

Diana R Tomchick

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.

109 papers	7,471 citations	50 h-index	85 g-index
117 ext. papers	8,505 ext. citations	11.9 avg, IF	5.55 L-index

#	Paper	IF	Citations
109	Potent Antimalarials with Development Potential Identified by Structure-Guided Computational Optimization of a Pyrrole-Based Dihydroorotate Dehydrogenase Inhibitor Series. <i>Journal of Medicinal Chemistry</i> , 2021 , 64, 6085-6136	8.3	3
108	Dynamic remodeling of host membranes by self-organizing bacterial effectors. <i>Science</i> , 2021 , 372, 935-941	39.3	4
107	Structure and dynamics of major histocompatibility class Ib molecule H2-M3 complexed with mitochondrial-derived peptides. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 1-13	3.6	
106	Alternative pathways utilize or circumvent putrescine for biosynthesis of putrescine-containing rhizoferrin. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100146	5.4	3
105	A distinct inhibitory mechanism of the V-ATPase by <i>Vibrio</i> VopQ revealed by cryo-EM. <i>Nature Structural and Molecular Biology</i> , 2020 , 27, 589-597	17.6	5
104	A effector kinase is activated by host inositol hexakisphosphate. <i>Journal of Biological Chemistry</i> , 2020 , 295, 6214-6224	5.4	8
103	Genetic and structural studies of RABL3 reveal an essential role in lymphoid development and function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 8563-8572	11.5	3
102	A Bacterial Effector Mimics a Host HSP90 Client to Undermine Immunity. <i>Cell</i> , 2019 , 179, 205-218.e21	56.2	25
101	Molecular Discrimination between Two Conformations of Sphingomyelin in Plasma Membranes. <i>Cell</i> , 2019 , 176, 1040-1053.e17	56.2	58
100	Bacterial pseudokinase catalyzes protein polyglutamylolation to inhibit the SidE-family ubiquitin ligases. <i>Science</i> , 2019 , 364, 787-792	33.3	65
99	High-resolution cryo-EM structures of the <i>E. coli</i> hemolysin ClyA oligomers. <i>PLoS ONE</i> , 2019 , 14, e0213423	3.7	23
98	Importin-9 wraps around the H2A-H2B core to act as nuclear importer and histone chaperone. <i>ELife</i> , 2019 , 8,	8.9	21
97	Identification and Mechanistic Understanding of Dihydroorotate Dehydrogenase Point Mutations in <i>Plasmodium falciparum</i> that Confer in Vitro Resistance to the Clinical Candidate DSM265. <i>ACS Infectious Diseases</i> , 2019 , 5, 90-101	5.5	23
96	Protein AMPylation by an Evolutionarily Conserved Pseudokinase. <i>Cell</i> , 2018 , 175, 809-821.e19	56.2	87
95	Trypanosomatid Deoxyhypusine Synthase Activity Is Dependent on Shared Active-Site Complementation between Pseudoenzyme Paralogs. <i>Structure</i> , 2018 , 26, 1499-1512.e5	5.2	11
94	Functional clues from the crystal structure of an orphan periplasmic ligand-binding protein from <i>Treponema pallidum</i> . <i>Protein Science</i> , 2017 , 26, 847-856	6.3	6
93	SAV1 promotes Hippo kinase activation through antagonizing the PP2A phosphatase STRIPAK. <i>ELife</i> , 2017 , 6,	8.9	63

