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	The RDâ€Connect Genomeâ€Phenome Analysis Platform: Accelerating diagnosis, research, and gene discovery for rare diseases. Human Mutation, 2022, , .	2.5	18
2	Systematic Collaborative Reanalysis of Genomic Data Improves Diagnostic Yield in Neurologic Rare Diseases. Journal of Molecular Diagnostics, 2022, 24, 529-542.	2.8	6
3	Dynamics of genome architecture and chromatin function during human B cell differentiation and neoplastic transformation. Nature Communications, 2021, 12, 651.	12.8	67
4	SPOTlight: seeded NMF regression to deconvolute spatial transcriptomics spots with single-cell transcriptomes. Nucleic Acids Research, 2021, 49, e50-e50.	14.5	338
5	Variation in predicted COVIDâ€19 risk among lemurs and lorises. American Journal of Primatology, 2021, 83, e23255.	1.7	7
6	Towards complete and error-free genome assemblies of all vertebrate species. Nature, 2021, 592, 737-746.	27.8	1,139
7	Solving patients with rare diseases through programmatic reanalysis of genome-phenome data. European Journal of Human Genetics, 2021, 29, 1337-1347.	2.8	34
8	A single-cell tumor immune atlas for precision oncology. Genome Research, 2021, 31, 1913-1926.	5.5	87
9	Framework for quality assessment of whole genome cancer sequences. Nature Communications, 2020, 11, 5040.	12.8	5
10	Chromatin activation as a unifying principle underlying pathogenic mechanisms in multiple myeloma. Genome Research, 2020, 30, 1217-1227.	5.5	35
11	Benchmarking single-cell RNA-sequencing protocols for cell atlas projects. Nature Biotechnology, 2020, 38, 747-755.	17.5	313
12	Improved Diagnosis of Rare Disease Patients through Systematic Detection of Runs of Homozygosity. Journal of Molecular Diagnostics, 2020, 22, 1205-1215.	2.8	14
13	Leveraging European infrastructures to access 1 million human genomes by 2022. Nature Reviews Genetics, 2019, 20, 693-701.	16.3	69
14	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
15	Recurrent somatic mutations reveal new insights into consequences of mutagenic processes in cancer. PLoS Computational Biology, 2019, 15, e1007496.	3.2	18
16	Single cell RNA-seq identifies the origins of heterogeneity in efficient cell transdifferentiation and reprogramming. ELife, 2019, 8, .	6.0	44
17	RD-Connect, NeurOmics and EURenOmics: collaborative European initiative for rare diseases. European Journal of Human Genetics, 2018, 26, 778-785.	2.8	55
18	Transcription Factors Drive Tet2-Mediated Enhancer Demethylation to Reprogram Cell Fate. Cell Stem Cell, 2018, 23, 727-741.e9.	11.1	156

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19	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. Nature Medicine, 2018, 24, 868-880.	30.7	157
20	Single-cell transcriptome conservation in cryopreserved cells and tissues. Genome Biology, 2017, 18, 45.	8.8	134
21	International Cooperation to Enable the Diagnosis of All Rare Genetic Diseases. American Journal of Human Genetics, 2017, 100, 695-705.	6.2	305
22	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. Genome Biology, 2016, 17, 251.	8.8	131
23	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
24	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
25	Genome sequence of the olive tree, Olea europaea. GigaScience, 2016, 5, 29.	6.4	201
26	Epigenomic analysis detects aberrant super-enhancer DNA methylation in human cancer. Genome Biology, 2016, 17, 11.	8.8	184
27	New technologies for DNA analysis â€“ a review of the READNA Project. New Biotechnology, 2016, 33, 311-330.	4.4	10
28	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. Nature Genetics, 2015, 47, 746-756.	21.4	278
29	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001.	12.8	266
30	Whole-epigenome analysis in multiple myeloma reveals DNA hypermethylation of B cell-specific enhancers. Genome Research, 2015, 25, 478-487.	5.5	118
31	Non-coding recurrent mutations in chronic lymphocytic leukaemia. Nature, 2015, 526, 519-524.	27.8	749
32	Comprehensive characterization of complex structural variations in cancer by directly comparing genome sequence reads. Nature Biotechnology, 2014, 32, 1106-1112.	17.5	74
33	Reproducibility of high-throughput mRNA and small RNA sequencing across laboratories. Nature Biotechnology, 2013, 31, 1015-1022.	17.5	251
34	Transcriptome and genome sequencing uncovers functional variation in humans. Nature, 2013, 501, 506-511.	27.8	1,857
35	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
36	DNA sequencing â€“ spanning the generations. New Biotechnology, 2013, 30, 366-372.	4.4	65

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37	Epigenomic analysis detects widespread gene-body DNA hypomethylation in chronic lymphocytic leukemia. Nature Genetics, 2012, 44, 1236-1242.	21.4	525
38	A mechanistic basis for amplification differences between samples and between genome regions. BMC Genomics, 2012, 13, 455.	2.8	40
39	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
40	BLUEPRINT to decode the epigenetic signature written in blood. Nature Biotechnology, 2012, 30, 224-226.	17.5	323
41	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. Nature, 2011, 475, 101-105.	27.8	1,364
42	Mutation discovery in mice by whole exome sequencing. Genome Biology, 2011, 12, R86.	9.6	102
43	ProteinSeq: High-Performance Proteomic Analyses by Proximity Ligation and Next Generation Sequencing. PLoS ONE, 2011, 6, e25583.	2.5	80
44	International network of cancer genome projects. Nature, 2010, 464, 993-998.	27.8	2,114
45	DNA sequencing by MALDI-TOF MS using alkali cleavage of RNA/DNA chimeras. Nucleic Acids Research, 2007, 35, e62-e62.	14.5	15
46	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
47	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
48	UPPER EXCITED STATE PHOTOCHEMISTRY OF DNA. Photochemistry and Photobiology, 1993, 58, 313-317.	2.5	19