

# Torbjörn Rognes

## List of Publications by Year in descending order

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Version: 2024-02-01

56  
papers

16,847  
citations

159358

30  
h-index

149479

56  
g-index

59  
all docs

59  
docs citations

59  
times ranked

24535  
citing authors

#	ARTICLE	IF	CITATIONS
1	The uracil-DNA glycosylase UNG protects the fitness of normal and cancer B cells expressing AID. <i>NAR Cancer</i> , 2021, 2, zcaa019.	1.6	10
2	Reduced metagenome sequencing for strain-resolution taxonomic profiles. <i>Microbiome</i> , 2021, 9, 79.	4.9	14
3	Exploring the role of the multiple sclerosis susceptibility gene <i>CLEC16A</i> in T cells. <i>Scandinavian Journal of Immunology</i> , 2021, 94, e13050.	1.3	4
4	Swarm v3: towards tera-scale amplicon clustering. <i>Bioinformatics</i> , 2021, 38, 267-269.	1.8	40
5	The CRCbiome study: a large prospective cohort study examining the role of lifestyle and the gut microbiome in colorectal cancer screening participants. <i>BMC Cancer</i> , 2021, 21, 930.	1.1	22
6	HMST-Seq-Analyzer: A new python tool for differential methylation and hydroxymethylation analysis in various DNA methylation sequencing data. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2877-2889.	1.9	4
7	NucBreak: location of structural errors in a genome assembly by using paired-end Illumina reads. <i>BMC Bioinformatics</i> , 2020, 21, 66.	1.2	5
8	Uracil Accumulation and Mutagenesis Dominated by Cytosine Deamination in CpG Dinucleotides in Mice Lacking UNG and SMUG1. <i>Scientific Reports</i> , 2017, 7, 7199.	1.6	43
9	NucDiff: in-depth characterization and annotation of differences between two sets of DNA sequences. <i>BMC Bioinformatics</i> , 2017, 18, 338.	1.2	43
10	The <i>Mycobacterium tuberculosis</i> transcriptional landscape under genotoxic stress. <i>BMC Genomics</i> , 2016, 17, 791.	1.2	33
11	cnvScan: a CNV screening and annotation tool to improve the clinical utility of computational CNV prediction from exome sequencing data. <i>BMC Genomics</i> , 2016, 17, 51.	1.2	24
12	Open-Source Sequence Clustering Methods Improve the State Of the Art. <i>MSystems</i> , 2016, 1, .	1.7	155
13	VSEARCH: a versatile open source tool for metagenomics. <i>PeerJ</i> , 2016, 4, e2584.	0.9	7,113
14	Transcriptome analysis of human OXR1 depleted cells reveals its role in regulating the p53 signaling pathway. <i>Scientific Reports</i> , 2015, 5, 17409.	1.6	43
15	Swarm v2: highly-scalable and high-resolution amplicon clustering. <i>PeerJ</i> , 2015, 3, e1420.	0.9	528
16	Non-homologous functions of the AlkB homologs. <i>Journal of Molecular Cell Biology</i> , 2015, 7, 494-504.	1.5	52
17	Normalization of RNA-Sequencing Data from Samples with Varying mRNA Levels. <i>PLoS ONE</i> , 2014, 9, e89158.	1.1	44
18	Swarm: robust and fast clustering method for amplicon-based studies. <i>PeerJ</i> , 2014, 2, e593.	0.9	828

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19	A new family of proteins related to the HEAT-like repeat DNA glycosylases with affinity for branched DNA structures. <i>Journal of Structural Biology</i> , 2013, 183, 66-75.	1.3	8
20	Single Transmembrane Peptide DinQ Modulates Membrane-Dependent Activities. <i>PLoS Genetics</i> , 2013, 9, e1003260.	1.5	56
21	Tiling array study of MNNG treated <i>Escherichia coli</i> reveals a widespread transcriptional response. <i>Scientific Reports</i> , 2013, 3, 3053.	1.6	7
22	Evolutionary Paths of the cAMP-Dependent Protein Kinase (PKA) Catalytic Subunits. <i>PLoS ONE</i> , 2013, 8, e60935.	1.1	46
23	<i>Alkbh1</i> and <i>Tzfp</i> repress a non-repeat piRNA cluster in pachytene spermatocytes. <i>Nucleic Acids Research</i> , 2012, 40, 10950-10963.	6.5	13
24	<i>ALKBH1</i> is a Histone H2A Dioxygenase Involved in Neural Differentiation. <i>Stem Cells</i> , 2012, 30, 2672-2682.	1.4	97
25	Identification and Characterization of Novel Mutations in the Human Gene Encoding the Catalytic Subunit Calpha of Protein Kinase A (PKA). <i>PLoS ONE</i> , 2012, 7, e34838.	1.1	10
26	<i>Schizosaccharomyces pombe</i> encodes a mutated AP endonuclease 1. <i>DNA Repair</i> , 2011, 10, 296-305.	1.3	8
27	The <i>ada</i> operon of <i>Mycobacterium tuberculosis</i> encodes two DNA methyltransferases for inducible repair of DNA alkylation damage. <i>DNA Repair</i> , 2011, 10, 595-602.	1.3	29
28	Faster Smith-Waterman database searches with inter-sequence SIMD parallelisation. <i>BMC Bioinformatics</i> , 2011, 12, 221.	1.2	163
29	A Two-tiered compensatory response to loss of DNA repair modulates aging and stress response pathways. <i>Aging</i> , 2010, 2, 133-159.	1.4	23
30	Continuous and Periodic Expansion of CAG Repeats in Huntington's Disease R6/1 Mice. <i>PLoS Genetics</i> , 2010, 6, e1001242.	1.5	68
31	Mice Lacking <i>Alkbh1</i> Display Sex-Ratio Distortion and Unilateral Eye Defects. <i>PLoS ONE</i> , 2010, 5, e13827.	1.1	57
32	Tiling Array Analysis of UV Treated <i>Escherichia coli</i> Predicts Novel Differentially Expressed Small Peptides. <i>PLoS ONE</i> , 2010, 5, e15356.	1.1	14
33	Custom Design and Analysis of High-Density Oligonucleotide Bacterial Tiling Microarrays. <i>PLoS ONE</i> , 2009, 4, e5943.	1.1	24
34	The disruptive positions in human G-quadruplex motifs are less polymorphic and more conserved than their neutral counterparts. <i>Nucleic Acids Research</i> , 2009, 37, 5749-5756.	6.5	58
35	Large-scale inference of the point mutational spectrum in human segmental duplications. <i>BMC Genomics</i> , 2009, 10, 43.	1.2	10
36	DNA Repair in Mammalian Cells. <i>Cellular and Molecular Life Sciences</i> , 2009, 66, 981-993.	2.4	498

