Joseph Rebehmed

List of Publications by Year
in descending order

23	470	840776 11	713466 21
papers	citations	h-index	g-index

23	23	23	890
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Protein flexibility in the light of structural alphabets. Frontiers in Molecular Biosciences, 2015, 2, 20.	3.5	71
2	Molecular modeling studies of N-substituted pyrrole derivativesâ€"Potential HIV-1 gp41 inhibitors. Bioorganic and Medicinal Chemistry, 2008, 16, 3039-3048.	3.0	68
3	Cisâ€"trans isomerization of omega dihedrals in proteins. Amino Acids, 2013, 45, 279-289.	2.7	60
4	PTM-SD: a database of structurally resolved and annotated posttranslational modifications in proteins. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau041-bau041.	3.0	44
5	Î²â€Bulges: Extensive structural analyses of Î²â€sheets irregularities. Protein Science, 2013, 22, 1366-1378.	7.6	27
6	Flexible computational docking studies of new aminoglycosides targeting RNA 16S bacterial ribosome site. European Journal of Medicinal Chemistry, 2008, 43, 1648-1656.	5.5	26
7	Discrete analyses of protein dynamics. Journal of Biomolecular Structure and Dynamics, 2020, 38, 2988-3002.	3.5	20
8	Evolution study of the Baeyerâ€"Villiger monooxygenases enzyme family: Functional importance of the highly conserved residues. Biochimie, 2013, 95, 1394-1402.	2.6	19
9	Expanding the SRI domain family: A common scaffold for binding the phosphorylated Câ€terminal domain of RNA polymerase II. FEBS Letters, 2014, 588, 4431-4437.	2.8	19
10	Investigation of the impact of PTMs on the protein backbone conformation. Amino Acids, 2019, 51, 1065-1079.	2.7	17
11	In silico prediction of protein flexibility with local structure approach. Biochimie, 2019, 165, 150-155.	2.6	15
12	iPBAvizu: a PyMOL plugin for an efficient 3D protein structure superimposition approach. Source Code for Biology and Medicine, 2019, 14, 5.	1.7	14
13	The respective roles of polar/nonpolar binary patterns and amino acid composition in protein regular secondary structures explored exhaustively using hydrophobic cluster analysis. Proteins: Structure, Function and Bioinformatics, 2016, 84, 624-638.	2.6	12
14	A topology-based investigation of protein interaction sites using Hydrophobic Cluster Analysis. Biochimie, 2019, 167, 68-80.	2.6	12
15	2D and 3D QSAR studies of diarylpyrimidine HIV-1 reverse transcriptase inhibitors. Journal of Computer-Aided Molecular Design, 2008, 22, 831-841.	2.9	10
16	Dynamics and deformability of Î±-, 310- and Ï€-helices. Archives of Biological Sciences, 2018, 70, 21-31.	0.5	10
17	Current status of PTMs structural databases: applications, limitations and prospects. Amino Acids, 2022, 54, 575-590.	2.7	9
18	Enhancing the Activity of a Dietzia sp. D5 Baeyerâ€Villiger Monooxygenase towards Cyclohexanone by Saturation Mutagenesis. ChemistrySelect, 2017, 2, 7169-7177.	1.5	7

#	Article	IF	Citations
19	Enzymatic Synthesis of Galactosylated Serine/Threonine Derivatives by Î²-Galactosidase from Escherichia coli. International Journal of Molecular Sciences, 2015, 16, 13714-13728.	4.1	4
20	Shaking the Î²-Bulges. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 14-18.	3.0	3
21	Editorial: Advances in Molecular Docking and Structure-Based Modelling. Frontiers in Molecular Biosciences, 2022, 9, 839826.	3.5	2
22	Combining In Silico Phylogenetic and Threading Approaches to Assist the in vitro Protein Engineering of BVMO Enzymes. Biophysical Journal, 2020, 118, 45a.	0.5	1
23	Efficient Protein Structure Alignment Methods Based on a Structural Alphabet. Biophysical Journal, 2014, 106, 54a.	0.5	0