Peter J Bond

List of Publications by Year
in descending order

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150 papers	7,325 citations	61687 45 h-index	75989 78 g-index
169 all docs	169 docs citations	169 times ranked	10968 citing authors

#	Article	IF	Citations
1	Glycosylation and Serological Reactivity of an Expression-enhanced SARS-CoV-2 Viral Spike Mimetic. Journal of Molecular Biology, 2022, 434, 167332.	2.0	22
2	Allosteric perspective on the mutability and druggability of the SARS-CoV-2 Spike protein. Structure, 2022, 30, 590-607.e4.	1.6	24
3	Bridging the N-terminal and middle domains in FliG of the flagellar rotor. Current Research in Structural Biology, 2022, 4, 59-67.	1.1	2
4	What have molecular simulations contributed to understanding of Gram-negative bacterial cell envelopes?. Microbiology (United Kingdom), 2022, 168, .	0.7	10
5	Motional clustering in supra-<mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" altimg="si29.svg"><mml:mrow><mml:msub><mml:mrow><mml:mi>Ï„</mml:mi></mml:mrow><mml:mrow><mml:mi mathvariant="normal">c</mml:mi></mml:mrow></mml:msub></mml:mrow></mml:math> conformational exchange influences NOE cross-relaxation rate. Journal of Magnetic Resonance, 2022, 338, 107196.	1.2	4
6	Uncovering cryptic pockets in the SARS-CoV-2 spike glycoprotein. Structure, 2022, 30, 1062-1074.e4.	1.6	21
7	Antibacterial and Anti-Inflammatory Effects of Apolipoprotein E. Biomedicines, 2022, 10, 1430.	1.4	8
8	Computational modelling of flavivirus dynamics: The ins and outs. Methods, 2021, 185, 28-38.	1.9	9
9	SARS-CoV-2 spike protein binds to bacterial lipopolysaccharide and boosts proinflammatory activity. Journal of Molecular Cell Biology, 2021, 12, 916-932.	1.5	121
10	A second shell residue modulates a conserved ATP-binding site with radically different affinities for ATP. Biochimica Et Biophysica Acta - General Subjects, 2021, 1865, 129766.	1.1	4
11	The impact of Gag non-cleavage site mutations on HIV-1 viral fitness from integrative modelling and simulations. Computational and Structural Biotechnology Journal, 2021, 19, 330-342.	1.9	7
12	Antibody affinity versus dengue morphology influences neutralization. PLoS Pathogens, 2021, 17, e1009331.	2.1	8
13	SARS-CoV-2 S protein:ACE2 interaction reveals novel allosteric targets. ELife, 2021, 10, .	2.8	100
14	The antibiotic darobactin mimics a Î²-strand to inhibit outer membrane insertase. Nature, 2021, 593, 125-129.	13.7	112
15	Site-Specific Steric Control of SARS-CoV-2 Spike Glycosylation. Biochemistry, 2021, 60, 2153-2169.	1.2	54
16	Somatic genetic rescue of a germline ribosome assembly defect. Nature Communications, 2021, 12, 5044.	5.8	44
17	Manipulating turn residues on de novo designed Î²-hairpin peptides for selectivity against drug-resistant bacteria. Acta Biomaterialia, 2021, 135, 214-224.	4.1	6
18	The nanotube express: Delivering a stapled peptide to the cell surface. Journal of Colloid and Interface Science, 2021, 604, 670-679.	5.0	3

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19	On the ion coupling mechanism of the MATE transporter ClbM. Biochimica Et Biophysica Acta - Biomembranes, 2020, 1862, 183137.	1.4	16
20	Flavivirus Cross-Reactivity to Dengue Nonstructural Protein 1 Antigen Detection Assays. Diagnostics, 2020, 10, 11.	1.3	16
21	Extending the Martini Coarse-Grained Force Field to N-Glycans. Journal of Chemical Information and Modeling, 2020, 60, 3864-3883.	2.5	30
