

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	Applications of saturation transfer difference NMR in biological systems. Drug Discovery Today, 2012, 17, 505-513.	6.4	126
2	NMR Structure of Pardaxin, a Pore-forming Antimicrobial Peptide, in Lipopolysaccharide Micelles. Journal of Biological Chemistry, 2010, 285, 3883-3895.	3.4	123
3	β -Amino Acids in Peptide Design. Crystal Structures and Solution Conformations of Peptide Helices Containing a β -Alanyl- β -Aminobutyryl Segment. Journal of the American Chemical Society, 1997, 119, 9087-9095.	13.7	120
4	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. Journal of the American Chemical Society, 2010, 132, 18417-18428.	13.7	104
5	Membrane Cholesterol Modulates Oligomeric Status and Peptide-Membrane Interaction of Severe Acute Respiratory Syndrome Coronavirus Fusion Peptide. Journal of Physical Chemistry B, 2019, 123, 10654-10662.	2.6	101
6	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
7	Designed β -Boomerang Antitendotoxic and Antimicrobial Peptides. Journal of Biological Chemistry, 2009, 284, 21991-22004.	3.4	94
8	Helical Hairpin Structure of a Potent Antimicrobial Peptide MSI-594 in Lipopolysaccharide Micelles by NMR Spectroscopy. Chemistry - A European Journal, 2009, 15, 2036-2040.	3.3	89
9	Multifunctional host defense peptides: functional and mechanistic insights from NMR structures of potent antimicrobial peptides. FEBS Journal, 2009, 276, 6465-6473.	4.7	88
10	NMR Structures and Interactions of Temporin-1Tl and Temporin-1Tb with Lipopolysaccharide Micelles. Journal of Biological Chemistry, 2011, 286, 24394-24406.	3.4	84
11	Design of short membrane selective antimicrobial peptides containing tryptophan and arginine residues for improved activity, salt resistance, and biocompatibility. Biotechnology and Bioengineering, 2014, 111, 37-49.	3.3	84
12	Structure and Interactions of Host Defense Antimicrobial Peptide Thanatin in Lipopolysaccharide Micelles Reveal Mechanism of Bacterial Cell Agglutination. Scientific Reports, 2017, 7, 17795.	3.3	81
13	Resurrecting Inactive Antimicrobial Peptides from the Lipopolysaccharide Trap. Antimicrobial Agents and Chemotherapy, 2014, 58, 1987-1996.	3.2	71
14	Polymyxin B nonapeptide: Conformations in water and in the lipopolysaccharide-bound state determined by two-dimensional NMR and molecular dynamics. Biopolymers, 1997, 41, 251-265.	2.4	63
15	α -Teflon-coated peptides: Hexafluoroacetone trihydrate as a structure stabilizer for peptides. , 1997, 42, 125-128.		63
16	Structural and thermodynamic analyses of the interaction between melittin and lipopolysaccharide. Biochimica Et Biophysica Acta - Biomembranes, 2007, 1768, 3282-3291.	2.6	58
17	Lipopolysaccharide bound structures of the active fragments of fowlicidin-1, a cathelicidin family of antimicrobial and antitendotoxic peptide from chicken, determined by transferred nuclear overhauser effect spectroscopy. Biopolymers, 2009, 92, 9-22.	2.4	56
18	Structure, activity and interactions of the cysteine deleted analog of tachyplesin-1 with lipopolysaccharide micelle: Mechanistic insights into outer-membrane permeabilization and endotoxin neutralization. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 1613-1624.	2.6	53

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19	Peptideâ€“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
20	High-Resolution Solution Structure of a Designed Peptide Bound to Lipopolysaccharide:â€“ Transferred Nuclear Overhauser Effects, Micelle Selectivity, and Anti-Endotoxic Activity,. <i>Biochemistry</i> , 2007, 46, 5864-5874.	2.5	49
21	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
22	Design, Engineering and Discovery of Novel Î±-Helical and Î²-Boomerang Antimicrobial Peptides against Drug Resistant Bacteria. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5773.	4.1	47
