

# Felicia S L Ng

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/639133/publications.pdf>

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13  
papers

1,020  
citations

933447

10  
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1125743

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docs citations

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times ranked

2444  
citing authors

#	ARTICLE	IF	CITATIONS
1	Combinatorial Transcriptional Control In Blood Stem/Progenitor Cells: Genome-wide Analysis of Ten Major Transcriptional Regulators. <i>Cell Stem Cell</i> , 2010, 7, 532-544.	11.1	623
2	CODEX: a next-generation sequencing experiment database for the haematopoietic and embryonic stem cell communities. <i>Nucleic Acids Research</i> , 2015, 43, D1117-D1123.	14.5	112
3	An experimentally validated network of nine haematopoietic transcription factors reveals mechanisms of cell state stability. <i>ELife</i> , 2016, 5, e11469.	6.0	61
4	LSD1 inhibition by tranylcypromine derivatives interferes with GFI1-mediated repression of PU.1 target genes and induces differentiation in AML. <i>Leukemia</i> , 2019, 33, 1411-1426.	7.2	53
5	Integrated genome-scale analysis of the transcriptional regulatory landscape in a blood stem/progenitor cell model. <i>Blood</i> , 2016, 127, e12-e23.	1.4	49
6	Anti-PD-L1 and anti-CD73 combination therapy promotes T cell response to EGFR-mutated NSCLC. <i>JCI Insight</i> , 2022, 7, .	5.0	42
7	Single-cell analyses of regulatory network perturbations using enhancer-targeting TALEs suggest novel roles for PU.1 during haematopoietic specification. <i>Development (Cambridge)</i> , 2014, 141, 4018-4030.	2.5	26
8	Constrained transcription factor spacing is prevalent and important for transcriptional control of mouse blood cells. <i>Nucleic Acids Research</i> , 2014, 42, 13513-13524.	14.5	21
9	Building an ENCODE-style data compendium on a shoestring. <i>Nature Methods</i> , 2013, 10, 926-926.	19.0	13
10	Establishing the stem cell state: insights from regulatory network analysis of blood stem cell development. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2012, 4, 285-295.	6.6	11
11	ConBind: motif-aware cross-species alignment for the identification of functional transcription factor binding sites. <i>Nucleic Acids Research</i> , 2016, 44, e72-e72.	14.5	7
12	Shared transcription factors contribute to distinct cell fates. <i>Transcription</i> , 2014, 5, e978173.	3.1	1
13	A graphical model approach visualizes regulatory relationships between genome-wide transcription factor binding profiles. <i>Briefings in Bioinformatics</i> , 2016, 19, bbw102.	6.5	1