

# Michal Sharon

## List of Publications by Year in descending order

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73  
papers

3,677  
citations

117453

34  
h-index

138251

58  
g-index

80  
all docs

80  
docs citations

80  
times ranked

4736  
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterizing Endogenous Protein Complexes with Biological Mass Spectrometry. <i>Chemical Reviews</i> , 2022, 122, 7386-7414.	23.0	24
2	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.	1.8	5
3	A counter-enzyme complex regulates glutamate metabolism in <i>Bacillus subtilis</i> . <i>Nature Chemical Biology</i> , 2022, 18, 161-170.	3.9	14
4	Biology of the Extracellular Proteasome. <i>Biomolecules</i> , 2022, 12, 619.	1.8	12
5	Surface-Induced Dissociation for Protein Complex Characterization. <i>Methods in Molecular Biology</i> , 2022, , 211-237.	0.4	3
6	Beyond cells: The extracellular circulating 20S proteasomes. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2021, 1867, 166041.	1.8	24
7	20S proteasomes secreted by the malaria parasite promote its growth. <i>Nature Communications</i> , 2021, 12, 1172.	5.8	45
8	Helicase-like functions in phosphate loop containing beta-alpha polypeptides. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	14
9	Cell communication and protein degradation: All in one parasitic package. <i>Journal of Extracellular Vesicles</i> , 2021, 10, e12116.	5.5	6
10	Intracellular Protein–Drug Interactions Probed by Direct Mass Spectrometry of Cell Lysates. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 19637-19642.	7.2	8
11	Intracellular Protein–Drug Interactions Probed by Direct Mass Spectrometry of Cell Lysates. <i>Angewandte Chemie</i> , 2021, 133, 19789-19794.	1.6	0
12	Direct–MS analysis of antibody–antigen complexes. <i>Proteomics</i> , 2021, 21, e2000300.	1.3	8
13	Albumin-EDTA-Vanadium Is a Powerful Anti-Proliferative Agent, Following Entrance into Glioma Cells via Caveolae-Mediated Endocytosis. <i>Pharmaceutics</i> , 2021, 13, 1557.	2.0	3
14	CSNAP, the smallest CSN subunit, modulates proteostasis through cullin-RING ubiquitin ligases. <i>Cell Death and Differentiation</i> , 2020, 27, 984-998.	5.0	19
15	Regulation of the 20S Proteasome by a Novel Family of Inhibitory Proteins. <i>Antioxidants and Redox Signaling</i> , 2020, 32, 636-655.	2.5	21
16	Software Requirements for the Analysis and Interpretation of Native Ion Mobility Mass Spectrometry Data. <i>Analytical Chemistry</i> , 2020, 92, 10881-10890.	3.2	17
17	Computational Strategies and Challenges for Using Native Ion Mobility Mass Spectrometry in Biophysics and Structural Biology. <i>Analytical Chemistry</i> , 2020, 92, 10872-10880.	3.2	24
18	Mass Spectrometry Analysis of Intact Proteins from Crude Samples. <i>Analytical Chemistry</i> , 2020, 92, 12741-12749.	3.2	15

