TorbjÃ¸rn Rognes

List of Publications by Year
in descending order

56 papers	16,847 citations	159585 30 h-index	149698 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. NAR Cancer, 2021, 2, zcaa019.	3.1	10
2	Reduced metagenome sequencing for strain-resolution taxonomic profiles. Microbiome, 2021, 9, 79.	11.1	14
3	Exploring the role of the multiple sclerosis susceptibility gene *CLEC16A* in T cells. Scandinavian Journal of Immunology, 2021, 94, e13050.	2.7	4
4	Swarm v3: towards tera-scale amplicon clustering. Bioinformatics, 2021, 38, 267-269.	4.1	40
5	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
6	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
7	NucBreak: location of structural errors in a genome assembly by using paired-end Illumina reads. BMC Bioinformatics, 2020, 21, 66.	2.6	5
8	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
9	NucDiff: in-depth characterization and annotation of differences between two sets of DNA sequences. BMC Bioinformatics, 2017, 18, 338.	2.6	43
10	The Mycobacterium tuberculosis transcriptional landscape under genotoxic stress. BMC Genomics, 2016, 17, 791.	2.8	33
11	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
12	Open-Source Sequence Clustering Methods Improve the State Of the Art. MSystems, 2016, 1, .	3.8	155
13	VSEARCH: a versatile open source tool for metagenomics. PeerJ, 2016, 4, e2584.	2.0	7,113
14	Transcriptome analysis of human OXR1 depleted cells reveals its role in regulating the p53 signaling pathway. Scientific Reports, 2015, 5, 17409.	3.3	43
15	Swarm v2: highly-scalable and high-resolution amplicon clustering. PeerJ, 2015, 3, e1420.	2.0	528
16	Non-homologous functions of the AlkB homologs. Journal of Molecular Cell Biology, 2015, 7, 494-504.	3.3	52
17	Normalization of RNA-Sequencing Data from Samples with Varying mRNA Levels. PLoS ONE, 2014, 9, e89158.	2.5	44
18	Swarm: robust and fast clustering method for amplicon-based studies. PeerJ, 2014, 2, e593.	2.0	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. Journal of Structural Biology, 2013, 183, 66-75.	2.8	8
20	Single Transmembrane Peptide DinQ Modulates Membrane-Dependent Activities. PLoS Genetics, 2013, 9, e1003260.	3.5	56
21	Tiling array study of MNNG treated Escherichia coli reveals a widespread transcriptional response. Scientific Reports, 2013, 3, 3053.	3.3	7
22	Evolutionary Paths of the cAMP-Dependent Protein Kinase (PKA) Catalytic Subunits. PLoS ONE, 2013, 8, e60935.	2.5	46
23	Alkbh1 and Tzfp repress a non-repeat piRNA cluster in pachytene spermatocytes. Nucleic Acids Research, 2012, 40, 10950-10963.	14.5	13
24	ALKBH1 is a Histone H2A Dioxygenase Involved in Neural Differentiation. Stem Cells, 2012, 30, 2672-2682.	3.2	97
25	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
26	Schizosaccharomyces pombe encodes a mutated AP endonuclease 1. DNA Repair, 2011, 10, 296-305.	2.8	8
27	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
28	Faster Smith-Waterman database searches with inter-sequence SIMD parallelisation. BMC Bioinformatics, 2011, 12, 221.	2.6	163
29	A Two-tiered compensatory response to loss of DNA repair modulates aging and stress response pathways. Aging, 2010, 2, 133-159.	3.1	23
30	Continuous and Periodic Expansion of CAG Repeats in Huntington's Disease R6/1 Mice. PLoS Genetics, 2010, 6, e1001242.	3.5	68
31	Mice Lacking Alkbh1 Display Sex-Ratio Distortion and Unilateral Eye Defects. PLoS ONE, 2010, 5, e13827.	2.5	57
32	Tiling Array Analysis of UV Treated Escherichia coli Predicts Novel Differentially Expressed Small Peptides. PLoS ONE, 2010, 5, e15356.	2.5	14
33	Custom Design and Analysis of High-Density Oligonucleotide Bacterial Tiling Microarrays. PLoS ONE, 2009, 4, e5943.	2.5	24
34	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
35	Large-scale inference of the point mutational spectrum in human segmental duplications. BMC Genomics, 2009, 10, 43.	2.8	10
36	DNA Repair in Mammalian Cells. Cellular and Molecular Life Sciences, 2009, 66, 981-993.	5.4	498

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37	Genome dynamics in major bacterial pathogens. FEMS Microbiology Reviews, 2009, 33, 453-470.	8.6	95
38	A universal assay for detection of oncogenic fusion transcripts by oligo microarray analysis. Molecular Cancer, 2009, 8, 5.	19.2	25
39	Characterization of novel mutations in the catalytic domain of the PCSK9 gene. Journal of Internal Medicine, 2008, 263, 420-431.	6.0	60
40	RNAmmer: consistent and rapid annotation of ribosomal RNA genes. Nucleic Acids Research, 2007, 35, 3100-3108.	14.5	5,357
41	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
42	Computational prediction of the effects of non-synonymous single nucleotide polymorphisms in human DNA repair genes. Neuroscience, 2007, 145, 1273-1279.	2.3	33
43	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
44	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
45	Computational Prediction of MicroRNAs Encoded in Viral and Other Genomes. Journal of Biomedicine and Biotechnology, 2006, 2006, 1-10.	3.0	6
46	Predicting non-coding RNA genes in Escherichia coli with boosted genetic programming. Nucleic Acids Research, 2005, 33, 3263-3270.	14.5	52
47	PARALIGN: rapid and sensitive sequence similarity searches powered by parallel computing technology. Nucleic Acids Research, 2005, 33, W535-W539.	14.5	37
48	Biased distribution of DNA uptake sequences towards genome maintenance genes. Nucleic Acids Research, 2004, 32, 1050-1058.	14.5	77
49	DNA repair by bacterial AlkB proteins. Research in Microbiology, 2003, 154, 531-538.	2.1	39
50	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
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. Nucleic Acids Research, 2002, 30, 4926-4936.	14.5	245
52	ParAlign: a parallel sequence alignment algorithm for rapid and sensitive database searches. Nucleic Acids Research, 2001, 29, 1647-1652.	14.5	49
53	Cell-cycle regulation, intracellular sorting and induced overexpression of the human NTH1 DNA glycosylase involved in removal of formamidopyrimidine residues from DNA. Mutation Research DNA Repair, 2000, 460, 95-104.	3.7	68
54	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

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55	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
56	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