

# 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	Comparative Analysis of Sulfonium <sup>+</sup> , Ammonium <sup>+</sup> , and Sulfur <sup>+</sup> Interactions and Relevance to SAM-Dependent Methyltransferases. <i>Journal of the American Chemical Society</i> , 2022, 144, 2535-2545.	13.7	2
2	From Protein Design to the Energy Landscape of a Cold Unfolding Protein. <i>Journal of Physical Chemistry B</i> , 2022, 126, 1212-1231.	2.6	3
3	Design and engineering of light-sensitive protein switches. <i>Current Opinion in Structural Biology</i> , 2022, 74, 102377.	5.7	7
4	A conserved set of mutations for stabilizing soluble envelope protein dimers from dengue and Zika viruses to advance the development of subunit vaccines. <i>Journal of Biological Chemistry</i> , 2022, 298, 102079.	3.4	2
5	<scp>AlphaFold</scp> accurately predicts distinct conformations based on the oligomeric state of a de novo designed protein. <i>Protein Science</i> , 2022, 31, .	7.6	6
6	Perturbing the energy landscape for improved packing during computational protein design. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 436-449.	2.6	85
7	Modifications to the Framework Regions Eliminate Chimeric Antigen Receptor Tonic Signaling. <i>Cancer Immunology Research</i> , 2021, 9, 441-453.	3.4	25
8	PyRosetta Jupyter Notebooks Teach Biomolecular Structure Prediction and Design. <i>The Biophysicist</i> , 2021, 2, 108-122.	0.3	8
9	Designed, highly expressing, thermostable dengue virus 2 envelope protein dimers elicit quaternary epitope antibodies. <i>Science Advances</i> , 2021, 7, eabg4084.	10.3	22
10	Designer proteins that competitively inhibit G $\beta$ q by targeting its effector site. <i>Journal of Biological Chemistry</i> , 2021, 297, 101348.	3.4	7
11	Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks. <i>Nature Communications</i> , 2021, 12, 6947.	12.8	16
12	A Computational Protocol for Regulating Protein Binding Reactions with a Light-Sensitive Protein Dimer. <i>Journal of Molecular Biology</i> , 2020, 432, 805-814.	4.2	6
13	Computer-based engineering of thermostabilized antibody fragments. <i>AIChE Journal</i> , 2020, 66, e16864.	3.6	12
14	An optogenetic switch for the Set2 methyltransferase provides evidence for transcription-dependent and -independent dynamics of H3K36 methylation. <i>Genome Research</i> , 2020, 30, 1605-1617.	5.5	10
15	Better together: Elements of successful scientific software development in a distributed collaborative community. <i>PLoS Computational Biology</i> , 2020, 16, e1007507.	3.2	27
16	Macromolecular modeling and design in Rosetta: recent methods and frameworks. <i>Nature Methods</i> , 2020, 17, 665-680.	19.0	513
17	Computational stabilization of T cell receptors allows pairing with antibodies to form bispecifics. <i>Nature Communications</i> , 2020, 11, 2330.	12.8	12
18	Dimerization of Dengue Virus E Subunits Impacts Antibody Function and Domain Focus. <i>Journal of Virology</i> , 2020, 94, .	3.4	9

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19	Advances in protein structure prediction and design. <i>Nature Reviews Molecular Cell Biology</i> , 2019, 20, 681-697.	37.0	489
20	Designing protein structures and complexes with the molecular modeling program Rosetta. <i>Journal of Biological Chemistry</i> , 2019, 294, 19436-19443.	3.4	27
21	Optogenetic control of cofilin and $\hat{\pm}$ TAT in living cells using Z-lock. <i>Nature Chemical Biology</i> , 2019, 15, 1183-1190.	8.0	36
22	Designing new protein structures and functions with the molecular modeling program Rosetta. <i>FASEB Journal</i> , 2019, 33, .	0.5	0
23	Comparative biochemical analysis of UHRF proteins reveals molecular mechanisms that uncouple UHRF2 from DNA methylation maintenance. <i>Nucleic Acids Research</i> , 2018, 46, 4405-4416.	14.5	25
