

Hui Lu

List of Publications by Year in descending order

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Version: 2024-02-01

135
papers

9,102
citations

76196

40
h-index

45213

90
g-index

140
all docs

140
docs citations

140
times ranked

11504
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive Analysis of Ubiquitously Expressed Genes in Humans from A Data-driven Perspective. <i>Genomics, Proteomics and Bioinformatics</i> , 2023, 21, 164-176.	3.0	9
2	Inferring Time-Lagged Causality Using the Derivative of Single-Cell Expression. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3348.	1.8	1
3	Weight spectrum and executive function in adolescents: the moderating role of negative emotions. <i>Child and Adolescent Psychiatry and Mental Health</i> , 2022, 16, 34.	1.2	5
4	Loosely-packed dynamical structures with partially-melted surface being the key for thermophilic argonaute proteins achieving high DNA-cleavage activity. <i>Nucleic Acids Research</i> , 2022, 50, 7529-7544.	6.5	9
5	Molecular dynamics provides new insights into the mechanism of calcium signal transduction and interdomain interactions in cardiac troponin. <i>FEBS Open Bio</i> , 2021, 11, 1841-1853.	1.0	5
6	Association of serum chemokine ligand 21 levels with asthma control in adults. <i>Clinics</i> , 2021, 76, e1713.	0.6	0
7	RePhine: An Integrative Method for Identification of Drug Response-related Transcriptional Regulators. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 534-548.	3.0	5
8	Improving glomerular filtration rate estimation by semi-supervised learning: a development and external validation study. <i>International Urology and Nephrology</i> , 2021, 53, 1649-1658.	0.6	1
9	Argonaute integrated single-tube PCR system enables supersensitive detection of rare mutations. <i>Nucleic Acids Research</i> , 2021, 49, e75-e75.	6.5	66
10	Evaluation Framework for Successful Artificial Intelligence-Enabled Clinical Decision Support Systems: Mixed Methods Study. <i>Journal of Medical Internet Research</i> , 2021, 23, e25929.	2.1	17
11	Demographics, in-hospital analysis, and prevalence of 33 rare diseases with effective treatment in Shanghai. <i>Orphanet Journal of Rare Diseases</i> , 2021, 16, 262.	1.2	4
12	Pitt-Hopkins syndrome: phenotypic and genotypic description of four unrelated patients and structural analysis of corresponding missense mutations. <i>Neurogenetics</i> , 2021, 22, 161-169.	0.7	4
13	Association of HIV infection and cognitive impairment in older adults: A meta-analysis. <i>Ageing Research Reviews</i> , 2021, 68, 101310.	5.0	11
14	Lymphocyte activation gene-3 is associated with programmed death-ligand 1 and programmed cell death protein 1 in small cell lung cancer. <i>Annals of Translational Medicine</i> , 2021, 9, 1468-1468.	0.7	10
15	DNA Damage Response and Repair Gene Alterations Increase Tumor Mutational Burden and Promote Poor Prognosis of Advanced Lung Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 708294.	1.3	15
16	Hemodynamic Phenotypes of Hypertension Based on Cardiac Output and Systemic Vascular Resistance. <i>American Journal of Medicine</i> , 2020, 133, e127-e139.	0.6	14
17	Nuclear Segmentation in Histopathological Images Using Two-Stage Stacked U-Nets With Attention Mechanism. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 573866.	2.0	31
18	Correlations Between Phenotypes and Biological Process Ontologies in Monogenic Human Diseases. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2020, 12, 547-554.	2.2	1

