

# Kathleen A Kennedy

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10880780/publications.pdf>

Version: 2024-02-01

10  
papers

754  
citations

1040056

9  
h-index

1372567

10  
g-index

10  
all docs

10  
docs citations

10  
times ranked

1770  
citing authors

#	ARTICLE	IF	CITATIONS
1	Function of C/EBP $\beta$ in a regulatory circuit that discriminates between transient and persistent TLR4-induced signals. <i>Nature Immunology</i> , 2009, 10, 437-443.	14.5	249
2	Uncovering a Macrophage Transcriptional Program by Integrating Evidence from Motif Scanning and Expression Dynamics. <i>PLoS Computational Biology</i> , 2008, 4, e1000021.	3.2	173
3	Systems analysis identifies an essential role for SHANK-associated RH domain-interacting protein (SHARPIN) in macrophage Toll-like receptor 2 (TLR2) responses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11536-11541.	7.1	67
4	Genome-wide histone acetylation data improve prediction of mammalian transcription factor binding sites. <i>Bioinformatics</i> , 2010, 26, 2071-2075.	4.1	63
5	Leishmania Promotes Its Own Virulence by Inducing Expression of the Host Immune Inhibitory Ligand CD200. <i>Cell Host and Microbe</i> , 2011, 9, 463-471.	11.0	62
6	Control of Parasitophorous Vacuole Expansion by LYST/Beige Restricts the Intracellular Growth of <i>Leishmania amazonensis</i> . <i>PLoS Pathogens</i> , 2008, 4, e1000179.	4.7	61
7	MalK Forms a Dimer Independent of Its Assembly into the MalFGK2 ATP-binding Cassette Transporter of <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 1999, 274, 6259-6264.	3.4	31
8	Multiscale representation of genomic signals. <i>Nature Methods</i> , 2014, 11, 689-694.	19.0	31
9	Evidence for Multiple Pathways in the Assembly of the <i>Escherichia coli</i> Maltose Transport Complex. <i>Journal of Biological Chemistry</i> , 2004, 279, 33290-33297.	3.4	15
10	Identifying novel transcription factors involved in the inflammatory response by using binding site motif scanning in genomic regions defined by histone acetylation. <i>PLoS ONE</i> , 2017, 12, e0184850.	2.5	2