Brian Kuhlman

List of Publications by Year
in descending order

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150 papers	16,968 citations	22153 59 h-index	17105 122 g-index
183 all docs	183 docs citations	183 times ranked	17036 citing authors

#	Article	IF	Citations
1	Rosetta3. Methods in Enzymology, 2011, 487, 545-574.	1.0	1,620
2	Design of a Novel Globular Protein Fold with Atomic-Level Accuracy. Science, 2003, 302, 1364-1368.	12.6	1,471
3	The Rosetta All-Atom Energy Function for Macromolecular Modeling and Design. Journal of Chemical Theory and Computation, 2017, 13, 3031-3048.	5.3	1,032
4	Proteinâ€"Protein Docking with Simultaneous Optimization of Rigid-body Displacement and Side-chain Conformations. Journal of Molecular Biology, 2003, 331, 281-299.	4.2	1,017
5	A genetically encoded photoactivatable Rac controls the motility of living cells. Nature, 2009, 461, 104-108.	27.8	960
6	Labelling and optical erasure of synaptic memory traces in the motor cortex. Nature, 2015, 525, 333-338.	27.8	546
7	Engineering an improved light-induced dimer (iLID) for controlling the localization and activity of signaling proteins. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 112-117.	7.1	533
8	Macromolecular modeling and design in Rosetta: recent methods and frameworks. Nature Methods, 2020, 17, 665-680.	19.0	513
9	Advances in protein structure prediction and design. Nature Reviews Molecular Cell Biology, 2019, 20, 681-697.	37.0	489
10	Serverification of Molecular Modeling Applications: The Rosetta Online Server That Includes Everyone (ROSIE). PLoS ONE, 2013, 8, e63906.	2.5	348
11	A Large Scale Test of Computational Protein Design: Folding and Stability of Nine Completely Redesigned Globular Proteins. Journal of Molecular Biology, 2003, 332, 449-460.	4.2	293
12	LOVTRAP: an optogenetic system for photoinduced protein dissociation. Nature Methods, 2016, 13, 755-758.	19.0	267
13	Generation of bispecific IgG antibodies by structure-based design of an orthogonal Fab interface. Nature Biotechnology, 2014, 32, 191-198.	17.5	210
14	Computer-based redesign of a protein folding pathway. Nature Structural Biology, 2001, 8, 602-605.	9.7	206
15	Combined Covalent-Electrostatic Model of Hydrogen Bonding Improves Structure Prediction with Rosetta. Journal of Chemical Theory and Computation, 2015, 11, 609-622.	5.3	204
16	Scientific Benchmarks for Guiding Macromolecular Energy Function Improvement. Methods in Enzymology, 2013, 523, 109-143.	1.0	195
17	RosettaDesign server for protein design. Nucleic Acids Research, 2006, 34, W235-W238.	14.5	184
18	Rapid E2-E3 Assembly and Disassembly Enable Processive Ubiquitylation of Cullin-RING Ubiquitin Ligase Substrates. Cell, 2009, 139, 957-968.	28.9	178

