

Diana R Tomchick

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|--------------------|-------------------------|-----------------|-----------------|
| 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 | A protein catalytic framework with an N-terminal nucleophile is capable of self-activation. <i>Nature</i> , 1995 , 378, 416-9 | 50.4 | 557 |
| 108 | Three-dimensional structure of the complexin/SNARE complex. <i>Neuron</i> , 2002 , 33, 397-409 | 13.9 | 327 |
| 107 | Pivotal role of water in the mechanism of P450BM-3. <i>Biochemistry</i> , 2001 , 40, 13456-65 | 3.2 | 293 |
| 106 | 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 |
| 105 | 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 |
| 104 | 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 |
| 103 | A long-duration dihydroorotate dehydrogenase inhibitor (DSM265) for prevention and treatment of malaria. <i>Science Translational Medicine</i> , 2015 , 7, 296ra111 | 17.5 | 194 |
| 102 | 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 |
| 101 | Structural basis of Rho GTPase-mediated activation of the formin mDia1. <i>Molecular Cell</i> , 2005 , 18, 273-81 | 17.6 | 188 |
| 100 | Crystal structure of a 12 ANK repeat stack from human ankyrinR. <i>EMBO Journal</i> , 2002 , 21, 6387-96 | 13 | 169 |
| 99 | 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 |
| 98 | p31comet blocks Mad2 activation through structural mimicry. <i>Cell</i> , 2007 , 131, 744-55 | 56.2 | 157 |
| 97 | 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 |
| 96 | 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 |
| 95 | 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 |
| 94 | Structural and energetic mechanisms of cooperative autoinhibition and activation of Vav1. <i>Cell</i> , 2010 , 140, 246-56 | 56.2 | 111 |
| 93 | Structural and functional characterization of second-coordination sphere mutants of soybean lipoxygenase-1. <i>Biochemistry</i> , 2001 , 40, 7509-17 | 3.2 | 110 |

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| 92 | 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 |
| 91 | 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 |
| 90 | 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 |
| 89 | 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 |
| 88 | The assembly of a GTPase-kinase signalling complex by a bacterial catalytic scaffold. <i>Nature</i> , 2011 , 469, 107-11 | 50.4 | 93 |
| 87 | Protein AMPylation by an Evolutionarily Conserved Pseudokinase. <i>Cell</i> , 2018 , 175, 809-821.e19 | 56.2 | 87 |
| 86 | Structural basis for a Munc13-1 homodimer to Munc13-1/RIM heterodimer switch. <i>PLoS Biology</i> , 2006 , 4, e192 | 9.7 | 84 |
| 85 | 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 |
| 84 | Structural Basis and IP6 Requirement for Pds5-Dependent Cohesin Dynamics. <i>Molecular Cell</i> , 2016 , 62, 248-259 | 17.6 | 78 |
| 83 | 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 |
| 82 | Structure and substrate recruitment of the human spindle checkpoint kinase Bub1. <i>Molecular Cell</i> , 2008 , 32, 394-405 | 17.6 | 72 |
| 81 | 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 |
| 80 | Strategies for macromolecular synchrotron crystallography. <i>Structure</i> , 2000 , 8, R105-10 | 5.2 | 70 |
| 79 | 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 |
| 78 | 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 |
| 77 | Mechanistic insights into neurotransmitter release and presynaptic plasticity from the crystal structure of Munc13-1 CCBMUN. <i>ELife</i> , 2017 , 6, | 8.9 | 68 |
| 76 | 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 |
| 75 | Bacterial pseudokinase catalyzes protein polyglutamylolation to inhibit the SidE-family ubiquitin ligases. <i>Science</i> , 2019 , 364, 787-792 | 33.3 | 65 |

