

# Stefan Pfeffer

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/403565/publications.pdf>

Version: 2024-02-01

44  
papers

3,395  
citations

201674

27  
h-index

254184

43  
g-index

53  
all docs

53  
docs citations

53  
times ranked

3674  
citing authors

#	ARTICLE	IF	CITATIONS
1	Modular assembly of the principal microtubule nucleator $\hat{\gamma}$ -TuRC. <i>Nature Communications</i> , 2022, 13, 473.	12.8	18
2	Bacterial ribosome collision sensing by a MutS DNA repair ATPase paralogue. <i>Nature</i> , 2022, 603, 509-514.	27.8	27
3	Ribosome-associated quality-control mechanisms from bacteria to humans. <i>Molecular Cell</i> , 2022, 82, 1451-1466.	9.7	58
4	The structure of the $\hat{\gamma}$ -TuRC: a 25-years-old molecular puzzle. <i>Current Opinion in Structural Biology</i> , 2021, 66, 15-21.	5.7	20
5	Mimicry of Canonical Translation Elongation Underlies Alanine Tail Synthesis in RQC. <i>Molecular Cell</i> , 2021, 81, 104-114.e6.	9.7	30
6	Microtubule nucleation: The waltz between $\hat{\gamma}$ -tubulin ring complex and associated proteins. <i>Current Opinion in Cell Biology</i> , 2021, 68, 124-131.	5.4	45
7	Reconstitution of the recombinant human $\hat{\gamma}$ -tubulin ring complex. <i>Open Biology</i> , 2021, 11, 200325.	3.6	11
8	The gamma-tubulin ring complex: Deciphering the molecular organization and assembly mechanism of a major vertebrate microtubule nucleator. <i>BioEssays</i> , 2021, 43, e2100114.	2.5	8
9	Deep learning improves macromolecule identification in 3D cellular cryo-electron tomograms. <i>Nature Methods</i> , 2021, 18, 1386-1394.	19.0	84
10	How to build a ribosome from RNA fragments in <i>Chlamydomonas</i> mitochondria. <i>Nature Communications</i> , 2021, 12, 7176.	12.8	27
11	Template-free detection and classification of membrane-bound complexes in cryo-electron tomograms. <i>Nature Methods</i> , 2020, 17, 209-216.	19.0	60
12	The cryo-EM structure of a $\hat{\gamma}$ -TuSC elucidates architecture and regulation of minimal microtubule nucleation systems. <i>Nature Communications</i> , 2020, 11, 5705.	12.8	7
13	Structural impact of K63 ubiquitin on yeast translocating ribosomes under oxidative stress. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 22157-22166.	7.1	21
14	Insights into the assembly and activation of the microtubule nucleator $\hat{\gamma}$ -TuRC. <i>Nature</i> , 2020, 578, 467-471.	27.8	106
15	MetAP-like Ebp1 occupies the human ribosomal tunnel exit and recruits flexible rRNA expansion segments. <i>Nature Communications</i> , 2020, 11, 776.	12.8	36
16	TRAM1 protein may support ER protein import by modulating the phospholipid bilayer near the lateral gate of the Sec61-channel. <i>Channels</i> , 2020, 14, 28-44.	2.8	13
17	A cryo-FIB lift-out technique enables molecular-resolution cryo-ET within native <i>Caenorhabditis elegans</i> tissue. <i>Nature Methods</i> , 2019, 16, 757-762.	19.0	165
18	Biogenic regions of cyanobacterial thylakoids form contact sites with the plasma membrane. <i>Nature Plants</i> , 2019, 5, 436-446.	9.3	114

