

# Oded Kleifeld

## List of Publications by Year in descending order

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Version: 2024-02-01

40  
papers

2,282  
citations

331670

21  
h-index

302126

39  
g-index

42  
all docs

42  
docs citations

42  
times ranked

3666  
citing authors

#	ARTICLE	IF	CITATIONS
1	Auxiliary ATP binding sites support DNA unwinding by RecBCD. <i>Nature Communications</i> , 2022, 13, 1806.	12.8	5
2	Global ubiquitinome profiling identifies NEDD4 as a regulator of Profilin 1 and actin remodelling in neural crest cells. <i>Nature Communications</i> , 2022, 13, 2018.	12.8	4
3	TRIM25 and DEAD-Box RNA Helicase DDX3X Cooperate to Regulate RIG-I-Mediated Antiviral Immunity. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9094.	4.1	9
4	A novel recognition site for polyubiquitin and ubiquitin-like signals in an unexpected region of proteasomal subunit Rpn1. <i>Journal of Biological Chemistry</i> , 2021, 297, 101052.	3.4	8
5	Ubiquitination and receptor-mediated mitophagy converge to eliminate oxidation-damaged mitochondria during hypoxia. <i>Redox Biology</i> , 2021, 45, 102047.	9.0	66
6	The 20S as a stand-alone proteasome in cells can degrade the ubiquitin tag. <i>Nature Communications</i> , 2021, 12, 6173.	12.8	66
7	Phosphoproteomic characterization of the signaling network resulting from activation of the chemokine receptor CCR2. <i>Journal of Biological Chemistry</i> , 2020, 295, 6518-6531.	3.4	16
8	Remodeling Membrane Binding by Mono-Ubiquitylation. <i>Biomolecules</i> , 2019, 9, 325.	4.0	7
9	Integration of Two In-depth Quantitative Proteomics Approaches Determines the Kallikrein-related Peptidase 7 (KLK7) Degradome in Ovarian Cancer Cell Secretome. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 818a-836.	3.8	16
10	Proteomic Identification of Interferon-Induced Proteins with Tetratricopeptide Repeats as Markers of M1 Macrophage Polarization. <i>Journal of Proteome Research</i> , 2018, 17, 1485-1499.	3.7	35
11	Proteotranscriptomic Measurements of E6-Associated Protein (E6AP) Targets in DU145 Prostate Cancer Cells. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1170-1183.	3.8	13
12	Activity-Based Probes Developed by Applying a Sequential Dehydroalanine Formation Strategy to Expressed Proteins Reveal a Potential $\beta$ -Globin-Modulating Deubiquitinase. <i>Angewandte Chemie</i> , 2018, 130, 5747-5751.	2.0	14
13	Determination of the small RNA GcvB regulon in the Gram-negative bacterial pathogen <i>Pasteurella multocida</i> and identification of the GcvB seed binding region. <i>Rna</i> , 2018, 24, 704-720.	3.5	26
14	Activity-Based Probes Developed by Applying a Sequential Dehydroalanine Formation Strategy to Expressed Proteins Reveal a Potential $\beta$ -Globin-Modulating Deubiquitinase. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 5645-5649.	13.8	41
15	Exploring the oncoproteomic response of human prostate cancer to therapeutic radiation using data-independent acquisition (DIA) mass spectrometry. <i>Prostate</i> , 2018, 78, 563-575.	2.3	23
16	Preassembled GPCR signaling complexes mediate distinct cellular responses to ultralow ligand concentrations. <i>Science Signaling</i> , 2018, 11, .	3.6	36
17	Cleavage of the leptin receptor by matrix metalloproteinase-2 promotes leptin resistance and obesity in mice. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	46
18	Biodosimetric transcriptional and proteomic changes are conserved in irradiated human tissue. <i>Radiation and Environmental Biophysics</i> , 2018, 57, 241-249.	1.4	8

