	Cancer and the nuclear pore complex. *Advances in Experimental Medicine and Biology*, **2014**, 773, 285-307	3.6	74
99	The nuclear pore complex-associated protein, Mlp2p, binds to the yeast spindle pole body and promotes its efficient assembly. *Journal of Cell Biology*, **2005**, 170, 225-35	7.3	68
98	Isolation and characterization of nuclear envelopes from the yeast Saccharomyces. *Journal of Cell Biology*, **1995**, 131, 19-31	7.3	67
97	The Evolution of Organellar Coat Complexes and Organization of the Eukaryotic Cell. *Annual Review of Biochemistry*, **2017**, 86, 637-657	29.1	65
96	Rrp17p is a eukaryotic exonuclease required for 5Vend processing of Pre-60S ribosomal RNA. *Molecular Cell*, **2009**, 36, 768-81	17.6	64
95	Interactome Mapping Reveals the Evolutionary History of the Nuclear Pore Complex. *PLoS Biology*, **2016**, 14, e1002365	9.7	64
94	Slide-and-exchange mechanism for rapid and selective transport through the nuclear pore complex. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, E2489-97	11.5	63
93	Isolation and characterization of subnuclear compartments from Trypanosoma brucei. Identification of a major repetitive nuclear lamina component. *Journal of Biological Chemistry*, **2001**, 276, 38261-71	5.4	60

92	Human cytomegalovirus UL29/28 protein interacts with components of the NuRD complex which promote accumulation of immediate-early RNA. *PLoS Pathogens*, **2010**, 6, e1000965	7.6	58
91	Integrative structure-function mapping of the nucleoporin Nup133 suggests a conserved mechanism for membrane anchoring of the nuclear pore complex. *Molecular and Cellular Proteomics*, **2014**, 13, 2911-26	7.6	54
90	Rapid, optimized interactomic screening. *Nature Methods*, **2015**, 12, 553-60	21.6	53
89	Nuclear pore complex biogenesis. *Current Opinion in Cell Biology*, **2009**, 21, 603-12	9	53
88	Molecular architecture and function of the SEA complex, a modulator of the TORC1 pathway. *Molecular and Cellular Proteomics*, **2014**, 13, 2855-70	7.6	52
87	Structure, dynamics, evolution, and function of a major scaffold component in the nuclear pore complex. *Structure*, **2013**, 21, 560-71	5.2	48
86	Enhancement of transport selectivity through nano-channels by non-specific competition. *PLoS Computational Biology*, **2010**, 6, e1000804	5	46
85	Nucleocytoplasmic transport: a role for nonspecific competition in karyopherin-nucleoporin interactions. *Molecular and Cellular Proteomics*, **2012**, 11, 31-46	7.6	46
84	Characterization of karyopherin cargoes reveals unique mechanisms of Kap121p-mediated nuclear import. *Molecular and Cellular Biology*, **2004**, 24, 8487-503	4.8	46
83	Revealing Higher Order Protein Structure Using Mass Spectrometry. *Journal of the American Society for Mass Spectrometry*, **2016**, 27, 952-65	3.5	45
82	Altering nuclear pore complex function impacts longevity and mitochondrial function in S. cerevisiae. *Journal of Cell Biology*, **2015**, 208, 729-44	7.3	43
81	A jumbo problem: mapping the structure and functions of the nuclear pore complex. *Current Opinion in Cell Biology*, **2012**, 24, 92-9	9	42
80	Genetic and biochemical evaluation of the importance of Cdc6 in regulating mitotic exit. *Molecular Biology of the Cell*, **2003**, 14, 4592-604	3.5	42
79	Kap121p-mediated nuclear import is required for mating and cellular differentiation in yeast. *Molecular and Cellular Biology*, **2002**, 22, 2544-55	4.8	41