23	Omega amino acids in peptide design: incorporation into helices. <i>Biopolymers</i> , 1996, 39, 769-777.	2.4	40
24	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
25	Hexafluoroacetone hydrate as a structure modifier in proteins: Characterization of a molten globule state of hen eggâ€“white lysozyme. <i>Protein Science</i> , 1997, 6, 1065-1073.	7.6	36
26	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 Ste50â€“Ste11 Complex. <i>Journal of Molecular Biology</i> , 2004, 344, 1071-1087.	4.2	36
27	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
28	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
29	Saltâ€“resistant short antimicrobial peptides. <i>Biopolymers</i> , 2016, 106, 345-356.	2.4	33
30	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
31	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
32	Î²â€“Hairpin Peptides: Heme Binding, Catalysis, and Structure in Detergent Micelles. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 6430-6434.	13.8	30
33	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
34	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
35	Inhibitory Activity and Structural Characterization of a C-Terminal Peptide Fragment Derived from the Prosegment of the Proprotein Convertase PC7â€“. <i>Biochemistry</i> , 2000, 39, 2868-2877.	2.5	27
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	Solid state and solution conformations of a helical peptide with a central gly-gly segment. , 1998, 38, 515-526.		26
38	pH-induced conformational transitions of a molten-globule-like state of the inhibitory prodomain of furin: Implications for zymogen activation. Protein Science, 2001, 10, 934-942.	7.6	26
39	NMR structural studies of the Ste11 SAM domain in the dodecyl phosphocholine micelle. Proteins: Structure, Function and Bioinformatics, 2009, 74, 328-343.	2.6	24
40	Designed Heme-Cage β -Sheet Miniproteins. Angewandte Chemie - International Edition, 2017, 56, 5904-5908.	13.8	23
41	Polymerization of the SAM domain of MAPKKK Ste11 from the budding yeast: Implications for efficient signaling through the MAPK cascades. Protein Science, 2005, 14, 828-835.	7.6	22
42	Interactions of a designed peptide with lipopolysaccharide: Bound conformation and anti-endotoxic activity. Biochemical and Biophysical Research Communications, 2008, 369, 853-857.	2.1	22
43	Designed multi-stranded heme binding β -sheet peptides in membrane. Chemical Science, 2016, 7, 2563-2571.	7.4	21
44	Piscidin-1-analogs with double L- and D-lysine residues exhibited different conformations in lipopolysaccharide but comparable anti-endotoxin activities. Scientific Reports, 2017, 7, 39925.	3.3	21
45	β -Boomerang Antimicrobial and Antiendotoxic Peptides: Lipidation and Disulfide Bond Effects on Activity and Structure. Pharmaceuticals, 2014, 7, 482-501.	3.8	20
46	α -Lollipop TM -shaped helical structure of a hybrid antimicrobial peptide of temporin B-lipopolysaccharide binding motif and mapping cationic residues in antibacterial activity. Biochimica Et Biophysica Acta - General Subjects, 2016, 1860, 1362-1372.	2.4	20
47	Enhanced Cholesterol-Dependent Hemifusion by Internal Fusion Peptide 1 of SARS Coronavirus-2 Compared to Its N-Terminal Counterpart. Biochemistry, 2021, 60, 559-562.	2.5	20
48	NMR structure and localization of a large fragment of the SARS-CoV fusion protein: Implications in viral cell fusion. Biochimica Et Biophysica Acta - Biomembranes, 2018, 1860, 407-415.	2.6	19
49	Structures and Interaction Analyses of Integrin β 2 Cytoplasmic Tails*. Journal of Biological Chemistry, 2011, 286, 43842-43854.	3.4	18
50	Designed Di-Heme Binding Helical Transmembrane Protein. ChemBioChem, 2014, 15, 1257-1262.	2.6	17
51	Lipopolysaccharide-affinity copolymer senses the rapid motility of swarmer bacteria to trigger antimicrobial drug release. Nature Communications, 2018, 9, 4277.	12.8	17
