

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	Discovery and Visualization of Uncharacterized Drug-Protein Adducts Using Mass Spectrometry. <i>Analytical Chemistry</i> , 2022, 94, 3501-3509.	6.5	7
2	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
3	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
4	Cullin-independent recognition of HHARI substrates by a dynamic RBR catalytic domain. <i>Structure</i> , 2022, , .	3.3	6
5	Microtubule-associated proteins and motors required for ectopic microtubule array formation in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2021, 218, .	2.9	5
6	CM1-driven assembly and activation of yeast $\hat{\gamma}$ -tubulin small complex underlies microtubule nucleation. <i>ELife</i> , 2021, 10, .	6.0	23
7	Microtubule pivoting enables mitotic spindle assembly in <i>S. cerevisiae</i> . <i>Journal of Cell Biology</i> , 2021, 220, .	5.2	5
8	VTT-006, an anti-mitotic compound, binds to the Ndc80 complex and suppresses cancer cell growth in vitro. <i>Oncoscience</i> , 2021, 8, 134-153.	2.2	1
9	Cdk1 Phosphorylation of the Dam1 Complex Strengthens Kinetochores-Microtubule Attachments. <i>Current Biology</i> , 2020, 30, 4491-4499.e5.	3.9	17
10	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
11	Reconstitution reveals two paths of force transmission through the kinetochore. <i>ELife</i> , 2020, 9, .	6.0	14
12	Kinetochore-associated Stu2 promotes chromosome biorientation in vivo. <i>PLoS Genetics</i> , 2019, 15, e1008423.	3.5	26
13	Seeing is believing: our evolving view of kinetochore structure, composition, and assembly. <i>Current Opinion in Cell Biology</i> , 2019, 60, 44-52.	5.4	19
14	Proxl (Protein Cross-Linking Database): A Public Server, QC Tools, and Other Major Updates. <i>Journal of Proteome Research</i> , 2019, 18, 759-764.	3.7	4
15	Tight bending of the Ndc80 complex provides intrinsic regulation of its binding to microtubules. <i>ELife</i> , 2019, 8, .	6.0	23
16	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
17	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
18	A Bifunctional Role for the UHRF1-UBL Domain in the Control of Hemi-methylated DNA-Dependent Histone Ubiquitylation. <i>Molecular Cell</i> , 2018, 72, 753-765.e6.	9.7	58

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19	Novel phosphorylation states of the yeast spindle pole body. <i>Biology Open</i> , 2018, 7, .	1.2	12
20	Differential inactivation mechanism and covalent adduct formation of ALDH1A1 and ALDH1A2 by WIN18,446. <i>FASEB Journal</i> , 2018, 32, 833.10.	0.5	0
21	Role of the Spc105 Complex in Organization and Microtubule Binding Activity of the Budding Yeast Kinetochore. <i>FASEB Journal</i> , 2018, 32, 533.105.	0.5	0
22	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
23	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
24	The Ndc80 complex bridges two Dam1 complex rings. <i>ELife</i> , 2017, 6, .	6.0	52
25	Computationally designed high specificity inhibitors delineate the roles of BCL2 family proteins in cancer. <i>ELife</i> , 2016, 5, .	6.0	65
26	Purification of Fluorescently Labeled <i>Saccharomyces cerevisiae</i> Spindle Pole Bodies. <i>Methods in Molecular Biology</i> , 2016, 1413, 189-195.	0.9	4
27	Coverslip Cleaning and Functionalization for Total Internal Reflection Fluorescence Microscopy. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.prot085548.	0.3	10
28	Preparation of Reactions for Imaging with Total Internal Reflection Fluorescence Microscopy. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.prot085563.	0.3	7
29	Single-Molecule Total Internal Reflection Fluorescence Microscopy. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.top077800.	0.3	22
30	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
31	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
32	Design of a hyperstable 60-subunit protein icosahedron. <i>Nature</i> , 2016, 535, 136-139.	27.8	373
33	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
34	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
35	Ring closure activates yeast $\hat{\gamma}$ TuRC for species-specific microtubule nucleation. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 132-137.	8.2	115
36	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, 1827-1836.	2.8	5