78	Affinity proteomics to study endogenous protein complexes: pointers, pitfalls, preferences and perspectives. *BioTechniques*, **2015**, 58, 103-19	2.5	39
77	Dissection of affinity captured LINE-1 macromolecular complexes. *ELife*, **2018**, 7,	8.9	38
76	SEA you later alli-GATOR--a dynamic regulator of the TORC1 stress response pathway. *Journal of Cell Science*, **2015**, 128, 2219-28	5.3	37
75	Improved methodology for the affinity isolation of human protein complexes expressed at near endogenous levels. *BioTechniques*, **2012**, 1-6	2.5	36

74	Enriching the pore: splendid complexity from humble origins. *Traffic*, **2014**, 15, 141-56	5.7	34
73	The mechanism of nucleocytoplasmic transport through the nuclear pore complex. *Cold Spring Harbor Symposia on Quantitative Biology*, **2010**, 75, 567-84	3.9	34
72	Yeast Rrp14p is required for ribosomal subunit synthesis and for correct positioning of the mitotic spindle during mitosis. *Nucleic Acids Research*, **2007**, 35, 1354-66	20.1	34
71	HIV-host interactome revealed directly from infected cells. *Nature Microbiology*, **2016**, 1, 16068	26.6	33
70	Thermodynamic characterization of the multivalent interactions underlying rapid and selective translocation through the nuclear pore complex. *Journal of Biological Chemistry*, **2018**, 293, 4555-4563	5.4	32
69	Molecular Architecture of the Major Membrane Ring Component of the Nuclear Pore Complex. *Structure*, **2017**, 25, 434-445	5.2	31
68	Protease accessibility laddering: a proteomic tool for probing protein structure. *Structure*, **2006**, 14, 653-60	5.2	30
67	The road to ribosomes. Filling potholes in the export pathway. *Journal of Cell Biology*, **2000**, 151, F23-6	7.3	30
66	Developing genetic tools to exploit Chaetomium thermophilum for biochemical analyses of eukaryotic macromolecular assemblies. *Scientific Reports*, **2016**, 6, 20937	4.9	29
65	The nuclear pore complex core scaffold and permeability barrier: variations of a common theme. *Current Opinion in Cell Biology*, **2017**, 46, 110-118	9	26
64	Pore timing: the evolutionary origins of the nucleus and nuclear pore complex. *F1000Research*, **2019**, 8,	3.6	24
63	Yeast spindle pole body components. *Cold Spring Harbor Symposia on Quantitative Biology*, **1991**, 56, 687-92	3.9	23
62	Pore relations: nuclear pore complexes and nucleocytoplasmic exchange. *Essays in Biochemistry*, **2000**, 36, 75-88	7.6	22
61	A Robust Workflow for Native Mass Spectrometric Analysis of Affinity-Isolated Endogenous Protein Assemblies. *Analytical Chemistry*, **2016**, 88, 2799-807	7.8	19
60	Nuclear pore complex evolution: a trypanosome Mlp analogue functions in chromosomal segregation but lacks transcriptional barrier activity. *Molecular Biology of the Cell*, **2014**, 25, 1421-36	3.5	19
59	Supervillin binding to myosin II and synergism with anillin are required for cytokinesis. *Molecular Biology of the Cell*, **2013**, 24, 3603-19	3.5	19
58	Telomeres, tethers and trypanosomes. *Nucleus*, **2012**, 3, 478-86	3.9	19
57	The Trypanosome Exocyst: A Conserved Structure Revealing a New Role in Endocytosis. *PLoS Pathogens*, **2017**, 13, e1006063	7.6	19

56	High-yield isolation and subcellular proteomic characterization of nuclear and subnuclear structures from trypanosomes. *Methods in Molecular Biology*, **2008**, 463, 77-92	1.4	19
55	One Ring to Rule them All? Structural and Functional Diversity in the Nuclear Pore Complex. *Trends in Biochemical Sciences*, **2021**, 46, 595-607	10.3	19
