

Trisha N Davis

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.

110
papers

5,926
citations

39
h-index

75
g-index

124
ext. papers

6,734
ext. citations

9.2
avg, IF

5.33
L-index

#	Paper	IF	Citations
110	CM1-driven assembly and activation of yeast β tubulin small complex underlies microtubule nucleation. <i>ELife</i> , 2021 , 10,	8.9	5
109	Microtubule pivoting enables mitotic spindle assembly in <i>S. cerevisiae</i> . <i>Journal of Cell Biology</i> , 2021 , 220,	7.3	1
108	VTT-006, an anti-mitotic compound, binds to the Ndc80 complex and suppresses cancer cell growth .. <i>Oncoscience</i> , 2021 , 8, 134-153	0.8	
107	Reconstitution reveals two paths of force transmission through the kinetochore. <i>ELife</i> , 2020 , 9,	8.9	5
106	Cdk1 Phosphorylation of the Dam1 Complex Strengthens Kinetochore-Microtubule Attachments. <i>Current Biology</i> , 2020 , 30, 4491-4499.e5	6.3	8
105	XMAP215 and β tubulin additively promote microtubule nucleation in purified solutions. <i>Molecular Biology of the Cell</i> , 2020 , 31, 2187-2194	3.5	6
104	Seeing is believing: our evolving view of kinetochore structure, composition, and assembly. <i>Current Opinion in Cell Biology</i> , 2019 , 60, 44-52	9	16
103	Kinetochore-associated Stu2 promotes chromosome biorientation in vivo. <i>PLoS Genetics</i> , 2019 , 15, e1008423	8.423	12
102	Tight bending of the Ndc80 complex provides intrinsic regulation of its binding to microtubules. <i>ELife</i> , 2019 , 8,	8.9	10
101	Proxl (Protein Cross-Linking Database): A Public Server, QC Tools, and Other Major Updates. <i>Journal of Proteome Research</i> , 2019 , 18, 759-764	5.6	0
100	Human Ska complex and Ndc80 complex interact to form a load-bearing assembly that strengthens kinetochore-microtubule attachments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 2740-2745	11.5	42
99	Identification of Wiskott-Aldrich syndrome protein (WASP) binding sites on the branched actin filament nucleator Arp2/3 complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E1409-E1418	11.5	21
98	Novel phosphorylation states of the yeast spindle pole body. <i>Biology Open</i> , 2018 , 7,	2.2	9
97	Differential inactivation mechanism and covalent adduct formation of ALDH1A1 and ALDH1A2 by WIN18,446. <i>FASEB Journal</i> , 2018 , 32, 833.10	0.9	
96	Role of the Spc105 Complex in Organization and Microtubule-Binding Activity of the Budding Yeast Kinetochore. <i>FASEB Journal</i> , 2018 , 32, 533.105	0.9	
95	A Bifunctional Role for the UHRF1 Δ UBL Domain in the Control of Hemi-methylated DNA-Dependent Histone Ubiquitylation. <i>Molecular Cell</i> , 2018 , 72, 753-765.e6	17.6	39
94	Direct measurement of the strength of microtubule attachment to yeast centrosomes. <i>Molecular Biology of the Cell</i> , 2017 , 28, 1853-1861	3.5	9

