

# Surajit Bhattacharjya

## List of Publications by Year in descending order

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79  
papers

2,770  
citations

159585

30  
h-index

206112

48  
g-index

82  
all docs

82  
docs citations

82  
times ranked

2951  
citing authors

#	ARTICLE	IF	CITATIONS
1	Linking dual mode of action of host defense antimicrobial peptide thanatin: Structures, lipopolysaccharide and LptAm binding of designed analogs. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2022, 1864, 183839.	2.6	10
2	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, 255, 151-160.	2.1	3
3	Atomic-Resolution Structures and Mode of Action of Clinically Relevant Antimicrobial Peptides. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4558.	4.1	11
4	Thanatin: An Emerging Host Defense Antimicrobial Peptide with Multiple Modes of Action. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1522.	4.1	48
5	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.	2.5	20
6	Binary and ternary complexes of FLNa-Ig21 with cytosolic tails of $\beta_2$ integrin reveal dual role of filamin mediated regulation. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2021, 1865, 130005.	2.4	2
7	<i>De Novo</i> -Designed $\beta$ -Sheet Heme Proteins. <i>Biochemistry</i> , 2021, 60, 431-439.	2.5	12
8	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.	2.5	3
9	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.	2.8	35
10	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.	2.6	13
11	Design, Engineering and Discovery of Novel $\alpha$ -Helical and $\beta$ -Boomerang Antimicrobial Peptides against Drug Resistant Bacteria. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5773.	4.1	47
12	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.	2.6	101
13	NMR Structure, Dynamics and Interactions of the Integrin $\beta_2$ Cytoplasmic Tail with Filamin Domain IgFLNa21. <i>Scientific Reports</i> , 2018, 8, 5490.	3.3	6
14	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.	2.6	19
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> , 2018, 3, 14650-14664.	3.5	10
16	Expanding heme-protein folding space using designed multi-heme $\beta$ -sheet mini-proteins. <i>Communications Chemistry</i> , 2018, 1, .	4.5	12
17	Interaction Analyses of 14-3-3 $\zeta$ , Dok1, and Phosphorylated Integrin $\beta_2$ Cytoplasmic Tails Reveal a Bi-molecular Switch in Integrin Regulation. <i>Journal of Molecular Biology</i> , 2018, 430, 4419-4430.	4.2	9
18	Lipopolysaccharide-affinity copolymer senses the rapid motility of swarmer bacteria to trigger antimicrobial drug release. <i>Nature Communications</i> , 2018, 9, 4277.	12.8	17

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19	Designed Heme-β-Sheet Miniproteins. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 5904-5908.	13.8	23
20	Designed Heme-β-Sheet Miniproteins. <i>Angewandte Chemie</i> , 2017, 129, 5998-6002.	2.0	9
21	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.	3.3	21
22	Structure and Interactions of Host Defense Antimicrobial Peptide Thanatin in Lipopolysaccharide Micelles Reveal Mechanism of Bacterial Cell Agglutination. <i>Scientific Reports</i> , 2017, 7, 17795.	3.3	81
23	<i>Pseudomonas aeruginosa</i> Psl Exopolysaccharide Interacts with the Antimicrobial Peptide LG21. <i>Water (Switzerland)</i> , 2017, 9, 681.	2.7	4
24	Salt-resistant short antimicrobial peptides. <i>Biopolymers</i> , 2016, 106, 345-356.	2.4	33
25	β-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> , 2016, 1860, 1362-1372.	2.4	20
26	Designed multi-stranded heme binding β-sheet peptides in membrane. <i>Chemical Science</i> , 2016, 7, 2563-2571.	7.4	21
27	Interaction Analyses of the Integrin β2 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> , 2016, 428, 4129-4142.	4.2	15
28	An Alternative Phosphorylation Switch in Integrin $\beta$ 2 (CD18) Tail for Dok1 Binding. <i>Scientific Reports</i> , 2015, 5, 11630.	3.3	15
29	NMR Structures and Interactions of Antimicrobial Peptides with Lipopolysaccharide: Connecting Structures to Functions. <i>Current Topics in Medicinal Chemistry</i> , 2015, 16, 4-15.	2.1	30
30	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, 721-730.	2.6	36
31	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.	2.5	7
32	β-Boomerang Antimicrobial and Antiendotoxic Peptides: Lipidation and Disulfide Bond Effects on Activity and Structure. <i>Pharmaceuticals</i> , 2014, 7, 482-501.	3.8	20
33	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.	3.3	84
34	Resurrecting Inactive Antimicrobial Peptides from the Lipopolysaccharide Trap. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 1987-1996.	3.2	71
35	Peptide- $\beta$ -perylene diimide functionalized magnetic nano-platforms for fluorescence turn-on detection and clearance of bacterial lipopolysaccharides. <i>Chemical Communications</i> , 2014, 50, 6200-6203.	4.1	52
36	Cysteine deleted protegrin-1 (CDP-1): Anti-bacterial activity, outer-membrane disruption and selectivity. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2014, 1840, 3006-3016.	2.4	27

