

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	Can AlphaFold2 predict the impact of missense mutations on structure?. Nature Structural and Molecular Biology, 2022, 29, 1-2.	8.2	170
2	Targeted protein degradation: from small molecules to complex organelles—a Keystone Symposia report. Annals of the New York Academy of Sciences, 2022, 1510, 79-99.	3.8	5
3	Nuclear destruction: A suicide mission by AKIRIN2 brings intact proteasomes into the nucleus. Molecular Cell, 2022, 82, 13-14.	9.7	5
4	Quality Control: Maintaining molecular order and preventing cellular chaos. Molecular Cell, 2022, 82, 1390-1397.	9.7	5
5	The CD8 α hinge is intrinsically disordered with a dynamic exchange that includes proline cis-trans isomerization. Journal of Magnetic Resonance, 2022, 340, 107234.	2.1	5
6	Proteasome substrate receptors and their therapeutic potential. Trends in Biochemical Sciences, 2022, 47, 950-964.	7.5	25
7	Proteasome interaction with ubiquitinated substrates: from mechanisms to therapies. FEBS Journal, 2021, 288, 5231-5251.	4.7	40
8	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
9	Editorial overview: Macromolecular assemblies: clues from structural insights. Current Opinion in Structural Biology, 2021, 67, vi-viii.	5.7	0
10	Inhibition of cytoplasmic EZH2 induces antitumor activity through stabilization of the DLC1 tumor suppressor protein. Nature Communications, 2021, 12, 6941.	12.8	5
11	Structure-guided bifunctional molecules hit a DEUBAD-lacking hRpn13 species upregulated in multiple myeloma. Nature Communications, 2021, 12, 7318.	12.8	18
12	Impact of Losing hRpn13 Pru or UCHL5 on Proteasome Clearance of Ubiquitinated Proteins and RA190 Cytotoxicity. Molecular and Cellular Biology, 2020, 40, .	2.3	21
13	Cryo-EM Reveals Unanchored M1-Ubiquitin Chain Binding at hRpn11 of the 26S Proteasome. Structure, 2020, 28, 1206-1217.e4.	3.3	17
14	Metabolic plasticity of IDH1-mutant glioma cell lines is responsible for low sensitivity to glutaminase inhibition. Cancer & Metabolism, 2020, 8, 23.	5.0	14
15	An Extended Conformation for K48 Ubiquitin Chains Revealed by the hRpn2:Rpn13:K48-Diubiquitin Structure. Structure, 2020, 28, 495-506.e3.	3.3	21
16	Structure of E3 ligase E6AP with a proteasome-binding site provided by substrate receptor hRpn10. Nature Communications, 2020, 11, 1291.	12.8	29
17	Ubiquitination. , 2020, , 1-11.		0
18	Ubiquitin in disguise unveils a cryptic binding site in 1.2-MDa anaphase-promoting complex/cyclosome. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17142-17144.	7.1	0

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19	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
20	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
21	Covalent Rpn13-Binding Inhibitors for the Treatment of Ovarian Cancer. <i>ACS Omega</i> , 2018, 3, 11917-11929.	3.5	25
22	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
23	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
24	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
25	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
26	<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
27	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
28	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
29	Myosin VI Contains a Compact Structural Motif that Binds to Ubiquitin Chains. <i>Cell Reports</i> , 2016, 14, 2683-2694.	6.4	49
30	Rpn1 provides adjacent receptor sites for substrate binding and deubiquitination by the proteasome. <i>Science</i> , 2016, 351, .	12.6	234
31	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
32	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
33	Gates, Channels, and Switches: Elements of the Proteasome Machine. <i>Trends in Biochemical Sciences</i> , 2016, 41, 77-93.	7.5	223
34	Artificial targeting of misfolded cytosolic proteins to endoplasmic reticulum as a mechanism for clearance. <i>Scientific Reports</i> , 2015, 5, 12088.	3.3	5
35	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
36	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

