

# Surajit Bhattacharjya

## List of Publications by Citations

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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	α-Amino Acids in Peptide Design. Crystal Structures and Solution Conformations of Peptide Helices Containing a β-Alanyl-β-Aminobutyryl Segment. <i>Journal of the American Chemical Society</i> , <b>1997</b> , 119, 9087-9095	16.4	113
77	Applications of saturation transfer difference NMR in biological systems. <i>Drug Discovery Today</i> , <b>2012</b> , 17, 505-13	8.8	111
76	NMR structure of pardaxin, a pore-forming antimicrobial peptide, in lipopolysaccharide micelles: mechanism of outer membrane permeabilization. <i>Journal of Biological Chemistry</i> , <b>2010</b> , 285, 3883-3895	5.4	105
75	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> , <b>2010</b> , 132, 18417-28	16.4	90
74	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> , <b>1997</b> , 29, 492-507	4.2	90
73	Designed beta-boomerang antiendotoxic and antimicrobial peptides: structures and activities in lipopolysaccharide. <i>Journal of Biological Chemistry</i> , <b>2009</b> , 284, 21991-22004	5.4	82
72	Helical hairpin structure of a potent antimicrobial peptide MSI-594 in lipopolysaccharide micelles by NMR spectroscopy. <i>Chemistry - A European Journal</i> , <b>2009</b> , 15, 2036-40	4.8	81
71	Multifunctional host defense peptides: functional and mechanistic insights from NMR structures of potent antimicrobial peptides. <i>FEBS Journal</i> , <b>2009</b> , 276, 6465-73	5.7	78
70	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> , <b>2011</b> , 286, 24394-406	5.4	73
69	Membrane Cholesterol Modulates Oligomeric Status and Peptide-Membrane Interaction of Severe Acute Respiratory Syndrome Coronavirus Fusion Peptide. <i>Journal of Physical Chemistry B</i> , <b>2019</b> , 123, 10654-10662	3.4	67
68	Design of short membrane selective antimicrobial peptides containing tryptophan and arginine residues for improved activity, salt-resistance, and biocompatibility. <i>Biotechnology and Bioengineering</i> , <b>2014</b> , 111, 37-49	4.9	65
67	"Teflon-coated peptides": hexafluoroacetone trihydrate as a structure stabilizer for peptides. <i>Biopolymers</i> , <b>1997</b> , 42, 125-8	2.2	58
66	Polymyxin B nonapeptide: Conformations in water and in the lipopolysaccharide-bound state determined by two-dimensional NMR and molecular dynamics. <i>Biopolymers</i> , <b>1997</b> , 41, 251-265	2.2	54
65	Resurrecting inactive antimicrobial peptides from the lipopolysaccharide trap. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2014</b> , 58, 1987-96	5.9	53
64	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> , <b>2009</b> , 92, 9-22	2.2	49
63	Structural and thermodynamic analyses of the interaction between melittin and lipopolysaccharide. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , <b>2007</b> , 1768, 3282-91	3.8	47
62	Structure and Interactions of α-Host Defense Antimicrobial Peptide Thanatin in Lipopolysaccharide Micelles Reveal Mechanism of Bacterial Cell Agglutination. <i>Scientific Reports</i> , <b>2017</b> , 7, 17795	4.9	42

