

Surajit Bhattacharjya

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

78
papers

2,209
citations

27
h-index

44
g-index

82
ext. papers

2,525
ext. citations

5
avg, IF

5.41
L-index

#	Paper	IF	Citations
78	NMR Structure and Localization of the Host Defense Peptide ThanatinM21F in Zwitterionic Dodecylphosphocholine Micelle: Implications in Antimicrobial and Hemolytic Activity.. <i>Journal of Membrane Biology</i> , 2022 , 1	2.3	0
77	Linking dual mode of action of host defense antimicrobial peptide thanatin: Structures, lipopolysaccharide and LptA binding of designed analogs.. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2021 , 1864, 183839	3.8	1
76	-Designed β Sheet Heme Proteins. <i>Biochemistry</i> , 2021 , 60, 431-439	3.2	3
75	Thanatin: An Emerging Host Defense Antimicrobial Peptide with Multiple Modes of Action. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	13
74	Enhanced Cholesterol-Dependent Hemifusion by Internal Fusion Peptide 1 of SARS Coronavirus-2 Compared to Its N-Terminal Counterpart. <i>Biochemistry</i> , 2021 , 60, 559-562	3.2	8
73	Binary and ternary complexes of FLNa-Ig21 with cytosolic tails of β integrin reveal dual role of filamin mediated regulation. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2021 , 1865, 130005	4	0
72	Salt Dependence Conformational Stability of the Dimeric SAM Domain of MAPKKK Ste11 from Budding Yeast: A Native-State H/D Exchange NMR Study. <i>Biochemistry</i> , 2020 , 59, 2849-2858	3.2	0
71	Mechanistic insights of host cell fusion of SARS-CoV-1 and SARS-CoV-2 from atomic resolution structure and membrane dynamics. <i>Biophysical Chemistry</i> , 2020 , 265, 106438	3.5	28
70	NMR structure and localization of the host defense antimicrobial peptide thanatin in zwitterionic dodecylphosphocholine micelle: Implications in antimicrobial activity. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2020 , 1862, 183432	3.8	4
69	Design, Engineering and Discovery of Novel β Helical and β Boomerang Antimicrobial Peptides against Drug Resistant Bacteria. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	22
68	Membrane Cholesterol Modulates Oligomeric Status and Peptide-Membrane Interaction of Severe Acute Respiratory Syndrome Coronavirus Fusion Peptide. <i>Journal of Physical Chemistry B</i> , 2019 , 123, 10654-10662	3.4	67
67	NMR Structure, Dynamics and Interactions of the Integrin β Cytoplasmic Tail with Filamin Domain IgFLNa21. <i>Scientific Reports</i> , 2018 , 8, 5490	4.9	5
66	NMR structure and localization of a large fragment of the SARS-CoV fusion protein: Implications in viral cell fusion. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2018 , 1860, 407-415	3.8	14
65	Cell-Selective Pore Forming Antimicrobial Peptides of the Prodomain of Human Furin: A Conserved Aromatic/Cationic Sequence Mapping, Membrane Disruption, and Atomic-Resolution Structure and Dynamics. <i>ACS Omega</i> , 2018 , 3, 14650-14664	3.9	6
64	Expanding heme-protein folding space using designed multi-heme β sheet mini-proteins. <i>Communications Chemistry</i> , 2018 , 1,	6.3	7
63	Interaction Analyses of 14-3-3 ζ Dok1, and Phosphorylated Integrin β Cytoplasmic Tails Reveal a Bi-molecular Switch in Integrin Regulation. <i>Journal of Molecular Biology</i> , 2018 , 430, 4419-4430	6.5	6
62	Lipopolysaccharide-affinity copolymer senses the rapid motility of swarmer bacteria to trigger antimicrobial drug release. <i>Nature Communications</i> , 2018 , 9, 4277	17.4	10

