David Komander

List of Publications by Year
in descending order

110 papers	23,441 citations	15504 65 h-index	24982 109 g-index
122 all docs	122 docs citations	122 times ranked	21466 citing authors

#	Article	IF	Citations
1	Activation mechanism of PINK1. Nature, 2022, 602, 328-335.	27.8	59
2	Insights Into Drug Repurposing, as Well as Specificity and Compound Properties of Piperidine-Based SARS-CoV-2 PLpro Inhibitors. Frontiers in Chemistry, 2022, 10, 861209.	3.6	11
3	Inhibitors of SARS-CoV-2 PLpro. Frontiers in Chemistry, 2022, 10, 876212.	3.6	38
4	LUBAC. Current Biology, 2022, 32, R506-R508.	3.9	7
5	The E3 ubiquitin ligase SCF(Fbxo7) mediates proteasomal degradation of UXT isoform 2 (UXT-V2) to inhibit the NF-Î°B signaling pathway. Biochimica Et Biophysica Acta - General Subjects, 2021, 1865, 129754.	2.4	11
6	The deubiquitylase USP9X controls ribosomal stalling. Journal of Cell Biology, 2021, 220, .	5.2	20
7	Ubiquitin signalling in neurodegeneration: mechanisms and therapeutic opportunities. Cell Death and Differentiation, 2021, 28, 570-590.	11.2	197
8	Linear ubiquitin chains break blood vessel branches. Cell Research, 2021, 31, 1045-1046.	12.0	0
9	Oligomerizationâ€driven MLKL ubiquitylation antagonizes necroptosis. EMBO Journal, 2021, 40, e103718.	7.8	39
10	USP28 deletion and small-molecule inhibition destabilizes c-MYC and elicits regression of squamous cell lung carcinoma. ELife, 2021, 10, .	6.0	25
11	Regulation of CYLD activity and specificity by phosphorylation and ubiquitin-binding CAP-Gly domains. Cell Reports, 2021, 37, 109777.	6.4	20
12	Dissecting distinct proteolytic activities of FMDV Lpro implicates cleavage and degradation of RLR signaling proteins, not its deISGylase/DUB activity, in type I interferon suppression. PLoS Pathogens, 2020, 16, e1008702.	4.7	26
13	Mechanism and inhibition of the papainâ€like protease, PLpro, of SARSâ€CoVâ€2. EMBO Journal, 2020, 39, e106275.	7.8	330
14	Global Landscape and Dynamics of Parkin and USP30-Dependent Ubiquitylomes in iNeurons during Mitophagic Signaling. Molecular Cell, 2020, 77, 1124-1142.e10.	9.7	143
15	OTULIN protects the liver against cell death, inflammation, fibrosis, and cancer. Cell Death and Differentiation, 2020, 27, 1457-1474.	11.2	45
16	Identification and characterization of diverse OTU deubiquitinases in bacteria. EMBO Journal, 2020, 39, e105127.	7.8	46
17	Dual role of a GTPase conformational switch for membrane fusion by mitofusin ubiquitylation. Life Science Alliance, 2020, 3, e201900476.	2.8	10
18	USP30 sets a trigger threshold for PINK1â€"PARKIN amplification of mitochondrial ubiquitylation. Life Science Alliance, 2020, 3, e202000768.	2.8	72

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19	Insights into ubiquitin chain architecture using Ub-clipping. Nature, 2019, 572, 533-537.	27.8	155
20	Regulation of the endosomal SNX27-retromer by OTULIN. Nature Communications, 2019, 10, 4320.	12.8	34
21	OTULIN deficiency in ORAS causes cell typeâ€specific LUBAC degradation, dysregulated TNF signalling and cell death. EMBO Molecular Medicine, 2019, 11, .	6.9	80
22	Distinct USP25 and USP28 Oligomerization States Regulate Deubiquitinating Activity. Molecular Cell, 2019, 74, 436-451.e7.	9.7	48
23	Evaluating enzyme activities and structures of DUBs. Methods in Enzymology, 2019, 618, 321-341.	1.0	19
24	Breaking the chains: deubiquitylating enzyme specificity begets function. Nature Reviews Molecular Cell Biology, 2019, 20, 338-352.	37.0	512
25	Irreversible inactivation of ISG15 by a viral leader protease enables alternative infection detection strategies. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 2371-2376.	7.1	68
26	Mind Bomb Regulates Cell Death during TNF Signaling by Suppressing RIPK1â€™s Cytotoxic Potential. Cell Reports, 2018, 23, 470-484.	6.4	42
27	Ubiquitin-Mediated Regulation of RIPK1 Kinase Activity Independent of IKK and MK2. Molecular Cell, 2018, 69, 566-580.e5.	9.7	102
28	Enzymatic Assembly of Ubiquitin Chains. Methods in Molecular Biology, 2018, 1844, 73-84.	0.9	29
29	A Chlamydia effector combining deubiquitination and acetylation activities induces Golgi fragmentation. Nature Microbiology, 2018, 3, 1377-1384.	13.3	55
30	Active site alanine mutations convert deubiquitinases into highâ€affinity ubiquitinâ€binding proteins. EMBO Reports, 2018, 19, .	4.5	43
31	Mechanism of parkin activation by PINK1. Nature, 2018, 559, 410-414.	27.8	271
32	Strange New World: Bacteria Catalyze Ubiquitylation via ADP Ribosylation. Cell Host and Microbe, 2017, 21, 127-129.	11.0	6
33	Mechanisms of Deubiquitinase Specificity and Regulation. Annual Review of Biochemistry, 2017, 86, 159-192.	11.1	698
34	LUBAC-synthesized linear ubiquitin chains restrict cytosol-invading bacteria by activating autophagy and NF-ÎºB. Nature Microbiology, 2017, 2, 17063.	13.3	182
35	Structure of PINK1 in complex with its substrate ubiquitin. Nature, 2017, 552, 51-56.	27.8	114
36	Ubiquitin Linkage-Specific Affimers Reveal Insights into K6-Linked Ubiquitin Signaling. Molecular Cell, 2017, 68, 233-246.e5.	9.7	153

