Sonja A Dames

List of Publications by Year
in descending order

29	905	687363 13	477307 29
papers	citations	h-index	g-index

30	30	30	1367
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	NMRâ€“ and MD simulationâ€“based structural characterization of the membrane-associating FATC domain of ataxia telangiectasia mutated. Journal of Biological Chemistry, 2019, 294, 7098-7112.	3.4	7
2	1H, 15N, and 13C chemical shift assignments of the micelle immersed FAT C-terminal (FATC) domains of the human protein kinases ataxia-telangiectasia mutated (ATM) and DNA-dependent protein kinase catalytic subunit (DNA-PKcs) fused to the B1 domain of streptococcal protein G (GB1). Biomolecular NMR Assignments, 2018, 12, 149-154.	0.8	1
3	<scp>NMR</scp> analysis of the backbone dynamics of the small <scp>GTP</scp>ase Rheb and its interaction with the regulatory protein <scp>FKBP</scp>38. FEBS Letters, 2018, 592, 130-146.	2.8	6
4	Target of rapamycin FATC domain as a general membrane anchor: The FKBPâ€12 like domain of FKBP38 as a case study. Protein Science, 2018, 27, 546-560.	7.6	4
5	Chemical shift assignment of the intrinsically disordered N-terminus and the rubredoxin domain in the folded metal bound and unfolded oxidized state of mycobacterial protein kinase G. Biomolecular NMR Assignments, 2016, 10, 401-406.	0.8	2
6	Oxidative Unfolding of the Rubredoxin Domain and the Natively Disordered N-terminal Region Regulate the Catalytic Activity of Mycobacterium tuberculosis Protein Kinase G. Journal of Biological Chemistry, 2016, 291, 27062-27072.	3.4	12
7	A Rigorous and Efficient Method To Reweight Very Large Conformational Ensembles Using Average Experimental Data and To Determine Their Relative Information Content. Journal of Chemical Theory and Computation, 2016, 12, 383-394.	5.3	43
8	One short cysteine-rich sequence pattern - two different disulfide-bonded structures - a molecular dynamics simulation study. Journal of Peptide Science, 2015, 21, 480-494.	1.4	1
9	Regulation of the Target of Rapamycin and Other Phosphatidylinositol 3-Kinase-Related Kinases by Membrane Targeting. Membranes, 2015, 5, 553-575.	3.0	13
10	Expression and purification of the natively disordered and redox sensitive metal binding regions of Mycobacterium tuberculosis protein kinase G. Protein Expression and Purification, 2015, 111, 68-74.	1.3	5
11	Subtype-Specific Modulation of Estrogen Receptorâ€“Coactivator Interaction by Phosphorylation. ACS Chemical Biology, 2015, 10, 475-484.	3.4	17
12	Characterization of residueâ€dependent differences in the peripheral membrane association of the FATC domain of the kinase â€˜target of rapamycinâ€™ by NMR and CD spectroscopy. FEBS Letters, 2014, 588, 1755-1766.	2.8	6
13	Characterization of the Immersion Properties of the Peripheral Membrane Anchor of the FATC Domain of the Kinase â€œTarget of Rapamycinâ€•by NMR, Oriented CD Spectroscopy, and MD Simulations. Journal of Physical Chemistry B, 2014, 118, 4817-4831.	2.6	14
14	NMR- and Circular Dichroism-monitored Lipid Binding Studies Suggest a General Role for the FATC Domain as Membrane Anchor of Phosphatidylinositol 3-Kinase-related Kinases (PIKK). Journal of Biological Chemistry, 2013, 288, 20046-20063.	3.4	17
15	The FKBPâ€“Rapamycin Binding Domain of Human TOR Undergoes Strong Conformational Changes in the Presence of Membrane Mimetics with and without the Regulator Phosphatidic Acid. Biochemistry, 2012, 51, 4909-4921.	2.5	20
16	A fast and simple method for probing the interaction of peptides and proteins with lipids and membraneâ€mimetics using GB1 fusion proteins and NMR spectroscopy. Protein Science, 2012, 21, 1566-1570.	7.6	12
17	1H, 15N, and 13C assignments of the N-terminal activation domain of Dictyostelium discoideum Formin C. Biomolecular NMR Assignments, 2011, 5, 47-49.	0.8	3
18	Structure, Dynamics, Lipid Binding, and Physiological Relevance of the Putative GTPase-binding Domain of Dictyostelium Formin C*. Journal of Biological Chemistry, 2011, 286, 36907-36920.	3.4	19

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19	Structural Basis for the Association of the Redox-sensitive Target of Rapamycin FATC Domain with Membrane-mimetic Micelles. Journal of Biological Chemistry, 2010, 285, 7766-7775.	3.4	20
20	A fast and simple method to prepare the FKBP-rapamycin binding domain of human target of rapamycin for NMR binding assays. Protein Expression and Purification, 2008, 59, 31-37.	1.3	3
21	Insights into the Low Adhesive Capacity of Human T-cadherin from the NMR Structure of Its N-terminal Extracellular Domain. Journal of Biological Chemistry, 2008, 283, 23485-23495.	3.4	28
22	Structure of the Cyclin T binding domain of Hexim1 and molecular basis for its recognition of P-TEFb. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 14312-14317.	7.1	55
23	NMR assignment of the Cyclin T-binding domain of human Hexim1. Journal of Biomolecular NMR, 2006, 36, 39-39.	2.8	2
24	The Solution Structure of the FATC Domain of the Protein Kinase Target of Rapamycin Suggests a Role for Redox-dependent Structural and Cellular Stability. Journal of Biological Chemistry, 2005, 280, 20558-20564.	3.4	111
25	Structural basis for Hif-1Â/CBP recognition in the cellular hypoxic response. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 5271-5276.	7.1	376
26	Contributions of the ionization states of acidic residues to the stability of the coiled coil domain of matrilin-1. FEBS Letters, 1999, 446, 75-80.	2.8	18
27	NMR structure of a parallel homotrimeric coiled coil. Nature Structural and Molecular Biology, 1998, 5, 687-691.	8.2	36
28	Heteronuclear NMR assignments and secondary structure of the coiled coil trimerization domain from cartilage matrix protein in oxidized and reduced forms. Protein Science, 1997, 6, 1734-1745.	7.6	40
29	A fragment of staphylococcal nuclease with an OBâ€fold structure shows hydrogenâ€exchange protection factors in the range reported for â€œmolten globulesâ€. Protein Science, 1996, 5, 1942-1946.	7.6	12