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37	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
38	Kojak: Efficient Analysis of Chemically Cross-Linked Protein Complexes. Journal of Proteome Research, 2015, 14, 2190-2198.	3.7	155
39	Regulation of outer kinetochore Ndc80 complex-based microtubule attachments by the central kinetochore Mis12/MIND complex. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5583-9.	7.1	40
40	Determining Protein Complex Structures Based on a Bayesian Model of in Vivo Förster Resonance Energy Transfer (FRET) Data. Molecular and Cellular Proteomics, 2014, 13, 2812-2823.	3.8	29
41	Kinetochore Biorientation in <i>Saccharomyces cerevisiae</i> Requires a Tightly Folded Conformation of the Ndc80 Complex. Genetics, 2014, 198, 1483-1493.	2.9	17
42	In-Line Separation by Capillary Electrophoresis Prior to Analysis by Top-Down Mass Spectrometry Enables Sensitive Characterization of Protein Complexes. Journal of Proteome Research, 2014, 13, 6078-6086.	3.7	57
43	Kinetochores require oligomerization of Dam1 complex to maintain microtubule attachments against tension and promote biorientation. Nature Communications, 2014, 5, 4951.	12.8	51
44	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
45	Coupling Unbiased Mutagenesis to High-throughput DNA Sequencing Uncovers Functional Domains in the Ndc80 Kinetochore Protein of <i>Saccharomyces cerevisiae</i> . Genetics, 2013, 195, 159-170.	2.9	21
46	Integrative phenomics reveals insight into the structure of phenotypic diversity in budding yeast. Genome Research, 2013, 23, 1496-1504.	5.5	138
47	The Ndc80 kinetochore complex directly modulates microtubule dynamics. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 16113-16118.	7.1	103
48	Dissecting DNA damage response pathways by analysing protein localization and abundance changes during DNA replication stress. Nature Cell Biology, 2012, 14, 966-976.	10.3	431
49	Mitosis puts sisters in a strained relationship: Force generation at the kinetochore. Experimental Cell Research, 2012, 318, 1361-1366.	2.6	6
50	Kinetochoresâ€™ gripping feat: conformational wave or biased diffusion?. Trends in Cell Biology, 2011, 21, 38-46.	7.9	45
51	An intein with genetically selectable markers provides a new approach to internally label proteins with GFP. BMC Biotechnology, 2011, 11, 71.	3.3	14
52	An assay to measure the affinity of proteins for microtubules by quantitative fluorescent microscopy. Analytical Biochemistry, 2011, 410, 313-315.	2.4	4
53	The Proteome Folding Project: Proteome-scale prediction of structure and function. Genome Research, 2011, 21, 1981-1994.	5.5	40
54	The Essential Ubc4/Ubc5 Function in Yeast Is HECT E3-dependent, and RING E3-dependent Pathways Require Only Monoubiquitin Transfer by Ubc4. Journal of Biological Chemistry, 2011, 286, 15165-15170.	3.4	25

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55	The Yeast Resource Center Public Image Repository: A large database of fluorescence microscopy images. <i>BMC Bioinformatics</i> , 2010, 11, 263.	2.6	34
56	Microtubule nucleating $\hat{\gamma}$ -TuSC assembles structures with 13-fold microtubule-like symmetry. <i>Nature</i> , 2010, 466, 879-882.	27.8	231
57	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
58	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
59	Laterally attached kinetochores recruit the checkpoint protein Bub1, but satisfy the spindle checkpoint. <i>Cell Cycle</i> , 2010, 9, 3619-3628.	2.6	23
60	Kip3, the yeast kinesin-8, is required for clustering of kinetochores at metaphase. <i>Cell Cycle</i> , 2010, 9, 2581-2588.	2.6	76
61	Reconstitution and Functional Analysis of Kinetochore Subcomplexes. <i>Methods in Cell Biology</i> , 2010, 95, 641-656.	1.1	19
62	Native Capillary Isoelectric Focusing for the Separation of Protein Complex Isoforms and Subcomplexes. <i>Analytical Chemistry</i> , 2010, 82, 6643-6651.	6.5	35
63	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
64	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
65	Identification of <i>Saccharomyces cerevisiae</i> Spindle Pole Body Remodeling Factors. <i>PLoS ONE</i> , 2010, 5, e15426.	2.5	12
66	Bir1 Is Required for the Tension Checkpoint. <i>Molecular Biology of the Cell</i> , 2009, 20, 915-923.	2.1	37
67	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
68	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
69	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
70	Insights into the Kinetochore. <i>Structure</i> , 2008, 16, 834-836.	3.3	2
71	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
72	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