93	The molecular architecture of the yeast spindle pole body core determined by Bayesian integrative modeling. <i>Molecular Biology of the Cell</i> , 2017 , 28, 3298-3314	3.5	32
92	The Ndc80 complex bridges two Dam1 complex rings. <i>ELife</i> , 2017 , 6,	8.9	35
91	Higher-order oligomerization of Spc110p drives β -tubulin ring complex assembly. <i>Molecular Biology of the Cell</i> , 2016 , 27, 2245-58	3.5	20
90	ProXL (Protein Cross-Linking Database): A Platform for Analysis, Visualization, and Sharing of Protein Cross-Linking Mass Spectrometry Data. <i>Journal of Proteome Research</i> , 2016 , 15, 2863-70	5.6	33
89	Design of a hyperstable 60-subunit protein dodecahedron. [corrected]. <i>Nature</i> , 2016 , 535, 136-9	50.4	243
88	Structure of β -tubulin small complex based on a cryo-EM map, chemical cross-links, and a remotely related structure. <i>Journal of Structural Biology</i> , 2016 , 194, 303-10	3.4	15
87	Computationally designed high specificity inhibitors delineate the roles of BCL2 family proteins in cancer. <i>ELife</i> , 2016 , 5,	8.9	52
86	Purification of Fluorescently Labeled <i>Saccharomyces cerevisiae</i> Spindle Pole Bodies. <i>Methods in Molecular Biology</i> , 2016 , 1413, 189-195	1.4	3
85	Coverslip Cleaning and Functionalization for Total Internal Reflection Fluorescence Microscopy. <i>Cold Spring Harbor Protocols</i> , 2016 , 2016,	1.2	7
84	Preparation of Reactions for Imaging with Total Internal Reflection Fluorescence Microscopy. <i>Cold Spring Harbor Protocols</i> , 2016 , 2016,	1.2	5
83	Single-Molecule Total Internal Reflection Fluorescence Microscopy. <i>Cold Spring Harbor Protocols</i> , 2016 , 2016,	1.2	12
82	Ring closure activates yeast γ -TuRC for species-specific microtubule nucleation. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 132-7	17.6	95
81	Visualization and dissemination of multidimensional proteomics data comparing protein abundance during <i>Caenorhabditis elegans</i> development. <i>Journal of the American Society for Mass Spectrometry</i> , 2015 , 26, 1827-36	3.5	5
80	Mason: a JavaScript web site widget for visualizing and comparing annotated features in nucleotide or protein sequences. <i>BMC Research Notes</i> , 2015 , 8, 70	2.3	4
79	Kojak: efficient analysis of chemically cross-linked protein complexes. <i>Journal of Proteome Research</i> , 2015 , 14, 2190-8	5.6	116
78	Regulation of outer kinetochore Ndc80 complex-based microtubule attachments by the central kinetochore Mis12/MIND complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E5583-9	11.5	31
77	The molecular architecture of the Dam1 kinetochore complex is defined by cross-linking based structural modelling. <i>Nature Communications</i> , 2015 , 6, 8673	17.4	36
76	In-line separation by capillary electrophoresis prior to analysis by top-down mass spectrometry enables sensitive characterization of protein complexes. <i>Journal of Proteome Research</i> , 2014 , 13, 6078-86	5.6	44

