

# Alberto Santos-Zavaleta

## List of Publications by Year in descending order

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27  
papers

5,281  
citations

304743

22  
h-index

526287

27  
g-index

29  
all docs

29  
docs citations

29  
times ranked

5770  
citing authors

#	ARTICLE	IF	CITATIONS
1	The EcoCyc database: reflecting new knowledge about <i>Escherichia coli</i> K-12. <i>Nucleic Acids Research</i> , 2017, 45, D543-D550.	14.5	541
2	EcoCyc: fusing model organism databases with systems biology. <i>Nucleic Acids Research</i> , 2013, 41, D605-D612.	14.5	505
3	RegulonDB version 9.0: high-level integration of gene regulation, coexpression, motif clustering and beyond. <i>Nucleic Acids Research</i> , 2016, 44, D133-D143.	14.5	450
4	EcoCyc: a comprehensive database of <i>Escherichia coli</i> biology. <i>Nucleic Acids Research</i> , 2011, 39, D583-D590.	14.5	444
5	RegulonDB v8.0: omics data sets, evolutionary conservation, regulatory phrases, cross-validated gold standards and more. <i>Nucleic Acids Research</i> , 2013, 41, D203-D213.	14.5	404
6	RegulonDB (version 6.0): gene regulation model of <i>Escherichia coli</i> K-12 beyond transcription, active (experimental) annotated promoters and Textpresso navigation. <i>Nucleic Acids Research</i> , 2007, 36, D120-D124.	14.5	395
7	RegulonDB (version 5.0): <i>Escherichia coli</i> K-12 transcriptional regulatory network, operon organization, and growth conditions. <i>Nucleic Acids Research</i> , 2006, 34, D394-D397.	14.5	325
8	RegulonDB v 10.5: tackling challenges to unify classic and high throughput knowledge of gene regulation in <i>E. coli</i> K-12. <i>Nucleic Acids Research</i> , 2019, 47, D212-D220.	14.5	322
9	EcoCyc: A comprehensive view of <i>Escherichia coli</i> biology. <i>Nucleic Acids Research</i> , 2009, 37, D464-D470.	14.5	320
10	RegulonDB version 7.0: transcriptional regulation of <i>Escherichia coli</i> K-12 integrated within genetic sensory response units (Gensor Units). <i>Nucleic Acids Research</i> , 2011, 39, D98-D105.	14.5	315
11	RegulonDB (version 4.0): transcriptional regulation, operon organization and growth conditions in <i>Escherichia coli</i> K-12. <i>Nucleic Acids Research</i> , 2004, 32, 303D-306.	14.5	231
12	RegulonDB (version 3.2): transcriptional regulation and operon organization in <i>Escherichia coli</i> K-12. <i>Nucleic Acids Research</i> , 2001, 29, 72-74.	14.5	201
13	Multidimensional annotation of the <i>Escherichia coli</i> K-12 genome. <i>Nucleic Acids Research</i> , 2007, 35, 7577-7590.	14.5	168
14	The EcoCyc Database in 2021. <i>Frontiers in Microbiology</i> , 2021, 12, 711077.	3.5	122
15	The EcoCyc Database. <i>EcoSal Plus</i> , 2014, 6, .	5.4	101
16	The EcoCyc Database. <i>EcoSal Plus</i> , 2018, 8, .	5.4	75
17	RegulonDB (version 3.0): transcriptional regulation and operon organization in <i>Escherichia coli</i> K-12. <i>Nucleic Acids Research</i> , 2000, 28, 65-67.	14.5	67
18	The comprehensive updated regulatory network of <i>Escherichia coli</i> K-12. <i>BMC Bioinformatics</i> , 2006, 7, 5.	2.6	63

#	ARTICLE	IF	CITATIONS
19	PromEC: An updated database of Escherichia coli mRNA promoters with experimentally identified transcriptional start sites. <i>Nucleic Acids Research</i> , 2001, 29, 277-0.	14.5	61
20	A unified resource for transcriptional regulation in Escherichia coli K-12 incorporating high-throughput-generated binding data into RegulonDB version 10.0. <i>BMC Biology</i> , 2018, 16, 91.	3.8	42
21	RegulonDB (version 2.0): a database on transcriptional regulation in Escherichia coli. <i>Nucleic Acids Research</i> , 1999, 27, 59-60.	14.5	38
22	Bioinformatics Resources for the Study of Gene Regulation in Bacteria. <i>Journal of Bacteriology</i> , 2009, 191, 23-31.	2.2	25
23	Evidence classification of high-throughput protocols and confidence integration in RegulonDB. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bas059.	3.0	23
24	Assisted curation of regulatory interactions and growth conditions of OxyR in E. coli K-12. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau049-bau049.	3.0	15
25	A comparative genome analysis of the RpoS sigma factor shows a high diversity of responses and origins. <i>Microbiology (United Kingdom)</i> , 2011, 157, 1393-1401.	1.8	11
26	Similarity corpus on microbial transcriptional regulation. <i>Journal of Biomedical Semantics</i> , 2019, 10, 8.	1.6	8
27	Tracing the phylogenetic history of the Crl regulon through the Bacteria and Archaea genomes. <i>BMC Genomics</i> , 2019, 20, 299.	2.8	8