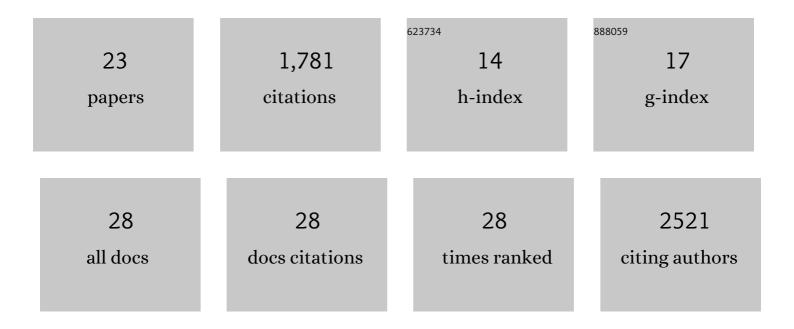
## Peter S Shen

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5390083/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Structural analysis of G protein β <sub>5</sub> subunit folding by the cytosolic chaperonin CCT/TRiC and its coâ€chaperone phosducinâ€like protein 1 reveal molecular mechanisms of chaperoneâ€mediated βâ€propeller protein folding. FASEB Journal, 2022, 36, .	0.5	0
2	Folding of the SARS oVâ€⊋ RNA Polymerase by the Cytosolic Chaperonin CCT. FASEB Journal, 2022, 36, .	0.5	0
3	Active conformation of the p97-p47 unfoldase complex. Nature Communications, 2022, 13, 2640.	12.8	18
4	Structural Determination of the CCT: $G\hat{I}^25$ folding intermediate. FASEB Journal, 2021, 35, .	0.5	0
5	Structural determination of the Dicer-2•R2D2 complex. Microscopy and Microanalysis, 2021, 27, 1122-1124.	0.4	0
6	The role of the ASPL-TFE3 fusion protein in Alveolar Soft Part Sarcoma. Microscopy and Microanalysis, 2021, 27, 1114-1116.	0.4	0
7	Negative charge in the RACK1 loop broadens the translational capacity of the human ribosome. Cell Reports, 2021, 36, 109663.	6.4	9
8	Determining the Structural Basis of Cofactor and Substrate Interactions with Cdc48. Microscopy and Microanalysis, 2020, 26, 578-579.	0.4	0
9	Rearranging AAA+ architecture to accommodate folded substrates. Nature Structural and Molecular Biology, 2020, 27, 225-226.	8.2	1
10	Structure of the Cdc48 segregase in the act of unfolding an authentic substrate. Science, 2019, 365, 502-505.	12.6	138
11	Structure of Vps4 with circular peptides and implications for translocation of two polypeptide chains by AAA+ ATPases. ELife, 2019, 8, .	6.0	41
12	The 2017 Nobel Prize in Chemistry: cryo-EM comes of age. Analytical and Bioanalytical Chemistry, 2018, 410, 2053-2057.	3.7	29
13	Dicer uses distinct modules for recognizing dsRNA termini. Science, 2018, 359, 329-334.	12.6	76
14	Vms1p is a release factor for the ribosome-associated quality control complex. Nature Communications, 2018, 9, 2197.	12.8	80
15	Structural basis of protein translocation by the Vps4-Vta1 AAA ATPase. ELife, 2017, 6, .	6.0	123
16	Structural inhibition of dynamin-mediated membrane fission by endophilin. ELife, 2017, 6, .	6.0	40
17	The AAA ATPase Vps4 binds ESCRT-III substrates through a repeating array of dipeptide-binding pockets. ELife, 2017, 6, .	6.0	80
18	The Structure of the Polycystic Kidney Disease Channel PKD2 in Lipid Nanodiscs. Cell, 2016, 167,	28.9	214

<sup>8</sup> 763-773.e11.

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#	Article	IF	CITATIONS
19	Rqc2p and 60 <i>S</i> ribosomal subunits mediate mRNA-independent elongation of nascent chains. Science, 2015, 347, 75-78.	12.6	245
20	Sequence and Structural Characterization of Great Salt Lake Bacteriophage CW02, a Member of the T7-Like Supergroup. Journal of Virology, 2012, 86, 7907-7917.	3.4	31
21	A Ribosome-Bound Quality Control Complex Triggers Degradation of Nascent Peptides and Signals Translation Stress. Cell, 2012, 151, 1042-1054.	28.9	536
22	The structure of avian polyomavirus reveals variably sized capsids, non-conserved inter-capsomere interactions, and a possible location of the minor capsid protein VP4. Virology, 2011, 411, 142-152.	2.4	26
23	Characterization of Pseudomonas chlororaphis myovirus 201ï•2-1 via genomic sequencing, mass spectrometry, and electron microscopy. Virology, 2008, 376, 330-338.	2.4	91