

# Jeetain Mittal

## 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.

126  
papers

9,130  
citations

47  
h-index

94  
g-index

139  
ext. papers

11,610  
ext. citations

6.3  
avg, IF

6.74  
L-index

#	Paper	IF	Citations
126	The living interface between synthetic biology and biomaterial design.. <i>Nature Materials</i> , <b>2022</b> , 21, 390-397	3.7	4
125	Tyrosine phosphorylation regulates hnRNPA2 granule protein partitioning and reduces neurodegeneration. <i>EMBO Journal</i> , <b>2021</b> , 40, e105001	13	15
124	Molecular interactions contributing to FUS SYGQ LC-RGG phase separation and co-partitioning with RNA polymerase II heptads. <i>Nature Structural and Molecular Biology</i> , <b>2021</b> , 28, 923-935	17.6	6
123	Reversible Kinetic Trapping of FUS Biomolecular Condensates. <i>Advanced Science</i> , <b>2021</b> , e2104247	13.6	1
122	Biomolecular Condensates: Sequence Determinants of Phase Separation, Microstructural Organization, Enzymatic Activity, and Material Properties. <i>Journal of Physical Chemistry B</i> , <b>2021</b> , 125, 3441-3451	3.4	11
121	Physics-based computational and theoretical approaches to intrinsically disordered proteins. <i>Current Opinion in Structural Biology</i> , <b>2021</b> , 67, 219-225	8.1	32
120	A predictive coarse-grained model for position-specific effects of post-translational modifications. <i>Biophysical Journal</i> , <b>2021</b> , 120, 1187-1197	2.9	27
119	Temperature-Controlled Reconfigurable Nanoparticle Binary Superlattices. <i>ACS Nano</i> , <b>2021</b> , 15, 8466-8473	13.7	3
118	Improved coarse-grained model for studying sequence dependent phase separation of disordered proteins. <i>Protein Science</i> , <b>2021</b> , 30, 1371-1379	6.3	21
117	Deep learning for characterizing the self-assembly of three-dimensional colloidal systems. <i>Soft Matter</i> , <b>2021</b> , 17, 989-999	3.6	3
116	Alteration of Microstructure in Biopolymeric Hydrogels Compositional Modification of Resilin-Like Polypeptides. <i>ACS Biomaterials Science and Engineering</i> , <b>2021</b> , 7, 4244-4257	5.5	2
115	Using a sequence-specific coarse-grained model for studying protein liquid-liquid phase separation. <i>Methods in Enzymology</i> , <b>2021</b> , 646, 1-17	1.7	7
114	N-terminal acetylation modestly enhances phase separation and reduces aggregation of the low-complexity domain of RNA-binding protein fused in sarcoma. <i>Protein Science</i> , <b>2021</b> , 30, 1337-1349	6.3	11
113	Biophysical studies of phase separation integrating experimental and computational methods. <i>Current Opinion in Structural Biology</i> , <b>2021</b> , 70, 78-86	8.1	4
112	Amphiphilic proteins coassemble into multiphasic condensates and act as biomolecular surfactants.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2021</b> , 118,	11.5	4
111	Self-Assembly of DNA-Functionalized Nanoparticles Guided by Binding Kinetics. <i>Journal of Physical Chemistry B</i> , <b>2020</b> , 124, 11593-11599	3.4	1
110	Molecular Details of Protein Condensates Probed by Microsecond Long Atomistic Simulations. <i>Journal of Physical Chemistry B</i> , <b>2020</b> , 124, 11671-11679	3.4	32

