Stephan Nickell

List of Publications by Year
in descending order

25 papers	2,606 citations	361045 20 h-index	610482 24 g-index
25 all docs	25 docs citations	25 times ranked	2688 citing authors

#	Article	IF	Citations
1	TOM software toolbox: acquisition and analysis for electron tomography. Journal of Structural Biology, 2005, 149, 227-234.	1.3	424
2	The structural basis of actin filament branching by the Arp2/3 complex. Journal of Cell Biology, 2008, 180, 887-895.	2.3	270
3	Identification of macromolecular complexes in cryoelectron tomograms of phantom cells. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 14153-14158.	3.3	246
4	Near-atomic resolution structural model of the yeast 26S proteasome. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 14870-14875.	3.3	242
5	A visual approach to proteomics. Nature Reviews Molecular Cell Biology, 2006, 7, 225-230.	16.1	212
6	Three-dimensional architecture of murine rod outer segments determined by cryoelectron tomography. Journal of Cell Biology, 2007, 177, 917-925.	2.3	192
7	The proteasomal subunit Rpn6 is a molecular clamp holding the core and regulatory subcomplexes together. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 149-154.	3.3	136
8	Structure of the 26S proteasome from Schizosaccharomyces pombe at subnanometer resolution. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 20992-20997.	3.3	130
9	Insights into the molecular architecture of the 26S proteasome. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 11943-11947.	3.3	116
10	Localization of the proteasomal ubiquitin receptors Rpn10 and Rpn13 by electron cryomicroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 1479-1484.	3.3	114
11	Pyrodictium cannulae enter the periplasmic space but do not enter the cytoplasm, as revealed by cryo-electron tomography. Journal of Structural Biology, 2003, 141, 34-42.	1.3	95
12	Maximum likelihood based classification of electron tomographic data. Journal of Structural Biology, 2011, 173, 77-85.	1.3	56
13	An atomic model AAA-ATPase/20S core particle sub-complex of the 26S proteasome. Biochemical and Biophysical Research Communications, 2009, 388, 228-233.	1.0	54
14	Unraveling the structure of membrane proteins in situ by transfer function corrected cryo-electron tomography. Journal of Structural Biology, 2012, 180, 488-496.	1.3	53
15	Toward an Integrated Structural Model of the 26S Proteasome. Molecular and Cellular Proteomics, 2010, 9, 1666-1677.	2.5	50
16	Computer controlled cryo-electron microscopy â€“ TOM2 a software package for high-throughput applications. Journal of Structural Biology, 2011, 175, 394-405.	1.3	49
17	Quantitative Proteome and Transcriptome Analysis of the Archaeon Thermoplasma acidophilum Cultured under Aerobic and Anaerobic Conditions. Journal of Proteome Research, 2010, 9, 4839-4850.	1.8	42
18	Structural analysis of the 26S proteasome by cryoelectron tomography. Biochemical and Biophysical Research Communications, 2007, 353, 115-120.	1.0	35

#	Article	IF	Citations
19	Automated cryoelectron microscopy of â€œsingle particlesâ€•applied to the 26S proteasome. FEBS Letters, 2007, 581, 2751-2756.	1.3	33
20	Localization of Protein Complexes by Pattern Recognition. Methods in Cell Biology, 2007, 79, 615-638.	0.5	27
21	Proteomics Analysis of Thermoplasma acidophilum with a Focus on Protein Complexes. Molecular and Cellular Proteomics, 2007, 6, 492-502.	2.5	16
22	Size distribution of native cytosolic proteins of Thermoplasma acidophilum. Proteomics, 2009, 9, 3783-3786.	1.3	9
23	Lipoprotein-like particles in a prokaryote: quinone droplets ofThermoplasma acidophilum. FEMS Microbiology Letters, 2016, 363, fnw169.	0.7	4
24	Exploring the Inner Space of Cells by Cryoelectron-Tomography. Microscopy and Microanalysis, 2004, 10, 152-153.	0.2	1
25	The State of the Art in Cryo-Electron Tomography. Microscopy and Microanalysis, 2003, 9, 174-175.	0.2	0