92	Exceptionally tight membrane-binding may explain the key role of the synaptotagmin-7 CA domain in asynchronous neurotransmitter release. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E8518-E8527	11.5	21
91	Mechanistic insights into neurotransmitter release and presynaptic plasticity from the crystal structure of Munc13-1 CCBMUN. <i>ELife</i> , 2017 , 6,	8.9	68
90	Author response: SAV1 promotes Hippo kinase activation through antagonizing the PP2A phosphatase STRIPAK 2017 ,		2
89	A Triazolopyrimidine-Based Dihydroorotate Dehydrogenase Inhibitor with Improved Drug-like Properties for Treatment and Prevention of Malaria. <i>ACS Infectious Diseases</i> , 2016 , 2, 945-957	5.5	55
88	Crystal structure of the cohesin loader Scc2 and insight into cohesinopathy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 12444-12449	11.5	61
87	Molecular insights into the enzymatic diversity of flavin-trafficking protein (Ftp; formerly ApbE) in flavoprotein biogenesis in the bacterial periplasm. <i>MicrobiologyOpen</i> , 2016 , 5, 21-38	3.4	20
86	Pathogenic C9ORF72 Antisense Repeat RNA Forms a Double Helix with Tandem C:C Mismatches. <i>Biochemistry</i> , 2016 , 55, 1283-6	3.2	24
85	Structural Basis and IP6 Requirement for Pds5-Dependent Cohesin Dynamics. <i>Molecular Cell</i> , 2016 , 62, 248-259	17.6	78
84	Bile salt receptor complex activates a pathogenic type III secretion system. <i>ELife</i> , 2016 , 5,	8.9	34
83	Relief of autoinhibition by conformational switch explains enzyme activation by a catalytically dead paralog. <i>ELife</i> , 2016 , 5,	8.9	16
82	Phosphorylation of spore coat proteins by a family of atypical protein kinases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E3482-91	11.5	40
81	Tetrahydro-2-naphthyl and 2-Indanyl Triazolopyrimidines Targeting Plasmodium falciparum Dihydroorotate Dehydrogenase Display Potent and Selective Antimalarial Activity. <i>Journal of Medicinal Chemistry</i> , 2016 , 59, 5416-31	8.3	36
80	A long-duration dihydroorotate dehydrogenase inhibitor (DSM265) for prevention and treatment of malaria. <i>Science Translational Medicine</i> , 2015 , 7, 296ra111	17.5	194
79	Evidence for Posttranslational Protein Flavinylation in the Syphilis Spirochete Treponema pallidum: Structural and Biochemical Insights from the Catalytic Core of a Periplasmic Flavin-Trafficking Protein. <i>MBio</i> , 2015 , 6, e00519-15	7.8	21
78	Dynamic binding mode of a Synaptotagmin-1-SNARE complex in solution. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 555-64	17.6	99
77	Coiled-coil coactivators play a structural role mediating interactions in hypoxia-inducible factor heterodimerization. <i>Journal of Biological Chemistry</i> , 2015 , 290, 7707-21	5.4	20
76	Structure and Ca ²⁺ -binding properties of the tandem C ₂ H domains of E-Syt2. <i>Structure</i> , 2014 , 22, 269-80	5.2	33
75	Identification of lysine residues in the Borrelia burgdorferi DbpA adhesin required for murine infection. <i>Infection and Immunity</i> , 2014 , 82, 3186-98	3.7	21