109	Identifying sequence perturbations to an intrinsically disordered protein that determine its phase-separation behavior. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 11421-11431	11.5	81
108	Symmetry-Based Crystal Structure Enumeration in Two Dimensions. <i>Journal of Physical Chemistry A</i> , <b>2020</b> , 124, 3276-3285	2.8	3
107	TDP-43 Helical structure tunes liquid-liquid phase separation and function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 5883-5894	11.5	119
106	Computational Investigation of Correlations in Adsorbate Entropy for Pure-Silica Zeolite Adsorbents. <i>Journal of Physical Chemistry C</i> , <b>2020</b> , 124,	3.8	2
105	Grand canonical inverse design of multicomponent colloidal crystals. <i>Soft Matter</i> , <b>2020</b> , 16, 3187-3194	3.6	10
104	Effect of Phosphorylation and O-GlcNAcylation on Proline-Rich Domains of Tau. <i>Journal of Physical Chemistry B</i> , <b>2020</b> , 124, 1909-1918	3.4	9
103	Hydropathy Patterning Complements Charge Patterning to Describe Conformational Preferences of Disordered Proteins. <i>Journal of Physical Chemistry Letters</i> , <b>2020</b> , 11, 3408-3415	6.4	34
102	Refining All-Atom Protein Force Fields for Polar-Rich, Prion-like, Low-Complexity Intrinsically Disordered Proteins. <i>Journal of Physical Chemistry B</i> , <b>2020</b> , 124, 9505-9512	3.4	13
101	Sequence dependent phase separation of protein-polynucleotide mixtures elucidated using molecular simulations. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, 12593-12603	20.1	34
100	Living cells as test tubes. <i>Nature Chemical Biology</i> , <b>2020</b> , 16, 934-935	11.7	3
99	Biomolecular Phase Separation: From Molecular Driving Forces to Macroscopic Properties. <i>Annual Review of Physical Chemistry</i> , <b>2020</b> , 71, 53-75	15.7	116
98	Size-dependent thermodynamic structural selection in colloidal crystallization. <i>Science Advances</i> , <b>2019</b> , 5, eaaw5912	14.3	8
97	Modelling and simulation of DNA-mediated self-assembly for superlattice design. <i>Molecular Simulation</i> , <b>2019</b> , 45, 1203-1210	2	5
96	Temperature-Controlled Liquid-Liquid Phase Separation of Disordered Proteins. <i>ACS Central Science</i> , <b>2019</b> , 5, 821-830	16.8	108
95	Using symmetry to elucidate the importance of stoichiometry in colloidal crystal assembly. <i>Nature Communications</i> , <b>2019</b> , 10, 2028	17.4	11
94	Simulation methods for liquid-liquid phase separation of disordered proteins. <i>Current Opinion in Chemical Engineering</i> , <b>2019</b> , 23, 92-98	5.4	47
93	Evolution of All-Atom Protein Force Fields to Improve Local and Global Properties. <i>Journal of Physical Chemistry Letters</i> , <b>2019</b> , 10, 2227-2234	6.4	39
92	Designing Molecular Building Blocks for the Self-assembly of Complex Porous Networks. <i>Molecular Systems Design and Engineering</i> , <b>2019</b> , 4,	4.6	7

91	Extension of the Einstein molecule method for solid free energy calculation to non-periodic and semi-periodic systems. <i>Journal of Chemical Physics</i> , <b>2019</b> , 151, 054105	3.9	3
90	A hybrid, bottom-up, structurally accurate, Go $\square$ -like coarse-grained protein model. <i>Journal of Chemical Physics</i> , <b>2019</b> , 151, 044111	3.9	12
89	Molecular interactions underlying liquid-liquid phase separation of the FUS low-complexity domain. <i>Nature Structural and Molecular Biology</i> , <b>2019</b> , 26, 637-648	17.6	211
88	Inferring properties of disordered chains from FRET transfer efficiencies. <i>Journal of Chemical Physics</i> , <b>2018</b> , 148, 123329	3.9	63
87	Mechanistic View of hnRNPA2 Low-Complexity Domain Structure, Interactions, and Phase Separation Altered by Mutation and Arginine Methylation. <i>Molecular Cell</i> , <b>2018</b> , 69, 465-479.e7	17.6	215
86	Looking at the Disordered Proteins through the Computational Microscope. <i>ACS Central Science</i> , <b>2018</b> , 4, 534-542	16.8	27
85	Lysines in the RNA Polymerase II C-Terminal Domain Contribute to TAF15 Fibril Recruitment. <i>Biochemistry</i> , <b>2018</b> , 57, 2549-2563	3.2	20
84	Assembly of three-dimensional binary superlattices from multi-flavored particles. <i>Soft Matter</i> , <b>2018</b> , 14, 6303-6312	3.6	11
83	Computational modeling highlights the role of the disordered Formin Homology 1 domain in profilin-actin transfer. <i>FEBS Letters</i> , <b>2018</b> , 592, 1804-1816	3.8	10
82	Sequence determinants of protein phase behavior from a coarse-grained model. <i>PLoS Computational Biology</i> , <b>2018</b> , 14, e1005941	5	209
81	Binary Superlattice Design by Controlling DNA-Mediated Interactions. <i>Langmuir</i> , <b>2018</b> , 34, 991-998	4	18
80	An optical nanoreporter of endolysosomal lipid accumulation reveals enduring effects of diet on hepatic macrophages in vivo. <i>Science Translational Medicine</i> , <b>2018</b> , 10,	17.5	47
79	Relation between single-molecule properties and phase behavior of intrinsically disordered proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, 9929-9934 <sup>115</sup> <sup>149</sup>		
78	Electrostatic Screening Modulates Analyte Binding and Emission of Carbon Nanotubes. <i>Journal of Physical Chemistry C</i> , <b>2018</b> , 122, 10592-10599	3.8	9
77	A Carbon Nanotube Reporter of miRNA Hybridization Events In Vivo. <i>Nature Biomedical Engineering</i> , <b>2017</b> , 1,	19	111
76	Interplay Between Membrane Composition and Structural Stability of Membrane-Bound hIAPP. <i>Journal of Physical Chemistry B</i> , <b>2017</b> , 121, 8661-8668	3.4	18
75	A Carbon Nanotube Optical Reporter Maps Endolysosomal Lipid Flux. <i>ACS Nano</i> , <b>2017</b> , 11, 10689-10703	16.7	52
74	Phosphorylation of the FUS low-complexity domain disrupts phase separation, aggregation, and toxicity. <i>EMBO Journal</i> , <b>2017</b> , 36, 2951-2967	13	365

