

Petra Wendler

List of Publications by Year in descending order

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31
papers

1,688
citations

394421

19
h-index

477307

29
g-index

34
all docs

34
docs citations

34
times ranked

2152
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure and function of the AAA+ nucleotide binding pocket. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2012, 1823, 2-14.	4.1	245
2	Structure and function of the AAA+ protein CbbX, a red-type Rubisco activase. <i>Nature</i> , 2011, 479, 194-199.	27.8	141
3	Head-to-tail interactions of the coiled-coil domains regulate ClpB activity and cooperation with Hsp70 in protein disaggregation. <i>ELife</i> , 2014, 3, e02481.	6.0	111
4	Blm3 is part of nascent proteasomes and is involved in a late stage of nuclear proteasome assembly. <i>EMBO Reports</i> , 2003, 4, 959-963.	4.5	107
5	Atypical AAA+ Subunit Packing Creates an Expanded Cavity for Disaggregation by the Protein-Remodeling Factor Hsp104. <i>Cell</i> , 2007, 131, 1366-1377.	28.9	107
6	Structure of green-type Rubisco activase from tobacco. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1366-1370.	8.2	97
7	Dodecameric Structure and ATPase Activity of the Human TIP48/TIP49 Complex. <i>Journal of Molecular Biology</i> , 2007, 366, 179-192.	4.2	92
8	Motor Mechanism for Protein Threading through Hsp104. <i>Molecular Cell</i> , 2009, 34, 81-92.	9.7	84
9	Structure of the VipA/B Type VI Secretion Complex Suggests a Contraction-State-Specific Recycling Mechanism. <i>Cell Reports</i> , 2014, 8, 20-30.	6.4	74
10	Structure and mechanism of the Swi2/Snf2 remodeller Mot1 in complex with its substrate TBP. <i>Nature</i> , 2011, 475, 403-407.	27.8	73
11	Molecular snapshots of the Pex1/6 AAA+ complex in action. <i>Nature Communications</i> , 2015, 6, 7331.	12.8	71
12	The Bipartite Nuclear Localization Sequence of Rpn2 Is Required for Nuclear Import of Proteasomal Base Complexes via Karyopherin β 2 and Proteasome Functions. <i>Journal of Biological Chemistry</i> , 2004, 279, 37751-37762.	3.4	62
13	Structure and mechanism of the Rubisco-assembly chaperone Raf1. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 720-728.	8.2	61
14	Cryo-EM structures reveal intricate Fe-S cluster arrangement and charging in <i>Rhodobacter capsulatus</i> formate dehydrogenase. <i>Nature Communications</i> , 2020, 11, 1912.	12.8	48
15	Mechanism of Enzyme Repair by the AAA+ Chaperone Rubisco Activase. <i>Molecular Cell</i> , 2017, 67, 744-756.e6.	9.7	47
16	AAA-ATPases in Protein Degradation. <i>Frontiers in Molecular Biosciences</i> , 2017, 4, 42.	3.5	46
17	Conserved Distal Loop Residues in the Hsp104 and ClpB Middle Domain Contact Nucleotide-binding Domain 2 and Enable Hsp70-dependent Protein Disaggregation. <i>Journal of Biological Chemistry</i> , 2014, 289, 848-867.	3.4	42
18	Proteasome assembly from 15S precursors involves major conformational changes and recycling of the Pba1/Pba2 chaperone. <i>Nature Communications</i> , 2015, 6, 6123.	12.8	42

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19	Structure and Function of p97 and Pex1/6 Type II AAA+ Complexes. <i>Frontiers in Molecular Biosciences</i> , 2017, 4, 33.	3.5	23
20	Structural comparison of contractile nanomachines. <i>AIMS Biophysics</i> , 2015, 2, 88-115.	0.6	20
21	Cryo electron microscopy structures of Hsp100 proteins: crowbars in or out? This paper is one of a selection of papers published in this special issue entitled 8th International Conference on AAA Proteins and has undergone the Journal's usual peer review process.. <i>Biochemistry and Cell Biology</i> , 2010, 88, 89-96.	2.0	19
22	Nuclear Transport of Yeast Proteasomes. <i>Frontiers in Molecular Biosciences</i> , 2019, 6, 34.	3.5	18
23	Structural Mapping of Missense Mutations in the Pex1/Pex6 Complex. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3756.	4.1	15
24	Current limits of structural biology: The transient interaction between cytochrome c and photosystem I. <i>Current Research in Structural Biology</i> , 2020, 2, 171-179.	2.2	13
25	Transformation of 2,2-dichlorodiisopropyl ether in mixed and pure culture. <i>Applied Microbiology and Biotechnology</i> , 2001, 56, 491-495.	3.6	9
26	Construction of Highly Ordered Glyco-Inside Nano-Assemblies through RAFT Dispersion Polymerization of Galactose-Decorated Monomer. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 11098-11103.	13.8	9
27	Antimicrobial Polymers of Linear and Bottlebrush Architecture: Probing the Membrane Interaction and Physicochemical Properties. <i>Macromolecular Rapid Communications</i> , 2022, 43, .	3.9	6
28	Protein Nanopore Membranes Prepared by a Simple Langmuir-Schaefer Approach. <i>Small</i> , 2021, 17, e2102975.	10.0	3
29	Construction of Highly Ordered Glyco-Inside Nano-Assemblies through RAFT Dispersion Polymerization of Galactose-Decorated Monomer. <i>Angewandte Chemie</i> , 2021, 133, 11198-11203.	2.0	1
30	Innentitelbild: Construction of Highly Ordered Glyco-Inside Nano-Assemblies through RAFT Dispersion Polymerization of Galactose-Decorated Monomer (Angew. Chem. 20/2021). <i>Angewandte Chemie</i> , 2021, 133, 11098-11098.	2.0	0
31	A RADD approach to probing AAA+ protein function. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 329-330.	8.2	0