TorbjÃ¸rn Rognes

List of Publications by Year
in descending order

56 papers	**16,847** citations	159585 **30** h-index
59 all docs	**59** docs citations	**59** times ranked

149698 **56** g-index

24535 citing authors

#	Article	IF	Citations
1	VSEARCH: a versatile open source tool for metagenomics. PeerJ, 2016, 4, e2584.	2.0	7,113
2	RNAmmer: consistent and rapid annotation of ribosomal RNA genes. Nucleic Acids Research, 2007, 35, 3100-3108.	14.5	5,357
3	Swarm: robust and fast clustering method for amplicon-based studies. PeerJ, 2014, 2, e593.	2.0	828
4	Swarm v2: highly-scalable and high-resolution amplicon clustering. PeerJ, 2015, 3, e1420.	2.0	528
5	DNA Repair in Mammalian Cells. Cellular and Molecular Life Sciences, 2009, 66, 981-993.	5.4	498
6	Opposite base-dependent reactions of a human base excision repair enzyme on DNA containing 7,8-dihydro-8-oxoguanine and abasic sites. EMBO Journal, 1997, 16, 6314-6322.	7.8	320
7	Human DNA glycosylases of the bacterial Fpg/MutM superfamily: an alternative pathway for the repair of 8-oxoguanine and other oxidation products in DNA. Nucleic Acids Research, 2002, 30, 4926-4936.	14.5	245
8	Faster Smith-Waterman database searches with inter-sequence SIMD parallelisation. BMC Bioinformatics, 2011, 12, 221.	2.6	163
9	Open-Source Sequence Clustering Methods Improve the State Of the Art. MSystems, 2016, 1, .	3.8	155
10	ALKBH1 is a Histone H2A Dioxygenase Involved in Neural Differentiation. Stem Cells, 2012, 30, 2672-2682.	3.2	97
11	Genome dynamics in major bacterial pathogens. FEMS Microbiology Reviews, 2009, 33, 453-470.	8.6	95
12	Biased distribution of DNA uptake sequences towards genome maintenance genes. Nucleic Acids Research, 2004, 32, 1050-1058.	14.5	77
13	Cell-cycle regulation, intracellular sorting and induced overexpression of the human NTH1 DNA glycosylase involved in removal of formamidopyrimidine residues from DNA. Mutation Research DNA Repair, 2000, 460, 95-104.	3.7	68
14	Continuous and Periodic Expansion of CAG Repeats in Huntington's Disease R6/1 Mice. PLoS Genetics, 2010, 6, e1001242.	3.5	68
15	Characterization of novel mutations in the catalytic domain of the PCSK9 gene. Journal of Internal Medicine, 2008, 263, 420-431.	6.0	60
16	Incision at hypoxanthine residues in DNA by a mammalian homologue of the Escherichia coli antimutator enzyme endonuclease V. Nucleic Acids Research, 2003, 31, 3893-3900.	14.5	58
17	The disruptive positions in human G-quadruplex motifs are less polymorphic and more conserved than their neutral counterparts. Nucleic Acids Research, 2009, 37, 5749-5756.	14.5	58
18	A new protein superfamily includes two novel 3-methyladenine DNA glycosylases fromBacillus cereus, AlkC and AlkD. Molecular Microbiology, 2006, 59, 1602-1609.	2.5	57

#	Article	IF	Citations
19	Mice Lacking Alkbh1 Display Sex-Ratio Distortion and Unilateral Eye Defects. PLoS ONE, 2010, 5, e13827.	2.5	57
20	Single Transmembrane Peptide DinQ Modulates Membrane-Dependent Activities. PLoS Genetics, 2013, 9, e1003260.	3.5	56
21	Predicting non-coding RNA genes in Escherichia coli with boosted genetic programming. Nucleic Acids Research, 2005, 33, 3263-3270.	14.5	52
22	Non-homologous functions of the AlkB homologs. Journal of Molecular Cell Biology, 2015, 7, 494-504.	3.3	52
23	ParAlign: a parallel sequence alignment algorithm for rapid and sensitive database searches. Nucleic Acids Research, 2001, 29, 1647-1652.	14.5	49
24	Evolutionary Paths of the cAMP-Dependent Protein Kinase (PKA) Catalytic Subunits. PLoS ONE, 2013, 8, e60935.	2.5	46
25	Normalization of RNA-Sequencing Data from Samples with Varying mRNA Levels. PLoS ONE, 2014, 9, e89158.	2.5	44
26	Transcriptome analysis of human OXR1 depleted cells reveals its role in regulating the p53 signaling pathway. Scientific Reports, 2015, 5, 17409.	3.3	43
27	Uracil Accumulation and Mutagenesis Dominated by Cytosine Deamination in CpG Dinucleotides in Mice Lacking UNG and SMUG1. Scientific Reports, 2017, 7, 7199.	3.3	43
28	NucDiff: in-depth characterization and annotation of differences between two sets of DNA sequences. BMC Bioinformatics, 2017, 18, 338.	2.6	43
29	Swarm v3: towards tera-scale amplicon clustering. Bioinformatics, 2021, 38, 267-269.	4.1	40
30	DNA repair by bacterial AlkB proteins. Research in Microbiology, 2003, 154, 531-538.	2.1	39
31	PARALIGN: rapid and sensitive sequence similarity searches powered by parallel computing technology. Nucleic Acids Research, 2005, 33, W535-W539.	14.5	37
32	Computational prediction of the effects of non-synonymous single nucleotide polymorphisms in human DNA repair genes. Neuroscience, 2007, 145, 1273-1279.	2.3	33
33	The Mycobacterium tuberculosis transcriptional landscape under genotoxic stress. BMC Genomics, 2016, 17, 791.	2.8	33
34	The ada operon of Mycobacterium tuberculosis encodes two DNA methyltransferases for inducible repair of DNA alkylation damage. DNA Repair, 2011, 10, 595-602.	2.8	29
35	Structural insight into repair of alkylated DNA by a new superfamily of DNA glycosylases comprising HEAT-like repeats. Nucleic Acids Research, 2007, 35, 2451-2459.	14.5	27
36	A universal assay for detection of oncogenic fusion transcripts by oligo microarray analysis. Molecular Cancer, 2009, 8, 5.	19.2	25

