

# Stephan

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/5233527/stephan-publications-by-year.pdf>

**Version:** 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

54  
papers

6,355  
citations

27  
h-index

58  
g-index

58  
ext. papers

8,346  
ext. citations

9.1  
avg, IF

5.48  
L-index

#	Paper	IF	Citations
54	Legal Action for Climate Protection Impulses on the international level from the German Federal Constitutional Court: the Court Order from March 2021 on the Unconstitutionality of the Federal German Climate Protection Act. <i>Brazilian Journal of Environmental Sciences (Online)</i> , <b>2022</b> , 57, 158-165	1	
53	Frequent mutations of FBXO11 highlight BCL6 as a therapeutic target in Burkitt lymphoma. <i>Blood Advances</i> , <b>2021</b> , 5, 5239-5257	7.8	1
52	Lifestyle weight-loss intervention may attenuate methylation aging: the CENTRAL MRI randomized controlled trial. <i>Clinical Epigenetics</i> , <b>2021</b> , 13, 48	7.7	2
51	Effects of lifestyle interventions on epigenetic signatures of liver fat: Central randomized controlled trial. <i>Liver International</i> , <b>2021</b> , 41, 2101-2111	7.9	3
50	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. <i>Leukemia</i> , <b>2021</b> , 35, 2002-2016	10.7	3
49	Absence of Non-Canonical, Inhibitory Splice Variants in B Cell Lymphomas Correlates With Sustained NF- $\kappa$ B Signaling. <i>Frontiers in Immunology</i> , <b>2021</b> , 12, 616451	8.4	2
48	MCPIP1 ribonuclease can bind and cleave mRNA in -amplified neuroblastoma cells. <i>RNA Biology</i> , <b>2021</b> , 18, 144-156	4.8	4
47	Transcription factor RFX7 governs a tumor suppressor network in response to p53 and stress. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, 7437-7456	20.1	4
46	The Evolving Faces of the SARS-CoV-2 Genome. <i>Viruses</i> , <b>2021</b> , 13,	6.2	5
45	Intronic tRNAs of mitochondrial origin regulate constitutive and alternative splicing. <i>Genome Biology</i> , <b>2020</b> , 21, 299	18.3	2
44	A probabilistic version of Sankoff's maximum parsimony algorithm. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2020</b> , 18, 2050004	1	1
43	Identification of RNA 3' ends and termination sites in. <i>RNA Biology</i> , <b>2020</b> , 17, 663-676	4.8	8
42	Reconstruction of rearranged T-cell receptor loci by whole genome and transcriptome sequencing gives insights into the initial steps of T-cell prolymphocytic leukemia. <i>Genes Chromosomes and Cancer</i> , <b>2020</b> , 59, 261-267	5	7
41	DNA methylation signature in blood mirrors successful weight-loss during lifestyle interventions: the CENTRAL trial. <i>Genome Medicine</i> , <b>2020</b> , 12, 97	14.4	9
40	Splicing Endonuclease Is an Important Player in rRNA and tRNA Maturation in Archaea. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 594838	5.7	3
39	DREAM and RB cooperate to induce gene repression and cell-cycle arrest in response to p53 activation. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 9087-9103	20.1	32
38	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. <i>Nature Communications</i> , <b>2019</b> , 10, 1459	17.4	49

