

# John Urban

## List of Publications by Year in descending order

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36  
papers

1,783  
citations

331670

21  
h-index

345221

36  
g-index

38  
all docs

38  
docs citations

38  
times ranked

1642  
citing authors

#	ARTICLE	IF	CITATIONS
1	Intrinsically disordered proteins: Ensembles at the limits of Anfinsen's dogma. <i>Biophysics Reviews</i> , 2022, 3, .	2.7	15
2	Engineering subtilisin proteases that specifically degrade active RAS. <i>Communications Biology</i> , 2021, 4, 299.	4.4	10
3	Protein conformational dynamics and phenotypic switching. <i>Biophysical Reviews</i> , 2021, 13, 1127-1138.	3.2	9
4	The structural basis of T-cell receptor (TCR) activation: An enduring enigma. <i>Journal of Biological Chemistry</i> , 2020, 295, 914-925.	3.4	58
5	A Non-genetic Mechanism Involving the Integrin $\beta$ 2/Paxillin Axis Contributes to Chemoresistance in Lung Cancer. <i>IScience</i> , 2020, 23, 101496.	4.1	27
6	Peptide-MHC Binding Reveals Conserved Allosteric Sites in MHC Class I- and Class II-Restricted T Cell Receptors (TCRs). <i>Journal of Molecular Biology</i> , 2020, 432, 166697.	4.2	12
7	The structural basis of T-cell receptor (TCR) activation: An enduring enigma. <i>Journal of Biological Chemistry</i> , 2020, 295, 914-925.	3.4	64
8	Structural and Dynamical Order of a Disordered Protein: Molecular Insights into Conformational Switching of PAGE4 at the Systems Level. <i>Biomolecules</i> , 2019, 9, 77.	4.0	19
9	Prostate-Associated Gene 4 (PAGE4): Leveraging the Conformational Dynamics of a Dancing Protein Cloud as a Therapeutic Target. <i>Journal of Clinical Medicine</i> , 2018, 7, 156.	2.4	10
10	Phenotypic Plasticity, Bet-Hedging, and Androgen Independence in Prostate Cancer: Role of Non-Genetic Heterogeneity. <i>Frontiers in Oncology</i> , 2018, 8, 50.	2.8	122
11	Peptide-MHC (pMHC) binding to a human antiviral T cell receptor induces long-range allosteric communication between pMHC- and CD3-binding sites. <i>Journal of Biological Chemistry</i> , 2018, 293, 15991-16005.	3.4	45
12	Structural metamorphism and polymorphism in proteins on the brink of thermodynamic stability. <i>Protein Science</i> , 2018, 27, 1557-1567.	7.6	34
13	PAGE4 and Conformational Switching: Insights from Molecular Dynamics Simulations and Implications for Prostate Cancer. <i>Journal of Molecular Biology</i> , 2018, 430, 2422-2438.	4.2	36
14	Phosphorylation-induced conformational dynamics in an intrinsically disordered protein and potential role in phenotypic heterogeneity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E2644-E2653.	7.1	72
15	Prostate-associated gene 4 (PAGE4), an intrinsically disordered cancer/testis antigen, is a novel therapeutic target for prostate cancer. <i>Asian Journal of Andrology</i> , 2016, 18, 695.	1.6	19
16	Subdomain Interactions Foster the Design of Two Protein Pairs with ~480% Sequence Identity but Different Folds. <i>Biophysical Journal</i> , 2015, 108, 154-162.	0.5	24
17	Identification of the Docking Site for CD3 on the T Cell Receptor $\beta$ Chain by Solution NMR. <i>Journal of Biological Chemistry</i> , 2015, 290, 19796-19805.	3.4	36
18	Phosphorylation-induced Conformational Ensemble Switching in an Intrinsically Disordered Cancer/Testis Antigen. <i>Journal of Biological Chemistry</i> , 2015, 290, 25090-25102.	3.4	55

#	ARTICLE	IF	CITATIONS
19	Implications of protein fold switching. <i>Current Opinion in Structural Biology</i> , 2013, 23, 314-316.	5.7	17
20	Solution NMR structure of a sheddase inhibitor prodomain from the malarial parasite <i>Plasmodium falciparum</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2810-2817.	2.6	7
21	Mutational Tipping Points for Switching Protein Folds and Functions. <i>Structure</i> , 2012, 20, 283-291.	3.3	87
22	The Cancer/Testis Antigen Prostate-associated Gene 4 (PAGE4) Is a Highly Intrinsically Disordered Protein. <i>Journal of Biological Chemistry</i> , 2011, 286, 13985-13994.	3.4	58
23	Proteins that switch folds. <i>Current Opinion in Structural Biology</i> , 2010, 20, 482-488.	5.7	170
24	A minimal sequence code for switching protein structure and function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 21149-21154.	7.1	219
25	NMR structures of two designed proteins with high sequence identity but different fold and function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 14412-14417.	7.1	98
26	The design and characterization of two proteins with 88% sequence identity but different structure and function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 11963-11968.	7.1	165
27	Hydrogen-Deuterium Exchange in Free and Prodomain-Complexed Subtilisin. <i>Biochemistry</i> , 2007, 46, 652-658.	2.5	13
28	An artificially evolved albumin binding module facilitates chemical shift epitope mapping of GA domain interactions with phylogenetically diverse albumins. <i>Protein Science</i> , 2007, 16, 1490-1494.	7.6	14
29	Structure, Dynamics, and Stability Variation in Bacterial Albumin Binding Modules: Implications for Species Specificity. <i>Biochemistry</i> , 2006, 45, 10102-10109.	2.5	36
30	Using Offset Recombinant Polymerase Chain Reaction To Identify Functional Determinants in a Common Family of Bacterial Albumin Binding Domains. <i>Biochemistry</i> , 2006, 45, 3263-3271.	2.5	19
31	Directed Evolution of Highly Homologous Proteins with Different Folds by Phage Display: Implications for the Protein Folding Code. <i>Biochemistry</i> , 2005, 44, 14045-14054.	2.5	46
32	Solution NMR Structures of IgG Binding Domains with Artificially Evolved High Levels of Sequence Identity but Different Folds. <i>Biochemistry</i> , 2005, 44, 14055-14061.	2.5	29
33	Solution Structure of the Pro-hormone Convertase 1 Pro-domain from <i>Mus musculus</i> . <i>Journal of Molecular Biology</i> , 2002, 320, 801-812.	4.2	43
34	Stability and Global Fold of the Mouse Prohormone Convertase 1 Pro-Domain. <i>Biochemistry</i> , 2001, 40, 5488-5495.	2.5	23
35	Assessment of Stability Differences in the Protein G B1 and B2 Domains From Hydrogen-Deuterium Exchange: Comparison with Calorimetric Data. <i>Biochemistry</i> , 1995, 34, 15291-15300.	2.5	58
36	Synthesis of backbone deuterium labelled [r(CGCGAAUUCGCG)] <sub>2</sub> and HPLC purification of synthetic RNA. <i>Nucleic Acids Research</i> , 1992, 20, 5131-5136.	14.5	10