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19	Outer membrane vesicles from <i>Neisseria gonorrhoeae</i> target PorB to mitochondria and induce apoptosis. <i>PLoS Pathogens</i> , 2018, 14, e1006945.	4.7	105
20	Dynamic structure and localization of G protein-coupled receptor (GPCR) complexes determines unique signalling outcomes. Proceedings for Annual Meeting of the Japanese Pharmacological Society, 2018, WCP2018, PO1-8-9.	0.0	0
21	Structure–function analyses of a pertussis-like toxin from pathogenic <i>Escherichia coli</i> reveal a distinct mechanism of inhibition of trimeric G-proteins. <i>Journal of Biological Chemistry</i> , 2017, 292, 15143-15158.	3.4	23
22	Clinical and Pharmacological Investigation of Myotoxicity in Sri Lankan Russell's Viper ( <i>Daboia</i> ) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	3.0	25
23	N-terminal domain of <i>Bothrops asper</i> Myotoxin II Enhances the Activity of Endothelin Converting Enzyme-1 and Neprilysin. <i>Scientific Reports</i> , 2016, 6, 22413.	3.3	8
24	Synthetic Uncleavable Ubiquitinated Proteins Dissect Proteasome Deubiquitination and Degradation, and Highlight Distinctive Fate of Tetraubiquitin. <i>Journal of the American Chemical Society</i> , 2016, 138, 16004-16015.	13.7	50
25	Studying Protein Ubiquitylation in Yeast. <i>Methods in Molecular Biology</i> , 2016, 1449, 117-142.	0.9	8
26	Structure of ubiquitylated-Rpn10 provides insight into its autoregulation mechanism. <i>Nature Communications</i> , 2016, 7, 12960.	12.8	34
27	Physicochemical properties that control protein aggregation also determine whether a protein is retained or released from necrotic cells. <i>Open Biology</i> , 2016, 6, 160098.	3.6	7
28	The RNA-Binding Chaperone Hfq Is an Important Global Regulator of Gene Expression in <i>Pasteurella multocida</i> and Plays a Crucial Role in Production of a Number of Virulence Factors, Including Hyaluronic Acid Capsule. <i>Infection and Immunity</i> , 2016, 84, 1361-1370.	2.2	40
29	Base-CP proteasome can serve as a platform for stepwise lid formation. <i>Bioscience Reports</i> , 2015, 35, .	2.4	18
30	Changes in protein abundance are observed in bacterial isolates from a natural host. <i>Frontiers in Cellular and Infection Microbiology</i> , 2015, 5, 71.	3.9	6
31	Disassembly of Lys11 and Mixed Linkage Polyubiquitin Conjugates Provides Insights into Function of Proteasomal Deubiquitinases Rpn11 and Ubp6. <i>Journal of Biological Chemistry</i> , 2015, 290, 4688-4704.	3.4	42
32	Conformational Changes during Pore Formation by the Perforin-Related Protein Pleurotolysin. <i>PLoS Biology</i> , 2015, 13, e1002049.	5.6	114
33	LysargiNase mirrors trypsin for protein C-terminal and methylation-site identification. <i>Nature Methods</i> , 2015, 12, 55-58.	19.0	128
34	Structural and mechanistic insight into alkane hydroxylation by <i>Pseudomonas putida</i> AlkB. <i>Biochemical Journal</i> , 2014, 460, 283-293.	3.7	18
35	Granzyme B Promotes Cytotoxic Lymphocyte Transmigration via Basement Membrane Remodeling. <i>Immunity</i> , 2014, 41, 960-972.	14.3	102
36	Oxidation of an Exposed Methionine Instigates the Aggregation of Glyceraldehyde-3-phosphate Dehydrogenase. <i>Journal of Biological Chemistry</i> , 2014, 289, 26922-26936.	3.4	41

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37	Reversible 26S Proteasome Disassembly upon Mitochondrial Stress. Cell Reports, 2014, 7, 1371-1380.	6.4	150
38	Identifying and quantifying proteolytic events and the natural N terminome by terminal amine isotopic labeling of substrates. Nature Protocols, 2011, 6, 1578-1611.	12.0	291
39	A Perturbed Ubiquitin Landscape Distinguishes Between Ubiquitin in Trafficking and in Proteolysis. Molecular and Cellular Proteomics, 2011, 10, M111.009753.	3.8	115
40	Isotopic labeling of terminal amines in complex samples identifies protein N-termini and protease cleavage products. Nature Biotechnology, 2010, 28, 281-288.	17.5	510