22	Concentration- and pH-Dependent Oligomerization of the Thrombin-Derived C-Terminal Peptide TCP-25. Biomolecules, 2020, 10, 1572.	1.8	9
23	Characterizing the Hydration Properties of Proton Binding Sites in the ATP Synthase c-Rings of Bacillus Species. Journal of Physical Chemistry B, 2020, 124, 7176-7183.	1.2	5
24	Molecular dynamics simulations of bacterial outer membrane lipid extraction: Adequate sampling?. Journal of Chemical Physics, 2020, 153, 044122.	1.2	10
25	Molecular simulations unravel the molecular principles that mediate selective permeability of carboxysome shell protein. Scientific Reports, 2020, 10, 17501.	1.6	52
26	A Benzene-Mapping Approach for Uncovering Cryptic Pockets in Membrane-Bound Proteins. Journal of Chemical Theory and Computation, 2020, 16, 5948-5959.	2.3	6
27	An Alternative HIV-1 Non-Nucleoside Reverse Transcriptase Inhibition Mechanism: Targeting the p51 Subunit. Molecules, 2020, 25, 5902.	1.7	5
28	3D reconstruction and flexibility of the hybrid engine Acetobacterium woodii F-ATP synthase. Biochemical and Biophysical Research Communications, 2020, 527, 518-524.	1.0	1
29	How Ligand Binding Affects the Dynamical Transition Temperature in Proteins. ChemPhysChem, 2020, 21, 916-926.	1.0	3
30	The Molecular Basis for Purine Binding Selectivity in the Bacterial ATP Synthase Ïµ Subunit. ChemBioChem, 2020, 21, 3249-3254.	1.3	5
31	Thrombin-derived C-terminal fragments aggregate and scavenge bacteria and their proinflammatory products. Journal of Biological Chemistry, 2020, 295, 3417-3430.	1.6	24
32	Not all therapeutic antibody isotypes are equal: the case of IgM versus IgG in Pertuzumab and Trastuzumab. Chemical Science, 2020, 11, 2843-2854.	3.7	23
33	Multiscale modelling and simulation of viruses. Current Opinion in Structural Biology, 2020, 61, 146-152.	2.6	26
34	Multiscale modeling of innate immune receptors: Endotoxin recognition and regulation by host defense peptides. Pharmacological Research, 2019, 147, 104372.	3.1	15
35	A T164S mutation in the dengue virus NS1 protein is associated with greater disease severity in mice. Science Translational Medicine, 2019, 11, .	5.8	32
36	Linker length affects photostability of protein-targeted sensor of cellular microviscosity. Methods and Applications in Fluorescence, 2019, 7, 044004.	1.1	8

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37	The structural basis for membrane assembly of immunoreceptor signalling complexes. Journal of Molecular Modeling, 2019, 25, 277.	0.8	3
38	Molecular basis of dengue virus serotype 2 morphological switch from 29Â°C to 37Â°C. PLoS Pathogens, 2019, 15, e1007996.	2.1	25
39	Directing GDNF-mediated neuronal signaling with proactively programmable cell-surface saccharide-free glycosaminoglycan mimetics. Chemical Communications, 2019, 55, 1259-1262.	2.2	0
40	Multiscale Modeling and Simulation Approaches to Lipidâ€“Protein Interactions. Methods in Molecular Biology, 2019, 2003, 1-30.	0.4	7
41	Structure and subunit arrangement of Mycobacterial F1FO ATP synthase and novel features of the unique mycobacterial subunit Î´. Journal of Structural Biology, 2019, 207, 199-208.	1.3	22
42	The disordered plant dehydrin Lti30 protects the membrane during water-related stress by cross-linking lipids. Journal of Biological Chemistry, 2019, 294, 6468-6482.	1.6	30
