John Orban

List of Publications by Year in descending order

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Version: 2024-02-01

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	A minimal sequence code for switching protein structure and function. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 21149-21154.	7.1	219
2	Proteins that switch folds. Current Opinion in Structural Biology, 2010, 20, 482-488.	5.7	170
3	The design and characterization of two proteins with 88% sequence identity but different structure and function. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 11963-11968.	7.1	165
4	Phenotypic Plasticity, Bet-Hedging, and Androgen Independence in Prostate Cancer: Role of Non-Genetic Heterogeneity. Frontiers in Oncology, 2018, 8, 50.	2.8	122
5	NMR structures of two designed proteins with high sequence identity but different fold and function. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 14412-14417.	7.1	98
6	Mutational Tipping Points for Switching Protein Folds and Functions. Structure, 2012, 20, 283-291.	3.3	87
7	Phosphorylation-induced conformational dynamics in an intrinsically disordered protein and potential role in phenotypic heterogeneity. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E2644-E2653.	7.1	72
8	The structural basis of T-cell receptor (TCR) activation: An enduring enigma. Journal of Biological Chemistry, 2020, 295, 914-925.	3.4	64
9	Assessment of Stability Differences in the Protein G B1 and B2 Domains From Hydrogen-Deuterium Exchange: Comparison with Calorimetric Data. Biochemistry, 1995, 34, 15291-15300.	2.5	58
10	The Cancer/Testis Antigen Prostate-associated Gene 4 (PAGE4) Is a Highly Intrinsically Disordered Protein. Journal of Biological Chemistry, 2011, 286, 13985-13994.	3.4	58
11	The structural basis of T-cell receptor (TCR) activation: An enduring enigma. Journal of Biological Chemistry, 2020, 295, 914-925.	3.4	58
12	Phosphorylation-induced Conformational Ensemble Switching in an Intrinsically Disordered Cancer/Testis Antigen. Journal of Biological Chemistry, 2015, 290, 25090-25102.	3.4	55
13	Directed Evolution of Highly Homologous Proteins with Different Folds by Phage Display:Â Implications for the Protein Folding Codeâ€. Biochemistry, 2005, 44, 14045-14054.	2.5	46
14	Peptideâ€“MHC (pMHC) binding to a human antiviral T cell receptor induces long-range allosteric communication between pMHC- and CD3-binding sites. Journal of Biological Chemistry, 2018, 293, 15991-16005.	3.4	45
15	Solution Structure of the Pro-hormone Convertase 1 Pro-domain from Mus musculus. Journal of Molecular Biology, 2002, 320, 801-812.	4.2	43
16	Structure, Dynamics, and Stability Variation in Bacterial Albumin Binding Modules:Â Implications for Species Specificityâ€,â€¡. Biochemistry, 2006, 45, 10102-10109.	2.5	36
17	Identification of the Docking Site for CD3 on the T Cell Receptor Î² Chain by Solution NMR. Journal of Biological Chemistry, 2015, 290, 19796-19805.	3.4	36
18	PAGE4 and Conformational Switching: Insights from Molecular Dynamics Simulations and Implications for Prostate Cancer. Journal of Molecular Biology, 2018, 430, 2422-2438.	4.2	36

#	Article	IF	Citations
19	Structural metamorphism and polymorphism in proteins on the brink of thermodynamic stability. Protein Science, 2018, 27, 1557-1567.	7.6	34
20	Solution NMR Structures of IgG Binding Domains with Artificially Evolved High Levels of Sequence Identity but Different Foldsâ€‚â€¡. Biochemistry, 2005, 44, 14055-14061.	2.5	29
21	A Non-genetic Mechanism Involving the Integrin Î²4/Paxillin Axis Contributes to Chemoresistance in Lung Cancer. IScience, 2020, 23, 101496.	4.1	27
22	Subdomain Interactions Foster the Design of Two Protein Pairs withÂâˆ¼80%ÂSequence Identity but Different Folds. Biophysical Journal, 2015, 108, 154-162.	0.5	24
23	Stability and Global Fold of the Mouse Prohormone Convertase 1 Pro-Domainâ€. Biochemistry, 2001, 40, 5488-5495.	2.5	23
24	Using Offset Recombinant Polymerase Chain Reaction To Identify Functional Determinants in a Common Family of Bacterial Albumin Binding Domains. Biochemistry, 2006, 45, 3263-3271.	2.5	19
25	Structural and Dynamical Order of a Disordered Protein: Molecular Insights into Conformational Switching of PAGE4 at the Systems Level. Biomolecules, 2019, 9, 77.	4.0	19
26	Prostate-associated gene 4 (PAGE4), an intrinsically disordered cancer/testis antigen, is a novel therapeutic target for prostate cancer. Asian Journal of Andrology, 2016, 18, 695.	1.6	19
27	Implications of protein fold switching. Current Opinion in Structural Biology, 2013, 23, 314-316.	5.7	17
28	Intrinsically disordered proteins: Ensembles at the limits of Anfinsen's dogma. Biophysics Reviews, 2022, 3, .	2.7	15
29	An artificially evolved albumin binding module facilitates chemical shift epitope mapping of GA domain interactions with phylogenetically diverse albumins. Protein Science, 2007, 16, 1490-1494.	7.6	14
30	Hydrogenâˆ’Deuterium Exchange in Free and Prodomain-Complexed Subtilisinâ€. Biochemistry, 2007, 46, 652-658.	2.5	13
31	Peptideâ€“MHC Binding Reveals Conserved Allosteric Sites in MHC Class I- and Class II-Restricted T Cell Receptors (TCRs). Journal of Molecular Biology, 2020, 432, 166697.	4.2	12
32	Synthesis of backbone deuterium labelled [r(CGCGAAUUCGCG)]2and HPLC purification of synthetic RNA. Nucleic Acids Research, 1992, 20, 5131-5136.	14.5	10
33	Prostate-Associated Gene 4 (PAGE4): Leveraging the Conformational Dynamics of a Dancing Protein Cloud as a Therapeutic Target. Journal of Clinical Medicine, 2018, 7, 156.	2.4	10
34	Engineering subtilisin proteases that specifically degrade active RAS. Communications Biology, 2021, 4, 299.	4.4	10
35	Protein conformational dynamics and phenotypic switching. Biophysical Reviews, 2021, 13, 1127-1138.	3.2	9
36	Solution NMR structure of a sheddase inhibitor prodomain from the malarial parasite Plasmodium falciparum. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2810-2817.	2.6	7