74	Full-length structure of a monomeric histidine kinase reveals basis for sensory regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 17839-44	11.5	60
73	Structure of cohesin subcomplex pinpoints direct shugoshin-Wapl antagonism in centromeric cohesion. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 864-70	17.6	104
72	Substrate-specific activation of the mitotic kinase Bub1 through intramolecular autophosphorylation and kinetochore targeting. <i>Structure</i> , 2014 , 22, 1616-27	5.2	23
71	Re-examining how complexin inhibits neurotransmitter release. <i>ELife</i> , 2014 , 3, e02391	8.9	49
70	Structural basis for autoactivation of human Mst2 kinase and its regulation by RASSF5. <i>Structure</i> , 2013 , 21, 1757-68	5.2	65
69	The bacterial effector VopL organizes actin into filament-like structures. <i>Cell</i> , 2013 , 155, 423-34	56.2	35
68	The TP0796 lipoprotein of <i>Treponema pallidum</i> is a bimetal-dependent FAD pyrophosphatase with a potential role in flavin homeostasis. <i>Journal of Biological Chemistry</i> , 2013 , 288, 11106-21	5.4	21
67	Structure of the human cohesin inhibitor Wapl. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 11355-60	11.5	48
66	Structural analysis of human Cdc20 supports multisite degron recognition by APC/C. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 18419-24	11.5	65
65	Structural, bioinformatic, and in vivo analyses of two <i>Treponema pallidum</i> lipoproteins reveal a unique TRAP transporter. <i>Journal of Molecular Biology</i> , 2012 , 416, 678-96	6.5	23
64	Structural and thermodynamic characterization of the interaction between two periplasmic <i>Treponema pallidum</i> lipoproteins that are components of a TPR-protein-associated TRAP transporter (TPAT). <i>Journal of Molecular Biology</i> , 2012 , 420, 70-86	6.5	20
63	Structure of human Mad1 C-terminal domain reveals its involvement in kinetochore targeting. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 6549-54	11.5	74
62	Structural and molecular characterization of iron-sensing hemerythrin-like domain within F-box and leucine-rich repeat protein 5 (FBXL5). <i>Journal of Biological Chemistry</i> , 2012 , 287, 7357-65	5.4	53
61	Biophysical and bioinformatic analyses implicate the <i>Treponema pallidum</i> Tp34 lipoprotein (Tp0971) in transition metal homeostasis. <i>Journal of Bacteriology</i> , 2012 , 194, 6771-81	3.5	14
60	Autoinhibition of Mint1 adaptor protein regulates amyloid precursor protein binding and processing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 3802-7	11.5	14
59	The assembly of a GTPase-kinase signalling complex by a bacterial catalytic scaffold. <i>Nature</i> , 2011 , 469, 107-11	50.4	93
58	The crystal structure of a Munc13 C-terminal module exhibits a remarkable similarity to vesicle tethering factors. <i>Structure</i> , 2011 , 19, 1443-55	5.2	68
57	A single active-site mutation of P450BM-3 dramatically enhances substrate binding and rate of product formation. <i>Biochemistry</i> , 2011 , 50, 8333-41	3.2	12

56	Mechanism of actin filament nucleation by the bacterial effector VopL. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 1068-74	17.6	49
55	Munc13 C2B domain is an activity-dependent Ca ²⁺ regulator of synaptic exocytosis. <i>Nature Structural and Molecular Biology</i> , 2010 , 17, 280-8	17.6	163
54	Crystal structure of the Formin mDia1 in autoinhibited conformation. <i>PLoS ONE</i> , 2010 , 5, e12896	3.7	32
53	Structural and functional analysis of the YAP-binding domain of human TEAD2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 7293-8	11.5	107
52	Evolution of substrate specificity within a diverse family of beta/alpha-barrel-fold basic amino acid decarboxylases: X-ray structure determination of enzymes with specificity for L-arginine and carboxynorspermidine. <i>Journal of Biological Chemistry</i> , 2010 , 285, 25708-19	5.4	20
51	Kinetic and structural insights into the mechanism of AMPylation by VopS Fic domain. <i>Journal of Biological Chemistry</i> , 2010 , 285, 20155-63	5.4	62
50	Structural and energetic mechanisms of cooperative autoinhibition and activation of Vav1. <i>Cell</i> , 2010 , 140, 246-56	56.2	111
49	Structural and mutational analysis of functional differentiation between synaptotagmins-1 and -7. <i>PLoS ONE</i> , 2010 , 5, e12544	3.7	23
48	Artificial ligand binding within the HIF2alpha PAS-B domain of the HIF2 transcription factor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 450-5	11.5	194
47	Localization and structure of the ankyrin-binding site on beta2-spectrin. <i>Journal of Biological Chemistry</i> , 2009 , 284, 6982-7	5.4	54
46	Structure and substrate recruitment of the human spindle checkpoint kinase Bub1. <i>Molecular Cell</i> , 2008 , 32, 394-405	17.6	72
45	Crystal structure of inhibitor-bound P450BM-3 reveals open conformation of substrate access channel. <i>Biochemistry</i> , 2008 , 47, 3662-70	3.2	31
44	Changes at the KinA PAS-A dimerization interface influence histidine kinase function. <i>Biochemistry</i> , 2008 , 47, 4051-64	3.2	49
43	Enzyme structure and dynamics affect hydrogen tunneling: the impact of a remote side chain (I553) in soybean lipoxygenase-1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 1146-51	11.5	139
42	Correction for Meyer et al., Enzyme structure and dynamics affect hydrogen tunneling: The impact of a remote side chain (I553) in soybean lipoxygenase-1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 19562-19562	11.5	2
41	Insights into mad2 regulation in the spindle checkpoint revealed by the crystal structure of the symmetric mad2 dimer. <i>PLoS Biology</i> , 2008 , 6, e50	9.7	71
40	Interactions of substrates at the surface of P450s can greatly enhance substrate potency. <i>Biochemistry</i> , 2007 , 46, 14010-7	3.2	28
39	Crystal structure of the RIM1alpha C2B domain at 1.7 Å resolution. <i>Biochemistry</i> , 2007 , 46, 8988-98	3.2	16

