

Trisha N Davis

List of Publications by Year in descending order

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110
papers

7,217
citations

71102

41
h-index

64796

79
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124
all docs

124
docs citations

124
times ranked

6990
citing authors

#	ARTICLE	IF	CITATIONS
1	Dissecting DNA damage response pathways by analysing protein localization and abundance changes during DNA replication stress. <i>Nature Cell Biology</i> , 2012, 14, 966-976.	10.3	431
2	Isolation of the yeast calmodulin gene: Calmodulin is an essential protein. <i>Cell</i> , 1986, 47, 423-431.	28.9	428
3	Design of a hyperstable 60-subunit protein icosahedron. <i>Nature</i> , 2016, 535, 136-139.	27.8	373
4	Two yeast forkhead genes regulate the cell cycle and pseudohyphal growth. <i>Nature</i> , 2000, 406, 90-94.	27.8	353
5	Can calmodulin function without binding calcium?. <i>Cell</i> , 1991, 65, 949-959.	28.9	309
6	A protein interaction map for cell polarity development. <i>Journal of Cell Biology</i> , 2001, 154, 549-576.	5.2	294
7	The Ndc80 Kinetochore Complex Forms Load-Bearing Attachments to Dynamic Microtubule Tips via Biased Diffusion. <i>Cell</i> , 2009, 136, 865-875.	28.9	262
8	Assigning Function to Yeast Proteins by Integration of Technologies. <i>Molecular Cell</i> , 2003, 12, 1353-1365.	9.7	248
9	Microtubule nucleating $\hat{\Gamma}^3$ -TuSC assembles structures with 13-fold microtubule-like symmetry. <i>Nature</i> , 2010, 466, 879-882.	27.8	231
10	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, 713-723.	5.2	193
11	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, 9873-9878.	7.1	177
12	Kojak: Efficient Analysis of Chemically Cross-Linked Protein Complexes. <i>Journal of Proteome Research</i> , 2015, 14, 2190-2198.	3.7	155
13	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, 832-837.	10.3	145
14	Integrative phenomics reveals insight into the structure of phenotypic diversity in budding yeast. <i>Genome Research</i> , 2013, 23, 1496-1504.	5.5	138
15	Phosphoregulation and depolymerization-driven movement of the Dam1 complex do not require ring formation. <i>Nature Cell Biology</i> , 2008, 10, 407-414.	10.3	136
16	The Organization of the Core Proteins of the Yeast Spindle Pole Body. <i>Molecular Biology of the Cell</i> , 2005, 16, 3341-3352.	2.1	121
17	Ring closure activates yeast $\hat{\Gamma}^3$ TuRC for species-specific microtubule nucleation. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 132-137.	8.2	115
18	Ctf3p, the Mis6 budding yeast homolog, interacts with Mcm22p and Mcm16p at the yeast outer kinetochore. <i>Genes and Development</i> , 2002, 16, 101-113.	5.9	111

