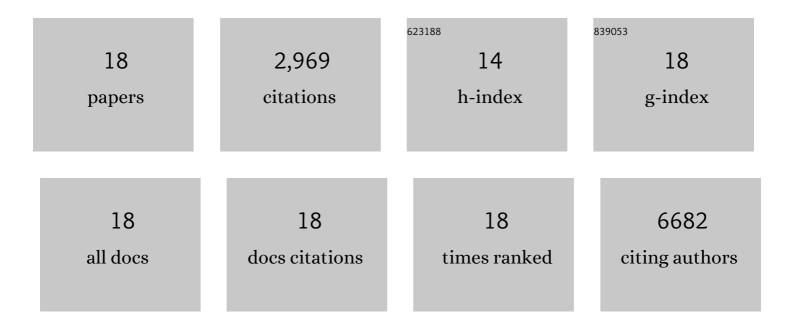
Matt E Oates

List of Publications by Year in descending order

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ΜΑΤΤ Ε ΟΛΤΕς

#	Article	IF	CITATIONS
1	The InterPro protein families database: the classification resource after 15 years. Nucleic Acids Research, 2015, 43, D213-D221.	6.5	1,205
2	D2P2: database of disordered protein predictions. Nucleic Acids Research, 2012, 41, D508-D516.	6.5	570
3	The genome of <i>Aiptasia</i> , a sea anemone model for coral symbiosis. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11893-11898.	3.3	359
4	A predictive computational framework for direct reprogramming between human cell types. Nature Genetics, 2016, 48, 331-335.	9.4	263
5	The SUPERFAMILY 2.0 database: a significant proteome update and a new webserver. Nucleic Acids Research, 2019, 47, D490-D494.	6.5	126
6	The SUPERFAMILY 1.75 database in 2014: a doubling of data. Nucleic Acids Research, 2015, 43, D227-D233.	6.5	74
7	Structured and disordered facets of the GPCR fold. Current Opinion in Structural Biology, 2014, 27, 129-137.	2.6	68
8	Molecular Principles of Gene Fusion Mediated Rewiring of Protein Interaction Networks in Cancer. Molecular Cell, 2016, 63, 579-592.	4.5	63
9	A Subset of Ubiquitin-Conjugating Enzymes Is Essential for Plant Immunity. Plant Physiology, 2017, 173, 1371-1390.	2.3	53
10	A daily-updated tree of (sequenced) life as a reference for genome research. Scientific Reports, 2013, 3, 2015.	1.6	47
11	Genome3D: exploiting structure to help users understand their sequences. Nucleic Acids Research, 2015, 43, D382-D386.	6.5	42
12	Evolution of the Calcium-Based Intracellular Signaling System. Genome Biology and Evolution, 2016, 8, 2118-2132.	1.1	35
13	â€~Why genes in pieces?'—revisited. Nucleic Acids Research, 2019, 47, 4970-4973.	6.5	17
14	Splice junctions are constrained by protein disorder. Nucleic Acids Research, 2015, 43, 4814-4822.	6.5	16
15	The Evolution of Human Cells in Terms of Protein Innovation. Molecular Biology and Evolution, 2014, 31, 1364-1374.	3.5	13
16	Three reasons protein disorder analysis makes more sense in the light of collagen. Protein Science, 2016, 25, 1030-1036.	3.1	7
17	A <scp>P</scp> roteome <scp>Q</scp> uality <scp>I</scp> ndex. Environmental Microbiology, 2015, 17, 4-9.	1.8	6
18	Function-selective domain architecture plasticity potentials in eukaryotic genome evolution. Biochimie, 2015, 119, 269-277.	1.3	5