Jeffrey J Gray

List of Publications by Year
in descending order

157 papers	13,755 citations	36203 51 h-index	26548 107 g-index
191 all docs	191 docs citations	191 times ranked	15495 citing authors

#	Article	IF	Citations
1	Rosetta3. Methods in Enzymology, 2011, 487, 545-574.	0.4	1,620
2	The Rosetta All-Atom Energy Function for Macromolecular Modeling and Design. Journal of Chemical Theory and Computation, 2017, 13, 3031-3048.	2.3	1,032
3	Proteinâ€“Protein Docking with Simultaneous Optimization of Rigid-body Displacement and Side-chain Conformations. Journal of Molecular Biology, 2003, 331, 281-299.	2.0	1,017
4	The interaction of proteins with solid surfaces. Current Opinion in Structural Biology, 2004, 14, 110-115.	2.6	740
5	PyRosetta: a script-based interface for implementing molecular modeling algorithms using Rosetta. Bioinformatics, 2010, 26, 689-691.	1.8	601
6	Macromolecular modeling and design in Rosetta: recent methods and frameworks. Nature Methods, 2020, 17, 665-680.	9.0	513
7	The RosettaDock server for local protein-protein docking. Nucleic Acids Research, 2008, 36, W233-W238.	6.5	508
8	Serverification of Molecular Modeling Applications: The Rosetta Online Server That Includes Everyone (ROSIE). PLoS ONE, 2013, 8, e63906.	1.1	348
9	A Comprehensive, High-Resolution Map of a Geneâ€™s Fitness Landscape. Molecular Biology and Evolution, 2014, 31, 1581-1592.	3.5	291
10	Benchmarking and Analysis of Protein Docking Performance in Rosetta v3.2. PLoS ONE, 2011, 6, e22477.	1.1	272
11	Modeling and docking of antibody structures with Rosetta. Nature Protocols, 2017, 12, 401-416.	5.5	236
12	Toward highâ€resolution homology modeling of antibody F_v regions and application to antibodyâ€“antigen docking. Proteins: Structure, Function and Bioinformatics, 2009, 74, 497-514.	1.5	198
13	Scientific Benchmarks for Guiding Macromolecular Energy Function Improvement. Methods in Enzymology, 2013, 523, 109-143.	0.4	195
14	Large-scale sequence and structural comparisons of human naive and antigen-experienced antibody repertoires. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E2636-45.	3.3	179
15	High-resolution proteinâ€“protein docking. Current Opinion in Structural Biology, 2006, 16, 183-193.	2.6	176
16	Targeting the CoREST complex with dual histone deacetylase and demethylase inhibitors. Nature Communications, 2018, 9, 53.	5.8	175
17	RosettaAntibody: antibody variable region homology modeling server. Nucleic Acids Research, 2009, 37, W474-W479.	6.5	157
18	Conformer Selection and Induced Fit in Flexible Backbone Proteinâ€“Protein Docking Using Computational and NMR Ensembles. Journal of Molecular Biology, 2008, 381, 1068-1087.	2.0	152