52	Solid state and solution conformations of a helical peptide with a central gly-gly segment. Biopolymers, 1996, 38, 515-526.	2.4	17
53	An Alternative Phosphorylation Switch in Integrin β 2 (CD18) Tail for Dok1 Binding. Scientific Reports, 2015, 5, 11630.	3.3	15
54	Interaction Analyses of the Integrin β 2 Cytoplasmic Tail with the F3 FERM Domain of Talin and 14-3-3 η Reveal a Ternary Complex with Phosphorylated Tail. Journal of Molecular Biology, 2016, 428, 4129-4142.	4.2	15

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55	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
56	Omega amino acids in peptide design: incorporation into helices. <i>Biopolymers</i> , 1996, 39, 769-777.	2.4	13
57	Structure and Binding Interface of the Cytosolic Tails of β 2 Integrin. <i>PLoS ONE</i> , 2012, 7, e41924.	2.5	12
58	β -Hairpin Peptides: Heme Binding, Catalysis, and Structure in Detergent Micelles. <i>Angewandte Chemie</i> , 2013, 125, 6558-6562.	2.0	12
59	Expanding heme-protein folding space using designed multi-heme β -sheet mini-proteins. <i>Communications Chemistry</i> , 2018, 1, .	4.5	12
60	<i>De Novo</i>-Designed β -Sheet Heme Proteins. <i>Biochemistry</i> , 2021, 60, 431-439.	2.5	12
61	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
62	Conformational analyses of a partially-folded bioactive prodomain of human furin. <i>Biopolymers</i> , 2007, 86, 329-344.	2.4	10
63	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
64	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
65	Designed Heme-Cage β -Sheet Miniproteins. <i>Angewandte Chemie</i> , 2017, 129, 5998-6002.	2.0	9
66	Interaction Analyses of 14-3-3 η , Dok1, and Phosphorylated Integrin β 2 Cytoplasmic Tails Reveal a Bi-molecular Switch in Integrin Regulation. <i>Journal of Molecular Biology</i> , 2018, 430, 4419-4430.	4.2	9
67	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
68	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
69	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
70	Folded conformations of antigenic peptides from riboflavin carrier protein in aqueous hexafluoroacetone. <i>Protein Science</i> , 1998, 7, 123-131.	7.6	6
71	An NMR-based identification of a peptide fragment from the β 2-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
72	NMR Structure, Dynamics and Interactions of the Integrin β 2 Cytoplasmic Tail with Filamin Domain IgFLNa21. <i>Scientific Reports</i> , 2018, 8, 5490.	3.3	6

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73	Sequence-specific ¹ H, ¹⁵ N and ¹³ C resonance assignments of the inhibitory prodomain of human furin. Journal of Biomolecular NMR, 2000, 16, 275-276.	2.8	4
74	Pseudomonas aeruginosa Psl Exopolysaccharide Interacts with the Antimicrobial Peptide LG21. Water (Switzerland), 2017, 9, 681.	2.7	4
75	Functional and structural characterization of the talin FOF1 domain. Biochemical and Biophysical Research Communications, 2010, 391, 159-165.	2.1	3
76	Salt Dependence Conformational Stability of the Dimeric SAM Domain of MAPKKK Ste11 from Budding Yeast: A Native-State H/D Exchange NMR Study. Biochemistry, 2020, 59, 2849-2858.	2.5	3
77	NMR Structure and Localization of the Host Defense Peptide ThanatinM21F in Zwitterionic Dodecylphosphocholine Micelle: Implications in Antimicrobial and Hemolytic Activity. Journal of Membrane Biology, 2022, 255, 151-160.	2.1	3
78	Binary and ternary complexes of FLNa-Ig21 with cytosolic tails of Î±MÃ2 integrin reveal dual role of filamin mediated regulation. Biochimica Et Biophysica Acta - General Subjects, 2021, 1865, 130005.	2.4	2
79	Characterization of the near native conformational states of the SAM domain of Ste11 protein by NMR spectroscopy. Proteins: Structure, Function and Bioinformatics, 2014, 82, 2957-2969.	2.6	1