73	Assembly of multi-flavored two-dimensional colloidal crystals. <i>Soft Matter</i> , <b>2017</b> , 13, 5397-5408	3.6	14
72	ALS Mutations Disrupt Phase Separation Mediated by $\beta$ -Helical Structure in the TDP-43 Low-Complexity C-Terminal Domain. <i>Structure</i> , <b>2016</b> , 24, 1537-49	5.2	409
71	Diffusive Dynamics of Contact Formation in Disordered Polypeptides. <i>Physical Review Letters</i> , <b>2016</b> , 116, 068102	7.4	19
70	Protein Composition Determines the Effect of Crowding on the Properties of Disordered Proteins. <i>Biophysical Journal</i> , <b>2016</b> , 111, 28-37	2.9	38
69	Surface force measurements and simulations of mussel-derived peptide adhesives on wet organic surfaces. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 4332-7	11.5	65
68	Self-assembly of trimer colloids: effect of shape and interaction range. <i>Soft Matter</i> , <b>2016</b> , 12, 4170-9	3.6	18
67	Effect of Nonionic Surfactant on Association/Dissociation Transition of DNA-Functionalized Colloids. <i>Langmuir</i> , <b>2016</b> , 32, 10017-10025	4	7
66	Equilibrium and nonequilibrium dynamics of soft sphere fluids. <i>Soft Matter</i> , <b>2015</b> , 11, 5274-81	3.6	10
65	Free energy surface of an intrinsically disordered protein: comparison between temperature replica exchange molecular dynamics and bias-exchange metadynamics. <i>Journal of Chemical Theory and Computation</i> , <b>2015</b> , 11, 2776-82	6.4	53
64	To What Extent Does Surface Hydrophobicity Dictate Peptide Folding and Stability near Surfaces?. <i>Langmuir</i> , <b>2015</b> , 31, 12223-30	4	19
63	Sequence- and Temperature-Dependent Properties of Unfolded and Disordered Proteins from Atomistic Simulations. <i>Journal of Physical Chemistry B</i> , <b>2015</b> , 119, 14622-30	3.4	49
62	Folding thermodynamics of $\beta$ -hairpins studied by replica-exchange molecular dynamics simulations. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2015</b> , 83, 1307-15	4.2	17
61	Computational study of trimer self-assembly and fluid phase behavior. <i>Journal of Chemical Physics</i> , <b>2015</b> , 142, 164901	3.9	22
60	Effect of O-Linked Glycosylation on the Equilibrium Structural Ensemble of Intrinsically Disordered Polypeptides. <i>Journal of Physical Chemistry B</i> , <b>2015</b> , 119, 15583-92	3.4	16
59	Temperature-dependent solvation modulates the dimensions of disordered proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 5213-8	11.5	125
58	Water transport through functionalized nanotubes with tunable hydrophobicity. <i>Journal of Chemical Physics</i> , <b>2014</b> , 141, 18C532	3.9	31
57	Disorder in cholesterol-binding functionality of CRAC peptides: a molecular dynamics study. <i>Journal of Physical Chemistry B</i> , <b>2014</b> , 118, 13169-74	3.4	25
56	Balanced Protein-Water Interactions Improve Properties of Disordered Proteins and Non-Specific Protein Association. <i>Journal of Chemical Theory and Computation</i> , <b>2014</b> , 10, 5113-5124	6.4	409

