

# Thomas E Wales

## List of Publications by Year in descending order

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73  
papers

4,211  
citations

172457

29  
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123424

61  
g-index

76  
all docs

76  
docs citations

76  
times ranked

5701  
citing authors

#	ARTICLE	IF	CITATIONS
1	Hydrogen exchange mass spectrometry for the analysis of protein dynamics. <i>Mass Spectrometry Reviews</i> , 2006, 25, 158-170.	5.4	767
2	Recommendations for performing, interpreting and reporting hydrogen deuterium exchange mass spectrometry (HDX-MS) experiments. <i>Nature Methods</i> , 2019, 16, 595-602.	19.0	452
3	High-Speed and High-Resolution UPLC Separation at Zero Degrees Celsius. <i>Analytical Chemistry</i> , 2008, 80, 6815-6820.	6.5	309
4	Substrate processing by the Cdc48 ATPase complex is initiated by ubiquitin unfolding. <i>Science</i> , 2019, 365, .	12.6	233
5	Identification and characterization of EX1 kinetics in H/D exchange mass spectrometry by peak width analysis. <i>Journal of the American Society for Mass Spectrometry</i> , 2006, 17, 1498-1509.	2.8	209
6	Design of stapled antimicrobial peptides that are stable, nontoxic and kill antibiotic-resistant bacteria in mice. <i>Nature Biotechnology</i> , 2019, 37, 1186-1197.	17.5	187
7	Tissue-Specific Oncogenic Activity of KRASA146T. <i>Cancer Discovery</i> , 2019, 9, 738-755.	9.4	127
8	Inhibition of Pro-Apoptotic BAX by a Noncanonical Interaction Mechanism. <i>Molecular Cell</i> , 2015, 57, 873-886.	9.7	116
9	Analytical Aspects of Hydrogen Exchange Mass Spectrometry. <i>Annual Review of Analytical Chemistry</i> , 2015, 8, 127-148.	5.4	112
10	Structure of the Cdc48 ATPase with its ubiquitin-binding cofactor Ufd1. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 616-622.	8.2	82
11	Inhibition of Flaviviruses by Targeting a Conserved Pocket on the Viral Envelope Protein. <i>Cell Chemical Biology</i> , 2018, 25, 1006-1016.e8.	5.2	68
12	Partial Unfolding of Diverse SH3 Domains on a Wide Timescale. <i>Journal of Molecular Biology</i> , 2006, 357, 1592-1604.	4.2	63
13	Developments in Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Analytical Chemistry</i> , 2021, 93, 567-582.	6.5	63
14	Conformational Locking upon Cooperative Assembly of Notch Transcription Complexes. <i>Structure</i> , 2012, 20, 340-349.	3.3	60
15	Evidence for Increased Exposure of the Notch1 Metalloprotease Cleavage Site upon Conversion to an Activated Conformation. <i>Structure</i> , 2011, 19, 546-554.	3.3	59
16	Considerations in the Analysis of Hydrogen Exchange Mass Spectrometry Data. <i>Methods in Molecular Biology</i> , 2013, 1007, 263-288.	0.9	58
17	Thermodynamic stability measurements on multimeric proteins using a new H/D exchange- and matrix-assisted laser desorption/ionization (MALDI) mass spectrometry-based method. <i>Protein Science</i> , 2002, 11, 841-851.	7.6	51
18	Structural Stability and Local Dynamics in Disease-Causing Mutants of Human Apolipoprotein A-I: What Makes the Protein Amyloidogenic?. <i>Journal of Molecular Biology</i> , 2016, 428, 449-462.	4.2	47