37	Improved annotation of protein-coding genes boundaries in metazoan mitochondrial genomes. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 10543-10552	20.1	70
36	DIEGO: detection of differential alternative splicing using Aitchison's geometry. <i>Bioinformatics</i> , <b>2018</b> , 34, 1066-1068	7.2	4
35	RBFOX2 and alternative splicing in B-cell lymphoma. <i>Blood Cancer Journal</i> , <b>2018</b> , 8, 77	7	3
34	Beyond the 3'UTR binding-microRNA-induced protein truncation via DNA binding. <i>Oncotarget</i> , <b>2018</b> , 9, 32855-32867	3.3	8
33	Noncoding RNA Transcripts during Differentiation of Induced Pluripotent Stem Cells into Hepatocytes. <i>Stem Cells International</i> , <b>2018</b> , 2018, 5692840	5	3
32	The DREAM complex through its subunit Lin37 cooperates with Rb to initiate quiescence. <i>ELife</i> , <b>2017</b> , 6,	8.9	24
31	Changes of bivalent chromatin coincide with increased expression of developmental genes in cancer. <i>Scientific Reports</i> , <b>2016</b> , 6, 37393	4.9	64
30	Temperature-responsive in vitro RNA structurome of <i>Yersinia pseudotuberculosis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 7237-42	11.5	55
29	Recurrent mTORC1-activating RRAGC mutations in follicular lymphoma. <i>Nature Genetics</i> , <b>2016</b> , 48, 183-836.3	6.3	116
28	metilene: fast and sensitive calling of differentially methylated regions from bisulfite sequencing data. <i>Genome Research</i> , <b>2016</b> , 26, 256-62	9.7	159
27	Differential transcriptional responses to Ebola and Marburg virus infection in bat and human cells. <i>Scientific Reports</i> , <b>2016</b> , 6, 34589	4.9	30
26	Alterations of microRNA and microRNA-regulated messenger RNA expression in germinal center B-cell lymphomas determined by integrative sequencing analysis. <i>Haematologica</i> , <b>2016</b> , 101, 1380-1389	6.6	31
25	DNA methylome analysis in Burkitt and follicular lymphomas identifies differentially methylated regions linked to somatic mutation and transcriptional control. <i>Nature Genetics</i> , <b>2015</b> , 47, 1316-1325	36.3	101
24	MINCR is a MYC-induced lncRNA able to modulate MYC's transcriptional network in Burkitt lymphoma cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, E5261-70	11.5	75
23	The PCBP1 gene encoding poly(rC) binding protein I is recurrently mutated in Burkitt lymphoma. <i>Genes Chromosomes and Cancer</i> , <b>2015</b> , 54, 555-64	5	21
22	The ViennaRNA web services. <i>Methods in Molecular Biology</i> , <b>2015</b> , 1269, 307-26	1.4	80
21	Energy-based RNA consensus secondary structure prediction in multiple sequence alignments. <i>Methods in Molecular Biology</i> , <b>2014</b> , 1097, 125-41	1.4	2
20	2D meets 4G: G-quadruplexes in RNA secondary structure prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2013</b> , 10, 832-44	3	31

19	Recurrent mutation of the ID3 gene in Burkitt lymphoma identified by integrated genome, exome and transcriptome sequencing. <i>Nature Genetics</i> , <b>2012</b> , 44, 1316-20	36.3	317
18	Folding RNA/DNA hybrid duplexes. <i>Bioinformatics</i> , <b>2012</b> , 28, 2530-1	7.2	14
17	ViennaRNA Package 2.0. <i>Algorithms for Molecular Biology</i> , <b>2011</b> , 6, 26	1.8	2351
16	Animal snoRNAs and scaRNAs with exceptional structures. <i>RNA Biology</i> , <b>2011</b> , 8, 938-46	4.8	27
15	A folding algorithm for extended RNA secondary structures. <i>Bioinformatics</i> , <b>2011</b> , 27, i129-36	7.2	46
14	RNA structure prediction. <i>Methods in Molecular Biology</i> , <b>2011</b> , 760, 307-23	1.4	3
13	RNPomics: defining the ncRNA transcriptome by cDNA library generation from ribonucleo-protein particles. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, e113	20.1	36
12	Nematode sbRNAs: homologs of vertebrate Y RNAs. <i>Journal of Molecular Evolution</i> , <b>2010</b> , 70, 346-58	3.1	27
11	From consensus structure prediction to RNA gene finding. <i>Briefings in Functional Genomics &amp; Proteomics</i> , <b>2009</b> , 8, 461-71		26
10	Strategies for measuring evolutionary conservation of RNA secondary structures. <i>BMC Bioinformatics</i> , <b>2008</b> , 9, 122	3.6	50
9	RNAalifold: improved consensus structure prediction for RNA alignments. <i>BMC Bioinformatics</i> , <b>2008</b> , 9, 474	3.6	390
8	The Vienna RNA websuite. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, W70-4	20.1	1339
7	Variations on RNA folding and alignment: lessons from Benasque. <i>Journal of Mathematical Biology</i> , <b>2008</b> , 56, 129-44	2	57
6	RNAs everywhere: genome-wide annotation of structured RNAs. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , <b>2007</b> , 308, 1-25	1.8	38
5	Local RNA base pairing probabilities in large sequences. <i>Bioinformatics</i> , <b>2006</b> , 22, 614-5	7.2	164
4	Partition function and base pairing probabilities of RNA heterodimers. <i>Algorithms for Molecular Biology</i> , <b>2006</b> , 1, 3	1.8	183
3	Thermodynamics of RNA-RNA binding. <i>Bioinformatics</i> , <b>2006</b> , 22, 1177-82	7.2	272
2	Identification of RNA 3' ends and termination sites in <i>Haloferax volcanii</i>		1

- 1 The failure of B cells to induce non-canonical MYD88 splice variants correlates with lymphomagenesis via sustained NF- $\kappa$ B signaling