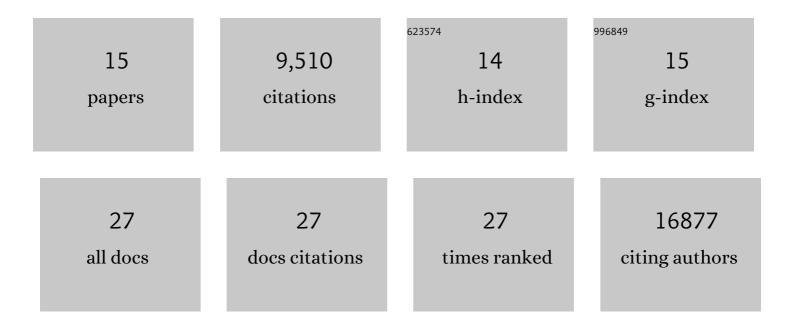
Stacia K Wyman

List of Publications by Year in descending order

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STACIA K WIVMAN

#	Article	IF	CITATIONS
1	ATF4 Regulates MYB to Increase γ-Globin in Response to Loss of β-Globin. Cell Reports, 2020, 32, 107993.	2.9	19
2	Controlled Cycling and Quiescence Enables Efficient HDR in Engraftment-Enriched Adult Hematopoietic Stem and Progenitor Cells. Cell Reports, 2020, 32, 108093.	2.9	54
3	The Histone Chaperone FACT Induces Cas9 Multi-turnover Behavior and Modifies Genome Manipulation in Human Cells. Molecular Cell, 2020, 79, 221-233.e5.	4.5	28
4	Timed inhibition of CDC7 increases CRISPR-Cas9 mediated templated repair. Nature Communications, 2020, 11, 2109.	5.8	84
5	CRISPR off-target detection with DISCOVER-seq. Nature Protocols, 2020, 15, 1775-1799.	5.5	45
6	SLC19A1 transports immunoreactive cyclic dinucleotides. Nature, 2019, 573, 434-438.	13.7	230
7	Oligogenic inheritance of a human heart disease involving a genetic modifier. Science, 2019, 364, 865-870.	6.0	142
8	Unbiased detection of CRISPR off-targets in vivo using DISCOVER-Seq. Science, 2019, 364, 286-289.	6.0	284
9	Post-transcriptional generation of miRNA variants by multiple nucleotidyl transferases contributes to miRNA transcriptome complexity. Genome Research, 2011, 21, 1450-1461.	2.4	269
10	Repertoire of microRNAs in Epithelial Ovarian Cancer as Determined by Next Generation Sequencing of Small RNA cDNA Libraries. PLoS ONE, 2009, 4, e5311.	1.1	223
11	Evaluation of the 8q24 Prostate Cancer Risk Locus and <i>MYC</i> Expression. Cancer Research, 2009, 69, 5568-5574.	0.4	110
12	Limitations and possibilities of small RNA digital gene expression profiling. Nature Methods, 2009, 6, 474-476.	9.0	280
13	MicroRNA Discovery and Profiling in Human Embryonic Stem Cells by Deep Sequencing of Small RNA Libraries. Stem Cells, 2008, 26, 2496-2505.	1.4	273
14	Circulating microRNAs as stable blood-based markers for cancer detection. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 10513-10518.	3.3	7,047
15	Methods for Obtaining and Analyzing Whole Chloroplast Genome Sequences. Methods in Enzymology, 2005, 395, 348-384.	0.4	410