43	Insights into water accessible pathways and the inactivation mechanism of proton translocation by the membrane-embedded domain of V-type ATPases. Biochimica Et Biophysica Acta - Biomembranes, 2019, 1861, 1004-1010.	1.4	10
44	Structure mapping of dengue and Zika viruses reveals functional long-range interactions. Nature Communications, 2019, 10, 1408.	5.8	104
45	Single-molecule studies of flavivirus envelope dynamics: Experiment and computation. Progress in Biophysics and Molecular Biology, 2019, 143, 38-51.	1.4	9
46	Energetic Fingerprinting of Ligand Binding to Paralogous Proteins: The Case of the Apoptotic Pathway. Journal of Chemical Information and Modeling, 2019, 59, 245-261.	2.5	4
47	Mechanism of Enhanced Immature Dengue Virus Attachment to Endosomal Membrane Induced by prM Antibody. Structure, 2019, 27, 253-267.e8.	1.6	36
48	Engineering an Osmosensor by Pivotal Histidine Positioning within Disordered Helices. Structure, 2019, 27, 302-314.e4.	1.6	11
49	Infectivity of Dengue Virus Serotypes 1 and 2 Is Correlated with E-Protein Intrinsic Dynamics but Not to Envelope Conformations. Structure, 2019, 27, 618-630.e4.	1.6	23
50	Evidence that TLR4 Is Not a Receptor for Saturated Fatty Acids but Mediates Lipid-Induced Inflammation by Reprogramming Macrophage Metabolism. Cell Metabolism, 2018, 27, 1096-1110.e5.	7.2	309
51	An Optical Technique for Mapping Microviscosity Dynamics in Cellular Organelles. ACS Nano, 2018, 12, 4398-4407.	7.3	125
52	A Thermodynamic Funnel Drives Bacterial Lipopolysaccharide Transfer in the TLR4 Pathway. Structure, 2018, 26, 1151-1161.e4.	1.6	32
53	The architecture of the OmpCâ€“MlaA complex sheds light on the maintenance of outer membrane lipid asymmetry in Escherichia coli. Journal of Biological Chemistry, 2018, 293, 11325-11340.	1.6	64
54	Partial Intrinsic Disorder Governs the Dengue Capsid Protein Conformational Ensemble. ACS Chemical Biology, 2018, 13, 1621-1630.	1.6	18

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55	Activation of Toll-like receptors nucleates assembly of the MyDDosome signaling hub. ELife, 2018, 7, .	2.8	83
56	Structural basis for endotoxin neutralisation and anti-inflammatory activity of thrombin-derived C-terminal peptides. Nature Communications, 2018, 9, 2762.	5.8	43
57	Facile saccharide-free mimetics that recapitulate key features of glycosaminoglycan sulfation patterns. Chemical Science, 2018, 9, 7940-7947.	3.7	10
58	A Funneled Conformational Landscape Governs Flavivirus Fusion Peptide Interaction with Lipid Membranes. Journal of Chemical Theory and Computation, 2018, 14, 3920-3932.	2.3	9
59	Influence of pH on the activity of thrombin-derived antimicrobial peptides. Biochimica Et Biophysica Acta - Biomembranes, 2018, 1860, 2374-2384.	1.4	25
60	Single mutations in the Îµ subunit from thermophilic Bacillus PS3 generate a high binding affinity site for ATP. PeerJ, 2018, 6, e5505.	0.9	3
61	Selective inhibitors of trypanosomal uridylyl transferase RET1 establish druggability of RNA post-transcriptional modifications. RNA Biology, 2017, 14, 611-619.	1.5	5
62	Full-length, Oligomeric Structure of Wzz Determined by Cryoelectron Microscopy Reveals Insights into Membrane-Bound States. Structure, 2017, 25, 806-815.e3.	1.6	31
63	Aggregation of thrombin-derived C-terminal fragments as a previously undisclosed host defense mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E4213-E4222.	3.3	49