24	Light-Dependent Cytoplasmic Recruitment Enhances the Dynamic Range of a Nuclear Import Photoswitch. <i>ChemBioChem</i> , 2018, 19, 1319-1325.	2.6	15
25	Physiological temperatures reduce dimerization of dengue and Zika virus recombinant envelope proteins. <i>Journal of Biological Chemistry</i> , 2018, 293, 8922-8933.	3.4	22
26	Protocols for Requirement-Driven Protein Design in the Rosetta Modeling Program. <i>Journal of Chemical Information and Modeling</i> , 2018, 58, 895-901.	5.4	20
27	Rapid Sampling of Hydrogen Bond Networks for Computational Protein Design. <i>Journal of Chemical Theory and Computation</i> , 2018, 14, 2751-2760.	5.3	36
28	Control of microtubule dynamics using an optogenetic microtubule plus end-actin cross-linker. <i>Journal of Cell Biology</i> , 2018, 217, 779-793.	5.2	24
29	We FRET so You Don't Have To: New Models of the Lipoprotein Lipase Dimer. <i>Biochemistry</i> , 2018, 57, 241-254.	2.5	11
30	Analysis of Relative Binding Affinity Predictions for Protein-Protein Complexes. <i>Biophysical Journal</i> , 2018, 114, 408a.	0.5	0
31	Engineering Improved Photoswitches for the Control of Nucleocytoplasmic Distribution. <i>ACS Synthetic Biology</i> , 2018, 7, 2898-2907.	3.8	17
32	Evolution of a highly active and enantiospecific metalloenzyme from short peptides. <i>Science</i> , 2018, 362, 1285-1288.	12.6	116
33	A Bifunctional Role for the UHRF1 $\hat{\Delta}$ UBL Domain in the Control of Hemi-methylated DNA-Dependent Histone Ubiquitylation. <i>Molecular Cell</i> , 2018, 72, 753-765.e6.	9.7	58
34	Engineering a Protein Binder Specific for p38 $\hat{\pm}$ with Interface Expansion. <i>Biochemistry</i> , 2018, 57, 4526-4535.	2.5	10
35	The Rosetta All-Atom Energy Function for Macromolecular Modeling and Design. <i>Journal of Chemical Theory and Computation</i> , 2017, 13, 3031-3048.	5.3	1,032
36	A Deep-Dive into the Rosetta Energy Function for Biological Macromolecules. <i>Biophysical Journal</i> , 2017, 112, 194a.	0.5	0

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37	Computational design of a specific heavy chain/light chain interface for expressing fully IgG bispecific antibodies. <i>Protein Science</i> , 2017, 26, 2021-2038.	7.6	22
38	Cells lay their own tracks: optogenetic Cdc42 activation stimulates fibronectin deposition supporting directed migration. <i>Journal of Cell Science</i> , 2017, 130, 2971-2983.	2.0	25
39	Structural Insights into Thioether Bond Formation in the Biosynthesis of Sactipeptides. <i>Journal of the American Chemical Society</i> , 2017, 139, 11734-11744.	13.7	119
40	Engineering a genetically encoded competitive inhibitor of the KEAP1/NRF2 interaction via structure-based design and phage display. <i>Protein Engineering, Design and Selection</i> , 2016, 29, gzv055.	2.1	21
41	Go in! Go out! Inducible control of nuclear localization. <i>Current Opinion in Chemical Biology</i> , 2016, 34, 62-71.	6.1	47
42	Probing the minimal determinants of zinc binding with computational protein design. <i>Protein Engineering, Design and Selection</i> , 2016, 29, 327-338.	2.1	17
43	Light-induced nuclear export reveals rapid dynamics of epigenetic modifications. <i>Nature Chemical Biology</i> , 2016, 12, 399-401.	8.0	89
44	Computational Design of Protein Linkers. <i>Methods in Molecular Biology</i> , 2016, 1414, 341-351.	0.9	3
45	Design of structurally distinct proteins using strategies inspired by evolution. <i>Science</i> , 2016, 352, 687-690.	12.6	132
46	Mechanism of Lysine 48 Selectivity during Polyubiquitin Chain Formation by the Ube2R1/2 Ubiquitin-Conjugating Enzyme. <i>Molecular and Cellular Biology</i> , 2016, 36, 1720-1732.	2.3	14
47	Lamellipodia are critical for haptotactic sensing and response. <i>Journal of Cell Science</i> , 2016, 129, 2329-42.	2.0	53
48	Computational Repacking of HIF-2 $\alpha$ Cavity Replaces Water-Based Stabilized Core. <i>Structure</i> , 2016, 24, 1918-1927.	3.3	6