38	Structural basis of histone demethylation by LSD1 revealed by suicide inactivation. <i>Nature Structural and Molecular Biology</i> , 2007 , 14, 535-9	17.6	152
37	Structural analysis of Xanthomonas XopD provides insights into substrate specificity of ubiquitin-like protein proteases. <i>Journal of Biological Chemistry</i> , 2007 , 282, 6773-82	5.4	59
36	Crystal structure of the Tp34 (TP0971) lipoprotein of treponema pallidum: implications of its metal-bound state and affinity for human lactoferrin. <i>Journal of Biological Chemistry</i> , 2007 , 282, 5944-58	5.4	39
35	p31comet blocks Mad2 activation through structural mimicry. <i>Cell</i> , 2007 , 131, 744-55	56.2	157
34	Structural and biochemical basis for polyamine binding to the Tp0655 lipoprotein of Treponema pallidum: putative role for Tp0655 (TpPotD) as a polyamine receptor. <i>Journal of Molecular Biology</i> , 2007 , 373, 681-94	6.5	36
33	A versatile conformational switch regulates reactivity in human branched-chain alpha-ketoacid dehydrogenase. <i>Structure</i> , 2006 , 14, 287-98	5.2	42
32	Structural insight into interactions between dihydrolipoamide dehydrogenase (E3) and E3 binding protein of human pyruvate dehydrogenase complex. <i>Structure</i> , 2006 , 14, 611-21	5.2	67
31	Dynamic evolution of the human immunodeficiency virus type 1 pathogenic factor, Nef. <i>Journal of Virology</i> , 2006 , 80, 1311-20	6.6	65
30	The PnrA (Tp0319; TmpC) lipoprotein represents a new family of bacterial purine nucleoside receptor encoded within an ATP-binding cassette (ABC)-like operon in Treponema pallidum. <i>Journal of Biological Chemistry</i> , 2006 , 281, 8072-81	5.4	49
29	Crystal structure of a type III pantothenate kinase: insight into the mechanism of an essential coenzyme A biosynthetic enzyme universally distributed in bacteria. <i>Journal of Bacteriology</i> , 2006 , 188, 5532-40	3.5	39
28	A proximal arginine R206 participates in switching of the Bradyrhizobium japonicum FixL oxygen sensor. <i>Journal of Molecular Biology</i> , 2006 , 360, 80-9	6.5	29
27	Structural basis for CoREST-dependent demethylation of nucleosomes by the human LSD1 histone demethylase. <i>Molecular Cell</i> , 2006 , 23, 377-87	17.6	252
26	Structural basis for a Munc13-1 homodimer to Munc13-1/RIM heterodimer switch. <i>PLoS Biology</i> , 2006 , 4, e192	9.7	84
25	Crystal structure of the RIM2 C2A-domain at 1.4 Å resolution. <i>Biochemistry</i> , 2005 , 44, 13533-42	3.2	18
24	Crystal structure of human dihydrolipoamide dehydrogenase: NAD ⁺ /NADH binding and the structural basis of disease-causing mutations. <i>Journal of Molecular Biology</i> , 2005 , 350, 543-52	6.5	95
23	Structural basis of Rho GTPase-mediated activation of the formin mDia1. <i>Molecular Cell</i> , 2005 , 18, 273-81	17.6	188
22	Structural basis of actin filament nucleation and processive capping by a formin homology 2 domain. <i>Nature</i> , 2005 , 433, 488-94	50.4	289
21	Structure of the photolyase-like domain of cryptochrome 1 from Arabidopsis thaliana. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 12142-7	11.5	251