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37	Mechanism and regulation of the Lys6-selective deubiquitinase USP30. Nature Structural and Molecular Biology, 2017, 24, 920-930.	8.2	173
38	Molecular basis of USP7 inhibition by selective small-molecule inhibitors. Nature, 2017, 550, 481-486.	27.8	332
39	A Linear Diubiquitin-Based Probe for Efficient and Selective Detection of the Deubiquitinating Enzyme OTULIN. Cell Chemical Biology, 2017, 24, 1299-1313.e7.	5.2	41
40	Synthesis of Poly-Ubiquitin Chains Using a Bifunctional Ubiquitin Monomer. Organic Letters, 2017, 19, 6490-6493.	4.6	21
41	An invisible ubiquitin conformation is required for efficient phosphorylation by <scp>PINK</scp> 1. EMBO Journal, 2017, 36, 3555-3572.	7.8	50
42	Recruitment of <scp>TBK</scp> 1 to cytosolâ€invading <i>Salmonella</i> induces <scp>WIPI</scp> 2â€dependent antibacterial autophagy. EMBO Journal, 2016, 35, 1779-1792.	7.8	107
43	Regulation of Met1â€linked polyubiquitin signalling by the deubiquitinase <scp>OTULIN</scp>. FEBS Journal, 2016, 283, 39-53.	4.7	27
44	CYLD Limits Lys63- and Met1-Linked Ubiquitin at Receptor Complexes to Regulate Innate Immune Signaling. Cell Reports, 2016, 14, 2846-2858.	6.4	128
45	A cascading activity-based probe sequentially targets E1â€"E2â€"E3 ubiquitin enzymes. Nature Chemical Biology, 2016, 12, 523-530.	8.0	122
46	Gsk3Î² and Tomm20 are substrates of the SCFFbxo7/PARK15 ubiquitin ligase associated with Parkinson's disease. Biochemical Journal, 2016, 473, 3563-3580.	3.7	45
47	Molecular basis of Lys11-polyubiquitin specificity in the deubiquitinase Cezanne. Nature, 2016, 538, 402-405.	27.8	129
48	The Deubiquitinase OTULIN Is an Essential Negative Regulator of Inflammation and Autoimmunity. Cell, 2016, 166, 1215-1230.e20.	28.9	259
49	SPATA2 Links CYLD to LUBAC, Activates CYLD, and Controls LUBAC Signaling. Molecular Cell, 2016, 63, 990-1005.	9.7	130
50	The Molecular Basis for Ubiquitin and Ubiquitin-like Specificities in Bacterial Effector Proteases. Molecular Cell, 2016, 63, 261-276.	9.7	119
51	The Salmonella Effector SpvD Is a Cysteine Hydrolase with a Serovar-specific Polymorphism Influencing Catalytic Activity, Suppression of Immune Responses, and Bacterial Virulence. Journal of Biological Chemistry, 2016, 291, 25853-25863.	3.4	35
52	Non-hydrolyzable Diubiquitin Probes Reveal Linkage-Specific Reactivity of Deubiquitylating Enzymes Mediated by S2 Pockets. Cell Chemical Biology, 2016, 23, 472-482.	5.2	90
53	Ubiquitin modifications. Cell Research, 2016, 26, 399-422.	12.0	1,357
54	Development of Diubiquitinâ€Based FRET Probes To Quantify Ubiquitin Linkage Specificity of Deubiquitinating Enzymes. ChemBioChem, 2016, 17, 816-820.	2.6	46

