

Shashi Bhushan

List of Publications by Year in descending order

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45
papers

2,450
citations

257450

24
h-index

265206

42
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45
all docs

45
docs citations

45
times ranked

3025
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of Monomeric Yeast and Mammalian Sec61 Complexes Interacting with the Translating Ribosome. <i>Science</i> , 2009, 326, 1369-1373.	12.6	263
2	Cryo-EM structure and rRNA model of a translating eukaryotic 80S ribosome at 5.5-Å resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19748-19753.	7.1	196
3	Î±-Helical nascent polypeptide chains visualized within distinct regions of the ribosomal exit tunnel. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 313-317.	8.2	187
4	Degradation of the Amyloid Î²-Protein by the Novel Mitochondrial Peptidosome, PreP. <i>Journal of Biological Chemistry</i> , 2006, 281, 29096-29104.	3.4	175
5	SecM-Stalled Ribosomes Adopt an Altered Geometry at the Peptidyl Transferase Center. <i>PLoS Biology</i> , 2011, 9, e1000581.	5.6	132
6	Localization of eukaryote-specific ribosomal proteins in a 5.5-Å cryo-EM map of the 80S eukaryotic ribosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19754-19759.	7.1	122
7	Nuclear Photosynthetic Gene Expression Is Synergistically Modulated by Rates of Protein Synthesis in Chloroplasts and Mitochondria. <i>Plant Cell</i> , 2006, 18, 970-991.	6.6	117
8	Characterization of a novel zinc metalloprotease involved in degrading targeting peptides in mitochondria and chloroplasts. <i>Plant Journal</i> , 2003, 36, 616-628.	5.7	106
9	Structural Basis for Translational Stalling by Human Cytomegalovirus and Fungal Arginine Attenuator Peptide. <i>Molecular Cell</i> , 2010, 40, 138-146.	9.7	106
10	The closed structure of presequence protease PreP forms a unique 10 000 Å ³ chamber for proteolysis. <i>EMBO Journal</i> , 2006, 25, 1977-1986.	7.8	93
11	Dual targeting and function of a protease in mitochondria and chloroplasts. <i>EMBO Reports</i> , 2003, 4, 1073-1077.	4.5	82
12	Identification and characterization of multiple rubisco activases in chemoautotrophic bacteria. <i>Nature Communications</i> , 2015, 6, 8883.	12.8	81
13	Two Novel Targeting Peptide Degrading Proteases, PrePs, in Mitochondria and Chloroplasts, so Similar and Still Different. <i>Journal of Molecular Biology</i> , 2005, 349, 847-860.	4.2	77
14	The role of the N-terminal domain of chloroplast targeting peptides in organellar protein import and miss-sorting. <i>FEBS Letters</i> , 2006, 580, 3966-3972.	2.8	73
15	Structural basis of RIP2 activation and signaling. <i>Nature Communications</i> , 2018, 9, 4993.	12.8	65
16	Catalysis, Subcellular Localization, Expression and Evolution of the Targeting Peptides Degrading Protease, AtPreP2. <i>Plant and Cell Physiology</i> , 2005, 46, 985-996.	3.1	56
17	Correcting for AFM tip induced topography convolutions in protein-DNA samples. <i>Ultramicroscopy</i> , 2012, 121, 8-15.	1.9	42
18	Unique localization of the plastid-specific ribosomal proteins in the chloroplast ribosome small subunit provides mechanistic insights into the chloroplastic translation. <i>Nucleic Acids Research</i> , 2017, 45, 8581-8595.	14.5	38