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37	Designed Diâ€Heme Binding Helical Transmembrane Protein. <i>ChemBioChem</i> , 2014, 15, 1257-1262.	2.6	17
38	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, 2957-2969.	2.6	1
39	Î²â€Hairpin Peptides: Heme Binding, Catalysis, and Structure in Detergent Micelles. <i>Angewandte Chemie</i> , 2013, 125, 6558-6562.	2.0	12
40	Î²â€Hairpin Peptides: Heme Binding, Catalysis, and Structure in Detergent Micelles. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 6430-6434.	13.8	30
41	NMR Structure of Temporin-1 Ta in Lipopolysaccharide Micelles: Mechanistic Insight into Inactivation by Outer Membrane. <i>PLoS ONE</i> , 2013, 8, e72718.	2.5	31
42	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, 1250-1260.	2.6	8
43	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, 1613-1624.	2.6	53
44	Structure and Binding Interface of the Cytosolic Tails of Î±XÎ²2 Integrin. <i>PLoS ONE</i> , 2012, 7, e41924.	2.5	12
45	Applications of saturation transfer difference NMR in biological systems. <i>Drug Discovery Today</i> , 2012, 17, 505-513.	6.4	126
46	Oligomeric structure of a cathelicidin antimicrobial peptide in dodecylphosphocholine micelle determined by NMR spectroscopy. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2011, 1808, 369-381.	2.6	38
47	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, 273-287.	2.4	29
48	Structures and Interaction Analyses of Integrin Î±MÎ²2 Cytoplasmic Tails*. <i>Journal of Biological Chemistry</i> , 2011, 286, 43842-43854.	3.4	18
49	NMR Structures and Interactions of Temporin-1Tl and Temporin-1Tb with Lipopolysaccharide Micelles. <i>Journal of Biological Chemistry</i> , 2011, 286, 24394-24406.	3.4	84
50	NMR Structure of Pardaxin, a Pore-forming Antimicrobial Peptide, in Lipopolysaccharide Micelles. <i>Journal of Biological Chemistry</i> , 2010, 285, 3883-3895.	3.4	123
51	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, 18417-18428.	13.7	104
52	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, 128-139.	2.6	31
53	Functional and structural characterization of the talin FOF1 domain. <i>Biochemical and Biophysical Research Communications</i> , 2010, 391, 159-165.	2.1	3
54	Designed Î²-Boomerang Antiendotoxic and Antimicrobial Peptides. <i>Journal of Biological Chemistry</i> , 2009, 284, 21991-22004.	3.4	94

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55	Helical Hairpin Structure of a Potent Antimicrobial Peptide MSI594 in Lipopolysaccharide Micelles by NMR Spectroscopy. <i>Chemistry - A European Journal</i> , 2009, 15, 2036-2040.	3.3	89
56	Lipopolysaccharide bound structures of the active fragments of fowlicidin1, a cathelicidin family of antimicrobial and antiendotoxic peptide from chicken, determined by transferred nuclear overhauser effect spectroscopy. <i>Biopolymers</i> , 2009, 92, 9-22.	2.4	56
57	NMR structural studies of the Ste11 SAM domain in the dodecyl phosphocholine micelle. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 328-343.	2.6	24
58	Multifunctional host defense peptides: functional and mechanistic insights from NMR structures of potent antimicrobial peptides. <i>FEBS Journal</i> , 2009, 276, 6465-6473.	4.7	88
59	Interactions of a designed peptide with lipopolysaccharide: Bound conformation and anti-endotoxic activity. <i>Biochemical and Biophysical Research Communications</i> , 2008, 369, 853-857.	2.1	22
60	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, 651-659.	2.5	8
61	Structural and thermodynamic analyses of the interaction between melittin and lipopolysaccharide. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2007, 1768, 3282-3291.	2.6	58
62	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, 5864-5874.	2.5	49
63	Conformational analyses of a partially-folded bioactive prodomain of human furin. <i>Biopolymers</i> , 2007, 86, 329-344.	2.4	10
64	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, 1145-1150.	2.1	6
65	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, 828-835.	7.6	22
66	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, 1071-1087.	4.2	36
67	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, 934-942.	7.6	26
68	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> , 2000, 16, 275-276.	2.8	4
69	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, 2868-2877.	2.5	27
70	Solid state and solution conformations of a helical peptide with a central gly-gly segment. , 1998, 38, 515-526.		26
71	Folded conformations of antigenic peptides from riboflavin carrier protein in aqueous hexafluoroacetone. <i>Protein Science</i> , 1998, 7, 123-131.	7.6	6
72	$^1\text{H}$ -Amino Acids in Peptide Design. Crystal Structures and Solution Conformations of Peptide Helices Containing a $\beta$ -Alanyl- $\beta$ -Aminobutyryl Segment. <i>Journal of the American Chemical Society</i> , 1997, 119, 9087-9095.	13.7	120

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73	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, 1065-1073.	7.6	36
74	Effects of organic solvents on protein structures: Observation of a structured helical core in hen egg-white lysozyme in aqueous dimethylsulfoxide. , 1997, 29, 492-507.		100
75	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.	2.4	63
76	Hexafluoroacetone trihydrate as a structure stabilizer for peptides. , 1997, 42, 125-128.		63
77	Omega amino acids in peptide design: incorporation into helices. <i>Biopolymers</i> , 1996, 39, 769-777.	2.4	40
78	Solid state and solution conformations of a helical peptide with a central gly-gly segment. <i>Biopolymers</i> , 1996, 38, 515-526.	2.4	17
79	Omega amino acids in peptide design: incorporation into helices. <i>Biopolymers</i> , 1996, 39, 769-777.	2.4	13