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19	Integrative Analysis of Membrane Proteome and MicroRNA Reveals Novel Lung Cancer Metastasis Biomarkers. <i>Frontiers in Genetics</i> , 2020, 11, 1023.	1.1	7
20	Closing Human Reference Genome Gaps: Identifying and Characterizing Gap-Closing Sequences. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2801-2809.	0.8	10
21	Relationship of Age With the Hemodynamic Parameters in Individuals With Elevated Blood Pressure. <i>Journal of the American Geriatrics Society</i> , 2020, 68, 1520-1528.	1.3	7
22	Improving accuracy of estimating glomerular filtration rate using artificial neural network: model development and validation. <i>Journal of Translational Medicine</i> , 2020, 18, 120.	1.8	6
23	Texture Synthesis Based Thyroid Nodule Detection From Medical Ultrasound Images: Interpreting and Suppressing the Adversarial Effect of In-place Manual Annotation. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 599.	2.0	15
24	Improving the Diagnosis of Phenylketonuria by Using a Machine Learning-Based Screening Model of Neonatal MRM Data. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 115.	1.6	12
25	Identifying and characterizing the effects of calendar and environmental conditions on pediatric admissions in Shanghai. <i>Journal of Big Data</i> , 2019, 6, .	6.9	1
26	Residue-Specific Force Field Improving the Sample of Intrinsically Disordered Proteins and Folded Proteins. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 4793-4805.	2.5	39
27	Functional Site Discovery From Incomplete Training Data: A Case Study With Nucleic Acid-Binding Proteins. <i>Frontiers in Genetics</i> , 2019, 10, 729.	1.1	1
28	Analysis of economic burden and its associated factors of twenty-three rare diseases in Shanghai. <i>Orphanet Journal of Rare Diseases</i> , 2019, 14, 233.	1.2	11
29	A Novel Joint Gene Set Analysis Framework Improves Identification of Enriched Pathways in Cross Disease Transcriptomic Analysis. <i>Frontiers in Genetics</i> , 2019, 10, 293.	1.1	2
30	VCFaCS: A web-based visualization tool for high-throughput variant data mining and management. <i>Molecular Genetics & Genomic Medicine</i> , 2019, 7, e00641.	0.6	12
31	Assessment of tumor mutation burden calculation from gene panel sequencing data. <i>OncoTargets and Therapy</i> , 2019, Volume 12, 3401-3409.	1.0	38
32	CellSim: a novel software to calculate cell similarity and identify their co-regulation networks. <i>BMC Bioinformatics</i> , 2019, 20, 111.	1.2	3
33	A statistical framework for cross-tissue transcriptome-wide association analysis. <i>Nature Genetics</i> , 2019, 51, 568-576.	9.4	262
34	Genomic analysis of a spinal muscular atrophy (SMA) discordant family identifies a novel mutation in TLL2, an activator of growth differentiation factor 8 (myostatin): a case report. <i>BMC Medical Genetics</i> , 2019, 20, 204.	2.1	8
35	A novel joint analysis framework improves identification of differentially expressed genes in cross disease transcriptomic analysis. <i>BioData Mining</i> , 2018, 11, 3.	2.2	12
36	Identification of human circadian genes based on time course gene expression profiles by using a deep learning method. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2018, 1864, 2274-2283.	1.8	13