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55	Cezanne regulates E2F1-dependent HIF2Î± expression. Journal of Cell Science, 2015, 128, 3082-93.	2.0	54
56	Ubiquitin Ser65 phosphorylation affects ubiquitin structure, chain assembly and hydrolysis. EMBO Journal, 2015, 34, 307-325.	7.8	258
57	Deubiquitinase-based analysis of ubiquitin chain architecture using Ubiquitin Chain Restriction (UbiCRest). Nature Protocols, 2015, 10, 349-361.	12.0	178
58	Assembly and Specific Recognition of K29- and K33-Linked Polyubiquitin. Molecular Cell, 2015, 58, 95-109.	9.7	162
59	Mechanism of phospho-ubiquitin-induced PARKIN activation. Nature, 2015, 524, 370-374.	27.8	356
60	Details of destruction, one molecule at a time. Science, 2015, 348, 183-184.	12.6	5
61	The JAMM in the proteasome. Nature Structural and Molecular Biology, 2014, 21, 346-348.	8.2	9
62	Lysine 27 Ubiquitination of the Mitochondrial Transport Protein Miro Is Dependent on Serine 65 of the Parkin Ubiquitin Ligase. Journal of Biological Chemistry, 2014, 289, 14569-14582.	3.4	152
63	Molecular Basis and Regulation of OTULIN-LUBAC Interaction. Molecular Cell, 2014, 54, 335-348.	9.7	158
64	Cezanne (<scp>OTUD</scp>7B) regulates <scp>HIF</scp>â€•1Î± homeostasis in a proteasomeâ€•independent manner. EMBO Reports, 2014, 15, 1268-1277.	4.5	78
65	OTU Deubiquitinases Reveal Mechanisms of Linkage Specificity and Enable Ubiquitin Chain Restriction Analysis. Cell, 2013, 154, 169-184.	28.9	470
66	OTULIN Restricts Met1-Linked Ubiquitination to Control Innate Immune Signaling. Molecular Cell, 2013, 50, 818-830.	9.7	209
67	Assembly, analysis and architecture of atypical ubiquitin chains. Nature Structural and Molecular Biology, 2013, 20, 555-565.	8.2	131
68	On Terminal Alkynes That Can React with Active-Site Cysteine Nucleophiles in Proteases. Journal of the American Chemical Society, 2013, 135, 2867-2870.	13.7	290
69	OTULIN Antagonizes LUBAC Signaling by Specifically Hydrolyzing Met1-Linked Polyubiquitin. Cell, 2013, 153, 1312-1326.	28.9	395
70	Structure of the human Parkin ligase domain in an autoinhibited state. EMBO Journal, 2013, 32, 2099-2112.	7.8	271
71	An essential role for the ATG8 ortholog LC3C in antibacterial autophagy. Autophagy, 2013, 9, 784-786.	9.1	25
72	Activation of the canonical IKK complex by K63/M1-linked hybrid ubiquitin chains. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 15247-15252.	7.1	373

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73	Unravelling the specificity in the ubiquitin system. FASEB Journal, 2013, 27, 553.26.	0.5	0
74	Ubiquitin chain conformation regulates recognition and activity of interacting proteins. Nature, 2012, 492, 266-270.	27.8	166
75	LC3C, Bound Selectively by a Noncanonical LIR Motif in NDP52, Is Required for Antibacterial Autophagy. Molecular Cell, 2012, 48, 329-342.	9.7	285
76	New Tools for Ubiquitin Signaling. Journal of Molecular Biology, 2012, 418, 129-130.	4.2	0
77	An ankyrin-repeat ubiquitin-binding domain determines TRABID's specificity for atypical ubiquitin chains. Nature Structural and Molecular Biology, 2012, 19, 62-71.	8.2	122
78	Atypical ubiquitylation â€" the unexplored world of polyubiquitin beyond Lys48 and Lys63 linkages. Nature Reviews Molecular Cell Biology, 2012, 13, 508-523.	37.0	558
79	The Ubiquitin Code. Annual Review of Biochemistry, 2012, 81, 203-229.	11.1	2,844
80	Polyubiquitin binding and crossâ€reactivity in the USP domain deubiquitinase USP21. EMBO Reports, 2011, 12, 350-357.	4.5	147
81	Emerging roles for Lys11-linked polyubiquitin in cellular regulation. Trends in Biochemical Sciences, 2011, 36, 355-63.	7.5	64
82	Molecular basis for ubiquitin and ISG15 cross-reactivity in viral ovarian tumor domains. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 2228-2233.	7.1	124
83	BIMEL, an intrinsically disordered protein, is degraded by 20S proteasomes in the absence of poly-ubiquitylation. Journal of Cell Science, 2011, 124, 969-977.	2.0	65
84	Lys11-linked ubiquitin chains adopt compact conformations and are preferentially hydrolyzed by the deubiquitinase Cezanne. Nature Structural and Molecular Biology, 2010, 17, 939-947.	8.2	294
85	A further case of Dopâ€ing in bacterial pupylation. EMBO Reports, 2010, 11, 722-723.	4.5	3
86	Engineered diubiquitin synthesis reveals Lys29-isopeptide specificity of an OTU deubiquitinase. Nature Chemical Biology, 2010, 6, 750-757.	8.0	269
87	The nuts and bolts of AGC protein kinases. Nature Reviews Molecular Cell Biology, 2010, 11, 9-22.	37.0	1,137
88	CYLD Tidies Up Dishevelled Signaling. Molecular Cell, 2010, 37, 589-590.	9.7	8
89	Analysis of the human E2 ubiquitin conjugating enzyme protein interaction network. Genome Research, 2009, 19, 1905-1911.	5.5	134
90	The emerging complexity of protein ubiquitination. Biochemical Society Transactions, 2009, 37, 937-953.	3.4	684

