

Vikas Nanda

List of Publications by Year in descending order

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98
papers

3,777
citations

159585

30
h-index

138484

58
g-index

103
all docs

103
docs citations

103
times ranked

4472
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural basis for the function and inhibition of an influenza virus proton channel. <i>Nature</i> , 2008, 451, 596-599.	27.8	549
2	Designing artificial enzymes by intuition and computation. <i>Nature Chemistry</i> , 2010, 2, 15-24.	13.6	232
3	Computational De Novo Design and Characterization of a Four-Helix Bundle Protein that Selectively Binds a Nonbiological Cofactor. <i>Journal of the American Chemical Society</i> , 2005, 127, 1346-1347.	13.7	167
4	Ez, a Depth-dependent Potential for Assessing the Energies of Insertion of Amino Acid Side-chains into Membranes: Derivation and Applications to Determining the Orientation of Transmembrane and Interfacial Helices. <i>Journal of Molecular Biology</i> , 2007, 366, 436-448.	4.2	143
5	Dimerization of the Transmembrane Domain of Integrin α IIb Subunit in Cell Membranes. <i>Journal of Biological Chemistry</i> , 2004, 279, 26666-26673.	3.4	137
6	De Novo Design of a Redox-Active Minimal Rubredoxin Mimic. <i>Journal of the American Chemical Society</i> , 2005, 127, 5804-5805.	13.7	126
7	A push-pull mechanism for regulating integrin function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 1424-1429.	7.1	118
8	Aromatic Interactions Promote Self-Association of Collagen Triple-Helical Peptides to Higher-Order Structures. <i>Biochemistry</i> , 2009, 48, 7959-7968.	2.5	102
9	A New Method for Determining the Local Environment and Orientation of Individual Side Chains of Membrane-Binding Peptides. <i>Journal of the American Chemical Society</i> , 2004, 126, 5078-5079.	13.7	101
10	The conformation of the pore region of the M2 proton channel depends on lipid bilayer environment. <i>Protein Science</i> , 2005, 14, 856-861.	7.6	91
11	Empirical lipid propensities of amino acid residues in multispan alpha helical membrane proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 59, 496-509.	2.6	85
12	Using α -Helical Coiled-Coils to Design Nanostructured Metalloporphyrin Arrays. <i>Journal of the American Chemical Society</i> , 2008, 130, 11921-11927.	13.7	63
13	De novo design of a non-natural fold for an iron-sulfur protein: Alpha-helical coiled-coil with a four-iron four-sulfur cluster binding site in its central core. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2010, 1797, 406-413.	1.0	60
14	Sequence Determinants of a Transmembrane Proton Channel: An Inverse Relationship between Stability and Function. <i>Journal of Molecular Biology</i> , 2005, 347, 169-179.	4.2	59
15	Self-Assembly of Left- and Right-Handed Molecular Screws. <i>Journal of the American Chemical Society</i> , 2013, 135, 18762-18765.	13.7	55
16	Potential Pitfalls and Solutions for Use of Fluorescent Fusion Proteins to Study the Lysosome. <i>PLoS ONE</i> , 2014, 9, e88893.	2.5	55
17	Circular Dichroism Spectroscopy of Collagen Fibrillogenesis: A New Use for an Old Technique. <i>Biophysical Journal</i> , 2016, 111, 2377-2386.	0.5	55
18	Aromatic interactions in homeodomains contribute to the low quantum yield of a conserved, buried tryptophan. , 2000, 40, 112-125.		54

