Gary Kleiger

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Perilous journey: a tour of the ubiquitin–proteasome system. Trends in Cell Biology, 2014, 24, 352-359.	7.9	271
2	Targeting of Ikaros to pericentromeric heterochromatin by direct DNA binding. Genes and Development, 2000, 14, 2146-2160.	5.9	230
3	Detection of sequential polyubiquitylation on a millisecond timescale. Nature, 2009, 462, 615-619.	27.8	189
4	GXXXG and AXXXA: Common α-Helical Interaction Motifs in Proteins, Particularly in Extremophilesâ€. Biochemistry, 2002, 41, 5990-5997.	2.5	181
5	Rapid E2-E3 Assembly and Disassembly Enable Processive Ubiquitylation of Cullin-RING Ubiquitin Ligase Substrates. Cell, 2009, 139, 957-968.	28.9	178
6	NEDD8Ânucleates a multivalent cullin–RING–UBE2D ubiquitin ligation assembly. Nature, 2020, 578, 461-466.	27.8	178
7	GXXXG and GXXXA Motifs Stabilize FAD and NAD(P)-binding Rossmann Folds Through Cα–Hâ⊄O Hydrogen Bonds and van der Waals Interactions. Journal of Molecular Biology, 2002, 323, 69-76.	4.2	168
8	Selective Dimerization of a C2H2 Zinc Finger Subfamily. Molecular Cell, 2003, 11, 459-470.	9.7	110
9	Essential Role for Ubiquitin-Ubiquitin-Conjugating Enzyme Interaction in Ubiquitin Discharge from Cdc34 to Substrate. Molecular Cell, 2011, 42, 75-83.	9.7	108
10	Ubiquitin ligation to F-box protein targets by SCF–RBR E3–E3 super-assembly. Nature, 2021, 590, 671-676.	27.8	97
11	E2 enzyme inhibition by stabilization of a low-affinity interface with ubiquitin. Nature Chemical Biology, 2014, 10, 156-163.	8.0	81
12	NEDD8 links cullin-RING ubiquitin ligase function to the p97 pathway. Nature Structural and Molecular Biology, 2012, 19, 511-516.	8.2	74
13	The 1.7 Ã crystal structure of BPI: a study of how two dissimilar amino acid sequences can adopt the same fold 1 1Edited by D. Rees. Journal of Molecular Biology, 2000, 299, 1019-1034.	4.2	50
14	Robust cullin-RING ligase function is established by a multiplicity of poly-ubiquitylation pathways. ELife, 2019, 8, .	6.0	36
15	The Acidic Tail of the Cdc34 Ubiquitin-conjugating Enzyme Functions in Both Binding to and Catalysis with Ubiquitin Ligase SCFCdc4. Journal of Biological Chemistry, 2009, 284, 36012-36023.	3.4	31
16	Linkage-specific ubiquitin chain formation depends on a lysine hydrocarbon ruler. Nature Chemical Biology, 2021, 17, 272-279.	8.0	26
17	3D Structure and Significance of the GΦXXG Helix Packing Motif in Tetramers of the E1β Subunit of Pyruvate Dehydrogenase from the ArcheonPyrobaculum aerophilumâ€,‡. Biochemistry, 2001, 40, 14484-14492.	2.5	21
18	Evaluation of a Diffusion-Driven Mechanism for Substrate Ubiquitination by the SCF-Cdc34 Ubiquitin Ligase Complex. Molecular Cell, 2006, 24, 523-534.	9.7	20

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19	Ubiquitin-conjugating Enzyme Cdc34 and Ubiquitin Ligase Skp1-Cullin-F-box Ligase (SCF) Interact through Multiple Conformations. Journal of Biological Chemistry, 2015, 290, 1106-1118.	3.4	20
20	Multimodal Mechanism of Action for the Cdc34 Acidic Loop. Journal of Biological Chemistry, 2013, 288, 34882-34896.	3.4	18
21	The extent of Ssa1/Ssa2 Hsp70 chaperone involvement in nuclear protein quality control degradation varies with the substrate. Molecular Biology of the Cell, 2020, 31, 221-233.	2.1	18
22	Mechanism of Lysine 48 Selectivity during Polyubiquitin Chain Formation by the Ube2R1/2 Ubiquitin-Conjugating Enzyme. Molecular and Cellular Biology, 2016, 36, 1720-1732.	2.3	14
23	Tag Team Ubiquitin Ligases. Cell, 2016, 166, 1080-1081.	28.9	14
24	The San1 Ubiquitin Ligase Functions Preferentially with Ubiquitin-conjugating Enzyme Ubc1 during Protein Quality Control. Journal of Biological Chemistry, 2016, 291, 18778-18790.	3.4	13
25	The San1 Ubiquitin Ligase Avidly Recognizes Misfolded Proteins through Multiple Substrate Binding Sites. Biomolecules, 2021, 11, 1619.	4.0	5
26	Using In Vitro Ubiquitylation Assays to Estimate the Affinities of Ubiquitin-Conjugating Enzymes for Their Ubiquitin Ligase Partners. Methods in Molecular Biology, 2018, 1844, 39-58.	0.9	2
27	Regulation of Cullin-RING E3 ligase dynamics by Inositol hexakisphosphate. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 6292-6294.	7.1	2
28	PFIT and PFRIT: Bioinformatic algorithms for detecting glycosidase function from structure and sequence. Protein Science, 2004, 13, 221-229.	7.6	1
29	Selfâ€regulating ubiquitin ligases. EMBO Journal, 2017, 36, 392-393.	7.8	1