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19	Mlc1p Is a Light Chain for the Unconventional Myosin Myo2p in <i>Saccharomyces cerevisiae</i> . <i>Journal of Cell Biology</i> , 1998, 142, 711-722.	5.2	104
20	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, 16113-16118.	7.1	103
21	The Structure of the $\hat{\gamma}$ -Tubulin Small Complex: Implications of Its Architecture and Flexibility for Microtubule Nucleation. <i>Molecular Biology of the Cell</i> , 2008, 19, 207-215.	2.1	96
22	Mps1 Phosphorylation of Dam1 Couples Kinetochores to Microtubule Plus Ends at Metaphase. <i>Current Biology</i> , 2006, 16, 1489-1501.	3.9	93
23	In vivo analysis of cohesin architecture using FRET in the budding yeast <i>Saccharomyces cerevisiae</i> . <i>EMBO Journal</i> , 2007, 26, 3783-3793.	7.8	92
24	A Genetic Analysis of Interactions with Spc110p Reveals Distinct Functions of Spc97p and Spc98p, Components of the Yeast $\hat{\gamma}$ -Tubulin Complex. <i>Molecular Biology of the Cell</i> , 1998, 9, 2201-2216.	2.1	81
25	Reconstitution and Characterization of Budding Yeast $\hat{\gamma}$ -Tubulin Complex. <i>Molecular Biology of the Cell</i> , 2002, 13, 1144-1157.	2.1	80
26	Kip3, the yeast kinesin-8, is required for clustering of kinetochores at metaphase. <i>Cell Cycle</i> , 2010, 9, 2581-2588.	2.6	76
27	Fluorescence resonance energy transfer using color variants of green fluorescent protein. <i>Methods in Enzymology</i> , 2002, 351, 34-49.	1.0	67
28	The centrosomal proteins pericentrin and kendrin are encoded by alternatively spliced products of one gene. <i>Genomics</i> , 2003, 82, 401-405.	2.9	65
29	Computationally designed high specificity inhibitors delineate the roles of BCL2 family proteins in cancer. <i>ELife</i> , 2016, 5, .	6.0	65
30	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.	7.1	65
31	A Bifunctional Role for the UHRF1 $\hat{\gamma}$ UBL Domain in the Control of Hemi-methylated DNA-Dependent Histone Ubiquitylation. <i>Molecular Cell</i> , 2018, 72, 753-765.e6.	9.7	58
32	Chl4p and Iml3p Are Two New Members of the Budding Yeast Outer Kinetochore. <i>Molecular Biology of the Cell</i> , 2003, 14, 460-476.	2.1	57
33	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, 6078-6086.	3.7	57
34	Protein localization in proteomics. <i>Current Opinion in Chemical Biology</i> , 2004, 8, 49-53.	6.1	54
35	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, 3261-3270.	2.5	53
36	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, 2575-2590.	2.1	52

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37	The Ndc80 complex bridges two Dam1 complex rings. <i>ELife</i> , 2017, 6, .	6.0	52
38	Kinetochores require oligomerization of Dam1 complex to maintain microtubule attachments against tension and promote biorientation. <i>Nature Communications</i> , 2014, 5, 4951.	12.8	51
39	The molecular architecture of the Dam1 kinetochore complex is defined by cross-linking based structural modelling. <i>Nature Communications</i> , 2015, 6, 8673.	12.8	51
40	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, 2863-2870.	3.7	51
41	Superfamily Assignments for the Yeast Proteome through Integration of Structure Prediction with the Gene Ontology. <i>PLoS Biology</i> , 2007, 5, e76.	5.6	48
42	Direct physical study of kinetochore-microtubule interactions by reconstitution and interrogation with an optical force clamp. <i>Methods</i> , 2010, 51, 242-250.	3.8	47
43	Kinetochores' gripping feat: conformational wave or biased diffusion?. <i>Trends in Cell Biology</i> , 2011, 21, 38-46.	7.9	45
44	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.	2.1	44
45	The <i>Saccharomyces cerevisiae</i> Spindle Pole Body Is a Dynamic Structure. <i>Molecular Biology of the Cell</i> , 2003, 14, 3494-3505.	2.1	43
46	Complete nucleotide sequence of the gene encoding the regulatory subunit of 3',5'-cyclic AMP-dependent protein kinase from the yeast <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 1987, 15, 368-369.	14.5	42
47	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, 20643-20652.	3.4	40
48	The Proteome Folding Project: Proteome-scale prediction of structure and function. <i>Genome Research</i> , 2011, 21, 1981-1994.	5.5	40
49	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.	7.1	40
50	Structural analysis of wild-type and mutant yeast calmodulins by limited proteolysis and electrospray ionization mass spectrometry. <i>Protein Science</i> , 1992, 1, 504-516.	7.6	39
51	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, 1065-1074.	2.1	39
52	Bir1 Is Required for the Tension Checkpoint. <i>Molecular Biology of the Cell</i> , 2009, 20, 915-923.	2.1	37
53	Native Capillary Isoelectric Focusing for the Separation of Protein Complex Isoforms and Subcomplexes. <i>Analytical Chemistry</i> , 2010, 82, 6643-6651.	6.5	35
54	The Yeast Resource Center Public Image Repository: A large database of fluorescence microscopy images. <i>BMC Bioinformatics</i> , 2010, 11, 263.	2.6	34