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19	Allosteric inhibition of antiapoptotic MCL-1. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 600-607.	8.2	46
20	Dynamic Regulation of Long-Chain Fatty Acid Oxidation by a Noncanonical Interaction between the MCL-1 BH3 Helix and VLCAD. <i>Molecular Cell</i> , 2018, 69, 729-743.e7.	9.7	45
21	Achieving a Graded Immune Response: BTK Adopts a Range of Active/Inactive Conformations Dictated by Multiple Interdomain Contacts. <i>Structure</i> , 2017, 25, 1481-1494.e4.	3.3	44
22	Dynamic Allostery Mediated by a Conserved Tryptophan in the Tec Family Kinases. <i>PLoS Computational Biology</i> , 2016, 12, e1004826.	3.2	40
23	Allosteric sensitization of proapoptotic BAX. <i>Nature Chemical Biology</i> , 2017, 13, 961-967.	8.0	40
24	Translocation of polyubiquitinated protein substrates by the hexameric Cdc48 ATPase. <i>Molecular Cell</i> , 2022, 82, 570-584.e8.	9.7	39
25	Membrane phospholipid bilayer as a determinant of monoacylglycerol lipase kinetic profile and conformational repertoire. <i>Protein Science</i> , 2013, 22, 774-787.	7.6	37
26	Partial cooperative unfolding in proteins as observed by hydrogen exchange mass spectrometry. <i>International Reviews in Physical Chemistry</i> , 2013, 32, 96-127.	2.3	36
27	Differential Sensitivity of Src-Family Kinases to Activation by SH3 Domain Displacement. <i>PLoS ONE</i> , 2014, 9, e105629.	2.5	35
28	The Energetic Contribution of Backbone~Backbone Hydrogen Bonds to the Thermodynamic Stability of a Hyperstable P22 Arc Repressor Mutant. <i>Journal of the American Chemical Society</i> , 2001, 123, 7709-7710.	13.7	34
29	Allosteric Loss-of-function Mutations in HIV-1 Nef from a Long-term Non-progressor. <i>Journal of Molecular Biology</i> , 2007, 374, 121-129.	4.2	34
30	Tuning a High Transmission Ion Guide to Prevent Gas-Phase Proton Exchange During H/D Exchange MS Analysis. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 662-668.	2.8	34
31	Structure, function, and inhibitor targeting of HIV-1 Nef-effector kinase complexes. <i>Journal of Biological Chemistry</i> , 2020, 295, 15158-15171.	3.4	34
32	Hydrogen-Deuterium Exchange Mass Spectrometry to Study Protein Complexes. <i>Methods in Molecular Biology</i> , 2018, 1764, 153-171.	0.9	33
33	Homogeneous Oligomers of Pro-apoptotic BAX Reveal Structural Determinants of Mitochondrial Membrane Permeabilization. <i>Molecular Cell</i> , 2020, 79, 68-83.e7.	9.7	32
34	Enhanced SH3/Linker Interaction Overcomes Abl Kinase Activation by Gatekeeper and Myristic Acid Binding Pocket Mutations and Increases Sensitivity to Small Molecule Inhibitors*. <i>Journal of Biological Chemistry</i> , 2013, 288, 6116-6129.	3.4	29
35	Identification of a Covalent Molecular Inhibitor of Anti-apoptotic BFL-1 by Disulfide Tethering. <i>Cell Chemical Biology</i> , 2020, 27, 647-656.e6.	5.2	28
36	Activation Loop Dynamics Determine the Different Catalytic Efficiencies of B Cell~ and T Cell~ Specific Tec Kinases. <i>Science Signaling</i> , 2013, 6, ra76.	3.6	27

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37	Insights into Notch3 Activation and Inhibition Mediated by Antibodies Directed against Its Negative Regulatory Region. <i>Journal of Molecular Biology</i> , 2013, 425, 3192-3204.	4.2	26
38	Cumulative deamidations of the major lens protein $\gamma$ -Crystallin increase its aggregation during unfolding and oxidation. <i>Protein Science</i> , 2020, 29, 1945-1963.	7.6	25
39	Differential impact of BTK active site inhibitors on the conformational state of full-length BTK. <i>ELife</i> , 2020, 9, .	6.0	25
40	Subzero Celsius separations in three-zone temperature controlled hydrogen deuterium exchange mass spectrometry. <i>Journal of Chromatography A</i> , 2017, 1523, 275-282.	3.7	24
41	Structural basis of the atypical activation mechanism of KRASV14I. <i>Journal of Biological Chemistry</i> , 2019, 294, 13964-13972.	3.4	24
42	Conformational Features of the Full-Length HIV and SIV Nef Proteins Determined by Mass Spectrometry. <i>Biochemistry</i> , 2006, 45, 7733-7739.	2.5	23
43	Hydrogen Exchange-Mass Spectrometry Measures Stapled Peptide Conformational Dynamics and Predicts Pharmacokinetic Properties. <i>Analytical Chemistry</i> , 2013, 85, 11185-11188.	6.5	21
44	Conformational Dynamics of the Escherichia coli DNA Polymerase Manager Proteins UmuD and UmuD <sup>2</sup> . <i>Journal of Molecular Biology</i> , 2010, 398, 40-53.	4.2	20
45	Lipid-targeting pleckstrin homology domain turns its autoinhibitory face toward the TEC kinases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 21539-21544.	7.1	19
46	HIV-1 Nef interaction influences the ATP-binding site of the Src-family kinase, Hck. <i>BMC Chemical Biology</i> , 2012, 12, 1.	1.6	18
47	Remodeling of HIV-1 Nef Structure by Src-Family Kinase Binding. <i>Journal of Molecular Biology</i> , 2018, 430, 310-321.	4.2	18
48	Active-Site Inhibitors Modulate the Dynamic Properties of Human Monoacylglycerol Lipase: A Hydrogen Exchange Mass Spectrometry Study. <i>Biochemistry</i> , 2013, 52, 5016-5026.	2.5	17
49	Dynamic and structural differences between heme oxygenase-1 and -2 are due to differences in their C-terminal regions. <i>Journal of Biological Chemistry</i> , 2019, 294, 8259-8272.	3.4	17
50	Structural Basis for Lipid Binding and Function by an Evolutionarily Conserved Protein, Serum Amyloid A. <i>Journal of Molecular Biology</i> , 2020, 432, 1978-1995.	4.2	16
51	The heme-regulatory motifs of heme oxygenase-2 contribute to the transfer of heme to the catalytic site for degradation. <i>Journal of Biological Chemistry</i> , 2020, 295, 5177-5191.	3.4	16
52	Site-Dependent Cysteine Lipidation Potentiates the Activation of Proapoptotic BAX. <i>Cell Reports</i> , 2020, 30, 3229-3239.e6.	6.4	15
53	Noncanonical Role of the PDZ4 Domain of the Adaptor Protein PDZK1 in the Regulation of the Hepatic High Density Lipoprotein Receptor Scavenger Receptor Class B, Type I (SR-BI). <i>Journal of Biological Chemistry</i> , 2013, 288, 19845-19860.	3.4	14
54	Membrane-Associated Conformation of HIV-1 Nef Investigated with Hydrogen Exchange Mass Spectrometry at a Langmuir Monolayer. <i>Analytical Chemistry</i> , 2015, 87, 7030-7035.	6.5	14