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37	Machine-Learning Prediction of Drug-Induced Cardiac Arrhythmia: Analysis of Gene Expression and Clustering. <i>Critical Reviews in Biomedical Engineering</i> , 2018, 46, 245-275.	0.5	2
38	Intrinsically disordered protein-specific force field <scp>CHARMM</scp>36<scp>IDPSFF</scp>. <i>Chemical Biology and Drug Design</i> , 2018, 92, 1722-1735.	1.5	62
39	A Herpes Simplex Virus Thymidine Kinase-Induced Mouse Model of Hepatocellular Carcinoma Associated with Up-Regulated Immune-Inflammatory-Related Signals. <i>Genes</i> , 2018, 9, 380.	1.0	8
40	Transcription Factors Contribute to Differential Expression in Cellular Pathways in Lung Adenocarcinoma and Lung Squamous Cell Carcinoma. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2018, 10, 836-847.	2.2	19
41	A new method to measure the semantic similarity from query phenotypic abnormalities to diseases based on the human phenotype ontology. <i>BMC Bioinformatics</i> , 2018, 19, 162.	1.2	10
42	Multi-omics facilitated variable selection in Cox-regression model for cancer prognosis prediction. <i>Methods</i> , 2017, 124, 100-107.	1.9	45
43	A disease similarity matrix based on the uniqueness of shared genes. <i>BMC Medical Genomics</i> , 2017, 10, 26.	0.7	28
44	16S rDNA Gene Sequencing Analysis in Functional Dyspepsia Treated With Fecal Microbiota Transplantation. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2017, 64, e80-e82.	0.9	4
45	Healthcare seeking behaviour among Chinese elderly. <i>International Journal of Health Care Quality Assurance</i> , 2017, 30, 248-259.	0.2	9
46	A Lesion-Based Response Prediction Model Using Pretherapy PET/CT Image Features for Y90 Radioembolization to Hepatic Malignancies. <i>Technology in Cancer Research and Treatment</i> , 2017, 16, 620-629.	0.8	13
47	RNA-seq Based Transcription Characterization of Fusion Breakpoints as a Potential Estimator for Its Oncogenic Potential. <i>BioMed Research International</i> , 2017, 2017, 1-8.	0.9	11
48	Classification of Benign and Malignant Thyroid Nodules Using a Combined Clinical Information and Gene Expression Signatures. <i>PLoS ONE</i> , 2016, 11, e0164570.	1.1	11
49	High-dimensional omics data analysis using a variable screening protocol with prior knowledge integration (SKI). <i>BMC Systems Biology</i> , 2016, 10, 118.	3.0	19
50	Meta-analysis of sex differences in gene expression in schizophrenia. <i>BMC Systems Biology</i> , 2016, 10, 9.	3.0	31
51	Gut microbiota community adaption during young children fecal microbiota transplantation by 16s rDNA sequencing. <i>Neurocomputing</i> , 2016, 206, 66-72.	3.5	4
52	Knowledge-based three-body potential for transcription factor binding site prediction. <i>IET Systems Biology</i> , 2016, 10, 23-29.	0.8	2
53	Efforts to reduce the disparity between permanent residents and temporary migrants: Stop TB experiences in Shanghai, China. <i>Tropical Medicine and International Health</i> , 2015, 20, 1033-1040.	1.0	12
54	Current inversions induced by resonant coupling to surface waves in a nanosized water pump. <i>Physical Review E</i> , 2015, 92, 053017.	0.8	10

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55	Network-based prediction and knowledge mining of disease genes. BMC Medical Genomics, 2015, 8, S9.	0.7	20
56	A novel essential domain perspective for exploring gene essentiality. Bioinformatics, 2015, 31, 2921-2929.	1.8	7
57	A three-gene panel that distinguishes benign from malignant thyroid nodules. International Journal of Cancer, 2015, 136, 1646-1654.	2.3	30
58	More Overweight Adolescents Think They Are Just Fine. American Journal of Preventive Medicine, 2015, 49, 670-677.	1.6	22
59	Acetylproteomic Analysis Reveals Functional Implications of Lysine Acetylation in Human Spermatozoa (sperm). Molecular and Cellular Proteomics, 2015, 14, 1009-1023.	2.5	70
60	Identification of cancer-related genes and motifs in the human gene regulatory network. IET Systems Biology, 2015, 9, 128-134.	0.8	6
61	Discovering Essential Domains in Essential Genes. Methods in Molecular Biology, 2015, 1279, 235-245.	0.4	1
62	On the Improvement of Free-Energy Calculation from Steered Molecular Dynamics Simulations Using Adaptive Stochastic Perturbation Protocols. PLoS ONE, 2014, 9, e101810.	1.1	13
63	Multiclass classification of sarcomas using pathway based feature selection method. Journal of Theoretical Biology, 2014, 362, 3-8.	0.8	16
64	Predicting essential genes for identifying potential drug targets in Aspergillus fumigatus. Computational Biology and Chemistry, 2014, 50, 29-40.	1.1	50
65	A New Exhaustive Method and Strategy for Finding Motifs in ChIP-Enriched Regions. PLoS ONE, 2014, 9, e86044.	1.1	34
66	Computational Methods for the Prediction of Microbial Essential Genes. Current Bioinformatics, 2014, 9, 89-101.	0.7	12
67	Quantum-Dot-Based Aptamer Beacons for $\{m K\}^{+}$ Detection. IEEE Sensors Journal, 2013, 13, 1549-1553.	2.4	8
68	The molecular basis of ceramide-1-phosphate recognition by C2 domains. Journal of Lipid Research, 2013, 54, 636-648.	2.0	34
69	Calcium Induced Regulation of Skeletal Troponin α Computational Insights from Molecular Dynamics Simulations. PLoS ONE, 2013, 8, e58313.	1.1	11
70	Do transportation subsidies and living allowances improve tuberculosis control outcomes among internal migrants in urban Shanghai, China?. Western Pacific Surveillance and Response Journal: WPSAR, 2013, 4, 19-24.	0.3	10
71	A structure-based protocol for learning the family-specific mechanisms of membrane-binding domains. Bioinformatics, 2012, 28, i431-i437.	1.8	4
72	Cholesterol modulates cell signaling and protein networking by specifically interacting with PDZ domain-containing scaffold proteins. Nature Communications, 2012, 3, 1249.	5.8	129

