Ivo Glynne Gut

List of Publications by Year
in descending order

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48 papers	12,208 citations	126907 33 h-index	189892 50 g-index
63 all docs	63 docs citations	63 times ranked	24059 citing authors

#	Article	IF	Citations
1	International network of cancer genome projects. Nature, 2010, 464, 993-998.	27.8	2,114
2	Transcriptome and genome sequencing uncovers functional variation in humans. Nature, 2013, 501, 506-511.	27.8	1,857
3	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. Nature, 2011, 475, 101-105.	27.8	1,364
4	Towards complete and error-free genome assemblies of all vertebrate species. Nature, 2021, 592, 737-746.	27.8	1,139
5	Non-coding recurrent mutations in chronic lymphocytic leukaemia. Nature, 2015, 526, 519-524.	27.8	749
6	Epigenomic analysis detects widespread gene-body DNA hypomethylation in chronic lymphocytic leukemia. Nature Genetics, 2012, 44, 1236-1242.	21.4	525
7	SPOTlight: seeded NMF regression to deconvolute spatial transcriptomics spots with single-cell transcriptomes. Nucleic Acids Research, 2021, 49, e50-e50.	14.5	338
8	BLUEPRINT to decode the epigenetic signature written in blood. Nature Biotechnology, 2012, 30, 224-226.	17.5	323
9	Benchmarking single-cell RNA-sequencing protocols for cell atlas projects. Nature Biotechnology, 2020, 38, 747-755.	17.5	313
10	International Cooperation to Enable the Diagnosis of All Rare Genetic Diseases. American Journal of Human Genetics, 2017, 100, 695-705.	6.2	305
11	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. Nature Genetics, 2015, 47, 746-756.	21.4	278
12	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001.	12.8	266
13	Reproducibility of high-throughput mRNA and small RNA sequencing across laboratories. Nature Biotechnology, 2013, 31, 1015-1022.	17.5	251
14	Genome sequence of the olive tree, Olea europaea. GigaScience, 2016, 5, 29.	6.4	201
15	Epigenomic analysis detects aberrant super-enhancer DNA methylation in human cancer. Genome Biology, 2016, 17, 11.	8.8	184
16	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. Nature Medicine, 2018, 24, 868-880.	30.7	157
17	Transcription Factors Drive Tet2-Mediated Enhancer Demethylation to Reprogram Cell Fate. Cell Stem Cell, 2018, 23, 727-741.e9.	11.1	156
18	Single-cell transcriptome conservation in cryopreserved cells and tissues. Genome Biology, 2017, 18, 45.	8.8	134

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19	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. Genome Biology, 2016, 17, 251.	8.8	131
20	Interaction of Triplet Photosensitizers with Nucleotides and DNA in Aqueous Solution at Room Temperature. Journal of the American Chemical Society, 1996, 118, 2366-2373.	13.7	127
21	Whole-epigenome analysis in multiple myeloma reveals DNA hypermethylation of B cell-specific enhancers. Genome Research, 2015, 25, 478-487.	5.5	118
22	Decoding the DNA Methylome of Mantle Cell Lymphoma in the Light of the Entire B Cell Lineage. Cancer Cell, 2016, 30, 806-821.	16.8	103
23	Mutation discovery in mice by whole exome sequencing. Genome Biology, 2011, 12, R86.	9.6	102
24	A single-cell tumor immune atlas for precision oncology. Genome Research, 2021, 31, 1913-1926.	5.5	87
25	ProteinSeq: High-Performance Proteomic Analyses by Proximity Ligation and Next Generation Sequencing. PLoS ONE, 2011, 6, e25583.	2.5	80
26	Comprehensive characterization of complex structural variations in cancer by directly comparing genome sequence reads. Nature Biotechnology, 2014, 32, 1106-1112.	17.5	74
27	Leveraging European infrastructures to access 1 million human genomes by 2022. Nature Reviews Genetics, 2019, 20, 693-701.	16.3	69
28	Dynamics of genome architecture and chromatin function during human B cell differentiation and neoplastic transformation. Nature Communications, 2021, 12, 651.	12.8	67
29	DNA sequencing â€“ spanning the generations. New Biotechnology, 2013, 30, 366-372.	4.4	65
30	RD-Connect, NeurOmics and EURenOmics: collaborative European initiative for rare diseases. European Journal of Human Genetics, 2018, 26, 778-785.	2.8	55
31	From Wetâ€Łab to Variations: Concordance and Speed of Bioinformatics Pipelines for Whole Genome and Whole Exome Sequencing. Human Mutation, 2016, 37, 1263-1271.	2.5	47
32	Single cell RNA-seq identifies the origins of heterogeneity in efficient cell transdifferentiation and reprogramming. ELife, 2019, 8, .	6.0	44
33	A mechanistic basis for amplification differences between samples and between genome regions. BMC Genomics, 2012, 13, 455.	2.8	40
34	Chromatin activation as a unifying principle underlying pathogenic mechanisms in multiple myeloma. Genome Research, 2020, 30, 1217-1227.	5.5	35
35	Solving patients with rare diseases through programmatic reanalysis of genome-phenome data. European Journal of Human Genetics, 2021, 29, 1337-1347.	2.8	34
36	UPPER EXCITED STATE PHOTOCHEMISTRY OF DNA. Photochemistry and Photobiology, 1993, 58, 313-317.	2.5	19

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37	Recurrent somatic mutations reveal new insights into consequences of mutagenic processes in cancer. PLoS Computational Biology, 2019, 15, e1007496.	3.2	18
38	The RDâ€Connect Genomeâ€Phenome Analysis Platform: Accelerating diagnosis, research, and gene discovery for rare diseases. Human Mutation, 2022, , .	2.5	18
39	SNP genotyping using alkali cleavage of RNA/DNA chimeras and MALDI time-of-flight mass spectrometry. Nucleic Acids Research, 2006, 34, e18-e18.	14.5	17
40	DNA sequencing by MALDI-TOF MS using alkali cleavage of RNA/DNA chimeras. Nucleic Acids Research, 2007, 35, e62-e62.	14.5	15
41	Improved Diagnosis of Rare Disease Patients through Systematic Detection of Runs of Homozygosity. Journal of Molecular Diagnostics, 2020, 22, 1205-1215.	2.8	14
42	New technologies for DNA analysis â€“ a review of the READNA Project. New Biotechnology, 2016, 33, 311-330.	4.4	10
43	Variation in predicted COVIDâ€19 risk among lemurs and lorises. American Journal of Primatology, 2021, 83, e23255.	1.7	7
44	High-Specificity Single-Tube Multiplex Genotyping Using Ribo-PAP PCR, Tag Primers, Alkali Cleavage of RNA/DNA Chimeras and MALDI-TOF MS. Human Mutation, 2013, 34, 266-273.	2.5	6
45	Systematic Collaborative Reanalysis of Genomic Data Improves Diagnostic Yield in Neurologic Rare Diseases. Journal of Molecular Diagnostics, 2022, 24, 529-542.	2.8	6
46	Framework for quality assessment of whole genome cancer sequences. Nature Communications, 2020, 11, 5040.	12.8	5
47	Ribo-polymerase chain reaction-A facile method for the preparation of chimeric RNA/DNA applied to DNA sequencing. Human Mutation, 2012, 33, 1010-1015.	2.5	3
48	High degree of polyclonality hinders somatic mutation calling in lung brush samples of COPD cases and controls. Scientific Reports, 2019, 9, 20158.	3.3	1