75	Kinetochores require oligomerization of Dam1 complex to maintain microtubule attachments against tension and promote biorientation. <i>Nature Communications</i> , 2014 , 5, 4951	17.4	39
74	SnipViz: a compact and lightweight web site widget for display and dissemination of multiple versions of gene and protein sequences. <i>BMC Research Notes</i> , 2014 , 7, 468	2.3	7
73	Determining protein complex structures based on a Bayesian model of in vivo Förster resonance energy transfer (FRET) data. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 2812-23	7.6	22
72	Kinetochore biorientation in <i>Saccharomyces cerevisiae</i> requires a tightly folded conformation of the Ndc80 complex. <i>Genetics</i> , 2014 , 198, 1483-93	4	17
71	Coupling unbiased mutagenesis to high-throughput DNA sequencing uncovers functional domains in the Ndc80 kinetochore protein of <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2013 , 195, 159-70	4	17
70	Integrative phenomics reveals insight into the structure of phenotypic diversity in budding yeast. <i>Genome Research</i> , 2013 , 23, 1496-504	9.7	114
69	Mitosis puts sisters in a strained relationship: force generation at the kinetochore. <i>Experimental Cell Research</i> , 2012 , 318, 1361-6	4.2	6
68	The Ndc80 kinetochore complex directly modulates microtubule dynamics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 16113-8	11.5	82
67	Dissecting DNA damage response pathways by analysing protein localization and abundance changes during DNA replication stress. <i>Nature Cell Biology</i> , 2012 , 14, 966-76	23.4	322
66	KinetochoresRgripping feat: conformational wave or biased diffusion?. <i>Trends in Cell Biology</i> , 2011 , 21, 38-46	18.3	43
65	An intein with genetically selectable markers provides a new approach to internally label proteins with GFP. <i>BMC Biotechnology</i> , 2011 , 11, 71	3.5	9
64	An assay to measure the affinity of proteins for microtubules by quantitative fluorescent microscopy. <i>Analytical Biochemistry</i> , 2011 , 410, 313-5	3.1	3
63	The Proteome Folding Project: proteome-scale prediction of structure and function. <i>Genome Research</i> , 2011 , 21, 1981-94	9.7	32
62	The essential Ubc4/Ubc5 function in yeast is HECT E3-dependent, and RING E3-dependent pathways require only monoubiquitin transfer by Ubc4. <i>Journal of Biological Chemistry</i> , 2011 , 286, 15165-70	5.4	20
61	Microtubule nucleating gamma-TuSC assembles structures with 13-fold microtubule-like symmetry. <i>Nature</i> , 2010 , 466, 879-82	50.4	187
60	Vesicle docking to the spindle pole body is necessary to recruit the exocyst during membrane formation in <i>Saccharomyces cerevisiae</i> . <i>Molecular Biology of the Cell</i> , 2010 , 21, 3693-707	3.5	15
59	Cooperation of the Dam1 and Ndc80 kinetochore complexes enhances microtubule coupling and is regulated by aurora B. <i>Journal of Cell Biology</i> , 2010 , 189, 713-23	7.3	157
58	Laterally attached kinetochores recruit the checkpoint protein Bub1, but satisfy the spindle checkpoint. <i>Cell Cycle</i> , 2010 , 9, 3619-28	4.7	18

57	Kip3, the yeast kinesin-8, is required for clustering of kinetochores at metaphase. <i>Cell Cycle</i> , 2010 , 9, 2581-8	4.7	55
56	Reconstitution and functional analysis of kinetochore subcomplexes. <i>Methods in Cell Biology</i> , 2010 , 95, 641-56	1.8	19
55	Native capillary isoelectric focusing for the separation of protein complex isoforms and subcomplexes. <i>Analytical Chemistry</i> , 2010 , 82, 6643-51	7.8	28
54	Isotope signatures allow identification of chemically cross-linked peptides by mass spectrometry: a novel method to determine interresidue distances in protein structures through cross-linking. <i>Journal of Proteome Research</i> , 2010 , 9, 3583-9	5.6	27
53	Direct physical study of kinetochore-microtubule interactions by reconstitution and interrogation with an optical force clamp. <i>Methods</i> , 2010 , 51, 242-50	4.6	41
52	The Yeast Resource Center Public Image Repository: A large database of fluorescence microscopy images. <i>BMC Bioinformatics</i> , 2010 , 11, 263	3.6	29
51	Identification of <i>Saccharomyces cerevisiae</i> spindle pole body remodeling factors. <i>PLoS ONE</i> , 2010 , 5, e15426	3.7	9
50	Bir1 is required for the tension checkpoint. <i>Molecular Biology of the Cell</i> , 2009 , 20, 915-23	3.5	31
49	The Ndc80 kinetochore complex forms load-bearing attachments to dynamic microtubule tips via biased diffusion. <i>Cell</i> , 2009 , 136, 865-75	56.2	215
48	Localization and orientation of the gamma-tubulin small complex components using protein tags as labels for single particle EM. <i>Journal of Structural Biology</i> , 2009 , 168, 571-4	3.4	25
47	Phosphoregulation and depolymerization-driven movement of the Dam1 complex do not require ring formation. <i>Nature Cell Biology</i> , 2008 , 10, 407-14	23.4	122
46	Insights into the kinetochore. <i>Structure</i> , 2008 , 16, 834-6	5.2	2
45	The structure of the gamma-tubulin small complex: implications of its architecture and flexibility for microtubule nucleation. <i>Molecular Biology of the Cell</i> , 2008 , 19, 207-15	3.5	79
44	Tension applied through the Dam1 complex promotes microtubule elongation providing a direct mechanism for length control in mitosis. <i>Nature Cell Biology</i> , 2007 , 9, 832-7	23.4	116
43	In vivo analysis of cohesin architecture using FRET in the budding yeast <i>Saccharomyces cerevisiae</i> . <i>EMBO Journal</i> , 2007 , 26, 3783-93	13	81
42	Rings, bracelets, sleeves, and chevrons: new structures of kinetochore proteins. <i>Trends in Cell Biology</i> , 2007 , 17, 377-82	18.3	22
41	Superfamily assignments for the yeast proteome through integration of structure prediction with the gene ontology. <i>PLoS Biology</i> , 2007 , 5, e76	9.7	42
40	12 Measuring the Proximity of Proteins in Living Cells by Fluorescence Resonance Energy Transfer between CFP and YFP. <i>Methods in Microbiology</i> , 2007 , 269-280	2.8	1