49	Tuning the Binding Affinities and Reversion Kinetics of a Light Inducible Dimer Allows Control of Transmembrane Protein Localization. <i>Biochemistry</i> , 2016, 55, 5264-5271.	2.5	68
50	LOVTRAP: an optogenetic system for photoinduced protein dissociation. <i>Nature Methods</i> , 2016, 13, 755-758.	19.0	267
51	Engineering and Application of LOV2-Based Photoswitches. <i>Methods in Enzymology</i> , 2016, 580, 169-190.	1.0	27
52	Boosting protein stability with the computational design of $\beta$ -sheet surfaces. <i>Protein Science</i> , 2016, 25, 702-710.	7.6	18
53	Dual RING E3 Architectures Regulate Multiubiquitination and Ubiquitin Chain Elongation by APC/C. <i>Cell</i> , 2016, 165, 1440-1453.	28.9	126
54	UbsRD: The Ubiquitin Structural Relational Database. <i>Journal of Molecular Biology</i> , 2016, 428, 679-687.	4.2	18

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55	Glutamine Triggers Acetylation-Dependent Degradation of Glutamine Synthetase via the Thalidomide Receptor Cereblon. <i>Molecular Cell</i> , 2016, 61, 809-820.	9.7	132
56	Computationally Designed Bispecific Antibodies using Negative State Repertoires. <i>Structure</i> , 2016, 24, 641-651.	3.3	54
57	Correlating <i>in Vitro</i> and <i>in Vivo</i> Activities of Light-Inducible Dimers: A Cellular Optogenetics Guide. <i>ACS Synthetic Biology</i> , 2016, 5, 53-64.	3.8	74
58	Hemi-methylated DNA regulates DNA methylation inheritance through allosteric activation of H3 ubiquitylation by UHRF1. <i>ELife</i> , 2016, 5, .	6.0	111
59	Ubiquitin-conjugating Enzyme Cdc34 and Ubiquitin Ligase Skp1-Cullin-F-box Ligase (SCF) Interact through Multiple Conformations. <i>Journal of Biological Chemistry</i> , 2015, 290, 1106-1118.	3.4	20
60	Data in support of UbSRD: The Ubiquitin Structural Relational Database. <i>Data in Brief</i> , 2015, 5, 605-615.	1.0	3
61	SwiftLib: rapid degenerate-codon-library optimization through dynamic programming. <i>Nucleic Acids Research</i> , 2015, 43, e34-e34.	14.5	53
62	Combined Covalent-Electrostatic Model of Hydrogen Bonding Improves Structure Prediction with Rosetta. <i>Journal of Chemical Theory and Computation</i> , 2015, 11, 609-622.	5.3	204
63	Engineering an improved light-induced dimer (iLID) for controlling the localization and activity of signaling proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 112-117.	7.1	533
64	Functional Class I and II Amino Acid-activating Enzymes Can Be Coded by Opposite Strands of the Same Gene. <i>Journal of Biological Chemistry</i> , 2015, 290, 19710-19725.	3.4	62
65	Fab-based bispecific antibody formats with robust biophysical properties and biological activity. <i>MAbs</i> , 2015, 7, 470-482.	5.2	53
66	Labelling and optical erasure of synaptic memory traces in the motor cortex. <i>Nature</i> , 2015, 525, 333-338.	27.8	546
67	Computational de novo design of a four-helix bundle protein. <i>Protein Science</i> , 2015, 24, 434-445.	7.6	24
68	Control of Protein Activity and Cell Fate Specification via Light-Mediated Nuclear Translocation. <i>PLoS ONE</i> , 2015, 10, e0128443.	2.5	95
69	Generation of bispecific IgG antibodies by structure-based design of an orthogonal Fab interface. <i>Nature Biotechnology</i> , 2014, 32, 191-198.	17.5	210
70	Requirements for 5' dRP/AP lyase activity in Ku. <i>Nucleic Acids Research</i> , 2014, 42, 11136-11143.	14.5	18
71	Strategies to control the binding mode of de novo designed protein interactions. <i>Current Opinion in Structural Biology</i> , 2013, 23, 639-646.	5.7	19
72	Scientific Benchmarks for Guiding Macromolecular Energy Function Improvement. <i>Methods in Enzymology</i> , 2013, 523, 109-143.	1.0	195

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73	Cages from coils. <i>Nature Biotechnology</i> , 2013, 31, 809-810.	17.5	9