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19	Designing Photoswitchable Peptides Using the AsLOV2 Domain. Chemistry and Biology, 2012, 19, 507-517.	6.0	176
20	Computational Design of a Single Amino Acid Sequence that Can Switch between Two Distinct Protein Folds. Journal of the American Chemical Society, 2006, 128, 1154-1161.	13.7	171
21	A comparison of successful and failed protein interface designs highlights the challenges of designing buried hydrogen bonds. Protein Science, 2013, 22, 74-82.	7.6	166
22	E2 conjugating enzymes must disengage from their E1 enzymes before E3-dependent ubiquitin and ubiquitin-like transfer. Nature Structural and Molecular Biology, 2005, 12, 933-934.	8.2	135
23	Design of structurally distinct proteins using strategies inspired by evolution. Science, 2016, 352, 687-690.	12.6	132
24	Glutamine Triggers Acetylation-Dependent Degradation of Glutamine Synthetase via the Thalidomide Receptor Cereblon. Molecular Cell, 2016, 61, 809-820.	9.7	132
25	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	4.2	131
26	Mechanism of ubiquitin ligation and lysine prioritization by a HECT E3. ELife, 2013, 2, e00828.	6.0	130
27	A â€œsolvated rotamerâ€•approach to modeling water-mediated hydrogen bonds at protein-protein interfaces. Proteins: Structure, Function and Bioinformatics, 2005, 58, 893-904.	2.6	129
28	Structure-Based Design of Supercharged, Highly Thermoresistant Antibodies. Chemistry and Biology, 2012, 19, 449-455.	6.0	127
29	Dual RING E3 Architectures Regulate Multiubiquitination and Ubiquitin Chain Elongation by APC/C. Cell, 2016, 165, 1440-1453.	28.9	126
30	Metal templated design of protein interfaces. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 1827-1832.	7.1	125
31	A Preliminary Survey of the Peptoid Folding Landscape. Journal of the American Chemical Society, 2009, 131, 16798-16807.	13.7	123
32	Structural Insights into Thioether Bond Formation in the Biosynthesis of Sactipeptides. Journal of the American Chemical Society, 2017, 139, 11734-11744.	13.7	119
33	Computational design of affinity and specificity at proteinâ€“protein interfaces. Current Opinion in Structural Biology, 2009, 19, 458-463.	5.7	117
34	COMPUTER-BASED DESIGN OF NOVEL PROTEIN STRUCTURES. Annual Review of Biophysics and Biomolecular Structure, 2006, 35, 49-65.	18.3	116
35	Evolution of a highly active and enantiospecific metalloenzyme from short peptides. Science, 2018, 362, 1285-1288.	12.6	116
36	Catalysis by a De Novo Zinc-Mediated Protein Interface: Implications for Natural Enzyme Evolution and Rational Enzyme Engineering. Biochemistry, 2012, 51, 3933-3940.	2.5	114

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37	High-resolution design of a protein loop. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 17668-17673.	7.1	113
38	Hemi-methylated DNA regulates DNA methylation inheritance through allosteric activation of H3 ubiquitylation by UHRF1. ELife, 2016, 5, .	6.0	111
39	Global analysis of the effects of temperature and denaturant on the folding and unfolding kinetics of the N-terminal domain of the protein L9 1 1Edited by P. E. Wright. Journal of Molecular Biology, 1998, 284, 1661-1670.	4.2	110
40	Design of protein conformational switches. Current Opinion in Structural Biology, 2006, 16, 525-530.	5.7	108
41	Essential Role for Ubiquitin-Ubiquitin-Conjugating Enzyme Interaction in Ubiquitin Discharge from Cdc34 to Substrate. Molecular Cell, 2011, 42, 75-83.	9.7	108
42	Incorporation of Noncanonical Amino Acids into Rosetta and Use in Computational Protein-Peptide Interface Design. PLoS ONE, 2012, 7, e32637.	2.5	98
43	Metal-Mediated Affinity and Orientation Specificity in a Computationally Designed Protein Homodimer. Journal of the American Chemical Society, 2012, 134, 375-385.	13.7	95
44	Control of Protein Activity and Cell Fate Specification via Light-Mediated Nuclear Translocation. PLoS ONE, 2015, 10, e0128443.	2.5	95
45	Structure-based Protocol for Identifying Mutations that Enhance Proteinâ€“Protein Binding Affinities. Journal of Molecular Biology, 2007, 371, 1392-1404.	4.2	90
46	Light-induced nuclear export reveals rapid dynamics of epigenetic modifications. Nature Chemical Biology, 2016, 12, 399-401.	8.0	89
47	Exploring folding free energy landscapes using computational protein design. Current Opinion in Structural Biology, 2004, 14, 89-95.	5.7	88
48	A Generic Program for Multistate Protein Design. PLoS ONE, 2011, 6, e20937.	2.5	88
49	A Minimal TrpRS Catalytic Domain Supports Sense/Antisense Ancestry of Class I and II Aminoacyl-tRNA Synthetases. Molecular Cell, 2007, 25, 851-862.	9.7	87
50	Perturbing the energy landscape for improved packing during computational protein design. Proteins: Structure, Function and Bioinformatics, 2021, 89, 436-449.	2.6	85
51	High-resolution Structural and Thermodynamic Analysis of Extreme Stabilization of Human Procarboxypeptidase by Computational Protein Design. Journal of Molecular Biology, 2007, 366, 1209-1221.	4.2	84
52	Site-specific monoubiquitination activates Ras by impeding GTPase-activating protein function. Nature Structural and Molecular Biology, 2013, 20, 46-52.	8.2	80
53	Global analysis of the thermal and chemical denaturation of the Nâ€terminal domain of the ribosomal protein L9 in H₂O and D₂O. Determination of the thermodynamic parameters, Î”HÂ°, Î”SÂ°, and Î”CÂ°_p, and evaluation of solvent isotope effects. Protein Science, 1998, 7, 2405-2412.	7.6	77
54	Correlating in Vitro and in Vivo Activities of Light-Inducible Dimers: AÂCellular Optogenetics Guide. ACS Synthetic Biology, 2016, 5, 53-64.	3.8	74

