

# Daniel N Itzhak

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4655355/publications.pdf>

Version: 2024-02-01

10  
papers

1,562  
citations

1039406

9  
h-index

1372195

10  
g-index

12  
all docs

12  
docs citations

12  
times ranked

3224  
citing authors

#	ARTICLE	IF	CITATIONS
1	Global, quantitative and dynamic mapping of protein subcellular localization. <i>ELife</i> , 2016, 5, .	2.8	469
2	Pervasive functional translation of noncanonical human open reading frames. <i>Science</i> , 2020, 367, 1140-1146.	6.0	400
3	Region and cell-type resolved quantitative proteomic map of the human heart. <i>Nature Communications</i> , 2017, 8, 1469.	5.8	213
4	The ER membrane protein complex interacts cotranslationally to enable biogenesis of multipass membrane proteins. <i>ELife</i> , 2018, 7, .	2.8	160
5	A Mass Spectrometry-Based Approach for Mapping Protein Subcellular Localization Reveals the Spatial Proteome of Mouse Primary Neurons. <i>Cell Reports</i> , 2017, 20, 2706-2718.	2.9	105
6	AP-4 vesicles contribute to spatial control of autophagy via RUSC-dependent peripheral delivery of ATG9A. <i>Nature Communications</i> , 2018, 9, 3958.	5.8	105
7	Small Molecule Enhancers of Endosome-to-Cytosol Import Augment Anti-tumor Immunity. <i>Cell Reports</i> , 2020, 32, 107905.	2.9	40
8	SHRED Is a Regulatory Cascade that Reprograms Ubr1 Substrate Specificity for Enhanced Protein Quality Control during Stress. <i>Molecular Cell</i> , 2018, 70, 1025-1037.e5.	4.5	36
9	Dynamic Organellar Maps for Spatial Proteomics. <i>Current Protocols in Cell Biology</i> , 2019, 83, e81.	2.3	14
10	SILAC-based quantitative mass spectrometry-based proteomics quantifies endoplasmic reticulum stress in whole HeLa cells. <i>DMM Disease Models and Mechanisms</i> , 2019, 12, .	1.2	10