61	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> , <b>2012</b> , 1818, 1613-24	3.8	42
60	High-resolution solution structure of a designed peptide bound to lipopolysaccharide: transferred nuclear Overhauser effects, micelle selectivity, and anti-endotoxic activity. <i>Biochemistry</i> , <b>2007</b> , 46, 5864-74	3.7	42
59	Peptide-erylene diimide functionalized magnetic nano-platforms for fluorescence turn-on detection and clearance of bacterial lipopolysaccharides. <i>Chemical Communications</i> , <b>2014</b> , 50, 6200-3	5.8	41
58	Omega amino acids in peptide design: incorporation into helices <b>1998</b> , 39, 769-777		38
57	Hexafluoroacetone hydrate as a structure modifier in proteins: characterization of a molten globule state of hen egg-white lysozyme. <i>Protein Science</i> , <b>1997</b> , 6, 1065-73	6.3	35
56	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> , <b>2004</b> , 344, 1071-87	6.5	32
55	Oligomeric structure of a cathelicidin antimicrobial peptide in dodecylphosphocholine micelle determined by NMR spectroscopy. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , <b>2011</b> , 1808, 369-81	3.8	30
54	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> , <b>2010</b> , 1798, 128-39	3.8	29
53	NMR structure of temporin-1 ta in lipopolysaccharide micelles: mechanistic insight into inactivation by outer membrane. <i>PLoS ONE</i> , <b>2013</b> , 8, e72718	3.7	29
52	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> , <b>2020</b> , 265, 106438	3.5	28
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> , <b>2015</b> , 1848, 721-30	3.8	26
50	pH-induced conformational transitions of a molten-globule-like state of the inhibitory prodomain of furin: implications for zymogen activation. <i>Protein Science</i> , <b>2001</b> , 10, 934-42	6.3	26
49	Inhibitory activity and structural characterization of a C-terminal peptide fragment derived from the prosegment of the proprotein convertase PC7. <i>Biochemistry</i> , <b>2000</b> , 39, 2868-77	3.2	26
48	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> , <b>2011</b> , 96, 273-87	2.2	25
47	NMR structural studies of the Ste11 SAM domain in the dodecyl phosphocholine micelle. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2009</b> , 74, 328-43	4.2	22
46	Solid state and solution conformations of a helical peptide with a central gly-gly segment <b>1998</b> , 38, 515-526		22
45	Design, Engineering and Discovery of Novel Helical and Boomerang Antimicrobial Peptides against Drug Resistant Bacteria. <i>International Journal of Molecular Sciences</i> , <b>2020</b> , 21,	6.3	22
44	Cysteine deleted protegrin-1 (CDP-1): anti-bacterial activity, outer-membrane disruption and selectivity. <i>Biochimica Et Biophysica Acta - General Subjects</i> , <b>2014</b> , 1840, 3006-16	4	21

43	Interactions of a designed peptide with lipopolysaccharide: Bound conformation and anti-endotoxic activity. <i>Biochemical and Biophysical Research Communications</i> , <b>2008</b> , 369, 853-7	3.4	21
42	NMR Structures and Interactions of Antimicrobial Peptides with Lipopolysaccharide: Connecting Structures to Functions. <i>Current Topics in Medicinal Chemistry</i> , <b>2016</b> , 16, 4-15	3	20
41	β-Hairpin peptides: heme binding, catalysis, and structure in detergent micelles. <i>Angewandte Chemie - International Edition</i> , <b>2013</b> , 52, 6430-4	16.4	19
40	Polymerization of the SAM domain of MAPKKK Ste11 from the budding yeast: implications for efficient signaling through the MAPK cascades. <i>Protein Science</i> , <b>2005</b> , 14, 828-35	6.3	18
39	Designed multi-stranded heme binding β-sheet peptides in membrane. <i>Chemical Science</i> , <b>2016</b> , 7, 2563-2574	3.4	18
38	Salt-resistant short antimicrobial peptides. <i>Biopolymers</i> , <b>2016</b> , 106, 345-56	2.2	17
37	Solid state and solution conformations of a helical peptide with a central gly-gly segment <b>1996</b> , 38, 515		17
36	Designed Heme-Cage β-Sheet Mini-proteins. <i>Angewandte Chemie - International Edition</i> , <b>2017</b> , 56, 5904-5908	3.4	16
35	Piscidin-1-analogs with double L- and D-lysine residues exhibited different conformations in lipopolysaccharide but comparable anti-endotoxin activities. <i>Scientific Reports</i> , <b>2017</b> , 7, 39925	4.9	16
34	β-Boomerang Antimicrobial and Antiendotoxic Peptides: Lipidation and Disulfide Bond Effects on Activity and Structure. <i>Pharmaceuticals</i> , <b>2014</b> , 7, 482-501	5.2	16
33	Designed di-heme binding helical transmembrane protein. <i>ChemBioChem</i> , <b>2014</b> , 15, 1257-62	3.8	15
32	Structures and interaction analyses of integrin $\alpha$ cytoplasmic tails. <i>Journal of Biological Chemistry</i> , <b>2011</b> , 286, 43842-43854	5.4	15
31	Lollipop-shaped helical structure of a hybrid antimicrobial peptide of temporin B-lipopolysaccharide binding motif and mapping cationic residues in antibacterial activity. <i>Biochimica Et Biophysica Acta - General Subjects</i> , <b>2016</b> , 1860, 1362-72	4	15
30	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> , <b>2018</b> , 1860, 407-415	3.8	14
29	An Alternative Phosphorylation Switch in Integrin $\alpha$ (CD18) Tail for Dok1 Binding. <i>Scientific Reports</i> , <b>2015</b> , 5, 11630	4.9	13
28	Interaction Analyses of the Integrin $\alpha$ Cytoplasmic Tail with the F3 FERM Domain of Talin and 14-3-3 $\sigma$ Reveal a Ternary Complex with Phosphorylated Tail. <i>Journal of Molecular Biology</i> , <b>2016</b> , 428, 4129-4142	6.5	13
27	Thanatin: An Emerging Host Defense Antimicrobial Peptide with Multiple Modes of Action. <i>International Journal of Molecular Sciences</i> , <b>2021</b> , 22,	6.3	13
26	Omega amino acids in peptide design: incorporation into helices <b>1996</b> , 39, 769		13