55	Interaction of single-stranded DNA with curved carbon nanotube is much stronger than with flat graphite. <i>Journal of the American Chemical Society</i> , <b>2014</b> , 136, 12947-57	16.4	50
54	Macromolecular crowding effects on coupled folding and binding. <i>Journal of Physical Chemistry B</i> , <b>2014</b> , 118, 12621-9	3.4	17
53	Modest influence of FRET chromophores on the properties of unfolded proteins. <i>Biophysical Journal</i> , <b>2014</b> , 107, 1654-60	2.9	25
52	Binding between DNA and carbon nanotubes strongly depends upon sequence and chirality. <i>Langmuir</i> , <b>2014</b> , 30, 3176-83	4	36
51	Role of solvation in pressure-induced helix stabilization. <i>Journal of Chemical Physics</i> , <b>2014</b> , 141, 22D522	3.9	15
50	Insights into DNA-mediated interparticle interactions from a coarse-grained model. <i>Journal of Chemical Physics</i> , <b>2014</b> , 141, 184901	3.9	18
49	Effect of molecular structure on fluid transport through carbon nanotubes. <i>Molecular Physics</i> , <b>2014</b> , 112, 2658-2664	1.7	1
48	Structural Stability and Binding Strength of a Designed Peptide-Carbon Nanotube Hybrid. <i>Journal of Physical Chemistry C</i> , <b>2013</b> , 117, 26255-26261	3.8	11
47	Ab Initio Crystallization of Alkanes: Structure and Kinetics of Nuclei Formation. <i>Macromolecules</i> , <b>2013</b> , 46, 9151-9157	5.5	15
46	Structural ensemble of an intrinsically disordered polypeptide. <i>Journal of Physical Chemistry B</i> , <b>2013</b> , 117, 118-24	3.4	64
45	Structural characteristics of oligomeric DNA strands adsorbed onto single-walled carbon nanotubes. <i>Journal of Physical Chemistry B</i> , <b>2013</b> , 117, 132-40	3.4	43
44	Protein-protein interactions in a crowded environment. <i>Biophysical Reviews</i> , <b>2013</b> , 5, 99-108	3.7	24
43	Molecular simulations indicate marked differences in the structure of amylin mutants, correlated with known aggregation propensity. <i>Journal of Physical Chemistry B</i> , <b>2013</b> , 117, 16066-75	3.4	37
42	Folding Kinetics and Unfolded State Dynamics of the GB1 Hairpin from Molecular Simulation. <i>Journal of Chemical Theory and Computation</i> , <b>2013</b> , 9, 1743-53	6.4	32
41	Crowding induced entropy-enthalpy compensation in protein association equilibria. <i>Physical Review Letters</i> , <b>2013</b> , 110, 208102	7.4	61
40	Residue-specific Helix propensities from molecular simulation. <i>Biophysical Journal</i> , <b>2012</b> , 102, 1462-7	2.9	72
39	DNA base dimers are stabilized by hydrogen-bonding interactions including non-Watson-Crick pairing near graphite surfaces. <i>Journal of Physical Chemistry B</i> , <b>2012</b> , 116, 12088-94	3.4	20
38	Molecular-basis of single-walled carbon nanotube recognition by single-stranded DNA. <i>Nano Letters</i> , <b>2012</b> , 12, 1464-9	11.5	98