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91	Molecular discrimination of structurally equivalent Lys 63â€linked and linear polyubiquitin chains. EMBO Reports, 2009, 10, 466-473.	4.5	513
92	Breaking the chains: structure and function of the deubiquitinases. Nature Reviews Molecular Cell Biology, 2009, 10, 550-563.	37.0	1,722
93	Two-sided ubiquitin binding explains specificity of the TAB2 NZF domain. Nature Structural and Molecular Biology, 2009, 16, 1328-1330.	8.2	177
94	Specific Recognition of Linear Ubiquitin Chains by NEMO Is Important for NF-Î°B Activation. Cell, 2009, 136, 1098-1109.	28.9	667
95	Recruitment of the Linear Ubiquitin Chain Assembly Complex Stabilizes the TNF-R1 Signaling Complex andÂIs Required for TNF-Mediated Gene Induction. Molecular Cell, 2009, 36, 831-844.	9.7	674
96	Dissection of USP catalytic domains reveals five common insertion points. Molecular BioSystems, 2009, 5, 1797.	2.9	135
97	Mechanism of multi-site phosphorylation from a ROCK-I:RhoE complex structure. EMBO Journal, 2008, 27, 3175-3185.	7.8	57
98	The Structure of the CYLD USP Domain Explains Its Specificity for Lys63-Linked Polyubiquitin and Reveals a B Box Module. Molecular Cell, 2008, 29, 451-464.	9.7	251
99	Mutation of the PDK1 PH Domain Inhibits Protein Kinase B/Akt, Leading to Small Size and Insulin Resistance. Molecular and Cellular Biology, 2008, 28, 3258-3272.	2.3	115
100	Structure of the A20 OTU domain and mechanistic insights into deubiquitination. Biochemical Journal, 2008, 409, 77-85.	3.7	165
101	Recognition of Polyubiquitin Isoforms by the Multiple Ubiquitin Binding Modules of Isopeptidase T. Journal of Biological Chemistry, 2008, 283, 19581-19592.	3.4	116
102	An Î±-Helical Extension of the ELMO1 Pleckstrin Homology Domain Mediates Direct Interaction to DOCK180 and Is Critical in Rac Signaling. Molecular Biology of the Cell, 2008, 19, 4837-4851.	2.1	85
103	Novel Inositol Phospholipid Headgroup Surrogate Crystallized in the Pleckstrin Homology Domain of Protein Kinase BÎ±. ACS Chemical Biology, 2007, 2, 242-246.	3.4	20
104	Role of T-loop Phosphorylation in PDK1 Activation, Stability, and Substrate Binding. Journal of Biological Chemistry, 2005, 280, 18797-18802.	3.4	36
105	Structural insights into the regulation of PDK1 by phosphoinositides and inositol phosphates. EMBO Journal, 2004, 23, 3918-3928.	7.8	167
106	Interactions of LY333531 and Other Bisindolyl Maleimide Inhibitors with PDK1. Structure, 2004, 12, 215-226.	3.3	79
107	Purification, crystallization and preliminary X-ray diffraction of a proteolytic fragment of PDK1 containing the pleckstrin homology domain. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 314-316.	2.5	4
108	Analysis of the LKB1-STRAD-MO25 complex. Journal of Cell Science, 2004, 117, 6365-6375.	2.0	130

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109	PDK1, the master regulator of AGC kinase signal transduction. Seminars in Cell and Developmental Biology, 2004, 15, 161-170.	5.0	715
110	High resolution crystal structure of the human PDK1 catalytic domain defines the regulatory phosphopeptide docking site. EMBO Journal, 2002, 21, 4219-4228.	7.8	176