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19	Phosphorylation-dependent inhibition of mineralization by osteopontin ASARM peptides is regulated by PHEX cleavage. Journal of Bone and Mineral Research, 2010, 25, 695-705.	3.1	151
20	Prediction of homoprotein and heteroprotein complexes by protein docking and templateâ€based modeling: A CASPâ€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2016, 84, 323-348.	1.5	148
21	An Integrated Framework Advancing Membrane Protein Modeling and Design. PLoS Computational Biology, 2015, 11, e1004398.	1.5	145
22	SnugDock: Paratope Structural Optimization during Antibody-Antigen Docking Compensates for Errors in Antibody Homology Models. PLoS Computational Biology, 2010, 6, e1000644.	1.5	139
23	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	2.0	131
24	Chiral acidic amino acids induce chiral hierarchical structure in calcium carbonate. Nature Communications, 2017, 8, 15066.	5.8	129
25	Structure-Based Design of Supercharged, Highly Thermoresistant Antibodies. Chemistry and Biology, 2012, 19, 449-455.	6.2	127
26	Efficient flexible backbone proteinâ€“protein docking for challenging targets. Bioinformatics, 2018, 34, 3461-3469.	1.8	121
27	Deep Learning in Protein Structural Modeling and Design. Patterns, 2020, 1, 100142.	3.1	119
28	Functional Loss of Semaphorin 3C and/or Semaphorin 3D and Their Epistatic Interaction with Ret Are Critical to Hirschsprung Disease Liability. American Journal of Human Genetics, 2015, 96, 581-596.	2.6	118
29	Structure Prediction of Proteinâ^'Solid Surface Interactions Reveals a Molecular Recognition Motif of Statherin for Hydroxyapatite. Journal of the American Chemical Society, 2007, 129, 13713-13722.	6.6	114
30	Enzyme Replacement Therapy Prevents Dental Defects in a Model of Hypophosphatasia. Journal of Dental Research, 2011, 90, 470-476.	2.5	106
31	Antibody structure prediction using interpretable deep learning. Patterns, 2022, 3, 100406.	3.1	106
32	Local motions in a benchmark of allosteric proteins. Proteins: Structure, Function and Bioinformatics, 2007, 67, 385-399.	1.5	103
33	Protein-protein docking predictions for the CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2003, 52, 118-122.	1.5	102
34	Allosteric Communication Occurs via Networks of Tertiary and Quaternary Motions in Proteins. PLoS Computational Biology, 2009, 5, e1000293.	1.5	98
35	Blind prediction performance of RosettaAntibody 3.0: Grafting, relaxation, kinematic loop modeling, and full CDR optimization. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1611-1623.	1.5	91
36	Contact rearrangements form coupled networks from local motions in allosteric proteins. Proteins: Structure, Function and Bioinformatics, 2008, 71, 455-466.	1.5	89

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37	Community-wide evaluation of methods for predicting the effect of mutations on protein-protein interactions. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1980-1987.	1.5	87
38	Computational modeling of membrane proteins. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1-24.	1.5	86
39	Nanostructure, osteopontin, and mechanical properties of calcitic avian eggshell. Science Advances, 2018, 4, eaar3219.	4.7	86
40	The Origin of CDR H3 Structural Diversity. Structure, 2015, 23, 302-311.	1.6	78
41	Analysis and Modeling of the Variable Region of Camelid Single-Domain Antibodies. Journal of Immunology, 2011, 186, 6357-6367.	0.4	75
42	Prediction of protein assemblies, the next frontier: The <scp>CASP14â€CAPRI</scp> experiment. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1800-1823.	1.5	73
43	Alternative Computational Protocols for Supercharging Protein Surfaces for Reversible Unfolding and Retention of Stability. PLoS ONE, 2013, 8, e64363.	1.1	73
44	Shape complementarity and hydrogen bond preferences in proteinâ€“protein interfaces: implications for antibody modeling and proteinâ€“protein docking. Bioinformatics, 2016, 32, 2451-2456.	1.8	70
45	An expanded benchmark for antibody-antigen docking and affinity prediction reveals insights into antibody recognition determinants. Structure, 2021, 29, 606-621.e5.	1.6	65
46	Rapid Calculation of Protein pKa Values Using Rosetta. Biophysical Journal, 2012, 103, 587-595.	0.2	61
47	Plasma Cells Are the Most Abundant Gluten Peptide MHC-expressing Cells in Inflamed Intestinal Tissues FromÂPatients With Celiac Disease. Gastroenterology, 2019, 156, 1428-1439.e10.	0.6	61
48	Modulation of Calcium Oxalate Dihydrate Growth by Selective Crystal-face Binding of Phosphorylated Osteopontin and Polyaspartate Peptide Showing Occlusion by Sectoral (Compositional) Zoning. Journal of Biological Chemistry, 2009, 284, 23491-23501.	1.6	60
49	Structural Diversity in the Type IV Pili of Multidrug-resistant Acinetobacter. Journal of Biological Chemistry, 2016, 291, 22924-22935.	1.6	60
50	Adding Diverse Noncanonical Backbones to Rosetta: Enabling Peptidomimetic Design. PLoS ONE, 2013, 8, e67051.	1.1	59
51	Protein Structure Prediction and Design in a Biologically Realistic Implicit Membrane. Biophysical Journal, 2020, 118, 2042-2055.	0.2	59
52	Real-Time PyMOL Visualization for Rosetta and PyRosetta. PLoS ONE, 2011, 6, e21931.	1.1	55
53	Solution- and Adsorbed-State Structural Ensembles Predicted for the Statherin-Hydroxyapatite System. Biophysical Journal, 2009, 96, 3082-3091.	0.2	54
54	Acidic C-terminal domains autoregulate the RNA chaperone Hfq. ELife, 2017, 6, .	2.8	53