74	Site-specific monoubiquitination activates Ras by impeding GTPase-activating protein function. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 46-52.	8.2	80
75	A comparison of successful and failed protein interface designs highlights the challenges of designing buried hydrogen bonds. <i>Protein Science</i> , 2013, 22, 74-82.	7.6	166
76	Supertertiary Structure of the MAGUK Core from PSD-95. <i>Structure</i> , 2013, 21, 402-413.	3.3	61
77	Using anchoring motifs for the computational design of protein-protein interactions. <i>Biochemical Society Transactions</i> , 2013, 41, 1141-1145.	3.4	9
78	A structural bioinformatics approach for identifying proteins predisposed to bind linear epitopes on pre-selected target proteins. <i>Protein Engineering, Design and Selection</i> , 2013, 26, 283-289.	2.1	4
79	Combined computational design of a zinc-binding site and a protein-protein interaction: One open zinc coordination site was not a robust hotspot for de novo ubiquitin binding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1245-1255.	2.6	10
80	Adding Diverse Noncanonical Backbones to Rosetta: Enabling Peptidomimetic Design. <i>PLoS ONE</i> , 2013, 8, e67051.	2.5	59
81	Serverification of Molecular Modeling Applications: The Rosetta Online Server That Includes Everyone (ROSIE). <i>PLoS ONE</i> , 2013, 8, e63906.	2.5	348
82	Alternative Computational Protocols for Supercharging Protein Surfaces for Reversible Unfolding and Retention of Stability. <i>PLoS ONE</i> , 2013, 8, e64363.	2.5	73
83	Mechanism of ubiquitin ligation and lysine prioritization by a HECT E3. <i>ELife</i> , 2013, 2, e00828.	6.0	130
84	Ras Activity Regulation by Monoubiquitination. <i>FASEB Journal</i> , 2013, 27, 1046.3.	0.5	0
85	Metal-Mediated Affinity and Orientation Specificity in a Computationally Designed Protein Homodimer. <i>Journal of the American Chemical Society</i> , 2012, 134, 375-385.	13.7	95
86	Redesigning the NEDD8 Pathway with a Bacterial Genetic Screen for Ubiquitin-Like Molecule Transfer. <i>Journal of Molecular Biology</i> , 2012, 418, 161-166.	4.2	2
87	A Systematic Computational Method to Predict and Enhance Antibody-Antigen Binding in the Absence of Antibody Crystal Structures. <i>Biophysical Journal</i> , 2012, 102, 621a.	0.5	0
88	Incorporation of Noncanonical Amino Acids into Rosetta and Use in Computational Protein-Peptide Interface Design. <i>PLoS ONE</i> , 2012, 7, e32637.	2.5	98
89	Computational protein design with explicit consideration of surface hydrophobic patches. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 825-838.	2.6	60
90	Catalysis by a De Novo Zinc-Mediated Protein Interface: Implications for Natural Enzyme Evolution and Rational Enzyme Engineering. <i>Biochemistry</i> , 2012, 51, 3933-3940.	2.5	114

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91	Structure-Based Design of Supercharged, Highly Thermoresistant Antibodies. <i>Chemistry and Biology</i> , 2012, 19, 449-455.	6.0	127
92	Designing Photoswitchable Peptides Using the AsLOV2 Domain. <i>Chemistry and Biology</i> , 2012, 19, 507-517.	6.0	176
93	Increasing Sequence Diversity with Flexible Backbone Protein Design: The Complete Redesign of a Protein Hydrophobic Core. <i>Structure</i> , 2012, 20, 1086-1096.	3.3	58
94	Computational Design of the Sequence and Structure of a Protein-Binding Peptide. <i>Journal of the American Chemical Society</i> , 2011, 133, 4190-4192.	13.7	44
95	A biosensor generated via high-throughput screening quantifies cell edge Src dynamics. <i>Nature Chemical Biology</i> , 2011, 7, 437-444.	8.0	72
96	Rosetta3. <i>Methods in Enzymology</i> , 2011, 487, 545-574.	1.0	1,620
97	Essential Role for Ubiquitin-Ubiquitin-Conjugating Enzyme Interaction in Ubiquitin Discharge from Cdc34 to Substrate. <i>Molecular Cell</i> , 2011, 42, 75-83.	9.7	108