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19	Computational Design of a Collagen A:B:C-Type Heterotrimer. <i>Journal of the American Chemical Society</i> , 2011, 133, 15260-15263.	13.7	52
20	Methacrylation Induces Rapid, Temperature-Dependent, Reversible Self-Assembly of Type-I Collagen. <i>Langmuir</i> , 2014, 30, 11204-11211.	3.5	51
21	Compositional Control of Higher Order Assembly Using Synthetic Collagen Peptides. <i>Journal of the American Chemical Society</i> , 2012, 134, 47-50.	13.7	50
22	Anoxic photochemical oxidation of siderite generates molecular hydrogen and iron oxides. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 10073-10077.	7.1	43
23	PET-RAFT and SAXS: High Throughput Tools To Study Compactness and Flexibility of Single-Chain Polymer Nanoparticles. <i>Macromolecules</i> , 2019, 52, 8295-8304.	4.8	43
24	Minimal Heterochiral <i>de Novo</i> Designed 4Fe-4S Binding Peptide Capable of Robust Electron Transfer. <i>Journal of the American Chemical Society</i> , 2018, 140, 11210-11213.	13.7	42
25	De novo design of symmetric ferredoxins that shuttle electrons in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 14557-14562.	7.1	41
26	Association of a Model Transmembrane Peptide Containing Gly in a Heptad Sequence Motif. <i>Biophysical Journal</i> , 2004, 87, 3421-3429.	0.5	39
27	Anoxic photogeochemical oxidation of manganese carbonate yields manganese oxide. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 22698-22704.	7.1	39
28	Computational Design of Thermostabilizing α -Amino Acid Substitutions. <i>Journal of the American Chemical Society</i> , 2011, 133, 18750-18759.	13.7	38
29	A knowledge-based potential highlights unique features of membrane α -helical and β -barrel protein insertion and folding. <i>Protein Science</i> , 2012, 21, 50-62.	7.6	36
30	Morphological Diversity and Polymorphism of Self-Assembling Collagen Peptides Controlled by Length of Hydrophobic Domains. <i>ACS Nano</i> , 2014, 8, 12514-12523.	14.6	35
31	<i>De Novo</i> Self-Assembling Collagen Heterotrimers Using Explicit Positive and Negative Design. <i>Biochemistry</i> , 2010, 49, 2307-2316.	2.5	34
32	Small protein folds at the root of an ancient metabolic network. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 7193-7199.	7.1	32
33	Polar Networks Control Oligomeric Assembly in Membranes. <i>Journal of the American Chemical Society</i> , 2006, 128, 4170-4171.	13.7	31
34	How electrostatic networks modulate specificity and stability of collagen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 6207-6212.	7.1	31
35	Empirical and computational design of iron-sulfur cluster proteins. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2012, 1817, 1256-1262.	1.0	30
36	Computational redesign of the lipid-facing surface of the outer membrane protein OmpA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 9632-9637.	7.1	30

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37	Dissecting Electrostatic Contributions to Folding and Self-Assembly Using Designed Multicomponent Peptide Systems. <i>Journal of the American Chemical Society</i> , 2016, 138, 4362-4367.	13.7	30
38	Structural and Dynamic Properties of Allergen and Non-Allergen Forms of Tropomyosin. <i>Structure</i> , 2018, 26, 997-1006.e5.	3.3	30
39	Simulated Evolution of Emergent Chiral Structures in Polyalanine. <i>Journal of the American Chemical Society</i> , 2004, 126, 14459-14467.	13.7	29
40	Energetic Selection of Topology in Ferredoxins. <i>PLoS Computational Biology</i> , 2012, 8, e1002463.	3.2	29
41	The orphan GPCR, Gpr161, regulates the retinoic acid and canonical Wnt pathways during neurulation. <i>Developmental Biology</i> , 2015, 402, 17-31.	2.0	29
42	Modular origins of biological electron transfer chains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1280-1285.	7.1	29
43	Melittin as model system for probing interactions between proteins and cyclodextrins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 275-287.	2.6	28
44	Computational Design of Heterochiral Peptides against a Helical Target. <i>Journal of the American Chemical Society</i> , 2006, 128, 809-816.	13.7	28
45	Are aromatic carbon donor hydrogen bonds linear in proteins?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 489-497.	2.6	28
46	Structural principles for computational and de novo design of 4Fe-4S metalloproteins. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2016, 1857, 531-538.	1.0	28
47	The role of protein homochirality in shaping the energy landscape of folding. <i>Protein Science</i> , 2007, 16, 1667-1675.	7.6	26
48	Quantifying structural relationships of metal-binding sites suggests origins of biological electron transfer. <i>Science Advances</i> , 2022, 8, eabj3984.	10.3	24
49	Empirical estimation of local dielectric constants: Toward atomistic design of collagen mimetic peptides. <i>Biopolymers</i> , 2015, 104, 360-370.	2.4	23
50	Self-assembled elastin-like polypeptide fusion protein coacervates as competitive inhibitors of advanced glycation end-products enhance diabetic wound healing. <i>Journal of Controlled Release</i> , 2021, 333, 176-187.	9.9	23
51	Synergistic Interactions between Aqueous and Membrane Domains of a Designed Protein Determine its Fold and Stability. <i>Journal of Molecular Biology</i> , 2005, 348, 1225-1233.	4.2	20
52	Do-it-yourself enzymes. <i>Nature Chemical Biology</i> , 2008, 4, 273-275.	8.0	20
53	The effects of protein crowding in bacterial photosynthetic membranes on the flow of quinone redox species between the photochemical reaction center and the ubiquinol-cytochrome c2 oxidoreductase. <i>Metalomics</i> , 2011, 3, 765.	2.4	20
54	Design principles for chlorophyll-binding sites in helical proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 463-476.	2.6	20