20	Structural evidence that the 32-kilodalton lipoprotein (Tp32) of <i>Treponema pallidum</i> is an L-methionine-binding protein. <i>Journal of Biological Chemistry</i> , 2004 , 279, 55644-50	5.4	33
19	Cross-talk between thiamin diphosphate binding and phosphorylation loop conformation in human branched-chain alpha-keto acid decarboxylase/dehydrogenase. <i>Journal of Biological Chemistry</i> , 2004 , 279, 32968-78	5.4	25
18	Structural basis for the evolutionary inactivation of Ca ²⁺ binding to synaptotagmin 4. <i>Nature Structural and Molecular Biology</i> , 2004 , 11, 844-9	17.6	80
17	Molecular mechanism for regulation of the human mitochondrial branched-chain alpha-ketoacid dehydrogenase complex by phosphorylation. <i>Structure</i> , 2004 , 12, 2185-96	5.2	50
16	Roles of His291-alpha and His146-beta in the reductive acylation reaction catalyzed by human branched-chain alpha-ketoacid dehydrogenase: refined phosphorylation loop structure in the active site. <i>Journal of Biological Chemistry</i> , 2003 , 278, 43402-10	5.4	14
15	Structure of Cdc42 in a complex with the GTPase-binding domain of the cell polarity protein, Par6. <i>EMBO Journal</i> , 2003 , 22, 1125-33	13	137
14	The purine repressor of <i>Bacillus subtilis</i> : a novel combination of domains adapted for transcription regulation. <i>Journal of Bacteriology</i> , 2003 , 185, 4087-98	3.5	31
13	Crystal structure of a 12 ANK repeat stack from human ankyrinR. <i>EMBO Journal</i> , 2002 , 21, 6387-96	13	169
12	Three-dimensional structure of the complexin/SNARE complex. <i>Neuron</i> , 2002 , 33, 397-409	13.9	327
11	Crystal structure of the 47-kDa lipoprotein of <i>Treponema pallidum</i> reveals a novel penicillin-binding protein. <i>Journal of Biological Chemistry</i> , 2002 , 277, 41857-64	5.4	42
10	Structure of human nicotinamide/nicotinic acid mononucleotide adenylyltransferase. Basis for the dual substrate specificity and activation of the oncolytic agent tiazofurin. <i>Journal of Biological Chemistry</i> , 2002 , 277, 13148-54	5.4	64
9	Structure of rat BCKD kinase: nucleotide-induced domain communication in a mitochondrial protein kinase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 11218-23	11.5	68
8	Structural and functional characterization of second-coordination sphere mutants of soybean lipoxygenase-1. <i>Biochemistry</i> , 2001 , 40, 7509-17	3.2	110
7	Pivotal role of water in the mechanism of P450BM-3. <i>Biochemistry</i> , 2001 , 40, 13456-65	3.2	293
6	Strategies for macromolecular synchrotron crystallography. <i>Structure</i> , 2000 , 8, R105-10	5.2	70
5	Adaptation of an enzyme to regulatory function: structure of <i>Bacillus subtilis</i> PyrR, a pyr RNA-binding attenuation protein and uracil phosphoribosyltransferase. <i>Structure</i> , 1998 , 6, 337-50	5.2	60
4	Mechanism of the synergistic end-product regulation of <i>Bacillus subtilis</i> glutamine phosphoribosylpyrophosphate amidotransferase by nucleotides. <i>Biochemistry</i> , 1997 , 36, 10718-26	3.2	43
3	Structure and function of the glutamine phosphoribosylpyrophosphate amidotransferase glutamine site and communication with the phosphoribosylpyrophosphate site. <i>Journal of Biological Chemistry</i> , 1996 , 271, 15549-57	5.4	62

- 2 A protein catalytic framework with an N-terminal nucleophile is capable of self-activation. *Nature*, **1995**, 378, 416-9 50.4 557
- 1 Photochemical synthesis and structural characterization of $(\eta\text{-C}_5\text{Me}_5)_3\text{Mo}_3(\text{CO})_4(\mu\text{-H})(\mu\text{-O})$: an unprecedented 46-electron trimolybdenum cluster containing a localized monoprotonated Mo \equiv Mo double bond. *Journal of Organometallic Chemistry*, **1988**, 340, C23-C30 2.3 7