98	Redesign of the PAK1 Autoinhibitory Domain for Enhanced Stability and Affinity in Biosensor Applications. <i>Journal of Molecular Biology</i> , 2011, 413, 513-522.	4.2	10
99	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. <i>Journal of Molecular Biology</i> , 2011, 414, 289-302.	4.2	131
100	Anchored Design of Protein-Protein Interfaces. <i>PLoS ONE</i> , 2011, 6, e20872.	2.5	67
101	From Computational Design to a Protein That Binds. <i>Science</i> , 2011, 332, 801-802.	12.6	9
102	Structural Determinants of Affinity Enhancement between GoLoco Motifs and G-Protein $\beta$ Subunit Mutants. <i>Journal of Biological Chemistry</i> , 2011, 286, 3351-3358.	3.4	17
103	Computational design of a symmetric homodimer using $\beta^2$ -strand assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 20562-20567.	7.1	71
104	A Generic Program for Multistate Protein Design. <i>PLoS ONE</i> , 2011, 6, e20937.	2.5	88
105	Computational design of second-site suppressor mutations at protein-protein interfaces. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 1055-1065.	2.6	31
106	Metal templated design of protein interfaces. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 1827-1832.	7.1	125
107	Engineering a protein-protein interface using a computationally designed library. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19296-19301.	7.1	59
108	Tryptophanyl-tRNA Synthetase Urzyme. <i>Journal of Biological Chemistry</i> , 2010, 285, 38590-38601.	3.4	58

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109	Kinetics of the Transfer of Ubiquitin from UbcH7 to E6AP. <i>Biochemistry</i> , 2010, 49, 1361-1363.	2.5	17
110	Computational Design of a PAK1 Binding Protein. <i>Journal of Molecular Biology</i> , 2010, 400, 257-270.	4.2	69
111	G Protein Mono-ubiquitination by the Rsp5 Ubiquitin Ligase. <i>Journal of Biological Chemistry</i> , 2009, 284, 8940-8950.	3.4	25
112	Computational design of affinity and specificity at protein-protein interfaces. <i>Current Opinion in Structural Biology</i> , 2009, 19, 458-463.	5.7	117
113	A genetically encoded photoactivatable Rac controls the motility of living cells. <i>Nature</i> , 2009, 461, 104-108.	27.8	960
114	A Preliminary Survey of the Peptoid Folding Landscape. <i>Journal of the American Chemical Society</i> , 2009, 131, 16798-16807.	13.7	123
115	Rapid E2-E3 Assembly and Disassembly Enable Processive Ubiquitylation of Cullin-RING Ubiquitin Ligase Substrates. <i>Cell</i> , 2009, 139, 957-968.	28.9	178
116	Crystal structures and increased stabilization of the protein G variants with switched folding pathways NuG1 and NuG2. <i>Protein Science</i> , 2009, 11, 2924-2931.	7.6	45
117	Future Challenges Of Computational Protein Design. , 2009, , .		2
118	Using quantum mechanics to improve estimates of amino acid side chain rotamer energies. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1637-1646.	2.6	27
119	Computer-Based Redesign of a $\beta^2$ Sandwich Protein Suggests that Extensive Negative Design Is Not Required for De Novo $\beta^2$ Sheet Design. <i>Structure</i> , 2008, 16, 1799-1805.	3.3	49
120	High-resolution design of a protein loop. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 17668-17673.	7.1	113
121	High-resolution Structural and Thermodynamic Analysis of Extreme Stabilization of Human Procarboxypeptidase by Computational Protein Design. <i>Journal of Molecular Biology</i> , 2007, 366, 1209-1221.	4.2	84
122	Sequence Determinants of E2-E6AP Binding Affinity and Specificity. <i>Journal of Molecular Biology</i> , 2007, 369, 419-428.	4.2	59
123	Structure-based Protocol for Identifying Mutations that Enhance Protein-Protein Binding Affinities. <i>Journal of Molecular Biology</i> , 2007, 371, 1392-1404.	4.2	90
124	A Minimal TrpRS Catalytic Domain Supports Sense/Antisense Ancestry of Class I and II Aminoacyl-tRNA Synthetases. <i>Molecular Cell</i> , 2007, 25, 851-862.	9.7	87