39	Mps1 phosphorylation of Dam1 couples kinetochores to microtubule plus ends at metaphase. <i>Current Biology</i> , 2006 , 16, 1489-501	6.3	77
38	Phosphorylation of the chromosomal passenger protein Bir1 is required for localization of Ndc10 to the spindle during anaphase and full spindle elongation. <i>Molecular Biology of the Cell</i> , 2006 , 17, 1065-74	3.5	37
37	The Dam1 kinetochore complex harnesses microtubule dynamics to produce force and movement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 9873-8	11.5	150
36	Protein Localization by Cell Imaging 2006 , 135-155		
35	The Yeast Resource Center Public Data Repository. <i>Nucleic Acids Research</i> , 2005 , 33, D378-82	20.1	25
34	A high-efficiency method to replace essential genes with mutant alleles in yeast. <i>Yeast</i> , 2005 , 22, 769-74	3.4	18
33	The organization of the core proteins of the yeast spindle pole body. <i>Molecular Biology of the Cell</i> , 2005 , 16, 3341-52	3.5	111
32	Analysis of a spindle pole body mutant reveals a defect in biorientation and illuminates spindle forces. <i>Molecular Biology of the Cell</i> , 2005 , 16, 141-52	3.5	24
31	Localization of proteins that are coordinately expressed with Cln2 during the cell cycle. <i>Yeast</i> , 2004 , 21, 793-800	3.4	25
30	Protein localization in proteomics. <i>Current Opinion in Chemical Biology</i> , 2004 , 8, 49-53	9.7	50
29	The centrosomal proteins pericentrin and kendrin are encoded by alternatively spliced products of one gene. <i>Genomics</i> , 2003 , 82, 401-5	4.3	55
28	Assigning function to yeast proteins by integration of technologies. <i>Molecular Cell</i> , 2003 , 12, 1353-65	17.6	236
27	Chl4p and iml3p are two new members of the budding yeast outer kinetochore. <i>Molecular Biology of the Cell</i> , 2003 , 14, 460-76	3.5	51
26	The <i>Saccharomyces cerevisiae</i> spindle pole body is a dynamic structure. <i>Molecular Biology of the Cell</i> , 2003 , 14, 3494-505	3.5	37
25	Fluorescence resonance energy transfer using color variants of green fluorescent protein. <i>Methods in Enzymology</i> , 2002 , 351, 34-49	1.7	51
24	Ctf3p, the Mis6 budding yeast homolog, interacts with Mcm22p and Mcm16p at the yeast outer kinetochore. <i>Genes and Development</i> , 2002 , 16, 101-13	12.6	99
23	Reconstitution and characterization of budding yeast gamma-tubulin complex. <i>Molecular Biology of the Cell</i> , 2002 , 13, 1144-57	3.5	74
22	Genetic analysis of yeast spindle pole bodies. <i>Methods in Cell Biology</i> , 2001 , 67, 95-111	1.8	