#	ARTICLE	IF	CITATIONS
37	Custom Design and Analysis of High-Density Oligonucleotide Bacterial Tiling Microarrays. PLoS ONE, 2009, 4, e5943.	2.5	24
38	cnvScan: a CNV screening and annotation tool to improve the clinical utility of computational CNV prediction from exome sequencing data. BMC Genomics, 2016, 17, 51.	2.8	24
39	A Two-tiered compensatory response to loss of DNA repair modulates aging and stress response pathways. Aging, 2010, 2, 133-159.	3.1	23
40	The CRCbiome study: a large prospective cohort study examining the role of lifestyle and the gut microbiome in colorectal cancer screening participants. BMC Cancer, 2021, 21, 930.	2.6	22
41	Slip Slidin' Away: A Duodecen-nial Review of Targeted Genes in Mismatch Repair Deficient Colorectal Cancer. Critical Reviews in Oncogenesis, 2007, 13, 229-257.	0.4	22
42	Reduced metagenome sequencing for strain-resolution taxonomic profiles. Microbiome, 2021, 9, 79.	11.1	14
43	Tiling Array Analysis of UV Treated Escherichia coli Predicts Novel Differentially Expressed Small Peptides. PLoS ONE, 2010, 5, e15356.	2.5	14
44	Alkbh1 and Tzfp repress a non-repeat piRNA cluster in pachytene spermatocytes. Nucleic Acids Research, 2012, 40, 10950-10963.	14.5	13
45	Base Removers and Strand Scissors: Different Strategies Employed in Base Excision and Strand Incision at Modified Base Residues in DNA. Cold Spring Harbor Symposia on Quantitative Biology, 2000, 65, 135-142.	1.1	13
46	SALSA: improved protein database searching by a new algorithm for assembly of sequence fragments into gapped alignments. Bioinformatics, 1998, 14, 839-845.	4.1	11
47	Large-scale inference of the point mutational spectrum in human segmental duplications. BMC Genomics, 2009, 10, 43.	2.8	10
48	The uracil-DNA glycosylase UNG protects the fitness of normal and cancer B cells expressing AID. NAR Cancer, 2021, 2, zcaa019.	3.1	10
49	Identification and Characterization of Novel Mutations in the Human Gene Encoding the Catalytic Subunit Calpha of Protein Kinase A (PKA). PLoS ONE, 2012, 7, e34838.	2.5	10
50	Schizosaccharomyces pombe encodes a mutated AP endonuclease 1. DNA Repair, 2011, 10, 296-305.	2.8	8
51	A new family of proteins related to the HEAT-like repeat DNA glycosylases with affinity for branched DNA structures. Journal of Structural Biology, 2013, 183, 66-75.	2.8	8
52	Tiling array study of MNNG treated Escherichia coli reveals a widespread transcriptional response. Scientific Reports, 2013, 3, 3053.	3.3	7
53	Computational Prediction of MicroRNAs Encoded in Viral and Other Genomes. Journal of Biomedicine and Biotechnology, 2006, 2006, 1-10.	3.0	6
54	NucBreak: location of structural errors in a genome assembly by using paired-end Illumina reads. BMC Bioinformatics, 2020, 21, 66.	2.6	5

#	Article	IF	Citations
55	HMST-Seq-Analyzer: A new python tool for differential methylation and hydroxymethylation analysis in various DNA methylation sequencing data. Computational and Structural Biotechnology Journal, 2020, 18, 2877-2889.	4.1	4
56	Exploring the role of the multiple sclerosis susceptibility gene *CLEC16A* in T cells. Scandinavian Journal of Immunology, 2021, 94, e13050.	2.7	4