Siobhan E Toal

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/8556353/publications.pdf

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25	536	623574	794469
papers	citations	14 h-index	19 g-index

28	28	28	386
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Water-Mediated Electronic Structure of Oligopeptides Probed by Their UV Circular Dichroism, Absorption Spectra, and Time-Dependent DFT Calculations. Journal of Physical Chemistry B, 2020, 124, 2579-2590.	1.2	17
2	Anticooperative Nearest-Neighbor Interactions between Residues in Unfolded Peptides andÂProteins. Biophysical Journal, 2018, 114, 1046-1057.	0.2	13
3	Anti-cooperative Nearest Neighbor Coupling Determines the Statistical Coil State of Peptides and Proteins at High Temperatures. Biophysical Journal, 2018, 114, 588a.	0.2	0
4	Investigating the Formation of a Repulsive Hydrogel of a Cationic 16mer Peptide at Low Ionic Strength in Water by Vibrational Spectroscopy and Rheology. Journal of Physical Chemistry B, 2016, 120, 10079-10090.	1.2	9
5	Construction and comparison of the statistical coil states of unfolded and intrinsically disordered proteins from nearest-neighbor corrected conformational propensities of short peptides. Molecular BioSystems, 2016, 12, 3294-3306.	2.9	17
6	Assessing N-Terminal Modifications on Alpha-Synuclein Structure and Function. Biophysical Journal, 2016, 110, 552a.	0.2	0
7	Demixing of water and ethanol causes conformational redistribution and gelation of the cationic GAG tripeptide. Chemical Communications, 2015, 51, 16498-16501.	2.2	28
8	Conformational Effects on Alanine Induced Induced by Various Alcohol Cosolvents. Biophysical Journal, 2015, 108, 230a.	0.2	0
9	Randomizing the Unfolded State of Peptides (and Proteins) by Nearest Neighbor Interactions between Unlike Residues. Chemistry - A European Journal, 2015, 21, 5173-5192.	1.7	27
10	Conformational Entropies of Unfolded Peptides: The Source of a Realistic Estimation of the Entropy of Unfolded Peptides and Proteins. Biophysical Journal, 2015, 108, 194a.	0.2	0
11	Assessing backbone solvation effects in the conformational propensities of amino acid residues in unfolded peptides. Physical Chemistry Chemical Physics, 2015, 17, 24917-24924.	1.3	41
12	Water-Centered Interpretation of Intrinsic pPII Propensities of Amino Acid Residues: In Vitro-Driven Molecular Dynamics Study. Journal of Physical Chemistry B, 2015, 119, 13237-13251.	1.2	33
13	Local Order in the Unfolded State: Conformational Biases and Nearest Neighbor Interactions. Biomolecules, 2014, 4, 725-773.	1.8	54
14	Entropy reduction in unfolded peptides (and proteins) due to conformational preferences of amino acid residues. Physical Chemistry Chemical Physics, 2014, 16, 22527-22536.	1.3	13
15	The TrpA protein of Trichodesmium erythraeum IMS101 is a non-fibril-forming collagen and a component of the outer sheath. Microbiology (United Kingdom), 2014, 160, 2148-2156.	0.7	5
16	Role of Enthalpyâ€“Entropy Compensation Interactions in Determining the Conformational Propensities of Amino Acid Residues in Unfolded Peptides.. Journal of Physical Chemistry B, 2014, 118, 1309-1318.	1.2	36
17	Disorder and order in unfolded and disordered peptides and proteins: A view derived from tripeptide conformational analysis. I. Tripeptides with long and predominantly hydrophobic side chains. Proteins: Structure, Function and Bioinformatics, 2013, 81, 955-967.	1.5	33
18	How do Nearest-Neighbor Interactions Effect the Conformational Distributions in Peptides?. Biophysical Journal, 2013, 104, 55a.	0.2	1

#	Article	IF	Citations
19	Investigating the Self-Aggregation of a Polyalanine Peptide: Kinetics and Isotope Edited Studies. Biophysical Journal, 2013, 104, 54a.	0.2	0
20	pH-Independence of Trialanine and the Effects of Termini Blocking in Short Peptides: A Combined Vibrational, NMR, UVCD, and Molecular Dynamics Study. Journal of Physical Chemistry B, 2013, 117, 3689-3706.	1.2	64
21	Disorder and order in unfolded and disordered peptides and proteins: A view derived from tripeptide conformational analysis. II. Tripeptides with short side chains populating asx and Î²â€type like turn conformations. Proteins: Structure, Function and Bioinformatics, 2013, 81, 968-983.	1.5	35
22	Ionized Trilysine: A Model System for Understanding the Nonrandom Structure of Poly-<scp>l</scp>-lysine and Lysine-Containing Motifs in Proteins. Journal of Physical Chemistry B, 2012, 116, 8084-8094.	1.2	14
23	Triaspartate: A Model System for Conformationally Flexible DDD Motifs in Proteins. Journal of Physical Chemistry B, 2012, 116, 5160-5171.	1.2	18
24	Conformational Changes of Trialanine Induced by Direct Interactions between Alanine Residues and Alcohols in Binary Mixtures of Water with Glycerol and Ethanol. Journal of the American Chemical Society, 2011, 133, 12728-12739.	6.6	29
25	Amino Acids with Hydrogenâ€Bonding Side Chains have an Intrinsic Tendency to Sample Various Turn Conformations in Aqueous Solution. Chemistry - A European Journal, 2011, 17, 6789-6797.	1.7	49