

# Ralf Zimmer

## List of Publications by Year in descending order

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Version: 2024-02-01

33  
papers

1,649  
citations

377584

21  
h-index

425179

34  
g-index

40  
all docs

40  
docs citations

40  
times ranked

2951  
citing authors

#	ARTICLE	IF	CITATIONS
1	Toward a gold standard for benchmarking gene set enrichment analysis. <i>Briefings in Bioinformatics</i> , 2021, 22, 545-556.	3.2	83
2	Vascular neutrophilic inflammation and immunothrombosis distinguish severe COVID-19 from influenza pneumonia. <i>Journal of Thrombosis and Haemostasis</i> , 2021, 19, 574-581.	1.9	80
3	Self-sustaining IL-8 loops drive a prothrombotic neutrophil phenotype in severe COVID-19. <i>JCI Insight</i> , 2021, 6, .	2.3	71
4	CNVRanger: association analysis of CNVs with gene expression and quantitative phenotypes. <i>Bioinformatics</i> , 2020, 36, 972-973.	1.8	17
5	MS-EmpiRe Utilizes Peptide-level Noise Distributions for Ultra-sensitive Detection of Differentially Expressed Proteins. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1880-1892.	2.5	27
6	YESdb: integrative analysis of environmental stress in yeast. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	1
7	Multi-Reference Spectral Library Yields Almost Complete Coverage of Heterogeneous LC-MS/MS Data Sets. <i>Journal of Proteome Research</i> , 2019, 18, 1553-1566.	1.8	5
8	Widespread modulation of gene expression by copy number variation in skeletal muscle. <i>Scientific Reports</i> , 2018, 8, 1399.	1.6	25
9	miR-103 promotes endothelial maladaptation by targeting IncWDR59. <i>Nature Communications</i> , 2018, 9, 2645.	5.8	57
10	Bioinformatics advances biology and medicine by turning big data troves into knowledge. <i>Informatik-Spektrum</i> , 2017, 40, 153-160.	1.0	2
11	EBF1 binds to EBNA2 and promotes the assembly of EBNA2 chromatin complexes in B cells. <i>PLoS Pathogens</i> , 2017, 13, e1006664.	2.1	25
12	Genome-Wide Detection of CNVs and Their Association with Meat Tenderness in Nelore Cattle. <i>PLoS ONE</i> , 2016, 11, e0157711.	1.1	59
13	Regulatory Implications of Non-Trivial Splicing: Isoform 3 of Rab1A Shows Enhanced Basal Activity and Is Not Controlled by Accessory Proteins. <i>Journal of Molecular Biology</i> , 2016, 428, 1544-1557.	2.0	5
14	Bioconductor's EnrichmentBrowser: seamless navigation through combined results of set- & network-based enrichment analysis. <i>BMC Bioinformatics</i> , 2016, 17, 45.	1.2	79
15	Count ratio model reveals bias affecting NGS fold changes. <i>Nucleic Acids Research</i> , 2015, 43, gkv696.	6.5	14
16	ContextMap 2: fast and accurate context-based RNA-seq mapping. <i>BMC Bioinformatics</i> , 2015, 16, 122.	1.2	54
17	Alternative Splicing in Next Generation Sequencing Data of <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2015, 10, e0140487.	1.1	41
18	Inactivation of Intergenic Enhancers by EBNA3A Initiates and Maintains Polycomb Signatures across a Chromatin Domain Encoding CXCL10 and CXCL9. <i>PLoS Pathogens</i> , 2013, 9, e1003638.	2.1	55

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19	A comprehensive gene regulatory network for the diauxic shift in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2013, 41, 8452-8463.	6.5	26
20	Mining RNA-Seq Data for Infections and Contaminations. <i>PLoS ONE</i> , 2013, 8, e73071.	1.1	13
21	Rigorous assessment of gene set enrichment tests. <i>Bioinformatics</i> , 2012, 28, 1480-1486.	1.8	27
22	A context-based approach to identify the most likely mapping for RNA-seq experiments. <i>BMC Bioinformatics</i> , 2012, 13, S9.	1.2	14
23	From sets to graphs: towards a realistic enrichment analysis of transcriptomic systems. <i>Bioinformatics</i> , 2011, 27, i366-i373.	1.8	64
24	FERN – a Java framework for stochastic simulation and evaluation of reaction networks. <i>BMC Bioinformatics</i> , 2008, 9, 356.	1.2	26
25	Alternative splicing and protein structure evolution. <i>Nucleic Acids Research</i> , 2008, 36, 550-558.	6.5	100
26	Bootstrapping the Interactome: Unsupervised Identification of Protein Complexes in Yeast. <i>Lecture Notes in Computer Science</i> , 2008, , 3-16.	1.0	48
27	RelEx-Relation extraction using dependency parse trees. <i>Bioinformatics</i> , 2007, 23, 365-371.	1.8	417
28	Toward the complete interactome. <i>Nature Biotechnology</i> , 2006, 24, 614-615.	9.4	15
29	Gene and protein nomenclature in public databases. <i>BMC Bioinformatics</i> , 2006, 7, 372.	1.2	41
30	A simple approach for protein name identification: prospects and limits. <i>BMC Bioinformatics</i> , 2005, 6, S15.	1.2	38
31	Expert knowledge without the expert: integrated analysis of gene expression and literature to derive active functional contexts. <i>Bioinformatics</i> , 2005, 21, ii259-ii267.	1.8	28
32	ToPNet--an application for interactive analysis of expression data and biological networks. <i>Bioinformatics</i> , 2004, 20, 1470-1471.	1.8	14
33	New methods for joint analysis of biological networks and expression data. <i>Bioinformatics</i> , 2004, 20, 1517-1521.	1.8	68