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| 74 | Structural basis for autoactivation of human Mst2 kinase and its regulation by RASSF5. <i>Structure</i> , 2013 , 21, 1757-68 | 5.2 | 65 |
| 73 | 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 |
| 72 | Dynamic evolution of the human immunodeficiency virus type 1 pathogenic factor, Nef. <i>Journal of Virology</i> , 2006 , 80, 1311-20 | 6.6 | 65 |
| 71 | 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 |
| 70 | SAV1 promotes Hippo kinase activation through antagonizing the PP2A phosphatase STRIPAK. <i>ELife</i> , 2017 , 6, | 8.9 | 63 |
| 69 | 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 |
| 68 | 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 |
| 67 | 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 |
| 66 | 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 |
| 65 | Adaptation of an enzyme to regulatory function: structure of Bacillus subtilis PyrR, a pyr RNA-binding attenuation protein and uracil phosphoribosyltransferase. <i>Structure</i> , 1998 , 6, 337-50 | 5.2 | 60 |
| 64 | 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 |
| 63 | Molecular Discrimination between Two Conformations of Sphingomyelin in Plasma Membranes. <i>Cell</i> , 2019 , 176, 1040-1053.e17 | 56.2 | 58 |
| 62 | 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 |
| 61 | Localization and structure of the ankyrin-binding site on beta2-spectrin. <i>Journal of Biological Chemistry</i> , 2009 , 284, 6982-7 | 5.4 | 54 |
| 60 | 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 |
| 59 | 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 |
| 58 | Mechanism of actin filament nucleation by the bacterial effector VopL. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 1068-74 | 17.6 | 49 |
| 57 | Changes at the KinA PAS-A dimerization interface influence histidine kinase function. <i>Biochemistry</i> , 2008 , 47, 4051-64 | 3.2 | 49 |

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| 56 | The PnrA (Tp0319; TmpC) lipoprotein represents a new family of bacterial purine nucleoside receptor encoded within an ATP-binding cassette (ABC)-like operon in <i>Treponema pallidum</i> . <i>Journal of Biological Chemistry</i> , 2006 , 281, 8072-81 | 5.4 | 49 |
| 55 | Re-examining how complexin inhibits neurotransmitter release. <i>ELife</i> , 2014 , 3, e02391 | 8.9 | 49 |
| 54 | 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 |
| 53 | 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 |
| 52 | A versatile conformational switch regulates reactivity in human branched-chain alpha-ketoacid dehydrogenase. <i>Structure</i> , 2006 , 14, 287-98 | 5.2 | 42 |
| 51 | 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 |
| 50 | 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 |
| 49 | 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 |
| 48 | Crystal structure of the Tp34 (TP0971) lipoprotein of <i>treponema pallidum</i> : implications of its metal-bound state and affinity for human lactoferrin. <i>Journal of Biological Chemistry</i> , 2007 , 282, 5944-58 | 5.4 | 39 |
| 47 | Structural and biochemical basis for polyamine binding to the Tp0655 lipoprotein of <i>Treponema pallidum</i> : putative role for Tp0655 (TpPotD) as a polyamine receptor. <i>Journal of Molecular Biology</i> , 2007 , 373, 681-94 | 6.5 | 36 |
| 46 | 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 |
| 45 | The bacterial effector VopL organizes actin into filament-like structures. <i>Cell</i> , 2013 , 155, 423-34 | 56.2 | 35 |
| 44 | Bile salt receptor complex activates a pathogenic type III secretion system. <i>ELife</i> , 2016 , 5, | 8.9 | 34 |
| 43 | Structure and Ca ²⁺ -binding properties of the tandem C ² domains of E-Syt2. <i>Structure</i> , 2014 , 22, 269-80 | 5.2 | 33 |
| 42 | 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 |
| 41 | Crystal structure of the Formin mDia1 in autoinhibited conformation. <i>PLoS ONE</i> , 2010 , 5, e12896 | 3.7 | 32 |
| 40 | Crystal structure of inhibitor-bound P450BM-3 reveals open conformation of substrate access channel. <i>Biochemistry</i> , 2008 , 47, 3662-70 | 3.2 | 31 |
| 39 | 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 |