25	Structure and binding interface of the cytosolic tails of $\alpha 5 \beta 1$ integrin. <i>PLoS ONE</i> , <b>2012</b> , 7, e41924	3.7	11
24	Lipopolysaccharide-affinity copolymer senses the rapid motility of swarmer bacteria to trigger antimicrobial drug release. <i>Nature Communications</i> , <b>2018</b> , 9, 4277	17.4	10
23	Hairpin Peptides: Heme Binding, Catalysis, and Structure in Detergent Micelles. <i>Angewandte Chemie</i> , <b>2013</b> , 125, 6558-6562	3.6	9
22	Conformational analyses of a partially-folded bioactive prodomain of human furin. <i>Biopolymers</i> , <b>2007</b> , 86, 329-44	2.2	9
21	Designed Heme-Cage $\beta$ Sheet Mini-proteins. <i>Angewandte Chemie</i> , <b>2017</b> , 129, 5998-6002	3.6	8
20	Enhanced Cholesterol-Dependent Hemifusion by Internal Fusion Peptide 1 of SARS Coronavirus-2 Compared to Its N-Terminal Counterpart. <i>Biochemistry</i> , <b>2021</b> , 60, 559-562	3.2	8
19	NMR characterization of the near native and unfolded states of the PTB domain of Dok1: alternate conformations and residual clusters. <i>PLoS ONE</i> , <b>2014</b> , 9, e90557	3.7	7
18	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> , <b>2008</b> , 47, 651-9	3.2	7
17	Expanding heme-protein folding space using designed multi-heme $\beta$ sheet mini-proteins. <i>Communications Chemistry</i> , <b>2018</b> , 1,	6.3	7
16	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> , <b>2012</b> , 1818, 1250-60	3.8	6
15	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> , <b>2018</b> , 3, 14650-14664	3.9	6
14	Interaction Analyses of 14-3-3 $\zeta$ Dok1, and Phosphorylated Integrin $\beta$ Cytoplasmic Tails Reveal a Bi-molecular Switch in Integrin Regulation. <i>Journal of Molecular Biology</i> , <b>2018</b> , 430, 4419-4430	6.5	6
13	NMR Structure, Dynamics and Interactions of the Integrin $\beta$ Cytoplasmic Tail with Filamin Domain IgFLNa21. <i>Scientific Reports</i> , <b>2018</b> , 8, 5490	4.9	5
12	Folded conformations of antigenic peptides from riboflavin carrier protein in aqueous hexafluoroacetone. <i>Protein Science</i> , <b>1998</b> , 7, 123-31	6.3	5
11	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> , <b>2006</b> , 347, 1145-50	3.4	5
10	Sequence-specific $^1\text{H}$ , $^{15}\text{N}$ and $^{13}\text{C}$ resonance assignments of the inhibitory prodomain of human furin. <i>Journal of Biomolecular NMR</i> , <b>2000</b> , 16, 275-6	3	4
9	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> , <b>2020</b> , 1862, 183432	3.8	4
8	Functional and structural characterization of the talin F0F1 domain. <i>Biochemical and Biophysical Research Communications</i> , <b>2010</b> , 391, 159-65	3.4	3

7	-Designed Sheet Heme Proteins. <i>Biochemistry</i> , <b>2021</b> , 60, 431-439	3.2	3
6	Characterization of the near native conformational states of the SAM domain of Ste11 protein by NMR spectroscopy. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2014</b> , 82, 2957-69	4.2	1
5	<i>Pseudomonas aeruginosa</i> Psl Exopolysaccharide Interacts with the Antimicrobial Peptide LG21. <i>Water (Switzerland)</i> , <b>2017</b> , 9, 681	3	1
4	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> , <b>2021</b> , 1864, 183839	3.8	1
3	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> , <b>2020</b> , 59, 2849-2858	3.2	0
2	Binary and ternary complexes of FLNa-Ig21 with cytosolic tails of $\alpha 5 \beta 1$ integrin reveal dual role of filamin mediated regulation. <i>Biochimica Et Biophysica Acta - General Subjects</i> , <b>2021</b> , 1865, 130005	4	0
1	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> , <b>2022</b> , 1	2.3	0