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55	Metal-activated histidine carbon donor hydrogen bonds contribute to metalloprotein folding and function. <i>Journal of Inorganic Biochemistry</i> , 2009, 103, 1054-1060.	3.5	18
56	Metal Stabilization of Collagen and de Novo Designed Mimetic Peptides. <i>Biochemistry</i> , 2015, 54, 4987-4997.	2.5	18
57	Design Strategies to Tune the Structural and Mechanical Properties of Synthetic Collagen Hydrogels. <i>Biomacromolecules</i> , 2021, 22, 3440-3450.	5.4	16
58	Mirrors in the PDB: left-handed β -turns guide design with D-amino acids. <i>BMC Structural Biology</i> , 2009, 9, 61.	2.3	14
59	Using D-amino acids to delineate the mechanism of protein folding: Application to Trp-cage. <i>Chemical Physics</i> , 2013, 422, 131-134.	1.9	14
60	Function-based assessment of structural similarity measurements using metal cofactor orientation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 648-656.	2.6	14
61	Biophysical analysis of the structural evolution of substrate specificity in RuBisCO. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 30451-30457.	7.1	14
62	Hydrophobic Clustering in Acid-Denatured IL-2 and Fluorescence of a Trp NH \cdots H-bond. <i>Biochemical and Biophysical Research Communications</i> , 2000, 279, 770-778.	2.1	13
63	Designing phenylalanine-based hybrid biological materials: controlling morphology via molecular composition. <i>Organic and Biomolecular Chemistry</i> , 2018, 16, 2499-2507.	2.8	13
64	Zeta Potential Prediction from Protein Structure in General Aqueous Electrolyte Solutions. <i>Langmuir</i> , 2020, 36, 13799-13803.	3.5	13
65	Marginal protein stability drives subcellular proteome isoelectric point. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 11778-11783.	7.1	12
66	Biallelic hypomorphic variants in ALDH1A2 cause a novel lethal human multiple congenital anomaly syndrome encompassing diaphragmatic, pulmonary, and cardiovascular defects. <i>Human Mutation</i> , 2021, 42, 506-519.	2.5	12
67	Circular Permutation Directs Orthogonal Assembly in Complex Collagen Peptide Mixtures. <i>Journal of Biological Chemistry</i> , 2013, 288, 31616-31623.	3.4	11
68	Rotational orientation of monomers within a designed homo-oligomer transmembrane helical bundle. <i>Protein Science</i> , 2005, 14, 1019-1024.	7.6	10
69	Sequence recombination improves target specificity in a redesigned collagen peptide α -type heterotrimer. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 386-393.	2.6	10
70	Design of net-charged α -type collagen heterotrimers. <i>Journal of Structural Biology</i> , 2014, 185, 163-167.	2.8	10
71	Hydrodynamic radius coincides with the slip plane position in the electrokinetic behavior of lysozyme. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 515-523.	2.6	10
72	Hetero-assembly of a dual β -amyloid variant peptide system. <i>Chemical Communications</i> , 2018, 54, 6380-6383.	4.1	10