#	ARTICLE	IF	CITATIONS
19	Functions and Mechanisms of the Human Ribosome-Translocon Complex. <i>Sub-Cellular Biochemistry</i> , 2019, 93, 83-141.	2.4	15
20	Structural basis for coupling protein transport and N-glycosylation at the mammalian endoplasmic reticulum. <i>Science</i> , 2018, 360, 215-219.	12.6	177
21	Plasma cell deficiency in human subjects with heterozygous mutations in Sec61 translocon alpha 1 subunit (SEC61A1). <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 1427-1438.	2.9	63
22	Cryo-FIB Lamella Milling: A Comprehensive Technique to Prepare Samples of Both Plunge- and High-pressure Frozen-hydrated Specimens for in situ Studies.. <i>Microscopy and Microanalysis</i> , 2018, 24, 820-821.	0.4	5
23	Unravelling molecular complexity in structural cell biology. <i>Current Opinion in Structural Biology</i> , 2018, 52, 111-118.	5.7	54
24	Proteomics reveals signal peptide features determining the client specificity in human TRAP-dependent ER protein import. <i>Nature Communications</i> , 2018, 9, 3765.	12.8	68
25	mTORC1 Controls Phase Separation and the Biophysical Properties of the Cytoplasm by Tuning Crowding. <i>Cell</i> , 2018, 174, 338-349.e20.	28.9	330
26	Structural Biology in Situ Using Cryo-Electron Subtomogram Analysis. <i>Biological and Medical Physics Series</i> , 2018, , 237-259.	0.4	3
27	Subtomogram analysis using the Volta phase plate. <i>Journal of Structural Biology</i> , 2017, 197, 94-101.	2.8	71
28	Dissecting the molecular organization of the translocon-associated protein complex. <i>Nature Communications</i> , 2017, 8, 14516.	12.8	131
29	Structure of the Human Mitochondrial Ribosome Studied In Situ by Cryoelectron Tomography. <i>Structure</i> , 2017, 25, 1574-1581.e2.	3.3	73
30	An Update on Sec61 Channel Functions, Mechanisms, and Related Diseases. <i>Frontiers in Physiology</i> , 2017, 8, 887.	2.8	117
31	Towards High Resolution in Cryo-Electron Tomography Subtomogram Analysis. <i>Microscopy and Microanalysis</i> , 2017, 23, 812-813.	0.4	1
32	Organization of the native ribosome-translocon complex at the mammalian endoplasmic reticulum membrane. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016, 1860, 2122-2129.	2.4	40
33	Visualizing the molecular sociology at the HeLa cell nuclear periphery. <i>Science</i> , 2016, 351, 969-972.	12.6	493
34	Sec61: A static framework for membrane-protein insertion. <i>Channels</i> , 2016, 10, 167-169.	2.8	5
35	Organization of the mitochondrial translation machinery studied in situ by cryoelectron tomography. <i>Nature Communications</i> , 2015, 6, 6019.	12.8	115
36	Structure of the native Sec61 protein-conducting channel. <i>Nature Communications</i> , 2015, 6, 8403.	12.8	169

#	ARTICLE	IF	CITATIONS
37	Protein Transport into the Human Endoplasmic Reticulum. <i>Journal of Molecular Biology</i> , 2015, 427, 1159-1175.	4.2	71
38	Structure of the mammalian oligosaccharyl-transferase complex in the native ER protein translocon. <i>Nature Communications</i> , 2014, 5, 3072.	12.8	127
39	Autofocused 3D Classification of Cryoelectron Subtomograms. <i>Structure</i> , 2014, 22, 1528-1537.	3.3	43
40	Automated detection of polysomes in cryoelectron tomography. , 2014, , .		1
41	Fast and accurate reference-free alignment of subtomograms. <i>Journal of Structural Biology</i> , 2013, 182, 235-245.	2.8	70
42	Detection and identification of macromolecular complexes in cryo-electron tomograms using support vector machines. , 2012, , .		11
43	PyTom: A python-based toolbox for localization of macromolecules in cryo-electron tomograms and subtomogram analysis. <i>Journal of Structural Biology</i> , 2012, 178, 177-188.	2.8	202
44	Structure and 3D Arrangement of Endoplasmic Reticulum Membrane-Associated Ribosomes. <i>Structure</i> , 2012, 20, 1508-1518.	3.3	79