61	Designed Heme-Cage β Sheet Miniproteins. <i>Angewandte Chemie - International Edition</i> , 2017 , 56, 5904-5908.4	16
60	Designed Heme-Cage β Sheet Miniproteins. <i>Angewandte Chemie</i> , 2017 , 129, 5998-6002	3.6 8
59	Piscidin-1-analogs with double L- and D-lysine residues exhibited different conformations in lipopolysaccharide but comparable anti-endotoxin activities. <i>Scientific Reports</i> , 2017 , 7, 39925	4.9 16
58	Structure and Interactions of AHost Defense Antimicrobial Peptide Thanatin in Lipopolysaccharide Micelles Reveal Mechanism of Bacterial Cell Agglutination. <i>Scientific Reports</i> , 2017 , 7, 17795	4.9 42
57	<i>Pseudomonas aeruginosa</i> Psl Exopolysaccharide Interacts with the Antimicrobial Peptide LG21. <i>Water (Switzerland)</i> , 2017 , 9, 681	3 1
56	NMR Structures and Interactions of Antimicrobial Peptides with Lipopolysaccharide: Connecting Structures to Functions. <i>Current Topics in Medicinal Chemistry</i> , 2016 , 16, 4-15	3 20
55	Salt-resistant short antimicrobial peptides. <i>Biopolymers</i> , 2016 , 106, 345-56	2.2 17
54	α -lipopolysaccharide binding motif and mapping cationic residues in antibacterial activity. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016 , 1860, 1362-72	4 15
53	Designed multi-stranded heme binding β sheet peptides in membrane. <i>Chemical Science</i> , 2016 , 7, 2563-2574	7.1 18
52	Interaction Analyses of the Integrin β Cytoplasmic Tail with the F3 FERM Domain of Talin and 14-3-3 σ Reveal a Ternary Complex with Phosphorylated Tail. <i>Journal of Molecular Biology</i> , 2016 , 428, 4129-4142	6.5 13
51	NMR structures and localization of the potential fusion peptides and the pre-transmembrane region of SARS-CoV: Implications in membrane fusion. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015 , 1848, 721-30	3.8 26
50	An Alternative Phosphorylation Switch in Integrin β (CD18) Tail for Dok1 Binding. <i>Scientific Reports</i> , 2015 , 5, 11630	4.9 13
49	Peptide-erythrosin diimide functionalized magnetic nano-platforms for fluorescence turn-on detection and clearance of bacterial lipopolysaccharides. <i>Chemical Communications</i> , 2014 , 50, 6200-3	5.8 41
48	Cysteine deleted protegrin-1 (CDP-1): anti-bacterial activity, outer-membrane disruption and selectivity. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2014 , 1840, 3006-16	4 21
47	Designed di-heme binding helical transmembrane protein. <i>ChemBioChem</i> , 2014 , 15, 1257-62	3.8 15
46	Characterization of the near native conformational states of the SAM domain of Ste11 protein by NMR spectroscopy. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014 , 82, 2957-69	4.2 1
45	NMR characterization of the near native and unfolded states of the PTB domain of Dok1: alternate conformations and residual clusters. <i>PLoS ONE</i> , 2014 , 9, e90557	3.7 7
44	β Boomerang Antimicrobial and Antiendotoxic Peptides: Lipidation and Disulfide Bond Effects on Activity and Structure. <i>Pharmaceuticals</i> , 2014 , 7, 482-501	5.2 16