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55	CAPRI rounds 3-5 reveal promising successes and future challenges for RosettaDock. Proteins: Structure, Function and Bioinformatics, 2005, 60, 181-186.	1.5	52
56	Structural Model of the mAb 806-EGFR Complex Using Computational Docking followed by Computational and Experimental Mutagenesis. Structure, 2006, 14, 401-414.	1.6	52
57	Improved prediction of antibody V_Lâ€“V_Horientation. Protein Engineering, Design and Selection, 2016, 29, 409-418.	1.0	52
58	De Novo Design of Peptideâ˜Calcite Biomineralization Systems. Journal of the American Chemical Society, 2010, 132, 12252-12262.	6.6	51
59	Enzymatic Excision of Uracil Residues in Nucleosomes Depends on the Local DNA Structure and Dynamics. Biochemistry, 2012, 51, 6028-6038.	1.2	50
60	Blind prediction of interfacial water positions in CAPRI. Proteins: Structure, Function and Bioinformatics, 2014, 82, 620-632.	1.5	50
61	Geometric potentials from deep learning improve prediction of CDR H3 loop structures. Bioinformatics, 2020, 36, i268-i275.	1.8	48
62	Webâ€accessible molecular modeling with Rosetta: The Rosetta Online Server that Includes Everyone (ROSIE). Protein Science, 2018, 27, 259-268.	3.1	47
63	A generalized approach to sampling backbone conformations with RosettaDock for CAPRI rounds 13â€“19. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3115-3123.	1.5	46
64	Pushing the Backbone in Protein-Protein Docking. Structure, 2016, 24, 1821-1829.	1.6	46
65	Accurate Structure Prediction of CDR H3 Loops Enabled by a Novel Structure-Based C-Terminal Constraint. Journal of Immunology, 2017, 198, 505-515.	0.4	43
66	Partial High-Resolution Structure of Phosphorylated and Non-phosphorylated Leucine-Rich Amelogenin Protein Adsorbed to Hydroxyapatite. Journal of Physical Chemistry C, 2011, 115, 13775-13785.	1.5	42
67	Adsorption of colloidal particles by Brownian dynamics simulation: Kinetics and surface structures. Journal of Chemical Physics, 2001, 114, 1366-1381.	1.2	41
68	Residueâ€centric modeling and design of saccharide and glycoconjugate structures. Journal of Computational Chemistry, 2017, 38, 276-287.	1.5	41
69	Chiral switching in biomineral suprastructures induced by homochiral <scp>l</scp> -amino acid. Science Advances, 2018, 4, eaas9819.	4.7	41
70	Advances to tackle backbone flexibility in protein docking. Current Opinion in Structural Biology, 2021, 67, 178-186.	2.6	41
71	Repertoire Analysis of Antibody CDR-H3 Loops Suggests Affinity Maturation Does Not Typically Result in Rigidification. Frontiers in Immunology, 2018, 9, 413.	2.2	39
72	Incorporating biochemical information and backbone flexibility in RosettaDock for CAPRI rounds 6â€“12. Proteins: Structure, Function and Bioinformatics, 2007, 69, 793-800.	1.5	37