37	Smoothing of the GB1 hairpin folding landscape by interfacial confinement. <i>Biophysical Journal</i> , <b>2012</b> , 103, 596-600	2.9	21
36	Inclusion of many-body effects in the additive CHARMM protein CMAP potential results in enhanced cooperativity of helix and hairpin formation. <i>Biophysical Journal</i> , <b>2012</b> , 103, 1045-51	2.9	105
35	Pair diffusion, hydrodynamic interactions, and available volume in dense fluids. <i>Journal of Chemical Physics</i> , <b>2012</b> , 137, 034110	3.9	17
34	Optimization of the additive CHARMM all-atom protein force field targeting improved sampling of the backbone and side-chain $\phi$ and $\psi$ dihedral angles. <i>Journal of Chemical Theory and Computation</i> , <b>2012</b> , 8, 3257-3273	6.4	2511
33	Water Transport through Nanotubes with Varying Interaction Strength between Tube Wall and Water. <i>Journal of Physical Chemistry Letters</i> , <b>2011</b> , 2, 2978-2983	6.4	81
32	Sequence-specific self-stitching motif of short single-stranded DNA on a single-walled carbon nanotube. <i>Journal of the American Chemical Society</i> , <b>2011</b> , 133, 13545-50	16.4	71
31	Free-energy landscape of the GB1 hairpin in all-atom explicit solvent simulations with different force fields: Similarities and differences. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2011</b> , 79, 1318-28	4.2	103
30	Modest protein-crowder attractive interactions can counteract enhancement of protein association by intermolecular excluded volume interactions. <i>Journal of Physical Chemistry B</i> , <b>2011</b> , 115, 2683-9	3.4	55
29	Microscopic events in hairpin folding from alternative unfolded ensembles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 11087-92	11.5	62
28	Dependence of protein folding stability and dynamics on the density and composition of macromolecular crowders. <i>Biophysical Journal</i> , <b>2010</b> , 98, 315-20	2.9	71
27	Tackling force-field bias in protein folding simulations: folding of Villin HP35 and Pin WW domains in explicit water. <i>Biophysical Journal</i> , <b>2010</b> , 99, L26-8	2.9	96
26	Protein simulations with an optimized water model: cooperative helix formation and temperature-induced unfolded state collapse. <i>Journal of Physical Chemistry B</i> , <b>2010</b> , 114, 14916-23	3.4	195
25	Balance between alpha and beta structures in ab initio protein folding. <i>Journal of Physical Chemistry B</i> , <b>2010</b> , 114, 8790-8	3.4	87
24	Macromolecular crowding effects on protein-protein binding affinity and specificity. <i>Journal of Chemical Physics</i> , <b>2010</b> , 133, 205101	3.9	56
23	Interfacial thermodynamics of confined water near molecularly rough surfaces. <i>Faraday Discussions</i> , <b>2010</b> , 146, 341-52; discussion 367-93, 395-401	3.6	70
22	Available states and available space: static properties that predict self-diffusivity of confined fluids. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , <b>2009</b> , 2009, P04006	1.9	41
21	Using compressibility factor as a predictor of confined hard-sphere fluid dynamics. <i>Journal of Physical Chemistry B</i> , <b>2009</b> , 113, 13800-4	3.4	12
20	Layering and position-dependent diffusive dynamics of confined fluids. <i>Physical Review Letters</i> , <b>2008</b> , 100, 145901	7.4	144

19	Static and dynamic correlations in water at hydrophobic interfaces. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 20130-5	11.5	121
18	Thermodynamics and kinetics of protein folding under confinement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 20233-8	11.5	131
17	Relationships between self-diffusivity, packing fraction, and excess entropy in simple bulk and confined fluids. <i>Journal of Physical Chemistry B</i> , <b>2007</b> , 111, 10054-63	3.4	88
16	Does confining the hard-sphere fluid between hard walls change its average properties?. <i>Journal of Chemical Physics</i> , <b>2007</b> , 126, 244708	3.9	61
15	Confinement, entropy, and single-particle dynamics of equilibrium hard-sphere mixtures. <i>Journal of Chemical Physics</i> , <b>2007</b> , 127, 154513	3.9	30
14	Thermodynamics predicts how confinement modifies the dynamics of the equilibrium hard-sphere fluid. <i>Physical Review Letters</i> , <b>2006</b> , 96, 177804	7.4	121
13	Excess-entropy-based anomalies for a waterlike fluid. <i>Journal of Chemical Physics</i> , <b>2006</b> , 125, 244502	3.9	146
12	Quantitative link between single-particle dynamics and static structure of supercooled liquids. <i>Journal of Physical Chemistry B</i> , <b>2006</b> , 110, 18147-50	3.4	93
11	Using Energy Landscapes To Predict the Properties of Thin Films $\square$ <i>Journal of Physical Chemistry B</i> , <b>2004</b> , 108, 19769-19779	3.4	20
10	Instability of thin liquid films by density variations: a new mechanism that mimics spinodal dewetting. <i>Physical Review Letters</i> , <b>2002</b> , 89, 186101	7.4	62
9	Instability and Dewetting of Thin Films Induced by Density Variations. <i>Langmuir</i> , <b>2002</b> , 18, 10213-10220	4	34
8	TDP-43 Helical structure tunes liquid-liquid phase separation and function		4
7	Hydropathy patterning complements charge patterning to describe conformational preferences of disordered proteins		2
6	Identifying Sequence Perturbations to an Intrinsically Disordered Protein that Determine Its Phase Separation Behavior		5
5	Tyrosine phosphorylation regulates hnRNPA2 granule protein partitioning & reduces neurodegeneration		2
4	A predictive coarse-grained model for position-specific effects of post-translational modifications on disordered protein phase separation		6
3	Sequence dependent co-phase separation of RNA-protein mixtures elucidated using molecular simulations		2
2	Molecular details of protein condensates probed by microsecond-long atomistic simulations		5



1 Amphiphilic proteins coassemble into multiphasic condensates and act as biomolecular surfactants

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