54	High-Efficiency Isolation of Nuclear Envelope Protein Complexes from Trypanosomes. *Methods in Molecular Biology*, **2016**, 1411, 67-80	1.4	19
53	Comprehensive structure and functional adaptations of the yeast nuclear pore complex.. *Cell*, **2021**,	56.2	18
52	Protein Complex Affinity Capture from Cryomilled Mammalian Cells. *Journal of Visualized Experiments*, **2016**,	1.6	16
51	Structure of the C-terminal domain of Saccharomyces cerevisiae Nup133, a component of the nuclear pore complex. *Proteins: Structure, Function and Bioinformatics*, **2011**, 79, 1672-7	4.2	16
50	A method for the rapid and efficient elution of native affinity-purified protein A tagged complexes. *Journal of Proteome Research*, **2005**, 4, 2250-6	5.6	16
49	Ciliary and nuclear transport: different places, similar routes?. *Developmental Cell*, **2012**, 22, 693-4	10.2	15
48	A novel coatomer-related SEA complex dynamically associates with the vacuole in yeast and is implicated in the response to nitrogen starvation. *Autophagy*, **2011**, 7, 1392-3	10.2	14
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46	Protein Complex Purification by Affinity Capture. *Cold Spring Harbor Protocols*, **2016**, 2016,	1.2	13
45	Co-dependence between trypanosome nuclear lamina components in nuclear stability and control of gene expression. *Nucleic Acids Research*, **2016**, 44, 10554-10570	20.1	13
44	Characterization of L1-Ribonucleoprotein Particles. *Methods in Molecular Biology*, **2016**, 1400, 311-38	1.4	13
43	A tense time for the nuclear envelope. *Cell*, **2002**, 108, 301-4	56.2	13
42	Malaria parasites use a soluble RhopH complex for erythrocyte invasion and an integral form for nutrient uptake. *ELife*, **2021**, 10,	8.9	13
41	Lineage-specific proteins essential for endocytosis in trypanosomes. *Journal of Cell Science*, **2017**, 130, 1379-1392	5.3	11
40	Comparative interactomics provides evidence for functional specialization of the nuclear pore complex. *Nucleus*, **2017**, 8, 340-352	3.9	11
39	Purification and analysis of endogenous human RNA exosome complexes. *Rna*, **2016**, 22, 1467-75	5.8	11

38	Optimizing selection of large animals for antibody production by screening immune response to standard vaccines. *Journal of Immunological Methods*, **2016**, 430, 56-60	2.5	11
37	The interactome challenge. *Journal of Cell Biology*, **2015**, 211, 729-32	7.3	11
36	Dissecting the Structural Dynamics of the Nuclear Pore Complex. *Molecular Cell*, **2021**, 81, 153-165.e7	17.6	11
35	Integrative structure and function of the yeast exocyst complex. *Protein Science*, **2020**, 29, 1486-1501	6.3	10
34	Improved native isolation of endogenous Protein A-tagged protein complexes. *BioTechniques*, **2013**, 54, 213-6	2.5	10
33	Proteomics on the rims: insights into the biology of the nuclear envelope and flagellar pocket of trypanosomes. *Parasitology*, **2012**, 139, 1158-67	2.7	10
32	Studying nuclear protein import in yeast. *Methods*, **2006**, 39, 291-308	4.6	10
31	Isolation of nuclear envelope from Saccharomyces cerevisiae. *Methods in Enzymology*, **2002**, 351, 394-408	1.7	10
30	Engineered high-affinity nanobodies recognizing staphylococcal Protein A and suitable for native isolation of protein complexes. *Analytical Biochemistry*, **2015**, 477, 92-4	3.1	9
29	Structures of the autoproteolytic domain from the Saccharomyces cerevisiae nuclear pore complex component, Nup145. *Proteins: Structure, Function and Bioinformatics*, **2010**, 78, 1992-8	4.2	9
