Michael V Airola

List of Publications by Year in Descending Order

25 papers	722 citations	13 h-index	26 g-index
30 ext. papers	900 ext. citations	6.8 avg, IF	4.28 L-index

#	Paper	IF	Citations
25	Measurement of neutral ceramidase activity in vitro and in vivo.. *Analytical Biochemistry*, **2022**, 643, 114577	3.1	
24	Structure and inhibition of Cryptococcus neoformans sterylglucosidase to develop antifungal agents. *Nature Communications*, **2021**, 12, 5885	17.4	1
23	Biallelic loss-of-function variants in PLD1 cause congenital right-sided cardiac valve defects and neonatal cardiomyopathy. *Journal of Clinical Investigation*, **2021**, 131,	15.9	4
22	Identification of Small-Molecule Inhibitors of Neutral Ceramidase (nCDase) via Target-Based High-Throughput Screening. *SLAS Discovery*, **2021**, 26, 113-121	3.4	2
21	Structure and regulation of human phospholipase D. *Advances in Biological Regulation*, **2021**, 79, 100783	6.2	7
20	The middle lipin domain adopts a membrane-binding dimeric protein fold. *Nature Communications*, **2021**, 12, 4718	17.4	2
19	Crystal structure of human PLD1 provides insight into activation by PI(4,5)P and RhoA. *Nature Chemical Biology*, **2020**, 16, 400-407	11.7	15
18	Crystal structure of a lipin/Pah phosphatidic acid phosphatase. *Nature Communications*, **2020**, 11, 1309	17.4	13
17	The juxtamembrane linker in neutral sphingomyelinase-2 functions as an intramolecular allosteric switch that activates the enzyme. *Journal of Biological Chemistry*, **2019**, 294, 7488-7502	5.4	10
16	Quantification of 3-ketodihydrosphingosine using HPLC-ESI-MS/MS to study SPT activity in yeast. *Journal of Lipid Research*, **2018**, 59, 162-170	6.3	10
15	Structure and Function of Lipins: Key Enzymes in Triglyceride Metabolism. *FASEB Journal*, **2018**, 32, 672.6	6.9	
14	Mek1 coordinates meiotic progression with DNA break repair by directly phosphorylating and inhibiting the yeast pachytene exit regulator Ndt80. *PLoS Genetics*, **2018**, 14, e1007832	6	14
13	How lipid droplets "TAG" along: Glycerolipid synthetic enzymes and lipid storage. *Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids*, **2017**, 1862, 1131-1145	5	52
12	Structure of human nSMase2 reveals an interdomain allosteric activation mechanism for ceramide generation. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, E5549-E5558	11.5	44
11	Structural Basis for Ceramide Recognition and Hydrolysis by Human Neutral Ceramidase. *Structure*, **2015**, 23, 1482-1491	5.2	37
10	P53-dependent upregulation of neutral sphingomyelinase-2: role in doxorubicin-induced growth arrest. *Cell Death and Disease*, **2015**, 6, e1947	9.8	48
9	Roles and regulation of neutral sphingomyelinase-2 in cellular and pathological processes. *Advances in Biological Regulation*, **2015**, 57, 24-41	6.2	109

List of Publications

8	Identification and biochemical characterization of an acid sphingomyelinase-like protein from the bacterial plant pathogen Ralstonia solanacearum that hydrolyzes ATP to AMP but not sphingomyelin to ceramide. *PLoS ONE*, **2014**, 9, e105830	3.7	6
7	Architecture of the soluble receptor Aer2 indicates an in-line mechanism for PAS and HAMP domain signaling. *Journal of Molecular Biology*, **2013**, 425, 886-901	6.5	34
6	Sphingolipid metabolism and neutral sphingomyelinases. *Handbook of Experimental Pharmacology*, **2013**, 57-76	3.2	99
5	HAMP domain conformers that propagate opposite signals in bacterial chemoreceptors. *PLoS Biology*, **2013**, 11, e1001479	9.7	44
4	Identifying divergent HAMP domains and poly-HAMP chains. *Journal of Biological Chemistry*, **2010**, 285, le7; author reply 1e8	5.4	6
3	Heme binding to the Mammalian circadian clock protein period 2 is nonspecific. *Biochemistry*, **2010**, 49, 4327-38	3.2	29
2	Co-expression of ferrochelatase allows for complete heme incorporation into recombinant proteins produced in E. coli. *Protein Expression and Purification*, **2010**, 73, 78-82	2	30
1	Structure of concatenated HAMP domains provides a mechanism for signal transduction. *Structure*, **2010**, 18, 436-48	5.2	105