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| 38 | 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 |
| 37 | Interactions of substrates at the surface of P450s can greatly enhance substrate potency. <i>Biochemistry</i> , 2007 , 46, 14010-7 | 3.2 | 28 |
| 36 | A Bacterial Effector Mimics a Host HSP90 Client to Undermine Immunity. <i>Cell</i> , 2019 , 179, 205-218.e21 | 56.2 | 25 |
| 35 | 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 |
| 34 | Pathogenic C9ORF72 Antisense Repeat RNA Forms a Double Helix with Tandem C:C Mismatches. <i>Biochemistry</i> , 2016 , 55, 1283-6 | 3.2 | 24 |
| 33 | High-resolution cryo-EM structures of the E. coli hemolysin ClyA oligomers. <i>PLoS ONE</i> , 2019 , 14, e0213423 | 3.7 | 23 |
| 32 | Substrate-specific activation of the mitotic kinase Bub1 through intramolecular autophosphorylation and kinetochore targeting. <i>Structure</i> , 2014 , 22, 1616-27 | 5.2 | 23 |
| 31 | Structural, bioinformatic, and in vivo analyses of two Treponema pallidum lipoproteins reveal a unique TRAP transporter. <i>Journal of Molecular Biology</i> , 2012 , 416, 678-96 | 6.5 | 23 |
| 30 | Structural and mutational analysis of functional differentiation between synaptotagmins-1 and -7. <i>PLoS ONE</i> , 2010 , 5, e12544 | 3.7 | 23 |
| 29 | Identification and Mechanistic Understanding of Dihydroorotate Dehydrogenase Point Mutations in Plasmodium falciparum that Confer in Vitro Resistance to the Clinical Candidate DSM265. <i>ACS Infectious Diseases</i> , 2019 , 5, 90-101 | 5.5 | 23 |
| 28 | 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 |
| 27 | 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 |
| 26 | 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 |
| 25 | The TP0796 lipoprotein of Treponema pallidum 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 |
| 24 | Importin-9 wraps around the H2A-H2B core to act as nuclear importer and histone chaperone. <i>ELife</i> , 2019 , 8, | 8.9 | 21 |
| 23 | 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 |
| 22 | 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 |
| 21 | Structural and thermodynamic characterization of the interaction between two periplasmic Treponema pallidum 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 |

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| 20 | 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 |
| 19 | Crystal structure of the RIM2 C2A-domain at 1.4 Å resolution. <i>Biochemistry</i> , 2005 , 44, 13533-42 | 3.2 | 18 |
| 18 | Crystal structure of the RIM1alpha C2B domain at 1.7 Å resolution. <i>Biochemistry</i> , 2007 , 46, 8988-98 | 3.2 | 16 |
| 17 | Relief of autoinhibition by conformational switch explains enzyme activation by a catalytically dead paralog. <i>ELife</i> , 2016 , 5, | 8.9 | 16 |
| 16 | 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 |
| 15 | 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 |
| 14 | 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 |
| 13 | 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 |
| 12 | 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 |
| 11 | A effector kinase is activated by host inositol hexakisphosphate. <i>Journal of Biological Chemistry</i> , 2020 , 295, 6214-6224 | 5.4 | 8 |
| 10 | Photochemical synthesis and structural characterization of (B-C5Me5)3Mo3(CO)4(μ-H)(μ-O): an unprecedented 46-electron trimolybdenum cluster containing a localized monoprotonated Mo?Mo double bond. <i>Journal of Organometallic Chemistry</i> , 1988 , 340, C23-C30 | 2.3 | 7 |
| 9 | 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 |
| 8 | 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 |
| 7 | Dynamic remodeling of host membranes by self-organizing bacterial effectors. <i>Science</i> , 2021 , 372, 935-941 | 9.3 | 4 |
| 6 | 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 |
| 5 | 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 |
| 4 | Alternative pathways utilize or circumvent putrescine for biosynthesis of putrescine-containing rhizoferrin. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100146 | 5.4 | 3 |
| 3 | 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 |

- 2 Author response: SAV1 promotes Hippo kinase activation through antagonizing the PP2A phosphatase STRIPAK **2017**, 2
- 1 Structure and dynamics of major histocompatibility class Ib molecule H2-M3 complexed with mitochondrial-derived peptides. *Journal of Biomolecular Structure and Dynamics*, **2021**, 1-13 3.6