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55	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, 3583-3589.	3.7	32
56	Localization of proteins that are coordinately expressed with Cln2 during the cell cycle. <i>Yeast</i> , 2004, 21, 793-800.	1.7	30
57	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.	7.1	30
58	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, 2812-2823.	3.8	29
59	Higher-order oligomerization of Spc110p drives $\hat{\gamma}$ -tubulin ring complex assembly. <i>Molecular Biology of the Cell</i> , 2016, 27, 2245-2258.	2.1	29
60	Yeast Mps1p Phosphorylates the Spindle Pole Component Spc110p in the N-terminal Domain. <i>Journal of Biological Chemistry</i> , 2001, 276, 17958-17967.	3.4	28
61	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, 236-244.	4.1	26
62	Kinetochores-associated Stu2 promotes chromosome biorientation in vivo. <i>PLoS Genetics</i> , 2019, 15, e1008423.	3.5	26
63	The Yeast Resource Center Public Data Repository. <i>Nucleic Acids Research</i> , 2004, 33, D378-D382.	14.5	25
64	Localization and orientation of the $\hat{\gamma}$ -Tubulin Small Complex components using protein tags as labels for single particle EM. <i>Journal of Structural Biology</i> , 2009, 168, 571-574.	2.8	25
65	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, 15165-15170.	3.4	25
66	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, 141-152.	2.1	24
67	Rings, bracelets, sleeves, and chevrons: new structures of kinetochore proteins. <i>Trends in Cell Biology</i> , 2007, 17, 377-382.	7.9	23
68	Laterally attached kinetochores recruit the checkpoint protein Bub1, but satisfy the spindle checkpoint. <i>Cell Cycle</i> , 2010, 9, 3619-3628.	2.6	23
69	Structure of $\hat{\gamma}$ -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, 303-310.	2.8	23
70	XMAP215 and $\hat{\gamma}$ -tubulin additively promote microtubule nucleation in purified solutions. <i>Molecular Biology of the Cell</i> , 2020, 31, 2187-2194.	2.1	23
71	CM1-driven assembly and activation of yeast $\hat{\gamma}$ -tubulin small complex underlies microtubule nucleation. <i>ELife</i> , 2021, 10, .	6.0	23
72	Tight bending of the Ndc80 complex provides intrinsic regulation of its binding to microtubules. <i>ELife</i> , 2019, 8, .	6.0	23

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73	A high-efficiency method to replace essential genes with mutant alleles in yeast. <i>Yeast</i> , 2005, 22, 769-774.	1.7	22
74	Single-Molecule Total Internal Reflection Fluorescence Microscopy. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.top077800.	0.3	22
75	Coupling Unbiased Mutagenesis to High-throughput DNA Sequencing Uncovers Functional Domains in the Ndc80 Kinetochores Protein of <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2013, 195, 159-170.	2.9	21
76	[21] Isolation of the yeast calmodulin gene using synthetic oligonucleotide probes. <i>Methods in Enzymology</i> , 1987, 139, 248-262.	1.0	19
77	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, 3693-3707.	2.1	19
78	Reconstitution and Functional Analysis of Kinetochores Subcomplexes. <i>Methods in Cell Biology</i> , 2010, 95, 641-656.	1.1	19
79	Seeing is believing: our evolving view of kinetochores structure, composition, and assembly. <i>Current Opinion in Cell Biology</i> , 2019, 60, 44-52.	5.4	19
80	Kinetochores Biorientation in <i>Saccharomyces cerevisiae</i> Requires a Tightly Folded Conformation of the Ndc80 Complex. <i>Genetics</i> , 2014, 198, 1483-1493.	2.9	17
81	Cdk1 Phosphorylation of the Dam1 Complex Strengthens Kinetochores-Microtubule Attachments. <i>Current Biology</i> , 2020, 30, 4491-4499.e5.	3.9	17
82	An intein with genetically selectable markers provides a new approach to internally label proteins with GFP. <i>BMC Biotechnology</i> , 2011, 11, 71.	3.3	14
83	Reconstitution reveals two paths of force transmission through the kinetochores. <i>ELife</i> , 2020, 9, .	6.0	14
84	The spindle pole body of <i>Saccharomyces cerevisiae</i> : Architecture and assembly of the core components. <i>Current Topics in Developmental Biology</i> , 1999, 49, 105-132.	2.2	13
85	Novel phosphorylation states of the yeast spindle pole body. <i>Biology Open</i> , 2018, 7, .	1.2	12
86	Identification of <i>Saccharomyces cerevisiae</i> Spindle Pole Body Remodeling Factors. <i>PLoS ONE</i> , 2010, 5, e15426.	2.5	12
87	Direct measurement of the strength of microtubule attachment to yeast centrosomes. <i>Molecular Biology of the Cell</i> , 2017, 28, 1853-1861.	2.1	11
88	Three interacting regions of the Ndc80 and Dam1 complexes support microtubule tip-coupling under load. <i>Journal of Cell Biology</i> , 2022, 221, .	5.2	11
89	Coverslip Cleaning and Functionalization for Total Internal Reflection Fluorescence Microscopy. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.prot085548.	0.3	10
90	Kinesin-14 motors participate in a force balance at microtubule plus-ends to regulate dynamic instability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	10