28	Crippling life support for SARS-CoV-2 and other viruses through synthetic lethality. *Journal of Cell Biology*, **2020**, 219,	7.3	9
27	Optimized Affinity Capture of Yeast Protein Complexes. *Cold Spring Harbor Protocols*, **2016**, 2016,	1.2	9
26	Deciphering the "Fuzzy" Interaction of FG Nucleoporins and Transport Factors Using Small-Angle Neutron Scattering. *Structure*, **2018**, 26, 477-484.e4	5.2	8
25	Native Elution of Yeast Protein Complexes Obtained by Affinity Capture. *Cold Spring Harbor Protocols*, **2016**, 2016,	1.2	8
24	Specialising the parasite nucleus: Pores, lamins, chromatin, and diversity. *PLoS Pathogens*, **2017**, 13, e1006170	7.6	7
23	Replication and single-cycle delivery of SARS-CoV-2 replicons. *Science*, **2021**, 374, 1099-1106	33.3	7
22	Density Gradient Ultracentrifugation to Isolate Endogenous Protein Complexes after Affinity Capture. *Cold Spring Harbor Protocols*, **2016**, 2016,	1.2	7
21	Affinity proteomic dissection of the human nuclear cap-binding complex interactome. *Nucleic Acids Research*, **2020**, 48, 10456-10469	20.1	7

20	Atomic structure of the nuclear pore complex targeting domain of a Nup116 homologue from the yeast, Candida glabrata. *Proteins: Structure, Function and Bioinformatics*, **2012**, 80, 2110-6	4.2	6
19	Integrative Structure Determination of Protein Assemblies by Satisfaction of Spatial Restraints. *Computational Biology*, **2008**, 99-114	0.7	6
18	Touching from a distance. *Nucleus*, **2014**, 5, 304-10	3.9	5
17	Interactions of nuclear transport factors and surface-conjugated FG nucleoporins: Insights and limitations. *PLoS ONE*, **2019**, 14, e0217897	3.7	4
16	Rapid isolation of functionally intact nuclei from the yeast Saccharomyces		4
15	Nanobody Repertoires for Exposing Vulnerabilities of SARS-CoV-2 **2021**,		4
14	Heh2/Man1 may be an evolutionarily conserved sensor of NPC assembly state. *Molecular Biology of the Cell*, **2021**, 32, 1359-1373	3.5	4
13	Involvement in surface antigen expression by a moonlighting FG-repeat nucleoporin in trypanosomes. *Molecular Biology of the Cell*, **2018**, 29, 1100-1110	3.5	3
12	Highly synergistic combinations of nanobodies that target SARS-CoV-2 and are resistant to escape. *ELife*, **2021**, 10,	8.9	3
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10	The peroxisome: a production in four acts. *Journal of Cell Biology*, **2008**, 181, 185-7	7.3	2
9	Cleave to leave: structural insights into the dynamic organization of the nuclear pore complex. *Molecular Cell*, **2002**, 10, 221-3	17.6	2
8	The structure and composition of the yeast NPC. *Results and Problems in Cell Differentiation*, **2002**, 35, 1-23	1.4	2
7	Analysis of Multivalent IDP Interactions: Stoichiometry, Affinity, and Local Concentration Effect Measurements. *Methods in Molecular Biology*, **2020**, 2141, 463-475	1.4	2
6	NPC mimics: probing the mechanism of nucleocytoplasmic transport. *Methods in Cell Biology*, **2014**, 122, 379-93	1.8	1
5	Heh2/Man1 may be an evolutionarily conserved sensor of NPC assembly state		1
4	Proteomic elucidation of the targets and primary functions of the picornavirus 2A protease.. *Journal of Biological Chemistry*, **2022**, 101882	5.4	1
3	Measuring protein turnover and exchange in yeast macromolecular assemblies. *STAR Protocols*, **2021**, 2, 100800	1.4	0

2	Affinity Isolation of Endogenous Saccharomyces Cerevisiae Nuclear Pore Complexes.. *Methods in Molecular Biology*, **2022**, 2502, 3-34	1.4	0
1	A 3D Physical Model of Karyopherin-β. *FASEB Journal*, **2012**, 26, lb268	0.9	