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55	Simple and Fast Maximally Deuterated Control (maxD) Preparation for Hydrogen-Deuterium Exchange Mass Spectrometry Experiments. <i>Analytical Chemistry</i> , 2022, 94, 10142-10150.	6.5	14
56	The conformational stability of pro-apoptotic BAX is dictated by discrete residues of the protein core. <i>Nature Communications</i> , 2021, 12, 4932.	12.8	13
57	Subtle Dynamic Changes Accompany Hck Activation by HIV-1 Nef and are Reversed by an Antiretroviral Kinase Inhibitor. <i>Biochemistry</i> , 2015, 54, 6382-6391.	2.5	12
58	The accuracy and precision of a new H/D exchange- and mass spectrometry-based technique for measuring the thermodynamic stability of proteins. <i>Analytica Chimica Acta</i> , 2003, 496, 225-232.	5.4	11
59	Hydrogen Exchange Mass Spectrometry of Related Proteins with Divergent Sequences: A Comparative Study of HIV-1 Nef Allelic Variants. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 1048-1061.	2.8	11
60	Hydrocarbon-Stitched Peptide Agonists of Glucagon-Like Peptide-1 Receptor. <i>ACS Chemical Biology</i> , 2020, 15, 1340-1348.	3.4	11
61	A Conserved Isoleucine Maintains the Inactive State of Bruton's Tyrosine Kinase. <i>Journal of Molecular Biology</i> , 2014, 426, 3656-3669.	4.2	10
62	A Conservative Point Mutation in a Dynamic Antigen-binding Loop of Human Immunoglobulin $\lambda$ 6 Light Chain Promotes Pathologic Amyloid Formation. <i>Journal of Molecular Biology</i> , 2021, 433, 167310.	4.2	9
63	Facile chemical synthesis and equilibrium unfolding properties of CopG. <i>Protein Science</i> , 2004, 13, 1918-1926.	7.6	8
64	Dynamics of the Src family tyrosine kinase SH3 domains. <i>Protein Science</i> , 2016, 25, 852-864.	7.6	8
65	Hydrogen deuterium exchange mass spectrometry applied to chaperones and chaperone-assisted protein folding. <i>Expert Review of Proteomics</i> , 2019, 16, 613-625.	3.0	6
66	Considerations in the Analysis of Hydrogen Exchange Mass Spectrometry Data. <i>Methods in Molecular Biology</i> , 2020, 2051, 407-435.	0.9	6
67	Targeting a helix-in-groove interaction between E1 and E2 blocks ubiquitin transfer. <i>Nature Chemical Biology</i> , 2020, 16, 1218-1226.	8.0	5
68	Structural basis for defective membrane targeting of mutant enzyme in human VLCAD deficiency. <i>Nature Communications</i> , 2022, 13, .	12.8	5
69	A redox switch regulates the structure and function of anti-apoptotic BFL-1. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 781-789.	8.2	4
70	The Conformational State of the BTK Substrate PLC $\gamma$ 3 Contributes to Ibrutinib Resistance. <i>Journal of Molecular Biology</i> , 2022, 434, 167422.	4.2	4
71	Identification of a Structural Determinant for Selective Targeting of HDMX. <i>Structure</i> , 2020, 28, 847-857.e5.	3.3	2
72	Remodeling of the Binding Site of Nucleoside Diphosphate Kinase Revealed by X-ray Structure and H/D Exchange. <i>Biochemistry</i> , 2019, 58, 1440-1449.	2.5	1

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73	Dynamics of the polymerase manager protein UmuD: DNA damage tolerance in E. coli. FASEB Journal, 2008, 22, 591.4.	0.5	0