43	Design of short membrane selective antimicrobial peptides containing tryptophan and arginine residues for improved activity, salt-resistance, and biocompatibility. <i>Biotechnology and Bioengineering</i> , 2014 , 111, 37-49	4.9	65
42	Resurrecting inactive antimicrobial peptides from the lipopolysaccharide trap. <i>Antimicrobial Agents and Chemotherapy</i> , 2014 , 58, 1987-96	5.9	53
41	Hairpin Peptides: Heme Binding, Catalysis, and Structure in Detergent Micelles. <i>Angewandte Chemie</i> , 2013 , 125, 6558-6562	3.6	9
40	Hairpin peptides: heme binding, catalysis, and structure in detergent micelles. <i>Angewandte Chemie - International Edition</i> , 2013 , 52, 6430-4	16.4	19
39	NMR structure of temporin-1 ta in lipopolysaccharide micelles: mechanistic insight into inactivation by outer membrane. <i>PLoS ONE</i> , 2013 , 8, e72718	3.7	29
38	Applications of saturation transfer difference NMR in biological systems. <i>Drug Discovery Today</i> , 2012 , 17, 505-13	8.8	111
37	Structural determinants of the specificity of a membrane binding domain of the scaffold protein Ste5 of budding yeast: implications in signaling by the scaffold protein in MAPK pathway. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 1250-60	3.8	6
36	Structure, activity and interactions of the cysteine deleted analog of tachyplesin-1 with lipopolysaccharide micelle: Mechanistic insights into outer-membrane permeabilization and endotoxin neutralization. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 1613-24	3.8	42
35	Structure and binding interface of the cytosolic tails of α integrin. <i>PLoS ONE</i> , 2012 , 7, e41924	3.7	11
34	Oligomeric structure of a cathelicidin antimicrobial peptide in dodecylphosphocholine micelle determined by NMR spectroscopy. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2011 , 1808, 369-81	3.8	30
33	Mapping residue-specific contacts of polymyxin B with lipopolysaccharide by saturation transfer difference NMR: insights into outer-membrane disruption and endotoxin neutralization. <i>Biopolymers</i> , 2011 , 96, 273-87	2.2	25
32	Structures and interaction analyses of integrin β cytoplasmic tails. <i>Journal of Biological Chemistry</i> , 2011 , 286, 43842-43854	5.4	15
31	NMR structures and interactions of temporin-1Tl and temporin-1Tb with lipopolysaccharide micelles: mechanistic insights into outer membrane permeabilization and synergistic activity. <i>Journal of Biological Chemistry</i> , 2011 , 286, 24394-406	5.4	73
30	NMR structure of pardaxin, a pore-forming antimicrobial peptide, in lipopolysaccharide micelles: mechanism of outer membrane permeabilization. <i>Journal of Biological Chemistry</i> , 2010 , 285, 3883-3895	5.4	105
29	Structure, interactions, and antibacterial activities of MSI-594 derived mutant peptide MSI-594F5A in lipopolysaccharide micelles: role of the helical hairpin conformation in outer-membrane permeabilization. <i>Journal of the American Chemical Society</i> , 2010 , 132, 18417-28	16.4	90
28	Micelle-bound structures and dynamics of the hinge deleted analog of melittin and its diastereomer: implications in cell selective lysis by D-amino acid containing antimicrobial peptides. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2010 , 1798, 128-39	3.8	29
27	Functional and structural characterization of the talin F0F1 domain. <i>Biochemical and Biophysical Research Communications</i> , 2010 , 391, 159-65	3.4	3
26	Designed beta-boomerang antiendotoxic and antimicrobial peptides: structures and activities in lipopolysaccharide. <i>Journal of Biological Chemistry</i> , 2009 , 284, 21991-22004	5.4	82