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37	Genome dynamics in major bacterial pathogens. <i>FEMS Microbiology Reviews</i> , 2009, 33, 453-470.	3.9	95
38	A universal assay for detection of oncogenic fusion transcripts by oligo microarray analysis. <i>Molecular Cancer</i> , 2009, 8, 5.	7.9	25
39	Characterization of novel mutations in the catalytic domain of the PCSK9 gene. <i>Journal of Internal Medicine</i> , 2008, 263, 420-431.	2.7	60
40	RNAmmer: consistent and rapid annotation of ribosomal RNA genes. <i>Nucleic Acids Research</i> , 2007, 35, 3100-3108.	6.5	5,357
41	Structural insight into repair of alkylated DNA by a new superfamily of DNA glycosylases comprising HEAT-like repeats. <i>Nucleic Acids Research</i> , 2007, 35, 2451-2459.	6.5	27
42	Computational prediction of the effects of non-synonymous single nucleotide polymorphisms in human DNA repair genes. <i>Neuroscience</i> , 2007, 145, 1273-1279.	1.1	33
43	Slip Slidin' Away: A Duodecennial Review of Targeted Genes in Mismatch Repair Deficient Colorectal Cancer. <i>Critical Reviews in Oncogenesis</i> , 2007, 13, 229-257.	0.2	22
44	A new protein superfamily includes two novel 3-methyladenine DNA glycosylases from <i>Bacillus cereus</i> , AlkC and AlkD. <i>Molecular Microbiology</i> , 2006, 59, 1602-1609.	1.2	57
45	Computational Prediction of MicroRNAs Encoded in Viral and Other Genomes. <i>Journal of Biomedicine and Biotechnology</i> , 2006, 2006, 1-10.	3.0	6
46	Predicting non-coding RNA genes in <i>Escherichia coli</i> with boosted genetic programming. <i>Nucleic Acids Research</i> , 2005, 33, 3263-3270.	6.5	52
47	PARALIGN: rapid and sensitive sequence similarity searches powered by parallel computing technology. <i>Nucleic Acids Research</i> , 2005, 33, W535-W539.	6.5	37
48	Biased distribution of DNA uptake sequences towards genome maintenance genes. <i>Nucleic Acids Research</i> , 2004, 32, 1050-1058.	6.5	77
49	DNA repair by bacterial AlkB proteins. <i>Research in Microbiology</i> , 2003, 154, 531-538.	1.0	39
50	Incision at hypoxanthine residues in DNA by a mammalian homologue of the <i>Escherichia coli</i> antimutator enzyme endonuclease V. <i>Nucleic Acids Research</i> , 2003, 31, 3893-3900.	6.5	58
51	Human DNA glycosylases of the bacterial Fpg/MutM superfamily: an alternative pathway for the repair of 8-oxoguanine and other oxidation products in DNA. <i>Nucleic Acids Research</i> , 2002, 30, 4926-4936.	6.5	245
52	ParAlign: a parallel sequence alignment algorithm for rapid and sensitive database searches. <i>Nucleic Acids Research</i> , 2001, 29, 1647-1652.	6.5	49
53	Cell-cycle regulation, intracellular sorting and induced overexpression of the human NTH1 DNA glycosylase involved in removal of formamidopyrimidine residues from DNA. <i>Mutation Research DNA Repair</i> , 2000, 460, 95-104.	3.8	68
54	Base Removers and Strand Scissors: Different Strategies Employed in Base Excision and Strand Incision at Modified Base Residues in DNA. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2000, 65, 135-142.	2.0	13

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55	SALSA: improved protein database searching by a new algorithm for assembly of sequence fragments into gapped alignments. <i>Bioinformatics</i> , 1998, 14, 839-845.	1.8	11
56	Opposite base-dependent reactions of a human base excision repair enzyme on DNA containing 7,8-dihydro-8-oxoguanine and abasic sites. <i>EMBO Journal</i> , 1997, 16, 6314-6322.	3.5	320