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73	Structure-based cross-docking analysis of antibodyâ€“antigen interactions. Scientific Reports, 2017, 7, 8145.	1.6	37
74	Toward a Structure Determination Method for Biomineral-Associated Protein Using Combined Solid-State NMR and Computational Structure Prediction. Structure, 2010, 18, 1678-1687.	1.6	36
75	Identification of Structural Mechanisms of HIV-1 Protease Specificity Using Computational Peptide Docking: Implications for Drug Resistance. Structure, 2009, 17, 1636-1648.	1.6	34
76	Modeling the structure of mAb 14B7 bound to the anthrax protective antigen. Proteins: Structure, Function and Bioinformatics, 2008, 70, 218-230.	1.5	32
77	Expanding the toolkit for membrane protein modeling in Rosetta. Bioinformatics, 2017, 33, 754-756.	1.8	32
78	Applying Linear Interaction Energy Method for Rational Design of Noncompetitive Allosteric Inhibitors of the Sarco- and Endoplasmic Reticulum Calcium-ATPase. Journal of Medicinal Chemistry, 2005, 48, 3005-3014.	2.9	31
79	Targeted DNA Methylation Using an Artificially Bisected M.HhaI Fused to Zinc Fingers. PLoS ONE, 2012, 7, e44852.	1.1	30
80	Microstructure Formation and Kinetics in the Random Sequential Adsorption of Polydisperse Tethered Nanoparticles Modeled as Hard Disks. Langmuir, 2001, 17, 2317-2328.	1.6	28
81	Neutron Reflectometry Studies of the Adsorbed Structure of the Amelogenin, LRAP. Journal of Physical Chemistry B, 2013, 117, 3098-3109.	1.2	28
82	Rheology and dynamics of sheared arrays of colloidal particles. Journal of Rheology, 1998, 42, 1121-1151.	1.3	27
83	Better together: Elements of successful scientific software development in a distributed collaborative community. PLoS Computational Biology, 2020, 16, e1007507.	1.5	27
84	Using the RosettaSurface Algorithm to Predict Protein Structure at Mineral Surfaces. Methods in Enzymology, 2013, 532, 343-366.	0.4	25
85	Nonequilibrium Phase Behavior during the Random Sequential Adsorption of Tethered Hard Disks. Physical Review Letters, 2000, 85, 4430-4433.	2.9	23
86	Structurally distinct toxicity inhibitors bind at common loci on Î²â€amyloid fibril. Protein Science, 2010, 19, 2291-2304.	3.1	23
87	Extending RosettaDock with water, sugar, and pH for prediction of complex structures and affinities for CAPRI rounds 20â€“27. Proteins: Structure, Function and Bioinformatics, 2013, 81, 2201-2209.	1.5	22
88	Interfacial Mineralâ€“Peptide Properties of a Mineral Binding Peptide from Osteonectin and Bone-like Apatite. Chemistry of Materials, 2015, 27, 5562-5569.	3.2	21
89	The structure of the colorectal cancer-associated enzyme GalNAc-T12 reveals how nonconserved residues dictate its function. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 20404-20410.	3.3	21
90	Structure-based non-canonical amino acid design to covalently crosslink an antibodyâ€“antigen complex. Journal of Structural Biology, 2014, 185, 215-222.	1.3	20

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91	Caulobacter crescentus Hfq structure reveals a conserved mechanism of RNA annealing regulation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10978-10987.	3.3	20
92	The structural basis of PTEN regulation by multi-site phosphorylation. Nature Structural and Molecular Biology, 2021, 28, 858-868.	3.6	20
93	Analysis of Protein Kinase Autophosphorylation Using Expressed Protein Ligation and Computational Modeling. Journal of the American Chemical Society, 2008, 130, 5667-5669.	6.6	19
94	Structure Prediction of Domain Insertion Proteins from Structures of Individual Domains. Structure, 2008, 16, 513-527.	1.6	18
95	Modeling oblong proteins and waterâ€mediated interfaces with RosettaDock in CAPRI rounds 28â€“35. Proteins: Structure, Function and Bioinformatics, 2017, 85, 479-486.	1.5	18
96	Robustification of RosettaAntibody and Rosetta SnugDock. PLoS ONE, 2021, 16, e0234282.	1.1	18
97	Protein-Protein Docking with Dynamic Residue Protonation States. PLoS Computational Biology, 2014, 10, e1004018.	1.5	17
98	Modulation of calcium oxalate dihydrate growth by phosphorylated osteopontin peptides. Journal of Structural Biology, 2018, 204, 131-144.	1.3	17
99	â€œHow Do We Do This at a Distance?!â€•A Descriptive Study of Remote Undergraduate Research Programs during COVID-19. CBE Life Sciences Education, 2022, 21, ar1.	1.1	17
100	Origin of anomalous multibody interactions. Nature, 1999, 402, 750-750.	13.7	16
101	Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks. Nature Communications, 2021, 12, 6947.	5.8	16
102	Novel sampling strategies and a coarseâ€grained score function for docking homomers, flexible heteromers, and oligosaccharides using Rosetta in CAPRI rounds 37â€“45. Proteins: Structure, Function and Bioinformatics, 2020, 88, 973-985.	1.5	15
103	Protein docking and steered molecular dynamics suggest alternative phospholamban-binding sites on the SERCA calcium transporter. Journal of Biological Chemistry, 2020, 295, 11262-11274.	1.6	15
104	A high-affinity human TCR-like antibody detects celiac disease gluten peptideâ€“MHC complexes and inhibits T cell activation. Science Immunology, 2021, 6, .	5.6	15
105	Development of a Broadly Accessible, Computationally Guided Biochemistry Course-Based Undergraduate Research Experience. Journal of Chemical Education, 2021, 98, 400-409.	1.1	15
106	A high throughput mutagenic analysis of yeast sumo structure and function. PLoS Genetics, 2017, 13, e1006612.	1.5	15
107	Glycoengineering of Esterase Activity through Metabolic Fluxâ€Based Modulation of Sialic Acid. ChemBioChem, 2017, 18, 1204-1215.	1.3	14
108	Effect of trisodium citrate treatment on hybridoma cell viability. Biotechnology Letters, 1991, 5, 295-298.	0.5	13