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19	Insight into the Autosomal-Dominant Inheritance Pattern of SOD1-Associated ALS from Native Mass Spectrometry. <i>Journal of Molecular Biology</i> , 2020, 432, 5995-6002.	2.0	6
20	Direct characterization of overproduced proteins by native mass spectrometry. <i>Nature Protocols</i> , 2020, 15, 236-265.	5.5	27
21	Comparative Structural Analysis of 20S Proteasome Ortholog Protein Complexes by Native Mass Spectrometry. <i>ACS Central Science</i> , 2020, 6, 573-588.	5.3	37
22	Optimizing antibody affinity and stability by the automated design of the variable light-heavy chain interfaces. <i>PLoS Computational Biology</i> , 2019, 15, e1007207.	1.5	77
23	The interdimeric interface controls function and stability of <i>Ureaplasma urealiticum</i> methionine S-adenosyltransferase. <i>Journal of Molecular Biology</i> , 2019, 431, 4796-4816.	2.0	12
24	Structural mass spectrometry approaches to study the 20S proteasome. <i>Methods in Enzymology</i> , 2019, 619, 179-223.	0.4	16
25	The Contribution of the 20S Proteasome to Proteostasis. <i>Biomolecules</i> , 2019, 9, 190.	1.8	98
26	Dissecting the molecular effects of cigarette smoke on proteasome function. <i>Journal of Proteomics</i> , 2019, 193, 1-9.	1.2	13
27	Conformational states during vinculin unlocking differentially regulate focal adhesion properties. <i>Scientific Reports</i> , 2018, 8, 2693.	1.6	40
28	Functional regulation of proteins by 20S proteasome proteolytic processing. <i>Cell Cycle</i> , 2018, 17, 393-394.	1.3	18
29	The application of ion-mobility mass spectrometry for structure/function investigation of protein complexes. <i>Current Opinion in Chemical Biology</i> , 2018, 42, 25-33.	2.8	103
30	Simple yet functional phosphate-loop proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11943-E11950.	3.3	70
31	Rapid characterization of secreted recombinant proteins by native mass spectrometry. <i>Communications Biology</i> , 2018, 1, 213.	2.0	24
32	Time-Resolved NMR Analysis of Proteolytic $\alpha$ -Synuclein Processing in vitro and in cellulo. <i>Proteomics</i> , 2018, 18, e1800056.	1.3	19
33	Estimating Interprotein Pairwise Interaction Energies in Cell Lysates from a Single Native Mass Spectrum. <i>Analytical Chemistry</i> , 2018, 90, 10090-10094.	3.2	17
34	Concentration-based self-assembly of phycocyanin. <i>Photosynthesis Research</i> , 2017, 134, 39-49.	1.6	16
35	Native Mass Spectrometry of Recombinant Proteins from Crude Cell Lysates. <i>Analytical Chemistry</i> , 2017, 89, 4398-4404.	3.2	47
36	Triple-Stage Mass Spectrometry Unravels the Heterogeneity of an Endogenous Protein Complex. <i>Analytical Chemistry</i> , 2017, 89, 4708-4715.	3.2	52

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37	Measuring inter-protein pairwise interaction energies from a single native mass spectrum by double-mutant cycle analysis. <i>Nature Communications</i> , 2017, 8, 212.	5.8	22
38	Post-translational regulation of p53 function through 20S proteasome-mediated cleavage. <i>Cell Death and Differentiation</i> , 2017, 24, 2187-2198.	5.0	42
39	Tuning the proteasome to brighten the end of the journey. <i>American Journal of Physiology - Cell Physiology</i> , 2016, 311, C793-C804.	2.1	24
40	Higher-order oligomerization promotes localization of SPOP to liquid nuclear speckles. <i>EMBO Journal</i> , 2016, 35, 1254-1275.	3.5	172
41	Mass spectrometry: a technique of many faces. <i>Quarterly Reviews of Biophysics</i> , 2016, 49, .	2.4	13
42	Structural Characterization of Missense Mutations Using High Resolution Mass Spectrometry: A Case Study of the Parkinson's-Related Protein, DJ-1. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 1062-1070.	1.2	16
43	CSNAP Is a Stoichiometric Subunit of the COP9 Signalosome. <i>Cell Reports</i> , 2015, 13, 585-598.	2.9	59
44	Exposing the subunit diversity and modularity of protein complexes by structural mass spectrometry approaches. <i>Proteomics</i> , 2015, 15, 2777-2791.	1.3	9
45	Chemical crosslinking and native mass spectrometry: A fruitful combination for structural biology. <i>Protein Science</i> , 2015, 24, 1193-1209.	3.1	112
46	Probing allosteric mechanisms using native mass spectrometry. <i>Current Opinion in Structural Biology</i> , 2015, 34, 7-16.	2.6	34
47	The Parkinson's-associated protein DJ-1 regulates the 20S proteasome. <i>Nature Communications</i> , 2015, 6, 6609.	5.8	112
48	The Evolutionary Potential of Phenotypic Mutations. <i>PLoS Genetics</i> , 2015, 11, e1005445.	1.5	45
49	Regulating the 20S Proteasome Ubiquitin-Independent Degradation Pathway. <i>Biomolecules</i> , 2014, 4, 862-884.	1.8	264
50	An Improved Rapid Mixing Device for Time-Resolved Electrospray Mass Spectrometry Measurements. <i>ChemistryOpen</i> , 2014, 3, 109-114.	0.9	14
51	Dynamic Regulation of the COP9 Signalosome in Response to DNA Damage. <i>Molecular and Cellular Biology</i> , 2014, 34, 1066-1076.	1.1	24
52	Regulation of focal adhesion formation by a vinculin-Arp2/3 hybrid complex. <i>Nature Communications</i> , 2014, 5, 3758.	5.8	106
53	An Iron-Containing Dodecameric Heptosyltransferase Family Modifies Bacterial Autotransporters in Pathogenesis. <i>Cell Host and Microbe</i> , 2014, 16, 351-363.	5.1	47
54	Exposing the subunit diversity within protein complexes: A mass spectrometry approach. <i>Methods</i> , 2013, 59, 270-277.	1.9	31

