Olivier Walker

List of Publications by Year
in descending order

37 papers	1,376 citations	361413 20 h-index	345221 36 g-index
37 all docs	37 docs citations	37 times ranked	1909 citing authors

#	Article	IF	Citations
1	NMR reveals the interplay between SilE and SilB model peptides in the context of silver resistance. Chemical Communications, 2021, 57, 8726-8729.	4.1	1
2	NLRP3 phosphorylation in its LRR domain critically regulates inflammasome assembly. Nature Communications, 2021, 12, 5862.	12.8	52
3	Accurate Prediction of Protein NMR Spin Relaxation by Means of Polarizable Force Fields. Application to Strongly Anisotropic Rotational Diffusion. Journal of Physical Chemistry B, 2020, 124, 5103-5112.	2.6	8
4	Molecular recognition of ubiquitin and Lys63-linked diubiquitin by STAM2 UIM-SH3 dual domain: the effect of its linker length and flexibility. Scientific Reports, 2019, 9, 14645.	3.3	3
5	Regulation of measles virus gene expression by P protein coiled-coil properties. Science Advances, 2019, 5, eaaw3702.	10.3	31
6	Ab Initio Prediction of NMR Spin Relaxation Parameters from Molecular Dynamics Simulations. Journal of Chemical Theory and Computation, 2018, 14, 1009-1019.	5.3	23
7	Alpha-helical folding of SilE models upon Ag(His)(Met) motif formation. Chemical Communications, 2018, 54, 10419-10422.	4.1	10
8	Computing the Rotational Diffusion of Biomolecules via Molecular Dynamics Simulation and Quaternion Orientations. Journal of Physical Chemistry B, 2017, 121, 1812-1823.	2.6	19
9	Model peptide studies of Ag⁺binding sites from the silver resistance protein SilE. Chemical Communications, 2017, 53, 6105-6108.	4.1	24
10	Structural Basis for the Inhibitory Effects of Ubistatins in the Ubiquitin-Proteasome Pathway. Structure, 2017, 25, 1839-1855.e11.	3.3	15
11	NMR Reveals the Interplay among the AMSH SH3 Binding Motif, STAM2, and Lys63-Linked Diubiquitin. Journal of Molecular Biology, 2016, 428, 4544-4558.	4.2	6
12	Linkage via K27 Bestows Ubiquitin Chains with Unique Properties among Polyubiquitins. Structure, 2016, 24, 423-436.	3.3	56
13	Francisella tularensis IglG Belongs to a Novel Family of PAAR-Like T6SS Proteins and Harbors a Unique N-terminal Extension Required for Virulence. PLoS Pathogens, 2016, 12, e1005821.	4.7	41
14	Funnel-Metadynamics and Solution NMR to Estimate Proteinâ€“Ligand Affinities. Journal of the American Chemical Society, 2015, 137, 1273-1281.	13.7	44
15	DNA-Damage-Inducible 1 Protein (Ddi1) Contains an Uncharacteristic Ubiquitin-like Domain that Binds Ubiquitin. Structure, 2015, 23, 542-557.	3.3	71
16	Versatile Roles of K63-Linked Ubiquitin Chains in Trafficking. Cells, 2014, 3, 1027-1088.	4.1	172
17	BcL-xL Conformational Changes upon Fragment Binding Revealed by NMR. PLoS ONE, 2013, 8, e64400.	2.5	9
18	Evidence for Cooperative and Domain-specific Binding of the Signal Transducing Adaptor Molecule 2 (STAM2) to Lys63-linked Diubiquitin. Journal of Biological Chemistry, 2012, 287, 18687-18699.	3.4	21

#	Article	IF	Citations
19	Competitive binding of UBPY and ubiquitin to the STAM2 SH3 domain revealed by NMR. FEBS Letters, 2012, 586, 3379-3384.	2.8	12
20	NMR Reveals a Different Mode of Binding of the Stam2 VHS Domain to Ubiquitin and Diubiquitin,. Biochemistry, 2011, 50, 48-62.	2.5	16
21	Exploring the Linkage Dependence of Polyubiquitin Conformations Using Molecular Modeling. Journal of Molecular Biology, 2010, 395, 803-814.	4.2	59
22	NMR Screening Applied to the Fragment-Based Generation of Inhibitors of Creatine Kinase Exploiting a New Interaction Proximate to the ATP Binding Site. Journal of Medicinal Chemistry, 2007, 50, 1865-1875.	6.4	19
23	Proteinâ€"protein interactions within peroxiredoxin systems. Photosynthesis Research, 2006, 89, 277-290.	2.9	25
24	Glutathionylation Induces the Dissociation of 1-Cys D-peroxiredoxin Non-covalent Homodimer. Journal of Biological Chemistry, 2006, 281, 31736-31742.	3.4	67
25	Glutathionylation Induces the Dissociation of 1-Cys D-peroxiredoxin Non-covalent Homodimer. Journal of Biological Chemistry, 2006, 281, 31736-31742.	3.4	20
26	NMR Reveals a Novel Glutaredoxinâ€"Glutaredoxin Interaction Interface. Journal of Molecular Biology, 2005, 353, 629-641.	4.2	24
27	Crystal Structure and Solution NMR Dynamics of a D (Type II) Peroxiredoxin Glutaredoxin and Thioredoxin Dependent:â€‰ A New Insight into the Peroxiredoxin Oligomerism. Biochemistry, 2005, 44, 1755-1767.	2.5	50
28	Efficient and accurate determination of the overall rotational diffusion tensor of a molecule from 15N relaxation data using computer program ROTDIF. Journal of Magnetic Resonance, 2004, 168, 336-345.	2.1	73
29	Determining domain orientation in macromolecules by using spin-relaxation and residual dipolar coupling measurements. Progress in Nuclear Magnetic Resonance Spectroscopy, 2004, 44, 189-214.	7.5	90
30	Heteronuclear Overhauser experiments for symmetric molecules. Magnetic Resonance in Chemistry, 2003, 41, 776-781.	1.9	9
31	Determination of the rotation-diffusion tensor orientation from NMR13C-1H cross-relaxation rates. Molecular Physics, 2002, 100, 2755-2761.	1.7	6
32	Structural Properties of Polyubiquitin Chains in Solution. Journal of Molecular Biology, 2002, 324, 637-647.	4.2	259
33	Determination of Carbon-13 Chemical Shielding Tensor in the Liquid State by Combining NMR Relaxation Experiments and Quantum Chemical Calculations. Journal of the American Chemical Society, 2002, 124, 865-873.	13.7	29
34	Solvent dependence of rotational anisotropy and molecular geometry as probed by NMR cross-relaxation rates. Chemical Physics Letters, 2002, 357, 103-107.	2.6	2
35	Synthesis and spectral study of (2R,11R)-2,11-bis{[(2-methoxyethoxy)methoxy]methyl}-1,10-dibenzyl-4,7,13,16-tetraoxa-1,10-diaza-cyclooctadecane. Magnetic Resonance in Chemistry, 2001, 39, 212-214.	n/a	1
36	Anisotropy of molecular reorientation and geometrical information as determined from short and long range13C-1H spin cross-relaxation rates. Molecular Physics, 1998, 94, 565-569.	1.7	2

#	Article	IF	Citations
37	Anisotropy of molecular reorientation and geometrical information as determined from short and long range 13C-1H spin cross-relaxation rates. Molecular Physics, 1998, 94, 565-569.	1.7	7