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109	Mechanism of Polyubiquitin Chain Recognition by the Human Ubiquitin Conjugating Enzyme Ube2g2. Journal of Biological Chemistry, 2011, 286, 3981-3991.	1.6	13
110	Flexible Backbone Assembly and Refinement of Symmetrical Homomeric Complexes. Structure, 2019, 27, 1041-1051.e8.	1.6	13
111	Truncation of the caspase-related subunit (Gpi8p) of Saccharomyces cerevisiae GPI transamidase: Dimerization revealed. Archives of Biochemistry and Biophysics, 2007, 462, 83-93.	1.4	12
112	Molecular Determinants for Protein Stabilization by Insertional Fusion to a Thermophilic Host Protein. ChemBioChem, 2015, 16, 2392-2402.	1.3	12
113	A cyber-linked undergraduate research experience in computational biomolecular structure prediction and design. PLoS Computational Biology, 2017, 13, e1005837.	1.5	12
114	A Benchmarking Study of Peptideâ€“Biomineral Interactions. Crystal Growth and Design, 2018, 18, 607-616.	1.4	12
115	A humanized yeast system to analyze cleavage of prelamin A by ZMPSTE24. Methods, 2019, 157, 47-55.	1.9	12
116	Computerâ€based engineering of thermostabilized antibody fragments. AICHE Journal, 2020, 66, e16864.	1.8	12
117	Development and Evaluation of GlycanDock: A Proteinâ€“Glycoligand Docking Refinement Algorithm in Rosetta. Journal of Physical Chemistry B, 2021, 125, 6807-6820.	1.2	12
118	Adsorption of Charge-Bidisperse Mixtures of Colloidal Particles. Langmuir, 2001, 17, 7935-7947.	1.6	11
119	Non-H3 CDR template selection in antibody modeling through machine learning. PeerJ, 2019, 7, e6179.	0.9	10
120	Shotgun scanning glycomutagenesis: A simple and efficient strategy for constructing and characterizing neoglycoproteins. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	9
121	Prediction of Calcite Morphology from Computational and Experimental Studies of Mutations of a De Novo-Designed Peptide. Langmuir, 2011, 27, 11520-11527.	1.6	8
122	Computed structures of point deletion mutants and their enzymatic activities. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2844-2860.	1.5	8
123	PyRosetta Jupyter Notebooks Teach Biomolecular Structure Prediction and Design. The Biophysicist, 2021, 2, 108-122.	0.1	8
124	Computational Predictions of the Mutant Behavior of AraC. Journal of Molecular Biology, 2010, 398, 462-470.	2.0	7
125	Colicin-Mediated Transport of DNA through the Iron Transporter FepA. MBio, 2021, 12, e0178721.	1.8	7
126	Comparison of NMR and crystal structures of membrane proteins and computational refinement to improve model quality. Proteins: Structure, Function and Bioinformatics, 2018, 86, 57-74.	1.5	6