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91	SnipViz: a compact and lightweight web site widget for display and dissemination of multiple versions of gene and protein sequences. BMC Research Notes, 2014, 7, 468.	1.4	7
92	Preparation of Reactions for Imaging with Total Internal Reflection Fluorescence Microscopy. Cold Spring Harbor Protocols, 2016, 2016, pdb.prot085563.	0.3	7
93	Discovery and Visualization of Uncharacterized Drug-Protein Adducts Using Mass Spectrometry. Analytical Chemistry, 2022, 94, 3501-3509.	6.5	7
94	Mitosis puts sisters in a strained relationship: Force generation at the kinetochore. Experimental Cell Research, 2012, 318, 1361-1366.	2.6	6
95	Cullin-independent recognition of HHARI substrates by a dynamic RBR catalytic domain. Structure, 2022, , .	3.3	6
96	Visualization and Dissemination of Multidimensional Proteomics Data Comparing Protein Abundance During <i>Caenorhabditis elegans</i> Development. Journal of the American Society for Mass Spectrometry, 2015, 26, 1827-1836.	2.8	5
97	Microtubule-associated proteins and motors required for ectopic microtubule array formation in <i>Saccharomyces cerevisiae</i> . Genetics, 2021, 218, .	2.9	5
98	Microtubule pivoting enables mitotic spindle assembly in <i>S. cerevisiae</i> . Journal of Cell Biology, 2021, 220, .	5.2	5
99	An assay to measure the affinity of proteins for microtubules by quantitative fluorescent microscopy. Analytical Biochemistry, 2011, 410, 313-315.	2.4	4
100	Mason: a JavaScript web site widget for visualizing and comparing annotated features in nucleotide or protein sequences. BMC Research Notes, 2015, 8, 70.	1.4	4
101	Purification of Fluorescently Labeled <i>Saccharomyces cerevisiae</i> Spindle Pole Bodies. Methods in Molecular Biology, 2016, 1413, 189-195.	0.9	4
102	Prox1 (Protein Cross-Linking Database): A Public Server, QC Tools, and Other Major Updates. Journal of Proteome Research, 2019, 18, 759-764.	3.7	4
103	Insights into the Kinetochore. Structure, 2008, 16, 834-836.	3.3	2
104	[10] Localization of calmodulin in budding yeast and fission yeast using green fluorescent protein. Methods in Enzymology, 1999, 302, 87-102.	1.0	1
105	Protein Localization by Cell Imaging. , 2006, , 135-155.		1
106	12 Measuring the Proximity of Proteins in Living Cells by Fluorescence Resonance Energy Transfer between CFP and YFP. Methods in Microbiology, 2007, , 269-280.	0.8	1
107	VTT-006, an anti-mitotic compound, binds to the Ndc80 complex and suppresses cancer cell growth in vitro. Oncoscience, 2021, 8, 134-153.	2.2	1
108	Genetic analysis of yeast spindle pole bodies. Methods in Cell Biology, 2001, 67, 95-111.	1.1	0

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109	Differential inactivation mechanism and covalent adduct formation of ALDH1A1 and ALDH1A2 by WIN18,446. FASEB Journal, 2018, 32, 833.10.	0.5	0
110	Role of the Spc105 Complex in Organization and Microtubule-Binding Activity of the Budding Yeast Kinetochore. FASEB Journal, 2018, 32, 533.105.	0.5	0