

Kylie J Walters

List of Publications by Year in descending order

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75
papers

5,145
citations

101543

36
h-index

91884

69
g-index

77
all docs

77
docs citations

77
times ranked

4733
citing authors

#	ARTICLE	IF	CITATIONS
1	Ubiquitin-binding domains " from structures to functions. <i>Nature Reviews Molecular Cell Biology</i> , 2009, 10, 659-671.	37.0	724
2	Proteasome subunit Rpn13 is a novel ubiquitin receptor. <i>Nature</i> , 2008, 453, 481-488.	27.8	553
3	Ubiquitin docking at the proteasome through a novel pleckstrin-homology domain interaction. <i>Nature</i> , 2008, 453, 548-552.	27.8	290
4	Rpn1 provides adjacent receptor sites for substrate binding and deubiquitination by the proteasome. <i>Science</i> , 2016, 351, .	12.6	234
5	Gates, Channels, and Switches: Elements of the Proteasome Machine. <i>Trends in Biochemical Sciences</i> , 2016, 41, 77-93.	7.5	223
6	Structural Studies of the Interaction between Ubiquitin Family Proteins and Proteasome Subunit S5a. <i>Biochemistry</i> , 2002, 41, 1767-1777.	2.5	211
7	Can AlphaFold2 predict the impact of missense mutations on structure?. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 1-2.	8.2	170
8	Structure of S5a Bound to Monoubiquitin Provides a Model for Polyubiquitin Recognition. <i>Journal of Molecular Biology</i> , 2005, 348, 727-739.	4.2	168
9	DNA-repair protein hHR23a alters its protein structure upon binding proteasomal subunit S5a. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 12694-12699.	7.1	137
10	A bis-Benzylidene Piperidone Targeting Proteasome Ubiquitin Receptor RPN13/ADRM1 as a Therapy for Cancer. <i>Cancer Cell</i> , 2013, 24, 791-805.	16.8	137
11	Structure of the S5a:K48-Linked Diubiquitin Complex and Its Interactions with Rpn13. <i>Molecular Cell</i> , 2009, 35, 280-290.	9.7	133
12	Chemical and structural studies provide a mechanistic basis for recognition of the MYC G-quadruplex. <i>Nature Communications</i> , 2018, 9, 4229.	12.8	131
13	Arylamine N-acetyltransferases: From Structure to Function. <i>Drug Metabolism Reviews</i> , 2008, 40, 479-510.	3.6	122
14	Structure of Proteasome Ubiquitin Receptor hRpn13 and Its Activation by the Scaffolding Protein hRpn2. <i>Molecular Cell</i> , 2010, 38, 404-415.	9.7	102
15	Prokaryotic Ubiquitin-Like Protein Pup Is Intrinsically Disordered. <i>Journal of Molecular Biology</i> , 2009, 392, 208-217.	4.2	97
16	Ubiquitin Recognition by the DNA Repair Protein hHR23a. <i>Biochemistry</i> , 2003, 42, 13529-13535.	2.5	90
17	Identification by NMR Spectroscopy of Residues at Contact Surfaces in Large, Slowly Exchanging Macromolecular Complexes. <i>Journal of the American Chemical Society</i> , 1999, 121, 9903-9904.	13.7	89
18	Characterizing Protein-Protein Complexes and Oligomers by Nuclear Magnetic Resonance Spectroscopy. <i>Methods in Enzymology</i> , 2001, 339, 238-258.	1.0	85