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55	Structure and Stability of the N-Terminal Domain of the Ribosomal Protein L9:â€‰ Evidence for Rapid Two-State Folding. Biochemistry, 1998, 37, 1025-1032.	2.5	73
56	Accurate computer-based design of a new backbone conformation in the second turn of protein L. Journal of Molecular Biology, 2002, 315, 471-477.	4.2	73
57	Alternative Computational Protocols for Supercharging Protein Surfaces for Reversible Unfolding and Retention of Stability. PLoS ONE, 2013, 8, e64363.	2.5	73
58	A biosensor generated via high-throughput screening quantifies cell edge Src dynamics. Nature Chemical Biology, 2011, 7, 437-444.	8.0	72
59	Computational design of a symmetric homodimer using Î²-strand assembly. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 20562-20567.	7.1	71
60	Computational Design of a PAK1 Binding Protein. Journal of Molecular Biology, 2010, 400, 257-270.	4.2	69
61	Tuning the Binding Affinities and Reversion Kinetics of a Light Inducible Dimer Allows Control of Transmembrane Protein Localization. Biochemistry, 2016, 55, 5264-5271.	2.5	68
62	Anchored Design of Protein-Protein Interfaces. PLoS ONE, 2011, 6, e20872.	2.5	67
63	Functional Class I and II Amino Acid-activating Enzymes Can Be Coded by Opposite Strands of the Same Gene. Journal of Biological Chemistry, 2015, 290, 19710-19725.	3.4	62
64	Supertertiary Structure of the MAGUK Core from PSD-95. Structure, 2013, 21, 402-413.	3.3	61
65	Computational protein design with explicit consideration of surface hydrophobic patches. Proteins: Structure, Function and Bioinformatics, 2012, 80, 825-838.	2.6	60
66	Sequence Determinants of E2-E6AP Binding Affinity and Specificity. Journal of Molecular Biology, 2007, 369, 419-428.	4.2	59
67	Engineering a proteinâ€“protein interface using a computationally designed library. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 19296-19301.	7.1	59
68	Adding Diverse Noncanonical Backbones to Rosetta: Enabling Peptidomimetic Design. PLoS ONE, 2013, 8, e67051.	2.5	59
69	Tryptophanyl-tRNA Synthetase Urzyme. Journal of Biological Chemistry, 2010, 285, 38590-38601.	3.4	58
70	Increasing Sequence Diversity with Flexible Backbone Protein Design: The Complete Redesign of a Protein Hydrophobic Core. Structure, 2012, 20, 1086-1096.	3.3	58
71	A Bifunctional Role for the UHRF1ÂUBL Domain in the Control of Hemi-methylated DNA-Dependent Histone Ubiquitylation. Molecular Cell, 2018, 72, 753-765.e6.	9.7	58
72	Computationally Designed Bispecific Antibodies using Negative State Repertoires. Structure, 2016, 24, 641-651.	3.3	54