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73	In Vivo Biogenesis of a De Novo Designed Iron-Sulfur Protein. ACS Synthetic Biology, 2020, 9, 3400-3407.	3.8	10
74	Automated use of mutagenesis data in structure prediction. Proteins: Structure, Function and Bioinformatics, 2005, 59, 454-466.	2.6	9
75	Protein tolerance to random circular permutation correlates with thermostability and local energetics of residue-residue contacts. Protein Engineering, Design and Selection, 2019, 32, 489-501.	2.1	9
76	Computational Design of Intermolecular Stability and Specificity in Protein Self-assembly. Methods in Enzymology, 2011, 487, 575-593.	1.0	8
77	Collagen mimetic peptide discs promote assembly of a broad range of natural protein fibers through hydrophobic interactions. Organic and Biomolecular Chemistry, 2017, 15, 5893-5898.	2.8	8
78	Control of Collagen Stability and Heterotrimer Specificity through Repulsive Electrostatic Interactions. Biomolecules, 2013, 3, 986-996.	4.0	7
79	Molecular Self-Assembly Strategy for Generating Catalytic Hybrid Polypeptides. PLoS ONE, 2016, 11, e0153700.	2.5	7
80	Searching for the Pareto frontier in multi-objective protein design. Biophysical Reviews, 2017, 9, 339-344.	3.2	6
81	Comparative dynamics of tropomyosin in vertebrates and invertebrates. Proteins: Structure, Function and Bioinformatics, 2020, 88, 265-273.	2.6	6
82	Design of a Fe ₄ S ₄ cluster into the core of a <i>de novo</i> four-helix bundle. Biotechnology and Applied Biochemistry, 2020, 67, 574-585.	3.1	6
83	Prediction and Design of Outer Membrane Protein-Protein Interactions. Methods in Molecular Biology, 2013, 1063, 183-196.	0.9	5
84	Nanosecond dynamics of influenza A/M2TM and an amantadine resistant mutant probed by time-dependent red shifts of a native tryptophan. Chemical Physics, 2013, 422, 73-79.	1.9	5
85	Evaluating pH-Induced Gastrointestinal Aggregation of Arachis hypogaea 1 Fragments as Potential Components of Peanut Allergy. Journal of Agricultural and Food Chemistry, 2013, 61, 8430-8435.	5.2	5
86	Computational Design of Metalloproteins. Methods in Molecular Biology, 2014, 1216, 233-249.	0.9	4
87	Getting to the bottom of the TIM barrel. Nature Chemical Biology, 2016, 12, 2-3.	8.0	4
88	Parallels between DNA and collagen – comparing elastic models of the double and triple helix. Scientific Reports, 2017, 7, 12802.	3.3	4
89	Catalytic linkage between caspase activity and proteostasis in <i>Archaea</i> . Environmental Microbiology, 2019, 21, 286-298.	3.8	4
90	Building bigger beta-barrels. ELife, 2019, 8, .	6.0	4

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91	Computational Simulation of Adapter Length-Dependent LASSO Probe Capture Efficiency. <i>Biomolecules</i> , 2019, 9, 199.	4.0	3
92	Lysosomal protein thermal stability does not correlate with cellular half-life: global observations and a case study of tripeptidyl-peptidase 1. <i>Biochemical Journal</i> , 2020, 477, 727-745.	3.7	3
93	Congenital Cataract in Gpr161vl/vl Mice Is Modified by Proximal Chromosome 15. <i>PLoS ONE</i> , 2017, 12, e0170724.	2.5	2
94	Temperature Dependent Reversible Self Assembly of Methacrylated Collagen Gels. , 2013, , .		0
95	Heterogeneous Epitaxy: Designed Peptides Scale Graphene's Surface. <i>Biophysical Journal</i> , 2016, 110, 2291-2292.	0.5	0
96	Anaerobic Expression and Purification of Holo-CCIS, an Artificial Iron-sulfur Protein. <i>Bio-protocol</i> , 2021, 11, e4169.	0.4	0
97	A folding insulator defines cryptic domains in tropomyosin. <i>Journal of Molecular Biology</i> , 2021, 433, 167281.	4.2	0
98	Biophysical Characterization of Iron-Sulfur Proteins. <i>Bio-protocol</i> , 2021, 11, e4202.	0.4	0