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19	Structure of BipA in GTP form bound to the ratcheted ribosome. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10944-10949.	7.1	37
20	Structural Basis for Linezolid Binding Site Rearrangement in the <i>Staphylococcus aureus</i> Ribosome. MBio, 2017, 8, .	4.1	37
21	Structures of Mycobacterium smegmatis 70S ribosomes in complex with HPF, tmRNA, and P-tRNA. Scientific Reports, 2018, 8, 13587.	3.3	37
22	Cryo-electron Microscopic Structure of SecA Protein Bound to the 70S Ribosome. Journal of Biological Chemistry, 2014, 289, 7190-7199.	3.4	35
23	Cryo-EM structure of the large subunit of the spinach chloroplast ribosome. Scientific Reports, 2016, 6, 35793.	3.3	35
24	Insights into the mechanism and regulation of the CbbQO-type Rubisco activase, a MoxR AAA+ ATPase. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 381-387.	7.1	33
25	Rational Engineering and Characterization of an mAb that Neutralizes Zika Virus by Targeting a Mutationally Constrained Quaternary Epitope. Cell Host and Microbe, 2018, 23, 618-627.e6.	11.0	28
26	Structure and subunit arrangement of Mycobacterial F1FO ATP synthase and novel features of the unique mycobacterial subunit F ₁ . Journal of Structural Biology, 2019, 207, 199-208.	2.8	22
27	AhpC of the mycobacterial antioxidant defense system and its interaction with its reducing partner Thioredoxin-C. Scientific Reports, 2017, 7, 5159.	3.3	20
28	Cryo-EM structure of the highly atypical cytoplasmic ribosome of <i>Euglena gracilis</i> . Nucleic Acids Research, 2020, 48, 11750-11761.	14.5	19
29	Dual targeting and function of a protease in mitochondria and chloroplasts. EMBO Reports, 2003, 4, 1073-1077.	4.5	18
30	Two novel mitochondrial and chloroplastic targeting-peptide-degrading peptidasomes in A. thaliana, AtPreP1 and AtPreP2. Biological Chemistry, 2006, 387, 1441-7.	2.5	16
31	Unique structural features of the Mycobacterium ribosome. Progress in Biophysics and Molecular Biology, 2020, 152, 15-24.	2.9	15
32	Functional Evolution in Orthologous Cell-encoded RNA-dependent RNA Polymerases. Journal of Biological Chemistry, 2016, 291, 9295-9309.	3.4	13
33	Structure of the GTP Form of Elongation Factor 4 (EF4) Bound to the Ribosome. Journal of Biological Chemistry, 2016, 291, 12943-12950.	3.4	11
34	A systematic assessment of mycobacterial F ₁ ATPase subunit F ₁ 's role in latent ATPase hydrolysis. FEBS Journal, 2021, 288, 818-836.	4.7	11
35	The stimulating role of subunit F in ATPase activity inside the A1-complex of the Methanosarcina mazei C ₁ A1AO ATP synthase. Biochimica Et Biophysica Acta - Bioenergetics, 2016, 1857, 177-187.	1.0	10
36	Atomic structure and enzymatic insights into the vancomycin-resistant Enterococcus faecalis (V583) alkylhydroperoxide reductase subunit C. Free Radical Biology and Medicine, 2018, 115, 252-265.	2.9	9

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37	Structure and function of Mycobacterium-specific components of F-ATP synthase subunits $\hat{\epsilon}$ and $\hat{\mu}$. Journal of Structural Biology, 2018, 204, 420-434.	2.8	9
38	Proteolytic mechanism of a novel mitochondrial and chloroplastic PreP peptidasome. Biological Chemistry, 2006, 387, 1087-90.	2.5	8
39	In Vitro and In Vivo Methods to Study Protein Import Into Plant Mitochondria. , 2007, 390, 131-150.		5
40	The structural features of Acetobacterium woodii F ₁ F ₀ -ATP synthase reveal the importance of the unique subunit $\hat{\epsilon}$ loop in Na ⁺ translocation and ATP synthesis. FEBS Journal, 2019, 286, 1894-1907.	4.7	4
41	In Vitro and In Vivo Protein Import Into Plant Mitochondria. Methods in Molecular Biology, 2007, 372, 297-314.	0.9	3
42	A complex between the Zika virion and the Fab of a broadly cross-reactive neutralizing monoclonal antibody revealed by cryo-EM and single particle analysis at 4.1 Å resolution. Journal of Structural Biology: X, 2020, 4, 100028.	1.3	3
43	Microtubule nucleation from a functionalised SiO ₂ EM grid. RSC Advances, 2013, 3, 7688.	3.6	1
44	Nascent polypeptide chains within the ribosomal tunnel analyzed by cryo-EM. , 2011, , 393-404.		0
45	In Vitro and In Vivo Methods to Study Protein Import Into Plant Mitochondria. , 0, , 131-150.		0