64	Progress in Molecular Dynamics Simulations of Gram-Negative Bacterial Cell Envelopes. Journal of Physical Chemistry Letters, 2017, 8, 2513-2518.	2.1	33
65	A Spring-Loaded Mechanism Governs the Clamp-like Dynamics of the Skp Chaperone. Structure, 2017, 25, 1079-1088.e3.	1.6	34
66	Polar N-terminal Residues Conserved in Type 2 Secretion Pseudopilins Determine Subunit Targeting and Membrane Extraction Steps during Fibre Assembly. Journal of Molecular Biology, 2017, 429, 1746-1765.	2.0	18
67	A polar SxxS motif drives assembly of the transmembrane domains of Toll-like receptor 4. Biochimica Et Biophysica Acta - Biomembranes, 2017, 1859, 2086-2095.	1.4	12
68	Editorial. Progress in Biophysics and Molecular Biology, 2017, 128, 1-2.	1.4	0
69	Multiscale molecular dynamics simulation approaches to the structure and dynamics of viruses. Progress in Biophysics and Molecular Biology, 2017, 128, 121-132.	1.4	31
70	Systematic analysis of protein identity between Zika virus and other arthropod-borne viruses. Bulletin of the World Health Organization, 2017, 95, 517-525I.	1.5	52
71	Protein-protein interactions in paralogues: Electrostatics modulates specificity on a conserved steric scaffold. PLoS ONE, 2017, 12, e0185928.	1.1	7
72	Dynamics of Crowded Vesicles: Local and Global Responses to Membrane Composition. PLoS ONE, 2016, 11, e0156963.	1.1	28

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73	Pushing the Envelope: Dengue Viral Membrane Coaxed into Shape by Molecular Simulations. Structure, 2016, 24, 1410-1420.	1.6	41
74	Characterizing the Conformational Landscape of Flavivirus Fusion Peptides via Simulation and Experiment. Scientific Reports, 2016, 6, 19160.	1.6	17
75	Impairing Cohesin Smc1/3 Head Engagement Compensates for the Lack of Eco1 Function. Structure, 2016, 24, 1991-1999.	1.6	23
76	Hydrocarbons Are Essential for Optimal Cell Size, Division, and Growth of Cyanobacteria. Plant Physiology, 2016, 172, 1928-1940.	2.3	53
77	OmpA: A Flexible Clamp for Bacterial Cell Wall Attachment. Structure, 2016, 24, 2227-2235.	1.6	76
78	Full-Length OmpA: Structure, Function, and Membrane Interactions Predicted by Molecular Dynamics Simulations. Biophysical Journal, 2016, 111, 1692-1702.	0.2	67
79	The severity of hereditary porphyria is modulated by the porphyrin exporter and Lan antigen ABCB6. Nature Communications, 2016, 7, 12353.	5.8	37
80	Energetics and Dynamics Across the Bcl-2-Regulated Apoptotic Pathway Reveal Distinct Evolutionary Determinants of Specificity and Affinity. Structure, 2016, 24, 2024-2033.	1.6	16
81	Bioinformatics and systems biology research update from the 15th International Conference on Bioinformatics (InCoB2016). BMC Bioinformatics, 2016, 17, 524.	1.2	3
82	Structural Basis of Pullulanase Membrane Binding and Secretion Revealed by X-Ray Crystallography, Molecular Dynamics and Biochemical Analysis. Structure, 2016, 24, 92-104.	1.6	26
83	The Structural Basis for Lipid and Endotoxin Binding in RP105-MD-1, and Consequences for Regulation of Host Lipopolysaccharide Sensitivity. Structure, 2016, 24, 200-211.	1.6	11
84	Energetics of Endotoxin Recognition in the Toll-Like Receptor 4 Innate Immune Response. Scientific Reports, 2015, 5, 17997.	1.6	25
85	Interaction of the Antimicrobial Peptide Polymyxin B1 with Both Membranes of E. coli: A Molecular Dynamics Study. PLoS Computational Biology, 2015, 11, e1004180.	1.5	134
86	The role of proteinâ€“protein interactions in Toll-like receptor function. Progress in Biophysics and Molecular Biology, 2015, 119, 72-83.	1.4	24