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127	Toward the computational design of protein crystals with improved resolution. Acta Crystallographica Section D: Structural Biology, 2019, 75, 1015-1027.	1.1	6
128	An Expanded Benchmark for Antibody-Antigen Docking and Affinity Prediction Reveals Insights into Antibody Recognition Determinants. SSRN Electronic Journal, 0, , .	0.4	6
129	Accurate positioning of functional residues with robotics-inspired computational protein design. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2115480119.	3.3	6
130	Diverse Scientific Benchmarks for Implicit Membrane Energy Functions. Journal of Chemical Theory and Computation, 2021, 17, 5248-5261.	2.3	5
131	Induced fit with replica exchange improves protein complex structure prediction. PLoS Computational Biology, 2022, 18, e1010124.	1.5	5
132	Simultaneous prediction of antibody backbone and side-chain conformations with deep learning. PLoS ONE, 2022, 17, e0258173.	1.1	5
133	Solid-State NMR Studies of Biomineralization Peptides and Proteins. ACS Symposium Series, 2012, , 77-96.	0.5	4
134	Rosetta-MPDock: A Novel Computational Tool for Protein-Protein Docking within the Membrane Bilayer. Biophysical Journal, 2015, 108, 250a.	0.2	4
135	A Parametric Rosetta Energy Function Analysis with LK Peptides on SAM Surfaces. Langmuir, 2018, 34, 5279-5289.	1.6	4
136	Structural Basis for Peptide Substrate Specificities of Glycosyltransferase GalNAc-T2. ACS Catalysis, 2021, 11, 2977-2991.	5.5	4
137	Correction to â€œThe Rosetta All-Atom Energy Function for Macromolecular Modeling and Designâ€• Journal of Chemical Theory and Computation, 2022, 18, 4594-4594.	2.3	4
138	Membrane Protein Engineering with Rosetta. Methods in Molecular Biology, 2021, 2315, 43-57.	0.4	3
139	Understanding the interactions between bone mineral crystals and their binding peptides derived from filamentous phage. Materials Today Advances, 2022, 15, 100263.	2.5	3
140	Efficient Flexible-Backbone Docking of Challenging Protein Complexes. Biophysical Journal, 2018, 114, 344a.	0.2	2
141	Big Data from Sparse Data: Diverse Scientific Benchmarks Reveal Optimization Imperatives for Implicit Membrane Energy Functions. Biophysical Journal, 2020, 118, 361a.	0.2	1
142	The Interaction of Proteins with Solid Surfaces. ChemInform, 2004, 35, no.	0.1	0
143	Fd Bacteriophage Coat Protein Structure Prediction and Design for the Assembly of Hydroxyapatite Nanorods and Bone Tissue Regeneration. Biophysical Journal, 2011, 100, 158a.	0.2	0
144	Towards Fast and Accurate Calculation of Protein pKa Values Exploiting Various Degrees of Conformational Flexibility. Biophysical Journal, 2012, 102, 169a-170a.	0.2	0

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145	A Systematic Computational Method to Predict and Enhance Antibody-Antigen Binding in the Absence of Antibody Crystal Structures. Biophysical Journal, 2012, 102, 621a.	0.2	0
146	Docking and Design of Oligosaccharides, Glycoproteins, and Glycolipids. Biophysical Journal, 2015, 108, 470a.	0.2	0
147	Characterization of Peptides Designed to Control Crystal Nucleation and Growth. Biophysical Journal, 2015, 108, 633a.	0.2	0
148	The Origin of CDR H3 Structural Diversity. Biophysical Journal, 2015, 108, 510a.	0.2	0
149	A Deep-Dive into the Rosetta Energy Function for Biological Macromolecules. Biophysical Journal, 2017, 112, 194a.	0.2	0
150	Evolution of CDR H3 Flexibility at an Immunomic Scale. Biophysical Journal, 2018, 114, 189a-190a.	0.2	0
151	Fast Implicit Potentials for Accurate Prediction and Design of Membrane Protein Structures. Biophysical Journal, 2018, 114, 345a.	0.2	0
152	Computational Design of High-Resolution Protein Crystals. Biophysical Journal, 2018, 114, 575a.	0.2	0
153	Cover Image, Volume 86, Issue 1. Proteins: Structure, Function and Bioinformatics, 2018, 86, C4.	1.5	0
154	Engineering immunity with quantitative tools. Molecular Systems Design and Engineering, 2019, 4, 677-678.	1.7	0
155	Toward Accurate Prediction and Design of Kinked Alpha Helices in Membrane Proteins. Biophysical Journal, 2019, 116, 58a.	0.2	0
156	Structure-Based Prediction of Polypeptide Substrate Specificities of Glycosyltransferases. Biophysical Journal, 2019, 116, 68a.	0.2	0
157	A Thermodynamically-Rigorous, Biologically-Driven Energy Function for Membrane Protein Modeling and Design. Biophysical Journal, 2019, 116, 58a.	0.2	0