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73	Genome-wide Functional Annotation of Dual-Specificity Protein- and Lipid-Binding Modules that Regulate Protein Interactions. <i>Molecular Cell</i> , 2012, 46, 226-237.	4.5	62
74	Template-based protein structure modeling using the RaptorX web server. <i>Nature Protocols</i> , 2012, 7, 1511-1522.	5.5	1,474
75	Mechanically Untying a Protein Slipknot: Multiple Pathways Revealed by Force Spectroscopy and Steered Molecular Dynamics Simulations. <i>Journal of the American Chemical Society</i> , 2012, 134, 10428-10435.	6.6	60
76	Comparison of SARS and NL63 Papain-Like Protease Binding Sites and Binding Site Dynamics: Inhibitor Design Implications. <i>Journal of Molecular Biology</i> , 2011, 414, 272-288.	2.0	23
77	Efficient free-energy-profile reconstruction using adaptive stochastic perturbation protocols. <i>Physical Review E</i> , 2011, 84, 056705.	0.8	4
78	Probing osmolyte participation in the unfolding transition state of a protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9759-9764.	3.3	13
79	An improved machine learning protocol for the identification of correct Sequest search results. <i>BMC Bioinformatics</i> , 2010, 11, 591.	1.2	4
80	Genome-wide sequence-based prediction of peripheral proteins using a novel semi-supervised learning technique. <i>BMC Bioinformatics</i> , 2010, 11, S6.	1.2	15
81	Boosting the prediction and understanding of DNA-binding domains from sequence. <i>Nucleic Acids Research</i> , 2010, 38, 3149-3158.	6.5	50
82	NAPS: a residue-level nucleic acid-binding prediction server. <i>Nucleic Acids Research</i> , 2010, 38, W431-W435.	6.5	66
83	Molecular Basis of the Potent Membrane-remodeling Activity of the Epsin 1 N-terminal Homology Domain. <i>Journal of Biological Chemistry</i> , 2010, 285, 531-540.	1.6	59
84	Probing static disorder in Arrhenius kinetics by single-molecule force spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 11336-11340.	3.3	65
85	Analysis of Combinatorial Regulation: Scaling of Partnerships between Regulators with the Number of Governed Targets. <i>PLoS Computational Biology</i> , 2010, 6, e1000755.	1.5	21
86	Visual Presentation as a Welcome Alternative to Textual Presentation of Gene Annotation Information. <i>Advances in Experimental Medicine and Biology</i> , 2010, 680, 709-715.	0.8	5
87	Structural feature extraction protocol for classifying reversible membrane binding protein domains. <i>BMC Bioinformatics</i> , 2009, 10, 6735-8.		1
88	CO-EXPRESSION AMONG CONSTITUENTS OF A MOTIF IN THE PROTEIN-PROTEIN INTERACTION NETWORK. <i>Journal of Bioinformatics and Computational Biology</i> , 2009, 07, 1-17.	0.3	11
89	Mechanical Signaling on the Single Protein Level Studied Using Steered Molecular Dynamics. <i>Cell Biochemistry and Biophysics</i> , 2009, 55, 141-152.	0.9	27
90	The PDZ2 domain of zonula occludens-1 and -2 is a phosphoinositide binding domain. <i>Cellular and Molecular Life Sciences</i> , 2009, 66, 3951-3966.	2.4	44