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19	UBL/LUBA Ubiquitin Receptor Proteins Bind a Common Tetraubiquitin Chain. <i>Journal of Molecular Biology</i> , 2006, 356, 1027-1035.	4.2	75
20	Structures of Rpn1 T1:Rad23 and hRpn13:hPLIC2 Reveal Distinct Binding Mechanisms between Substrate Receptors and Shuttle Factors of the Proteasome. <i>Structure</i> , 2016, 24, 1257-1270.	3.3	72
21	Structure of the Rpn13-Rpn2 complex provides insights for Rpn13 and Uch37 as anticancer targets. <i>Nature Communications</i> , 2017, 8, 15540.	12.8	67
22	A Simple Method to Distinguish Intermonomer Nuclear Overhauser Effects in Homodimeric Proteins with C2 Symmetry. <i>Journal of the American Chemical Society</i> , 1997, 119, 5958-5959.	13.7	58
23	Multitasking with ubiquitin through multivalent interactions. <i>Trends in Biochemical Sciences</i> , 2010, 35, 352-360.	7.5	52
24	Structure and mobility of the PUT3 dimer. <i>Nature Structural Biology</i> , 1997, 4, 744-750.	9.7	51
25	A critical role for the loop region of the basic helix-loop-helix/leucine zipper protein Mlx in DNA binding and glucose-regulated transcription. <i>Nucleic Acids Research</i> , 2006, 35, 35-44.	14.5	51
26	The Proteasome Ubiquitin Receptor hRpn13 and Its Interacting Deubiquitinating Enzyme Uch37 Are Required for Proper Cell Cycle Progression. <i>Journal of Biological Chemistry</i> , 2016, 291, 8773-8783.	3.4	50
27	Myosin VI Contains a Compact Structural Motif that Binds to Ubiquitin Chains. <i>Cell Reports</i> , 2016, 14, 2683-2694.	6.4	49
28	Ubiquitin and its binding domains. <i>Frontiers in Bioscience - Landmark</i> , 2012, 17, 2140.	3.0	47
29	NMR-based Model Reveals the Structural Determinants of Mammalian Arylamine N-Acetyltransferase Substrate Specificity. <i>Journal of Molecular Biology</i> , 2006, 363, 188-200.	4.2	43
30	Mouse N-acetyltransferase type 2, the homologue of human N-acetyltransferase type 1. <i>Biochemical Pharmacology</i> , 2008, 75, 1550-1560.	4.4	43
31	Structural Insights into Proteasome Activation by the 19S Regulatory Particle. <i>Biochemistry</i> , 2013, 52, 3618-3628.	2.5	43
32	Arylamine N-Acetyltransferases: Characterization of the Substrate Specificities and Molecular Interactions of Environmental Arylamines with Human NAT1 and NAT2. <i>Chemical Research in Toxicology</i> , 2007, 20, 1300-1308.	3.3	42
33	Diverse functions of myosin VI elucidated by an isoform-specific α -helix domain. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 300-308.	8.2	42
34	Ubiquitin family proteins and their relationship to the proteasome: a structural perspective. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2004, 1695, 73-87.	4.1	41
35	Structure of hRpn10 Bound to UBQLN2 UBL Illustrates Basis for Complementarity between Shuttle Factors and Substrates at the Proteasome. <i>Journal of Molecular Biology</i> , 2019, 431, 939-955.	4.2	41
36	Proteasome interaction with ubiquitinated substrates: from mechanisms to therapies. <i>FEBS Journal</i> , 2021, 288, 5231-5251.	4.7	40

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37	Arylamine N-acetyltransferase Aggregation and Constitutive Ubiquitylation. <i>Journal of Molecular Biology</i> , 2006, 361, 482-492.	4.2	38
38	Ubiquitin Receptor Proteins hHR23a and hPLIC2 Interact. <i>Journal of Molecular Biology</i> , 2007, 365, 1093-1101.	4.2	38
39	Defining how Ubiquitin Receptors hHR23a and S5a Bind Polyubiquitin. <i>Journal of Molecular Biology</i> , 2007, 369, 168-176.	4.2	38
40	Clathrin light chain A drives selective myosin VI recruitment to clathrin-coated pits under membrane tension. <i>Nature Communications</i> , 2019, 10, 4974.	12.8	38
41	Characterization of Dynamic Ubr-Proteasome Subcomplexes by In vivo Cross-linking (X) Assisted Bimolecular Tandem Affinity Purification (XBAP) and Label-free Quantitation. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2279-2292.	3.8	33
42	Structure of E3 ligase E6AP with a proteasome-binding site provided by substrate receptor hRpn10. <i>Nature Communications</i> , 2020, 11, 1291.	12.8	29
43	Covalent Rpn13-Binding Inhibitors for the Treatment of Ovarian Cancer. <i>ACS Omega</i> , 2018, 3, 11917-11929.	3.5	25
44	Proteasome substrate receptors and their therapeutic potential. <i>Trends in Biochemical Sciences</i> , 2022, 47, 950-964.	7.5	25
45	A High Affinity hRpn2-Derived Peptide That Displaces Human Rpn13 from Proteasome in 293T Cells. <i>PLoS ONE</i> , 2015, 10, e0140518.	2.5	24
46	Conformational Dynamics of the Rpt6 ATPase in Proteasome Assembly and Rpn14 Binding. <i>Structure</i> , 2013, 21, 753-765.	3.3	21
47	Structural Plasticity Allows UCH37 to Be Primed by RPN13 or Locked Down by INO80G. <i>Molecular Cell</i> , 2015, 57, 767-768.	9.7	21
48	Impact of Losing hRpn13 Pru or UCHL5 on Proteasome Clearance of Ubiquitinated Proteins and RA190 Cytotoxicity. <i>Molecular and Cellular Biology</i> , 2020, 40, .	2.3	21
49	An Extended Conformation for K48 Ubiquitin Chains Revealed by the hRpn2:Rpn13:K48-Diubiquitin Structure. <i>Structure</i> , 2020, 28, 495-506.e3.	3.3	21
50	Structure-guided bifunctional molecules hit a DEUBAD-lacking hRpn13 species upregulated in multiple myeloma. <i>Nature Communications</i> , 2021, 12, 7318.	12.8	18
51	Identifying and Studying Ubiquitin Receptors by NMR. <i>Methods in Molecular Biology</i> , 2012, 832, 279-303.	0.9	17
52	Novel TDP2-ubiquitin interactions and their importance for the repair of topoisomerase II-mediated DNA damage. <i>Nucleic Acids Research</i> , 2016, 44, gkw719.	14.5	17
53	Cryo-EM Reveals Unanchored M1-Ubiquitin Chain Binding at hRpn11 of the 26S Proteasome. <i>Structure</i> , 2020, 28, 1206-1217.e4.	3.3	17
54	Metabolic plasticity of IDH1-mutant glioma cell lines is responsible for low sensitivity to glutaminase inhibition. <i>Cancer & Metabolism</i> , 2020, 8, 23.	5.0	14

