

Markus Wiederstein

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

4,926
citations

516215

16
h-index

794141

19
g-index

23
all docs

23
docs citations

23
times ranked

7909
citing authors

#	ARTICLE	IF	CITATIONS
1	Bet v 1 from birch pollen is a hypoallergen with vitamin D3 in the pocket. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2021, 76, 3801-3804.	2.7	8
2	Protein Structure Analysis and Prediction with Statistical Scoring Functions. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8665.	1.8	0
3	Friend or Foe: Lipid Droplets as Organelles for Protein and Lipid Storage in Cellular Stress Response, Aging and Disease. <i>Molecules</i> , 2020, 25, 5053.	1.7	39
4	Retinoic acid loading of the major birch pollen allergen Bet v 1 may improve specific allergen immunotherapy: In silico, in vitro and in vivo data in BALB/c mice. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2020, 75, 2073-2077.	2.7	23
5	TopMatch-web: pairwise matching of large assemblies of protein and nucleic acid chains in 3D. <i>Nucleic Acids Research</i> , 2020, 48, W31-W35.	6.5	19
6	Synergistic cross-talk of hedgehog and interleukin-6 signaling drives growth of basal cell carcinoma. <i>International Journal of Cancer</i> , 2018, 143, 2943-2954.	2.3	23
7	Nanoparticle-allergen interactions mediate human allergic responses: protein corona characterization and cellular responses. <i>Particle and Fibre Toxicology</i> , 2015, 13, 3.	2.8	52
8	Structure-Based Characterization of Multiprotein Complexes. <i>Structure</i> , 2014, 22, 1063-1070.	1.6	48
9	Comprehensive analysis of alterations in the miRNome in response to photodynamic treatment. <i>Journal of Photochemistry and Photobiology B: Biology</i> , 2013, 120, 74-81.	1.7	25
10	Detection of Spatial Correlations in Protein Structures and Molecular Complexes. <i>Structure</i> , 2012, 20, 718-728.	1.6	65
11	Effective Techniques for Protein Structure Mining. <i>Methods in Molecular Biology</i> , 2011, 857, 33-54.	0.4	3
12	COPS—a novel workbench for explorations in fold space. <i>Nucleic Acids Research</i> , 2009, 37, W539-W544.	6.5	25
13	A discrete view on fold space. <i>Bioinformatics</i> , 2008, 24, 870-871.	1.8	16
14	A note on difficult structure alignment problems. <i>Bioinformatics</i> , 2008, 24, 426-427.	1.8	114
15	QSCOP—SCOP quantified by structural relationships. <i>Bioinformatics</i> , 2007, 23, 513-514.	1.8	18
16	ProSA-web: interactive web service for the recognition of errors in three-dimensional structures of proteins. <i>Nucleic Acids Research</i> , 2007, 35, W407-W410.	6.5	4,244
17	Directed in silico Mutagenesis. , 2005, , 153-175.		1
18	Protein Sequence Randomization: Efficient Estimation of Protein Stability Using Knowledge-based Potentials. <i>Journal of Molecular Biology</i> , 2005, 345, 1199-1212.	2.0	57

#	ARTICLE	IF	CITATIONS
19	Validation and classification of protein structures. Acta Crystallographica Section A: Foundations and Advances, 2005, 61, c42-c42.	0.3	0
20	Assessment of the CASP4 fold recognition category. Proteins: Structure, Function and Bioinformatics, 2001, 45, 55-67.	1.5	61
21	Characterization of novel proteins based on known protein structures 1 Edited by R. Huber. Journal of Molecular Biology, 2000, 296, 1139-1152.	2.0	43
22	Sustained performance of knowledge-based potentials in fold recognition. Proteins: Structure, Function and Bioinformatics, 1999, 37, 112-120.	1.5	42