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91	A Single-Molecule Perspective on the Role of Solvent Hydrogen Bonds in Protein Folding and Chemical Reactions. <i>ChemPhysChem</i> , 2008, 9, 2836-2847.	1.0	39
92	Stabilization Provided by Neighboring Strands Is Critical for the Mechanical Stability of Proteins. <i>Biophysical Journal</i> , 2008, 95, 3935-3942.	0.2	33
93	Solvent molecules bridge the mechanical unfolding transition state of a protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 3185-3190.	3.3	73
94	Differential Roles of Phosphatidylserine, PtdIns(4,5)P2, and PtdIns(3,4,5)P3 in Plasma Membrane Targeting of C2 Domains. <i>Journal of Biological Chemistry</i> , 2008, 283, 26047-26058.	1.6	75
95	Mining knowledge for the methylation status of CpG islands using alternating decision trees. , 2008, 2008, 3787-90.		7
96	Intelligible machine learning with malibu. , 2008, 2008, 3795-8.		8
97	Machine Learning for Protein Structure and Function Prediction. <i>Annual Reports in Computational Chemistry</i> , 2008, , 41-66.	0.9	6
98	Single-molecule force spectroscopy reveals a mechanically stable protein fold and the rational tuning of its mechanical stability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 9278-9283.	3.3	117
99	MeTaDoR: a comprehensive resource for membrane targeting domains and their host proteins. <i>Bioinformatics</i> , 2007, 23, 3110-3112.	1.8	21
100	Finding new structural and sequence attributes to predict possible disease association of single amino acid polymorphism (SAP). <i>Bioinformatics</i> , 2007, 23, 1444-1450.	1.8	55
101	Prediction of Specific Protein-DNA Recognition by Knowledge-based Two-body and Three-body Interaction Potentials. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society</i> , 2007, 2007, 5017-20.	0.5	4
102	Residue-level prediction of DNA-binding sites and its application on DNA-binding protein predictions. <i>FEBS Letters</i> , 2007, 581, 1058-1066.	1.3	61
103	Computer simulation of I27 translocation through ClpY reveals a critical role of protein mechanical strength and local stability. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society</i> , 2007, 2007, 1213-6.	0.5	3
104	Contour Length and Refolding Rate of a Small Protein Controlled by Engineered Disulfide Bonds. <i>Biophysical Journal</i> , 2007, 92, 225-233.	0.2	285
105	Learning to Translate Sequence and Structure to Function: Identifying DNA Binding and Membrane Binding Proteins. <i>Annals of Biomedical Engineering</i> , 2007, 35, 1043-1052.	1.3	16
106	Structural Bioinformatics Prediction of Membrane-binding Proteins. <i>Journal of Molecular Biology</i> , 2006, 359, 486-495.	2.0	58
107	Improved protein fold assignment using support vector machines. <i>International Journal of Bioinformatics Research and Applications</i> , 2006, 1, 319.	0.1	6
108	Improved protein fold assignment using support vector machines. <i>International Journal of Bioinformatics Research and Applications</i> , 2005, 1, 319.	0.1	8