87	Membrane Recognition and Dynamics of the RNA Degradosome. PLoS Genetics, 2015, 11, e1004961.	1.5	93
88	Revisiting the Interaction between the Chaperone Skp and Lipopolysaccharide. Biophysical Journal, 2015, 108, 1516-1526.	0.2	12
89	Understanding Dengue Virus Capsid Protein Disordered N-Terminus and pep14-23-Based Inhibition. ACS Chemical Biology, 2015, 10, 517-526.	1.6	45
90	Molecular Dynamics Simulations of Membrane Proteins. Methods in Molecular Biology, 2015, 1215, 91-108.	0.4	13

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91	The Structural Basis for Activation and Inhibition of ZAP-70 Kinase Domain. PLoS Computational Biology, 2015, 11, e1004560.	1.5	12
92	Ab Initio Folding of Glycophorin A and Acetylcholine M2 Transmembrane Segments Via Simplified Environment Molecular Simulations. , 2015, , 115-139.		0
93	A Study on Fe2+Ââ€“ Î±-Helical-Rich Keratin Complex Formation Using Isothermal Titration Calorimetry and Molecular Dynamics Simulation. Journal of Pharmaceutical Sciences, 2014, 103, 1224-1232.	1.6	8
94	Free Energy Predictions of Ligand Binding to an Î±-Helix Using Steered Molecular Dynamics and Umbrella Sampling Simulations. Journal of Chemical Information and Modeling, 2014, 54, 2093-2104.	2.5	19
95	Efficient Characterization of Protein Cavities within Molecular Simulation Trajectories: trj_cavity. Journal of Chemical Theory and Computation, 2014, 10, 2151-2164.	2.3	129
96	Molecular and thermodynamic basis for EGCGâ€Keratin interactionâ€part II: Experimental investigation. AICHE Journal, 2013, 59, 4824-4827.	1.8	9
97	Molecular and thermodynamic basis for EGCGâ€Keratin interactionâ€part I: Molecular dynamics simulations. AICHE Journal, 2013, 59, 4816-4823.	1.8	9
98	Selective inhibition of the unfolded protein response: targeting catalytic sites for Schiff base modification. Molecular BioSystems, 2013, 9, 2408.	2.9	26
99	Multiscale Molecular Dynamics Simulations of Membrane Proteins. Methods in Molecular Biology, 2013, 924, 635-657.	0.4	16
100	Design, Synthesis, and Biological Evaluation of an Allosteric Inhibitor of HSET that Targets Cancer Cells with Supernumerary Centrosomes. Chemistry and Biology, 2013, 20, 1399-1410.	6.2	94
101	The Structural Basis for Endotoxin-induced Allosteric Regulation of the Toll-like Receptor 4 (TLR4) Innate Immune Receptor. Journal of Biological Chemistry, 2013, 288, 36215-36225.	1.6	51
102	The Simulation Approach to Lipidâ€“Protein Interactions. Methods in Molecular Biology, 2013, 974, 435-455.	0.4	4
103	Dynamics of the Antigen-binding Grooves in CD1 Proteins. Journal of Biological Chemistry, 2013, 288, 19528-19536.	1.6	16
104	Minor pseudopilin self-assembly primes type II secretion pseudopilus elongation. EMBO Journal, 2012, 31, 1041-1053.	3.5	94
105	The molecular basis for selective inhibition of unconventional mRNA splicing by an IRE1-binding small molecule. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E869-78.	3.3	476
106	A-Ring Dihalogenation Increases the Cellular Activity of Combretastatin-Templated Tetrazoles. ACS Medicinal Chemistry Letters, 2012, 3, 177-181.	1.3	42
107	Computational Prediction of Metabolism: Sites, Products, SAR, P450 Enzyme Dynamics, and Mechanisms. Journal of Chemical Information and Modeling, 2012, 52, 617-648.	2.5	246