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55	Allosteric mechanisms can be distinguished using structural mass spectrometry. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 7235-7239.	3.3	131
56	Biosensor based on DNA directed immobilization of enzymes onto optically sensitive porous Si. Materials Research Society Symposia Proceedings, 2013, 1569, 195-200.	0.1	1
57	Structural MS Pulls Its Weight. Science, 2013, 340, 1059-1060.	6.0	54
58	Thermo-resistant intrinsically disordered proteins are efficient 20S proteasome substrates. Molecular BioSystems, 2012, 8, 368-373.	2.9	39
59	A Mutually Inhibitory Feedback Loop between the 20S Proteasome and Its Regulator, NQO1. Molecular Cell, 2012, 47, 76-86.	4.5	97
60	Capturing protein structural kinetics by mass spectrometry. Chemical Society Reviews, 2011, 40, 3627.	18.7	29
61	T-wave Ion Mobility-mass Spectrometry: Basic Experimental Procedures for Protein Complex Analysis. Journal of Visualized Experiments, 2010, , .	0.2	37
62	How far can we go with structural mass spectrometry of protein complexes?. Journal of the American Society for Mass Spectrometry, 2010, 21, 487-500.	1.2	79
63	Analyzing Large Protein Complexes by Structural Mass Spectrometry. Journal of Visualized Experiments, 2010, , .	0.2	38
64	Gas-Phase Compaction and Unfolding of Protein Structures. Analytical Chemistry, 2010, 82, 9484-9491.	3.2	38
65	Structure and Function of a Novel Type of ATP-dependent Clp Protease. Journal of Biological Chemistry, 2009, 284, 13519-13532.	1.6	62
66	Symmetrical Modularity of the COP9 Signalosome Complex Suggests its Multifunctionality. Structure, 2009, 17, 31-40.	1.6	133
67	Subunit Architecture of Intact Protein Complexes from Mass Spectrometry and Homology Modeling. Accounts of Chemical Research, 2008, 41, 617-627.	7.6	123
68	Mass Spectrometry Reveals the Missing Links in the Assembly Pathway of the Bacterial 20 S Proteasome. Journal of Biological Chemistry, 2007, 282, 18448-18457.	1.6	50
69	The Role of Mass Spectrometry in Structure Elucidation of Dynamic Protein Complexes. Annual Review of Biochemistry, 2007, 76, 167-193.	5.0	337
70	Evidence for Micellar Structure in the Gas Phase. Journal of the American Chemical Society, 2007, 129, 8740-8746.	6.6	54
71	Structural Organization of the 19S Proteasome Lid: Insights from MS of Intact Complexes. PLoS Biology, 2006, 4, e267.	2.6	176
72	Proteasome Assembly Triggers a Switch Required for Active-Site Maturation. Structure, 2006, 14, 1179-1188.	1.6	31

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73	20S Proteasomes Have the Potential to Keep Substrates in Store for Continual Degradation. Journal of Biological Chemistry, 2006, 281, 9569-9575.	1.6	65