

# Peter S Shen

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5390083/publications.pdf>

Version: 2024-02-01

23  
papers

1,781  
citations

623734

14  
h-index

888059

17  
g-index

28  
all docs

28  
docs citations

28  
times ranked

2521  
citing authors

#	ARTICLE	IF	CITATIONS
1	A Ribosome-Bound Quality Control Complex Triggers Degradation of Nascent Peptides and Signals Translation Stress. <i>Cell</i> , 2012, 151, 1042-1054.	28.9	536
2	Rqc2p and 60S ribosomal subunits mediate mRNA-independent elongation of nascent chains. <i>Science</i> , 2015, 347, 75-78.	12.6	245
3	The Structure of the Polycystic Kidney Disease Channel PKD2 in Lipid Nanodiscs. <i>Cell</i> , 2016, 167, 763-773.e11.	28.9	214
4	Structure of the Cdc48 segregase in the act of unfolding an authentic substrate. <i>Science</i> , 2019, 365, 502-505.	12.6	138
5	Structural basis of protein translocation by the Vps4-Vta1 AAA ATPase. <i>ELife</i> , 2017, 6, .	6.0	123
6	Characterization of Pseudomonas chlororaphis myovirus 2011-2-1 via genomic sequencing, mass spectrometry, and electron microscopy. <i>Virology</i> , 2008, 376, 330-338.	2.4	91
7	Vms1p is a release factor for the ribosome-associated quality control complex. <i>Nature Communications</i> , 2018, 9, 2197.	12.8	80
8	The AAA ATPase Vps4 binds ESCRT-III substrates through a repeating array of dipeptide-binding pockets. <i>ELife</i> , 2017, 6, .	6.0	80
9	Dicer uses distinct modules for recognizing dsRNA termini. <i>Science</i> , 2018, 359, 329-334.	12.6	76
10	Structure of Vps4 with circular peptides and implications for translocation of two polypeptide chains by AAA+ ATPases. <i>ELife</i> , 2019, 8, .	6.0	41
11	Structural inhibition of dynamin-mediated membrane fission by endophilin. <i>ELife</i> , 2017, 6, .	6.0	40
12	Sequence and Structural Characterization of Great Salt Lake Bacteriophage CW02, a Member of the T7-Like Supergroup. <i>Journal of Virology</i> , 2012, 86, 7907-7917.	3.4	31
13	The 2017 Nobel Prize in Chemistry: cryo-EM comes of age. <i>Analytical and Bioanalytical Chemistry</i> , 2018, 410, 2053-2057.	3.7	29
14	The structure of avian polyomavirus reveals variably sized capsids, non-conserved inter-capsomere interactions, and a possible location of the minor capsid protein VP4. <i>Virology</i> , 2011, 411, 142-152.	2.4	26
15	Active conformation of the p97-p47 unfoldase complex. <i>Nature Communications</i> , 2022, 13, 2640.	12.8	18
16	Negative charge in the RACK1 loop broadens the translational capacity of the human ribosome. <i>Cell Reports</i> , 2021, 36, 109663.	6.4	9
17	Rearranging AAA+ architecture to accommodate folded substrates. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 225-226.	8.2	1
18	Determining the Structural Basis of Cofactor and Substrate Interactions with Cdc48. <i>Microscopy and Microanalysis</i> , 2020, 26, 578-579.	0.4	0

#	ARTICLE	IF	CITATIONS
19	Structural Determination of the CCT:G <sup>25</sup> folding intermediate. FASEB Journal, 2021, 35, .	0.5	0
20	Structural determination of the Dicer-2 <sup>R2D2</sup> complex. Microscopy and Microanalysis, 2021, 27, 1122-1124.	0.4	0
21	The role of the ASPL-TFE3 fusion protein in Alveolar Soft Part Sarcoma. Microscopy and Microanalysis, 2021, 27, 1114-1116.	0.4	0
22	Structural analysis of G protein $\gamma$ subunit folding by the cytosolic chaperonin CCT/TRiC and its co-chaperone phosphatidylethanolamine transfer protein 1 reveal molecular mechanisms of chaperone-mediated $\gamma$ propeller protein folding. FASEB Journal, 2022, 36, .	0.5	0
23	Folding of the SARS-CoV-2 RNA Polymerase by the Cytosolic Chaperonin CCT. FASEB Journal, 2022, 36, .	0.5	0