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73	SwiftLib: rapid degenerate-codon-library optimization through dynamic programming. Nucleic Acids Research, 2015, 43, e34-e34.	14.5	53
74	Fab-based bispecific antibody formats with robust biophysical properties and biological activity. MAbs, 2015, 7, 470-482.	5.2	53
75	Lamellipodia are critical for haptotactic sensing and response. Journal of Cell Science, 2016, 129, 2329-42.	2.0	53
76	Computer-Based Redesign of a Î² Sandwich Protein Suggests that Extensive Negative Design Is Not Required for De Novo Î² Sheet Design. Structure, 2008, 16, 1799-1805.	3.3	49
77	An exceptionally stable helix from the ribosomal protein L9: implications for protein folding and stability. Journal of Molecular Biology, 1997, 270, 640-647.	4.2	47
78	Go in! Go out! Inducible control of nuclear localization. Current Opinion in Chemical Biology, 2016, 34, 62-71.	6.1	47
79	Crystal structures and increased stabilization of the protein G variants with switched folding pathways NuG1 and NuG2. Protein Science, 2009, 11, 2924-2931.	7.6	45
80	Computational Design of the Sequence and Structure of a Protein-Binding Peptide. Journal of the American Chemical Society, 2011, 133, 4190-4192.	13.7	44
81	Cooperative folding of a protein mini domain: the peripheral subunit-binding domain of the pyruvate dehydrogenase multienzyme complex 1 1Edited by P. E. Wright. Journal of Molecular Biology, 1998, 276, 479-489.	4.2	39
82	A Conformational Transition State Accompanies Tryptophan Activation by B. stearothermophilus Tryptophanyl-tRNA Synthetase. Structure, 2007, 15, 1272-1284.	3.3	37
83	Rapid Sampling of Hydrogen Bond Networks for Computational Protein Design. Journal of Chemical Theory and Computation, 2018, 14, 2751-2760.	5.3	36
84	Optogenetic control of cofilin and Î±TAT in living cells using Z-lock. Nature Chemical Biology, 2019, 15, 1183-1190.	8.0	36
85	Protein design simulations suggest that side-chain conformational entropy is not a strong determinant of amino acid environmental preferences. Proteins: Structure, Function and Bioinformatics, 2005, 62, 739-748.	2.6	31
86	Computational design of secondâ€site suppressor mutations at proteinâ€“protein interfaces. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1055-1065.	2.6	31
87	Mis-translation of a Computationally Designed Protein Yields an Exceptionally Stable Homodimer: Implications for Protein Engineering and Evolution. Journal of Molecular Biology, 2006, 362, 1004-1024.	4.2	29
88	Using quantum mechanics to improve estimates of amino acid side chain rotamer energies. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1637-1646.	2.6	27
89	Engineering and Application of LOV2-Based Photoswitches. Methods in Enzymology, 2016, 580, 169-190.	1.0	27
90	Designing protein structures and complexes with the molecular modeling program Rosetta. Journal of Biological Chemistry, 2019, 294, 19436-19443.	3.4	27

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91	Better together: Elements of successful scientific software development in a distributed collaborative community. PLoS Computational Biology, 2020, 16, e1007507.	3.2	27
92	Effects of varying the local propensity to form secondary structure on the stability and folding kinetics of a rapid folding mixed Î±/Î² protein: characterization of a truncation mutant of the N-terminal domain of the ribosomal protein L9 1 1Edited by P. E. Wright. Journal of Molecular Biology, 1999, 289, 167-174.	4.2	26
93	G Protein Mono-ubiquitination by the Rsp5 Ubiquitin Ligase. Journal of Biological Chemistry, 2009, 284, 8940-8950.	3.4	25
94	Cells lay their own tracks: optogenetic Cdc42 activation stimulates fibronectin deposition supporting directed migration. Journal of Cell Science, 2017, 130, 2971-2983.	2.0	25
95	Comparative biochemical analysis of UHRF proteins reveals molecular mechanisms that uncouple UHRF2 from DNA methylation maintenance. Nucleic Acids Research, 2018, 46, 4405-4416.	14.5	25
96	Modifications to the Framework Regions Eliminate Chimeric Antigen Receptor Tonic Signaling. Cancer Immunology Research, 2021, 9, 441-453.	3.4	25
97	Computational de novo design of a fourâ€helix bundle proteinâ€"<scp>DND</scp>_4<scp>HB</scp>. Protein Science, 2015, 24, 434-445.	7.6	24
98	Control of microtubule dynamics using an optogenetic microtubule plus endâ€"F-actin cross-linker. Journal of Cell Biology, 2018, 217, 779-793.	5.2	24
99	Computational design of a specific heavy chain/Îº light chain interface for expressing fully IgG bispecific antibodies. Protein Science, 2017, 26, 2021-2038.	7.6	22
100	Physiological temperatures reduce dimerization of dengue and Zika virus recombinant envelope proteins. Journal of Biological Chemistry, 2018, 293, 8922-8933.	3.4	22
101	Designed, highly expressing, thermostable dengue virus 2 envelope protein dimers elicit quaternary epitope antibodies. Science Advances, 2021, 7, eabg4084.	10.3	22
102	Engineering a genetically encoded competitive inhibitor of the KEAP1â€"NRF2 interaction via structure-based design and phage display. Protein Engineering, Design and Selection, 2016, 29, gzv055.	2.1	21
103	Ubiquitin-conjugating Enzyme Cdc34 and Ubiquitin Ligase Skp1-Cullin-F-box Ligase (SCF) Interact through Multiple Conformations. Journal of Biological Chemistry, 2015, 290, 1106-1118.	3.4	20
104	Protocols for Requirement-Driven Protein Design in the Rosetta Modeling Program. Journal of Chemical Information and Modeling, 2018, 58, 895-901.	5.4	20
105	Strategies to control the binding mode of de novo designed protein interactions. Current Opinion in Structural Biology, 2013, 23, 639-646.	5.7	19
106	Requirements for 5â€²dRP/AP lyase activity in Ku. Nucleic Acids Research, 2014, 42, 11136-11143.	14.5	18
107	Boosting protein stability with the computational design of Î²â€sheet surfaces. Protein Science, 2016, 25, 702-710.	7.6	18
108	UbSRD: The Ubiquitin Structural Relational Database. Journal of Molecular Biology, 2016, 428, 679-687.	4.2	18