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73	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.	0.8	1
74	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
75	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
76	Rings, bracelets, sleeves, and chevrons: new structures of kinetochore proteins. <i>Trends in Cell Biology</i> , 2007, 17, 377-382.	7.9	23
77	Protein Localization by Cell Imaging. , 2006, , 135-155.		1
78	Mps1 Phosphorylation of Dam1 Couples Kinetochores to Microtubule Plus Ends at Metaphase. <i>Current Biology</i> , 2006, 16, 1489-1501.	3.9	93
79	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
80	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
81	A high-efficiency method to replace essential genes with mutant alleles in yeast. <i>Yeast</i> , 2005, 22, 769-774.	1.7	22
82	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
83	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
84	The Yeast Resource Center Public Data Repository. <i>Nucleic Acids Research</i> , 2004, 33, D378-D382.	14.5	25
85	Localization of proteins that are coordinately expressed with Cln2 during the cell cycle. <i>Yeast</i> , 2004, 21, 793-800.	1.7	30
86	Protein localization in proteomics. <i>Current Opinion in Chemical Biology</i> , 2004, 8, 49-53.	6.1	54
87	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
88	Assigning Function to Yeast Proteins by Integration of Technologies. <i>Molecular Cell</i> , 2003, 12, 1353-1365.	9.7	248
89	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
90	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

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91	Fluorescence resonance energy transfer using color variants of green fluorescent protein. <i>Methods in Enzymology</i> , 2002, 351, 34-49.	1.0	67
92	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
93	Reconstitution and Characterization of Budding Yeast $\hat{1}^3$ -Tubulin Complex. <i>Molecular Biology of the Cell</i> , 2002, 13, 1144-1157.	2.1	80
94	Genetic analysis of yeast spindle pole bodies. <i>Methods in Cell Biology</i> , 2001, 67, 95-111.	1.1	0
95	A protein interaction map for cell polarity development. <i>Journal of Cell Biology</i> , 2001, 154, 549-576.	5.2	294
96	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
97	Two yeast forkhead genes regulate the cell cycle and pseudohyphal growth. <i>Nature</i> , 2000, 406, 90-94.	27.8	353
98	[10] Localization of calmodulin in budding yeast and fission yeast using green fluorescent protein. <i>Methods in Enzymology</i> , 1999, 302, 87-102.	1.0	1
99	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
100	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
101	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
102	A Genetic Analysis of Interactions with Spc110p Reveals Distinct Functions of Spc97p and Spc98p, Components of the Yeast $\hat{1}^3$ -Tubulin Complex. <i>Molecular Biology of the Cell</i> , 1998, 9, 2201-2216.	2.1	81
103	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
104	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
105	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
106	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
107	Can calmodulin function without binding calcium?. <i>Cell</i> , 1991, 65, 949-959.	28.9	309
108	Complete nucleotide sequence of the gene encoding the regulatory subunit of 3 \hat{a} \hat{e} ² ,5 \hat{a} \hat{e} ² -cyclic AMP-dependent protein kinase from the yeast <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 1987, 15, 368-369.	14.5	42

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109	[21] Isolation of the yeast calmodulin gene using synthetic oligonucleotide probes. Methods in Enzymology, 1987, 139, 248-262.	1.0	19
110	Isolation of the yeast calmodulin gene: Calmodulin is an essential protein. Cell, 1986, 47, 423-431.	28.9	428