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109	Correlation between gene expression profiles and protein-protein interactions within and across genomes. <i>Bioinformatics</i> , 2005, 21, 2730-2738.	1.8	160
110	Structure Based Prediction of Binding Residues on DNA-binding Proteins. , 2005, 2005, 2611-4.		14
111	Development of a Grid-based Statistical Potential for Protein Structure Prediction. , 2005, 2005, 6064-7.		2
112	Kernel-based machine learning protocol for predicting DNA-binding proteins. <i>Nucleic Acids Research</i> , 2005, 33, 6486-6493.	6.5	142
113	Chemistry on a Single Protein, Vascular Cell Adhesion Molecule-1, during Forced Unfolding. <i>Journal of Biological Chemistry</i> , 2004, 279, 45865-45874.	1.6	53
114	Application of statistical potentials to protein structure refinement from low resolution ab initio models. <i>Biopolymers</i> , 2003, 70, 575-584.	1.2	40
115	The mechanical stability of ubiquitin is linkage dependent. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 738-743.	3.6	436
116	Development of Unified Statistical Potentials Describing Protein-Protein Interactions. <i>Biophysical Journal</i> , 2003, 84, 1895-1901.	0.2	137
117	Multimeric Threading-Based Prediction of Protein-Protein Interactions on a Genomic Scale: Application to the <i>Saccharomyces cerevisiae</i> Proteome. <i>Genome Research</i> , 2003, 13, 1146-1154.	2.4	102
118	Unfolding of titin domains studied by molecular dynamics simulations. , 2003, , 513-521.		1
119	Ab initio protein structure prediction on a genomic scale: Application to the <i>Mycoplasma genitalium</i> genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 5993-5998.	3.3	41
120	MULTIPROSPECTOR: An algorithm for the prediction of protein-protein interactions by multimeric threading. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 49, 350-364.	1.5	239
121	Reverse engineering of the giant muscle protein titin. <i>Nature</i> , 2002, 418, 998-1002.	13.7	487
122	Unfolding of titin domains studied by molecular dynamics simulations. <i>Journal of Muscle Research and Cell Motility</i> , 2002, 23, 513-521.	0.9	61
123	Simulated Refolding of Stretched Titin Immunoglobulin Domains. <i>Biophysical Journal</i> , 2001, 81, 2268-2277.	0.2	48
124	A distance-dependent atomic knowledge-based potential for improved protein structure selection. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 44, 223-232.	1.5	282
125	The Key Event in Force-Induced Unfolding of Titin's Immunoglobulin Domains. <i>Biophysical Journal</i> , 2000, 79, 51-65.	0.2	282
126	Computer Modeling of Force-Induced Titin Domain Unfolding. <i>Advances in Experimental Medicine and Biology</i> , 2000, 481, 143-162.	0.8	18

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127	Steered Molecular Dynamics. Lecture Notes in Computational Science and Engineering, 1999, , 39-65.	0.1	240
128	Steered molecular dynamics simulation of conformational changes of immunoglobulin domain I27 interpret atomic force microscopy observations. Chemical Physics, 1999, 247, 141-153.	0.9	145
129	Mechanical unfolding intermediates in titin modules. Nature, 1999, 402, 100-103.	13.7	789
130	Steered molecular dynamics simulations of force-induced protein domain unfolding. , 1999, 35, 453-463.		246
131	Steered molecular dynamics simulations of force-induced protein domain unfolding. , 1999, 35, 453.		1
132	Steered molecular dynamics simulations of force-induced protein domain unfolding. Proteins: Structure, Function and Bioinformatics, 1999, 35, 453-463.	1.5	8
133	Quantum dynamics of the femtosecond photoisomerization of retinal in bacteriorhodopsin. Faraday Discussions, 1998, 110, 447-462.	1.6	83
134	Unfolding of Titin Immunoglobulin Domains by Steered Molecular Dynamics Simulation. Biophysical Journal, 1998, 75, 662-671.	0.2	658
135	Three Electronic State Model of the Primary Phototransformation of Bacteriorhodopsin. Biophysical Journal, 1998, 75, 1689-1699.	0.2	61