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109	Kinetics of the Transfer of Ubiquitin from UbcH7 to E6AP. Biochemistry, 2010, 49, 1361-1363.	2.5	17
110	Structural Determinants of Affinity Enhancement between GoLoco Motifs and G-Protein Î± Subunit Mutants. Journal of Biological Chemistry, 2011, 286, 3351-3358.	3.4	17
111	Probing the minimal determinants of zinc binding with computational protein design. Protein Engineering, Design and Selection, 2016, 29, 327-338.	2.1	17
112	Engineering Improved Photoswitches for the Control of Nucleocytoplasmic Distribution. ACS Synthetic Biology, 2018, 7, 2898-2907.	3.8	17
113	Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks. Nature Communications, 2021, 12, 6947.	12.8	16
114	An adaptive dynamic programming algorithm for the side chain placement problem. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2005, , 16-27.	0.7	16
115	Maintaining solvent accessible surface area under rotamer substitution for protein design. Journal of Computational Chemistry, 2007, 28, 1336-1341.	3.3	15
116	Lightâ€Dependent Cytoplasmic Recruitment Enhances the Dynamic Range of a Nuclear Import Photoswitch. ChemBioChem, 2018, 19, 1319-1325.	2.6	15
117	Mechanism of Lysine 48 Selectivity during Polyubiquitin Chain Formation by the Ube2R1/2 Ubiquitin-Conjugating Enzyme. Molecular and Cellular Biology, 2016, 36, 1720-1732.	2.3	14
118	AN ADAPTIVE DYNAMIC PROGRAMMING ALGORITHM FOR THE SIDE CHAIN PLACEMENT PROBLEM. , 2004, , .		14
119	Rotamer-Pair Energy Calculations Using a Trie Data Structure. Lecture Notes in Computer Science, 2005, , 389-400.	1.3	12
120	Computerâ€based engineering of thermostabilized antibody fragments. AICHE Journal, 2020, 66, e16864.	3.6	12
121	Computational stabilization of T cell receptors allows pairing with antibodies to form bispecifics. Nature Communications, 2020, 11, 2330.	12.8	12
122	We FRET so You Donâ€™t Have To: New Models of the Lipoprotein Lipase Dimer. Biochemistry, 2018, 57, 241-254.	2.5	11
123	Redesign of the PAK1 Autoinhibitory Domain for Enhanced Stability and Affinity in Biosensor Applications. Journal of Molecular Biology, 2011, 413, 513-522.	4.2	10
124	Combined computational design of a zincâ€binding site and a proteinâ€“protein interaction: One open zinc coordination site was not a robust hotspot for de novo ubiquitin binding. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1245-1255.	2.6	10
125	Engineering a Protein Binder Specific for p38Î± with Interface Expansion. Biochemistry, 2018, 57, 4526-4535.	2.5	10
126	An optogenetic switch for the Set2 methyltransferase provides evidence for transcription-dependent and -independent dynamics of H3K36 methylation. Genome Research, 2020, 30, 1605-1617.	5.5	10