108	Increased endothelial cell selectivity of triazole-bridged dihalogenated A-ring analogues of combretastatin Aâ€“1. Bioorganic and Medicinal Chemistry, 2012, 20, 1749-1759.	1.4	18

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109	Molecular Dynamics Simulations of DNA within a Nanopore: Argincâ˜Phosphate Tethering and a Binding/Sliding Mechanism for Translocation. Biochemistry, 2011, 50, 3777-3783.	1.2	26
110	Exploring the conformational dynamics and membrane interactions of PorB from C. glutamicum: A multi-scale molecular dynamics simulation study. Biochimica Et Biophysica Acta - Biomembranes, 2011, 1808, 1746-1752.	1.4	6
111	From in silico target prediction to multi-target drug design: Current databases, methods and applications. Journal of Proteomics, 2011, 74, 2554-2574.	1.2	243
112	Molecular Mechanism of Selective Recruitment of Syk Kinases by the Membrane Antigen-Receptor Complex. Journal of Biological Chemistry, 2011, 286, 25872-25881.	1.6	16
113	Structural and energetic basis for H+ versus Na+ binding selectivity in ATP synthase Fo rotors. Biochimica Et Biophysica Acta - Bioenergetics, 2010, 1797, 763-772.	0.5	58
114	Antimicrobial and Cell-Penetrating Peptides: Structure, Assembly and Mechanisms of Membrane Lysis via Atomistic and Coarse-Grained Molecular Dynamic Simulations. Protein and Peptide Letters, 2010, 17, 1313-1327.	0.4	37
115	Coarseâ€Grain Simulations of the Râ€SNARE Fusion Protein in its Membrane Environment Detect Longâ€Lived Conformational Subâ€States. ChemPhysChem, 2009, 10, 1548-1552.	1.0	30
116	Complete Ion-Coordination Structure in the Rotor Ring of Na+-Dependent F-ATP Synthases. Journal of Molecular Biology, 2009, 391, 498-507.	2.0	98
117	Predicted structural basis for CD1c presentation of mycobacterial branched polyketides and long lipopeptide antigens. Molecular Immunology, 2009, 47, 253-260.	1.0	11
118	Interaction of Monotopic Membrane Enzymes with a Lipid Bilayer: A Coarse-Grained MD Simulation Studyâ€. Biochemistry, 2009, 48, 2135-2145.	1.2	44
119	Outer membrane proteins: comparing X-ray and NMR structures by MD simulations in lipid bilayers. European Biophysics Journal, 2008, 37, 131-141.	1.2	22
120	DNA and lipid bilayers: self-assembly and insertion. Journal of the Royal Society Interface, 2008, 5, 241-250.	1.5	64
121	Coarse-Grained MD Simulations of Membrane Protein-Bilayer Self-Assembly. Structure, 2008, 16, 621-630.	1.6	199
122	Molecular Dynamics Simulations of Membrane Proteins. Methods in Molecular Biology, 2008, 443, 147-160.	0.4	26
123	Coarse-Grained Molecular Dynamics Simulations of the Energetics of Helix Insertion into a Lipid Bilayer. Biochemistry, 2008, 47, 11321-11331.	1.2	87
124	Coarse-Grained Simulations of the Membrane-Active Antimicrobial Peptide Maculatin 1.1. Biophysical Journal, 2008, 95, 3802-3815.	0.2	68
125	Self-Assembly of a Simple Membrane Protein: Coarse-Grained Molecular Dynamics Simulations of the Influenza M2 Channel. Biophysical Journal, 2008, 95, 3790-3801.	0.2	69
126	OmpA: Gating and dynamics via molecular dynamics simulations. Biochimica Et Biophysica Acta - Biomembranes, 2008, 1778, 1871-1880.	1.4	53

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127	Helixâ^'Helix Interactions in Membrane Proteins: Coarse-Grained Simulations of Glycophorin A Helix Dimerization. Biochemistry, 2008, 47, 10503-10512.	1.2	82
128	Coarse-grained simulation: a high-throughput computational approach to membrane proteins. Biochemical Society Transactions, 2008, 36, 27-32.	1.6	117