125	Maintaining solvent accessible surface area under rotamer substitution for protein design. <i>Journal of Computational Chemistry</i> , 2007, 28, 1336-1341.	3.3	15
126	A Conformational Transition State Accompanies Tryptophan Activation by B. stearothermophilus Tryptophanyl-tRNA Synthetase. <i>Structure</i> , 2007, 15, 1272-1284.	3.3	37



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127	COMPUTER-BASED DESIGN OF NOVEL PROTEIN STRUCTURES. Annual Review of Biophysics and Biomolecular Structure, 2006, 35, 49-65.	18.3	116
128	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
129	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
130	Design of protein conformational switches. Current Opinion in Structural Biology, 2006, 16, 525-530.	5.7	108
131	RosettaDesign server for protein design. Nucleic Acids Research, 2006, 34, W235-W238.	14.5	184
132	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
133	A "solvated rotamer" approach to modeling water-mediated hydrogen bonds at protein-protein interfaces. Proteins: Structure, Function and Bioinformatics, 2005, 58, 893-904.	2.6	129
134	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
135	Rotamer-Pair Energy Calculations Using a Trie Data Structure. Lecture Notes in Computer Science, 2005, , 389-400.	1.3	12
136	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
137	Exploring folding free energy landscapes using computational protein design. Current Opinion in Structural Biology, 2004, 14, 89-95.	5.7	88
138	AN ADAPTIVE DYNAMIC PROGRAMMING ALGORITHM FOR THE SIDE CHAIN PLACEMENT PROBLEM. , 2004, , .		14
139	Design of a Novel Globular Protein Fold with Atomic-Level Accuracy. Science, 2003, 302, 1364-1368.	12.6	1,471
140	Protein-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
141	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
142	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
143	Computer-based redesign of a protein folding pathway. Nature Structural Biology, 2001, 8, 602-605.	9.7	206
144	Effects of varying the local propensity to form secondary structure on the stability and folding kinetics of a rapid folding mixed $\alpha/\beta$ protein: characterization of a truncation mutant of the N-terminal domain of the ribosomal protein L9. Edited by P. E. Wright. Journal of Molecular Biology, 1999, 289, 167-174.	4.2	26

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145	Amide proton exchange measurements as a probe of the stability and dynamics of the N-terminal domain of the ribosomal protein L9: Comparison with the intact protein. <i>Protein Science</i> , 1998, 7, 1994-1997.	7.6	7
146	Global analysis of the thermal and chemical denaturation of the N-terminal domain of the ribosomal protein L9 in H <sub>2</sub> O and D <sub>2</sub> O. Determination of the thermodynamic parameters, $\Delta H^\circ$ , $\Delta S^\circ$ , and $\Delta C_p^\circ$ , and evaluation of solvent isotope effects. <i>Protein Science</i> , 1998, 7, 2405-2412.	7.6	77
147	Structure and Stability of the N-Terminal Domain of the Ribosomal Protein L9: Evidence for Rapid Two-State Folding. <i>Biochemistry</i> , 1998, 37, 1025-1032.	2.5	73
148	Cooperative folding of a protein mini domain: the peripheral subunit-binding domain of the pyruvate dehydrogenase multienzyme complex 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1998, 276, 479-489.	4.2	39
149	Global analysis of the effects of temperature and denaturant on the folding and unfolding kinetics of the N-terminal domain of the protein L9 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1998, 284, 1661-1670.	4.2	110
150	An exceptionally stable helix from the ribosomal protein L9: implications for protein folding and stability. <i>Journal of Molecular Biology</i> , 1997, 270, 640-647.	4.2	47