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127	From Computational Design to a Protein That Binds. Science, 2011, 332, 801-802.	12.6	9
128	Cages from coils. Nature Biotechnology, 2013, 31, 809-810.	17.5	9
129	Using anchoring motifs for the computational design of proteinâ€“protein interactions. Biochemical Society Transactions, 2013, 41, 1141-1145.	3.4	9
130	Dimerization of Dengue Virus E Subunits Impacts Antibody Function and Domain Focus. Journal of Virology, 2020, 94, .	3.4	9
131	PyRosetta Jupyter Notebooks Teach Biomolecular Structure Prediction and Design. The Biophysicist, 2021, 2, 108-122.	0.3	8
132	Amide proton exchange measurements as a probe of the stability and dynamics of the nâ€terminal domain of the ribosomal protein L9: Comparison with the intact protein. Protein Science, 1998, 7, 1994-1997.	7.6	7
133	Designer proteins that competitively inhibit GÎ±q by targeting its effector site. Journal of Biological Chemistry, 2021, 297, 101348.	3.4	7
134	Design and engineering of light-sensitive protein switches. Current Opinion in Structural Biology, 2022, 74, 102377.	5.7	7
135	Computational Repacking of HIF-2Î± Cavity Replaces Water-Based Stabilized Core. Structure, 2016, 24, 1918-1927.	3.3	6
136	A Computational Protocol for Regulating Protein Binding Reactions with a Light-Sensitive Protein Dimer. Journal of Molecular Biology, 2020, 432, 805-814.	4.2	6
137	<scp>AlphaFold</scp> accurately predicts distinct conformations based on the oligomeric state of a de novo designed protein. Protein Science, 2022, 31, .	7.6	6
138	A structural bioinformatics approach for identifying proteins predisposed to bind linear epitopes on pre-selected target proteins. Protein Engineering, Design and Selection, 2013, 26, 283-289.	2.1	4
139	Data in support of UbSRD: The Ubiquitin Structural Relational Database. Data in Brief, 2015, 5, 605-615.	1.0	3
140	Computational Design of Protein Linkers. Methods in Molecular Biology, 2016, 1414, 341-351.	0.9	3
141	From Protein Design to the Energy Landscape of a Cold Unfolding Protein. Journal of Physical Chemistry B, 2022, 126, 1212-1231.	2.6	3
142	Future Challenges Of Computational Protein Design. , 2009, , .		2
143	Redesigning the NEDD8 Pathway with a Bacterial Genetic Screen for Ubiquitin-Like Molecule Transfer. Journal of Molecular Biology, 2012, 418, 161-166.	4.2	2
144	Comparative Analysis of Sulfoniumâ˜Ï€, Ammoniumâ˜Ï€, and Sulfurâ˜Ï€ Interactions and Relevance to SAM-Dependent Methyltransferases. Journal of the American Chemical Society, 2022, 144, 2535-2545.	13.7	2

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145	A conserved set of mutations for stabilizing soluble envelope protein dimers from dengue and Zika viruses to advance the development of subunit vaccines. Journal of Biological Chemistry, 2022, 298, 102079.	3.4	2
146	A Systematic Computational Method to Predict and Enhance Antibody-Antigen Binding in the Absence of Antibody Crystal Structures. Biophysical Journal, 2012, 102, 621a.	0.5	0
147	A Deep-Dive into the Rosetta Energy Function for Biological Macromolecules. Biophysical Journal, 2017, 112, 194a.	0.5	0
148	Analysis of Relative Binding Affinity Predictions for Protein-Protein Complexes. Biophysical Journal, 2018, 114, 408a.	0.5	0
149	Ras Activity Regulation by Monoubiquitination. FASEB Journal, 2013, 27, 1046.3.	0.5	0
150	Designing new protein structures and functions with the molecular modeling program Rosetta. FASEB Journal, 2019, 33, .	0.5	0