21	A protein interaction map for cell polarity development. <i>Journal of Cell Biology</i> , 2001 , 154, 549-71	7.3	268
20	Yeast Mps1p phosphorylates the spindle pole component Spc110p in the N-terminal domain. <i>Journal of Biological Chemistry</i> , 2001 , 276, 17958-67	5.4	23
19	Two yeast forkhead genes regulate the cell cycle and pseudohyphal growth. <i>Nature</i> , 2000 , 406, 90-4	50.4	306
18	The spindle pole body of <i>Saccharomyces cerevisiae</i> : architecture and assembly of the core components. <i>Current Topics in Developmental Biology</i> , 2000 , 49, 105-32	5.3	12
17	Localization of calmodulin in budding yeast and fission yeast using green fluorescent protein. <i>Methods in Enzymology</i> , 1999 , 302, 87-102	1.7	1
16	The fork head transcription factor Hcm1p participates in the regulation of SPC110, which encodes the calmodulin-binding protein in the yeast spindle pole body. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 1998 , 1448, 236-44	4.9	23
15	Mlc1p is a light chain for the unconventional myosin Myo2p in <i>Saccharomyces cerevisiae</i> . <i>Journal of Cell Biology</i> , 1998 , 142, 711-22	7.3	102
14	A genetic analysis of interactions with Spc110p reveals distinct functions of Spc97p and Spc98p, components of the yeast gamma-tubulin complex. <i>Molecular Biology of the Cell</i> , 1998 , 9, 2201-16	3.5	77
13	A mutational analysis identifies three functional regions of the spindle pole component Spc110p in <i>Saccharomyces cerevisiae</i> . <i>Molecular Biology of the Cell</i> , 1997 , 8, 2575-90	3.5	51
12	Ca ²⁺ binding to calmodulin and its role in <i>Schizosaccharomyces pombe</i> as revealed by mutagenesis and NMR spectroscopy. <i>Journal of Biological Chemistry</i> , 1995 , 270, 20643-52	5.4	34
11	Similarities and differences between yeast and vertebrate calmodulin: an examination of the calcium-binding and structural properties of calmodulin from the yeast <i>Saccharomyces cerevisiae</i> . <i>Biochemistry</i> , 1993 , 32, 3261-70	3.2	50
10	Structural analysis of wild-type and mutant yeast calmodulins by limited proteolysis and electrospray ionization mass spectrometry. <i>Protein Science</i> , 1992 , 1, 504-16	6.3	36
9	Can calmodulin function without binding calcium?. <i>Cell</i> , 1991 , 65, 949-59	56.2	280
8	Complete nucleotide sequence of the gene encoding the regulatory subunit of 3R5Rcyclic AMP-dependent protein kinase from the yeast <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 1987 , 15, 368-9	20.1	37
7	Isolation of the yeast calmodulin gene using synthetic oligonucleotide probes. <i>Methods in Enzymology</i> , 1987 , 139, 248-62	1.7	16
6	Isolation of the yeast calmodulin gene: calmodulin is an essential protein. <i>Cell</i> , 1986 , 47, 423-31	56.2	389
5	Spc110 N-Terminal Domains Act Independently to Mediate Stable β Tubulin Small Complex Binding and β Tubulin Ring Complex Assembly		1
4	XMAP215 and β tubulin additively promote microtubule nucleation in purified solutions		2

- 3 CM1-driven assembly and activation of Yeast β -Tubulin Small Complex underlies microtubule nucleation 1
- 2 A Stu2-mediated intrinsic tension-sensing pathway promotes chromosome biorientation in vivo 1
- 1 Discovery and visualization of uncharacterized drug-protein adducts using mass spectrometry 1