25	Helical hairpin structure of a potent antimicrobial peptide MSI-594 in lipopolysaccharide micelles by NMR spectroscopy. <i>Chemistry - A European Journal</i> , 2009 , 15, 2036-40	4.8	81
24	Lipopolysaccharide bound structures of the active fragments of fowlicidin-1, a cathelicidin family of antimicrobial and antiendotoxic peptide from chicken, determined by transferred nuclear Overhauser effect spectroscopy. <i>Biopolymers</i> , 2009 , 92, 9-22	2.2	49
23	NMR structural studies of the Ste11 SAM domain in the dodecyl phosphocholine micelle. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 74, 328-43	4.2	22
22	Multifunctional host defense peptides: functional and mechanistic insights from NMR structures of potent antimicrobial peptides. <i>FEBS Journal</i> , 2009 , 276, 6465-73	5.7	78
21	Interactions of a designed peptide with lipopolysaccharide: Bound conformation and anti-endotoxic activity. <i>Biochemical and Biophysical Research Communications</i> , 2008 , 369, 853-7	3.4	21
20	Equilibrium unfolding of the dimeric SAM domain of MAPKKK Ste11 from the budding yeast: role of the interfacial residues in structural stability and binding. <i>Biochemistry</i> , 2008 , 47, 651-9	3.2	7
19	Conformational analyses of a partially-folded bioactive prodomain of human furin. <i>Biopolymers</i> , 2007 , 86, 329-44	2.2	9
18	Structural and thermodynamic analyses of the interaction between melittin and lipopolysaccharide. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2007 , 1768, 3282-91	3.8	47
17	High-resolution solution structure of a designed peptide bound to lipopolysaccharide: transferred nuclear Overhauser effects, micelle selectivity, and anti-endotoxic activity. <i>Biochemistry</i> , 2007 , 46, 5864-74	3.2	42
16	An NMR-based identification of a peptide fragment from the beta-subunit of a G-protein showing specific interactions with the GBB domain of the Ste20 kinase in budding yeast. <i>Biochemical and Biophysical Research Communications</i> , 2006 , 347, 1145-50	3.4	5
15	Polymerization of the SAM domain of MAPKKK Ste11 from the budding yeast: implications for efficient signaling through the MAPK cascades. <i>Protein Science</i> , 2005 , 14, 828-35	6.3	18
14	Solution structure of the dimeric SAM domain of MAPKKK Ste11 and its interactions with the adaptor protein Ste50 from the budding yeast: implications for Ste11 activation and signal transmission through the Ste50-Ste11 complex. <i>Journal of Molecular Biology</i> , 2004 , 344, 1071-87	6.5	32
13	pH-induced conformational transitions of a molten-globule-like state of the inhibitory prodomain of furin: implications for zymogen activation. <i>Protein Science</i> , 2001 , 10, 934-42	6.3	26
12	Sequence-specific ¹ H, ¹⁵ N and ¹³ C resonance assignments of the inhibitory prodomain of human furin. <i>Journal of Biomolecular NMR</i> , 2000 , 16, 275-6	3	4
11	Inhibitory activity and structural characterization of a C-terminal peptide fragment derived from the prosegment of the proprotein convertase PC7. <i>Biochemistry</i> , 2000 , 39, 2868-77	3.2	26
10	Solid state and solution conformations of a helical peptide with a central gly-gly segment 1998 , 38, 515-526		22
9	Omega amino acids in peptide design: incorporation into helices 1998 , 39, 769-777		38
8	Folded conformations of antigenic peptides from riboflavin carrier protein in aqueous hexafluoroacetone. <i>Protein Science</i> , 1998 , 7, 123-31	6.3	5

7	Ω-Amino Acids in Peptide Design. Crystal Structures and Solution Conformations of Peptide Helices Containing a Ω-Alanyl-Ω-Aminobutyryl Segment. <i>Journal of the American Chemical Society</i> , 1997 , 119, 9087-9095	16.4	113
6	Hexafluoroacetone hydrate as a structure modifier in proteins: characterization of a molten globule state of hen egg-white lysozyme. <i>Protein Science</i> , 1997 , 6, 1065-73	6.3	35
5	Effects of organic solvents on protein structures: observation of a structured helical core in hen egg-white lysozyme in aqueous dimethylsulfoxide. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997 , 29, 492-507	4.2	90
4	Polymyxin B nonapeptide: Conformations in water and in the lipopolysaccharide-bound state determined by two-dimensional NMR and molecular dynamics. <i>Biopolymers</i> , 1997 , 41, 251-265	2.2	54
3	"Teflon-coated peptides": hexafluoroacetone trihydrate as a structure stabilizer for peptides. <i>Biopolymers</i> , 1997 , 42, 125-8	2.2	58
2	Solid state and solution conformations of a helical peptide with a central gly-gly segment 1996 , 38, 515		17
1	Omega amino acids in peptide design: incorporation into helices 1996 , 39, 769		13