

Linda J Ball

List of Publications by Year in descending order

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34
papers

2,183
citations

394421

19
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454955

30
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36
all docs

36
docs citations

36
times ranked

3543
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural changes of TasA in biofilm formation of <i>Bacillus subtilis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 3237-3242.	7.1	97
2	Structural insight into protein-aided bacterial biofilm formation. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, e206-e206.	0.1	0
3	Structural Insights into the Activation of the RhoA GTPase by the Lymphoid Blast Crisis (Lbc) Oncoprotein. Journal of Biological Chemistry, 2014, 289, 23992-24004.	3.4	10
4	Resonance assignments of the human AKAP13-PH domain and stabilizing DH helix. Biomolecular NMR Assignments, 2009, 3, 215-218.	0.8	3
5	Backbone and sidechain 1H, 13C and 15N resonance assignments of the Bright/ARID domain from the human JARID1C (SMCX) protein. Biomolecular NMR Assignments, 2008, 2, 9-11.	0.8	16
6	Structural diversity in the RGS domain and its interaction with heterotrimeric G protein β -subunits. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 6457-6462.	7.1	174
7	The scientific impact of the Structural Genomics Consortium: a protein family and ligand-centered approach to medically-relevant human proteins. Journal of Structural and Functional Genomics, 2007, 8, 107-119.	1.2	66
8	Resonance assignment of the RGS domain of human RGS10. Journal of Biomolecular NMR, 2007, 38, 191-191.	2.8	0
9	Backbone and sidechain 1H, 13C and 15N resonance assignments of the RGS domain from human RGS14. Biomolecular NMR Assignments, 2007, 1, 95-97.	0.8	0
10	Chemical screening methods to identify ligands that promote protein stability, protein crystallization, and structure determination. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 15835-15840.	7.1	526
11	Structural and Biochemical Study of Effector Molecule Recognition by the E.coli Glyoxylate and Allantoin Utilization Regulatory Protein AllR. Journal of Molecular Biology, 2006, 358, 810-828.	4.2	24
12	NMR assignment of human RGS18. Journal of Biomolecular NMR, 2006, 36, 72-72.	2.8	1
13	Quantitative study of the effects of chemical shift tolerances and rates of SA cooling on structure calculation from automatically assigned NOE data. Journal of Magnetic Resonance, 2005, 175, 92-102.	2.1	31
14	Recognition of Proline-Rich Motifs by Protein-Protein-Interaction Domains. Angewandte Chemie - International Edition, 2005, 44, 2852-2869.	13.8	236
15	EVH1/WH1 Domains. , 2005, , 73-101.		1
16	Recognition of Proline-Rich Motifs by Protein-Protein-Interaction Domains. ChemInform, 2005, 36, no.	0.0	0
17	Solution Structure of Human Cofilin. Journal of Biological Chemistry, 2004, 279, 4840-4848.	3.4	122
18	Letter to the Editor: Backbone and Sidechain 1H, 13C and 15N Resonance Assignments of Human Cofilin. Journal of Biomolecular NMR, 2004, 29, 429-430.	2.8	1

#	ARTICLE	IF	CITATIONS
19	Letter to the Editor: ^1H , ^{13}C and ^{15}N Resonance Assignment of the Human Spred2 EVH1 Domain. <i>Journal of Biomolecular NMR</i> , 2004, 29, 435-436.	2.8	4
20	Letter to the Editor: ^1H , ^{13}C and ^{15}N resonance assignments of the C-terminal BRCT domain from human BRCA1. <i>Journal of Biomolecular NMR</i> , 2004, 30, 221-222.	2.8	1
21	Solution Structure, Backbone Dynamics, and Association Behavior of the C-Terminal BRCT Domain from the Breast Cancer-Associated Protein BRCA1. <i>Biochemistry</i> , 2004, 43, 15983-15995.	2.5	26
22	The SEP domain of p47 acts as a reversible competitive inhibitor of cathepsin L. <i>FEBS Letters</i> , 2004, 576, 358-362.	2.8	18
23	Design of N-substituted Peptomer Ligands for EVH1 Domains. <i>Journal of Biological Chemistry</i> , 2003, 278, 36810-36818.	3.4	22
24	Relaxation, Equilibrium Oligomerization, and Molecular Symmetry of the VASP (336-380) EVH2 Tetramer. <i>Biochemistry</i> , 2002, 41, 11143-11151.	2.5	27
25	EVH1 domains: structure, function and interactions. <i>FEBS Letters</i> , 2002, 513, 45-52.	2.8	132
26	Normalization of nomenclature for peptide motifs as ligands of modular protein domains. <i>FEBS Letters</i> , 2002, 513, 141-144.	2.8	118
27	The NMR structure of the 47-kDa dimeric enzyme 3,4-dihydroxy-2-butanone-4-phosphate synthase and ligand binding studies reveal the location of the active site. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 13025-13030.	7.1	33
28	Bridging the gap: A set of selective ^1H - ^{15}N -correlations to link sequential neighbors of prolines. <i>Journal of Biomolecular NMR</i> , 2000, 17, 331-335.	2.8	18
29	Dual epitope recognition by the VASP EVH1 domain modulates polyproline ligand specificity and binding affinity. <i>EMBO Journal</i> , 2000, 19, 4903-4914.	7.8	120
30	Application of amino acid type-specific ^1H - and ^{14}N -labeling in a ^2H -, ^{15}N -labeled background to a 47 kDa homodimer: potential for NMR structure determination of large proteins. <i>Journal of Biomolecular NMR</i> , 1999, 14, 79-83.	2.8	33
31	Solution structure of the receptor tyrosine kinase EphB2 SAM domain and identification of two distinct homotypic interaction sites. <i>Protein Science</i> , 1999, 8, 1954-1961.	7.6	73
32	The origin of the β -domain intermediate in the folding of hen lysozyme. <i>Journal of Molecular Biology</i> , 1998, 277, 997-1005.	4.2	53
33	Structure of the chromatin binding (chromo) domain from mouse modifier protein 1. <i>EMBO Journal</i> , 1997, 16, 2473-2481.	7.8	160
34	Zinc co-ordination in the DNA-binding domain of the yeast transcriptional activator PPR1. <i>FEBS Letters</i> , 1995, 358, 278-282.	2.8	15