129	Bilayer deformation by the Kv channel voltage sensor domain revealed by self-assembly simulations. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 2631-2636.	3.3	100
130	Coarse-grained molecular dynamics simulations of membrane proteins and peptides. Journal of Structural Biology, 2007, 157, 593-605.	1.3	303
131	Membrane Simulations of OpcA: Gating in the Loops?. Biophysical Journal, 2007, 92, L23-L25.	0.2	34
132	MD Simulations of Mistic:â€‰ Conformational Stability in Detergent Micelles and Water. Biochemistry, 2006, 45, 9053-9058.	1.2	18
133	Anionic Phospholipid Interactions with the Potassium Channel KcsA: Simulation Studies. Biophysical Journal, 2006, 90, 822-830.	0.2	77
134	Transmembrane Helixâ^'Helix Interactions:â€‰ Comparative Simulations of the Glycophorin A Dimer. Biochemistry, 2006, 45, 14298-14310.	1.2	65
135	Modeling and simulations of a bacterial outer membrane protein: OprF from Pseudomonas aeruginosa. Proteins: Structure, Function and Bioinformatics, 2006, 63, 6-15.	1.5	27
136	Insertion and Assembly of Membrane Proteins via Simulation. Journal of the American Chemical Society, 2006, 128, 2697-2704.	6.6	314
137	Membrane protein dynamics and detergent interactions within a crystal: A simulation study of OmpA. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 9518-9523.	3.3	38
138	Cysteine-scanning Mutagenesis and Disulfide Mapping Studies of the Conserved Domain of the Twin-arginine Translocase TatB Component*. Journal of Biological Chemistry, 2006, 281, 34072-34085.	1.6	60
139	Membrane Protein Simulations: Modelling a Complex Environment. , 2006, , 3-20.		0
140	Membrane protein structure quality in molecular dynamics simulation. Journal of Molecular Graphics and Modelling, 2005, 24, 157-165.	1.3	58
141	Molecular Dynamics Simulations of GlpF in a Micelle vs in a Bilayer:Â Conformational Dynamics of a Membrane Protein as a Function of Environment. Journal of Physical Chemistry B, 2005, 109, 575-582.	1.2	35
142	Conformational sampling and dynamics of membrane proteins from 10-nanosecond computer simulations. Proteins: Structure, Function and Bioinformatics, 2004, 57, 783-791.	1.5	92
143	Lipid-Protein Interactions of Integral Membrane Proteins: A Comparative Simulation Study. Biophysical Journal, 2004, 87, 3737-3749.	0.2	104
144	MD Simulations of Spontaneous Membrane Protein/Detergent Micelle Formation. Journal of the American Chemical Society, 2004, 126, 15948-15949.	6.6	85

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145	The simulation approach to bacterial outer membrane proteins (Review). Molecular Membrane Biology, 2004, 21, 151-161.	2.0	61
146	Lipid/Protein Interactions and the Membrane/Water Interfacial Region. Journal of the American Chemical Society, 2003, 125, 14966-14967.	6.6	57
147	Membrane Protein Dynamics versus Environment: Simulations of OmpA in a Micelle and in a Bilayer. Journal of Molecular Biology, 2003, 329, 1035-1053.	2.0	130
148	Membrane Protein Simulations: Ion Channels And Bacterial Outer Membrane Proteins. Advances in Protein Chemistry, 2003, 66, 159-193.	4.4	49
149	OmpA: A Pore or Not a Pore? Simulation and Modeling Studies. Biophysical Journal, 2002, 83, 763-775.	0.2	92
150	Infectivity of Dengue Virus Serotypes 1 and 2 is Correlated to E Protein Intrinsic Dynamics But Not to Envelope Conformations. SSRN Electronic Journal, 0, , .	0.4	0