## David J Aceti

## List of Publications by Citations

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25 g-index

25 ext. papers ext. citations avg, IF L-index

#	Paper	IF	Citations
25	Structure and mechanism of mouse cysteine dioxygenase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2006</b> , 103, 3084-9	11.5	157
24	Protocols for production of selenomethionine-labeled proteins in 2-L polyethylene terephthalate bottles using auto-induction medium. <i>Protein Expression and Purification</i> , <b>2005</b> , 40, 256-67	2	99
23	Auto-induction medium for the production of [U-15N]- and [U-13C, U-15N]-labeled proteins for NMR screening and structure determination. <i>Protein Expression and Purification</i> , <b>2005</b> , 40, 268-78	2	81
22	Sweetness determinant sites of brazzein, a small, heat-stable, sweet-tasting protein. <i>Archives of Biochemistry and Biophysics</i> , <b>2000</b> , 376, 259-65	4.1	77
21	High-throughput purification and quality assurance of Arabidopsis thaliana proteins for eukaryotic structural genomics. <i>Journal of Structural and Functional Genomics</i> , <b>2005</b> , 6, 143-7		65
20	Efficient production of recombinant brazzein, a small, heat-stable, sweet-tasting protein of plant origin. <i>Archives of Biochemistry and Biophysics</i> , <b>2000</b> , 376, 252-8	4.1	64
19	Comparison of cell-based and cell-free protocols for producing target proteins from the Arabidopsis thaliana genome for structural studies. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2005</b> , 59, 633-43	4.2	52
18	Critical regions for the sweetness of brazzein. FEBS Letters, 2003, 544, 33-7	3.8	49
17	Mutations in FLS2 Ser-938 dissect signaling activation in FLS2-mediated Arabidopsis immunity. <i>PLoS Pathogens</i> , <b>2013</b> , 9, e1003313	7.6	44
16	Transcriptional regulation of Streptomyces coelicolor pathway-specific antibiotic regulators by the absA and absB loci. <i>Journal of Bacteriology</i> , <b>1998</b> , 180, 3100-6	3.5	43
15	Small-scale, semi-automated purification of eukaryotic proteins for structure determination. <i>Journal of Structural and Functional Genomics</i> , <b>2007</b> , 8, 153-66		27
14	The Center for Eukaryotic Structural Genomics. <i>Journal of Structural and Functional Genomics</i> , <b>2009</b> , 10, 165-79		25
13	Structure of the putative 32 kDa myrosinase-binding protein from Arabidopsis (At3g16450.1) determined by SAIL-NMR. <i>FEBS Journal</i> , <b>2008</b> , 275, 5873-84	5.7	25
12	Applications of Parametrized NMR Spin Systems of Small Molecules. <i>Analytical Chemistry</i> , <b>2018</b> , 90, 10	64,6810	649;
11	Crystal structure of At2g03760, a putative steroid sulfotransferase from Arabidopsis thaliana. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2004</b> , 57, 854-7	4.2	14
10	Structural and functional characterization of a novel phosphatase from the Arabidopsis thaliana gene locus At1g05000. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2008</b> , 73, 241-53	4.2	13
9	Expression platforms for producing eukaryotic proteins: a comparison of E. coli cell-based and wheat germ cell-free synthesis, affinity and solubility tags, and cloning strategies. <i>Journal of Structural and Functional Genomics</i> , <b>2015</b> , 16, 67-80		10

## LIST OF PUBLICATIONS

8	Structural and functional characterization of CalS11, a TDP-rhamnose 3[-O-methyltransferase involved in calicheamicin biosynthesis. <i>ACS Chemical Biology</i> , <b>2013</b> , 8, 1632-9	4.9	10
7	X-ray structure of Arabidopsis At1g77680, 12-oxophytodienoate reductase isoform 1. <i>Proteins:</i> Structure, Function and Bioinformatics, <b>2005</b> , 61, 206-8	4.2	7
6	Solution structure of the 2A protease from a common cold agent, human rhinovirus C2, strain W12. <i>PLoS ONE</i> , <b>2014</b> , 9, e97198	3.7	7
5	Cell-free translation and purification of Arabidopsis thaliana regulator of G signaling 1 protein. <i>Protein Expression and Purification</i> , <b>2016</b> , 126, 33-41	2	7
4	Microbiology and biochemistry of the methanogenic archaeobacteria. <i>Advances in Space Research</i> , <b>1989</b> , 9, 101-105	2.4	6
3	(1)H, (13)C and (15)N backbone assignment of a 32 kDa hypothetical protein from Arabidopsis thaliana, At3g16450.1. <i>Journal of Biomolecular NMR</i> , <b>2004</b> , 30, 357-8	3	2
2	Backbone resonance assignments and secondary structure of Ebola nucleoprotein 600-739 construct. <i>Biomolecular NMR Assignments</i> , <b>2019</b> , 13, 315-319	0.7	1
1	Fragment screening targeting Ebola virus nucleoprotein C-terminal domain identifies lead candidates. <i>Antiviral Research</i> , <b>2020</b> , 180, 104822	10.8	1