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55	Measuring ubiquitin chain linkage: Rap80 uses a molecular ruler mechanism for ubiquitin linkage specificity. <i>EMBO Journal</i> , 2009, 28, 2307-2308.	7.8	12
56	The SH3 domain of a M7 interacts with its C-terminal proline-rich region. <i>Protein Science</i> , 2007, 16, 189-196.	7.6	10
57	Ufd1 Exhibits Dual Ubiquitin Binding Modes. <i>Structure</i> , 2005, 13, 943-944.	3.3	7
58	Letter to the Editor: Chemical shift assignments of the (poly)ubiquitin-binding region of the proteasome subunit S5a. <i>Journal of Biomolecular NMR</i> , 2004, 30, 231-232.	2.8	6
59	In support of the BMRB. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 854-860.	8.2	6
60	Artificial targeting of misfolded cytosolic proteins to endoplasmic reticulum as a mechanism for clearance. <i>Scientific Reports</i> , 2015, 5, 12088.	3.3	5
61	Inhibition of cytoplasmic EZH2 induces antitumor activity through stabilization of the DLC1 tumor suppressor protein. <i>Nature Communications</i> , 2021, 12, 6941.	12.8	5
62	Targeted protein degradation: from small molecules to complex organelles—a Keystone Symposia report. <i>Annals of the New York Academy of Sciences</i> , 2022, 1510, 79-99.	3.8	5
63	Nuclear destruction: A suicide mission by AKIRIN2 brings intact proteasomes into the nucleus. <i>Molecular Cell</i> , 2022, 82, 13-14.	9.7	5
64	Quality Control: Maintaining molecular order and preventing cellular chaos. <i>Molecular Cell</i> , 2022, 82, 1390-1397.	9.7	5
65	The CD8 α hinge is intrinsically disordered with a dynamic exchange that includes proline cis-trans isomerization. <i>Journal of Magnetic Resonance</i> , 2022, 340, 107234.	2.1	5
66	<i>Mycobacterium tuberculosis</i> copper-regulated protein SocB is an intrinsically disordered protein that folds upon interaction with a synthetic phospholipid bilayer. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 193-200.	2.6	4
67	Rpn10 Protects the Proteasome from Dsk2. <i>Molecular Cell</i> , 2008, 32, 459-460.	9.7	3
68	Probing the catalytic potential of the hamster arylamine N-acetyltransferase 2 catalytic triad by site-directed mutagenesis of the proximal conserved residue, Tyr190. <i>FEBS Journal</i> , 2009, 276, 6928-6941.	4.7	3
69	Insights into how protein dynamics affects arylamine N-acetyltransferase catalysis. <i>Biochemical and Biophysical Research Communications</i> , 2009, 385, 395-401.	2.1	3
70	Policing Parkin with a UblD. <i>EMBO Journal</i> , 2011, 30, 2757-2758.	7.8	2
71	¹ H, ¹⁵ N, ¹³ C resonance assignments for <i>Saccharomyces cerevisiae</i> Rad23 UBL domain. <i>Biomolecular NMR Assignments</i> , 2016, 10, 291-295.	0.8	1
72	Ubiquitin in disguise unveils a cryptic binding site in 1.2-MDa anaphase-promoting complex/cyclosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17142-17144.	7.1	0

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73	An optimized protocol for acquiring and processing cryo-EM data of human 26S proteasome with M1-Ub6. STAR Protocols, 2021, 2, 100278.	1.2	0
74	Editorial overview: Macromolecular assemblies: clues from structural insights. Current Opinion in Structural Biology, 2021, 67, vi-viii.	5.7	0
75	Ubiquitination. , 2020, , 1-11.		0