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37	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
38	Conformational Dynamics of the Rpt6 ATPase in Proteasome Assembly and Rpn14 Binding. <i>Structure</i> , 2013, 21, 753-765.	3.3	21
39	Structural Insights into Proteasome Activation by the 19S Regulatory Particle. <i>Biochemistry</i> , 2013, 52, 3618-3628.	2.5	43
40	Identifying and Studying Ubiquitin Receptors by NMR. <i>Methods in Molecular Biology</i> , 2012, 832, 279-303.	0.9	17
41	In support of the BMRB. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 854-860.	8.2	6
42	Ubiquitin and its binding domains. <i>Frontiers in Bioscience - Landmark</i> , 2012, 17, 2140.	3.0	47
43	Policing Parkin with a UblD. <i>EMBO Journal</i> , 2011, 30, 2757-2758.	7.8	2
44	Multitasking with ubiquitin through multivalent interactions. <i>Trends in Biochemical Sciences</i> , 2010, 35, 352-360.	7.5	52
45	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
46	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
47	Ubiquitin-binding domains – from structures to functions. <i>Nature Reviews Molecular Cell Biology</i> , 2009, 10, 659-671.	37.0	724
48	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
49	Insights into how protein dynamics affects arylamine N-acetyltransferase catalysis. <i>Biochemical and Biophysical Research Communications</i> , 2009, 385, 395-401.	2.1	3
50	Prokaryotic Ubiquitin-Like Protein Pup Is Intrinsically Disordered. <i>Journal of Molecular Biology</i> , 2009, 392, 208-217.	4.2	97
51	Structure of the S5a:K48-Linked Diubiquitin Complex and Its Interactions with Rpn13. <i>Molecular Cell</i> , 2009, 35, 280-290.	9.7	133
52	Ubiquitin docking at the proteasome through a novel pleckstrin-homology domain interaction. <i>Nature</i> , 2008, 453, 548-552.	27.8	290
53	Proteasome subunit Rpn13 is a novel ubiquitin receptor. <i>Nature</i> , 2008, 453, 481-488.	27.8	553
54	Mouse N-acetyltransferase type 2, the homologue of human N-acetyltransferase type 1. <i>Biochemical Pharmacology</i> , 2008, 75, 1550-1560.	4.4	43

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55	Arylamine N-acetyltransferases: From Structure to Function. <i>Drug Metabolism Reviews</i> , 2008, 40, 479-510.	3.6	122
56	Rpn10 Protects the Proteasome from Dsk2. <i>Molecular Cell</i> , 2008, 32, 459-460.	9.7	3
57	Ubiquitin Receptor Proteins hHR23a and hPLIC2 Interact. <i>Journal of Molecular Biology</i> , 2007, 365, 1093-1101.	4.2	38
58	Defining how Ubiquitin Receptors hHR23a and S5a Bind Polyubiquitin. <i>Journal of Molecular Biology</i> , 2007, 369, 168-176.	4.2	38
59	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
60	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
61	UBL/LUBA Ubiquitin Receptor Proteins Bind a Common Tetraubiquitin Chain. <i>Journal of Molecular Biology</i> , 2006, 356, 1027-1035.	4.2	75
62	Arylamine N-acetyltransferase Aggregation and Constitutive Ubiquitylation. <i>Journal of Molecular Biology</i> , 2006, 361, 482-492.	4.2	38
63	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
64	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
65	Ufd1 Exhibits Dual Ubiquitin Binding Modes. <i>Structure</i> , 2005, 13, 943-944.	3.3	7
66	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
67	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
68	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
69	Ubiquitin Recognition by the DNA Repair Protein hHR23a. <i>Biochemistry</i> , 2003, 42, 13529-13535.	2.5	90
70	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
71	Structural Studies of the Interaction between Ubiquitin Family Proteins and Proteasome Subunit S5a. <i>Biochemistry</i> , 2002, 41, 1767-1777.	2.5	211
72	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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73	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
74	A Simple Method to Distinguish Intermonomer Nuclear Overhauser Effects in Homodimeric Proteins with C2Symmetry. <i>Journal of the American Chemical Society</i> , 1997, 119, 5958-5959.	13.7	58
75	Structure and mobility of the PUT3 dimer. <i>Nature Structural Biology</i> , 1997, 4, 744-750.	9.7	51