

# Ivo Gut

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11470288/publications.pdf>

Version: 2024-02-01

21  
papers

12,707  
citations

361413

20  
h-index

713466

21  
g-index

25  
all docs

25  
docs citations

25  
times ranked

22662  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide association defines more than 30 distinct susceptibility loci for Crohn's disease. <i>Nature Genetics</i> , 2008, 40, 955-962.	21.4	2,422
2	International network of cancer genome projects. <i>Nature</i> , 2010, 464, 993-998.	27.8	2,114
3	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. <i>Nature</i> , 2011, 475, 101-105.	27.8	1,364
4	A susceptibility locus for lung cancer maps to nicotinic acetylcholine receptor subunit genes on 15q25. <i>Nature</i> , 2008, 452, 633-637.	27.8	1,169
5	Exome sequencing identifies recurrent mutations of the splicing factor SF3B1 gene in chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2012, 44, 47-52.	21.4	893
6	A genome-wide association study of global gene expression. <i>Nature Genetics</i> , 2007, 39, 1202-1207.	21.4	882
7	Non-coding recurrent mutations in chronic lymphocytic leukaemia. <i>Nature</i> , 2015, 526, 519-524.	27.8	749
8	Epigenomic analysis detects widespread gene-body DNA hypomethylation in chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2012, 44, 1236-1242.	21.4	525
9	Lung cancer susceptibility locus at 5p15.33. <i>Nature Genetics</i> , 2008, 40, 1404-1406.	21.4	514
10	Novel Crohn Disease Locus Identified by Genome-Wide Association Maps to a Gene Desert on 5p13.1 and Modulates Expression of PTGER4. <i>PLoS Genetics</i> , 2007, 3, e58.	3.5	506
11	Common variants at five new loci associated with early-onset inflammatory bowel disease. <i>Nature Genetics</i> , 2009, 41, 1335-1340.	21.4	459
12	BLUEPRINT to decode the epigenetic signature written in blood. <i>Nature Biotechnology</i> , 2012, 30, 224-226.	17.5	323
13	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. <i>Genome Research</i> , 2014, 24, 212-226.	5.5	175
14	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. <i>Nature Medicine</i> , 2018, 24, 868-880.	30.7	157
15	Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. <i>Cell Reports</i> , 2018, 24, 2784-2794.	6.4	104
16	Genomewide Association Study of a Rapid Progression Cohort Identifies New Susceptibility Alleles for AIDS (ANRS Genomewide Association Study 03). <i>Journal of Infectious Diseases</i> , 2009, 200, 1194-1201.	4.0	99
17	Multiple Cohort Genetic Association Study Reveals CXCR6 as a New Chemokine Receptor Involved in Long-Term Nonprogression to AIDS. <i>Journal of Infectious Diseases</i> , 2010, 202, 908-915.	4.0	82
18	Dynamics of genome architecture and chromatin function during human B cell differentiation and neoplastic transformation. <i>Nature Communications</i> , 2021, 12, 651.	12.8	67

#	ARTICLE	IF	CITATIONS
19	Distinct Trends of DNA Methylation Patterning in the Innate and Adaptive Immune Systems. Cell Reports, 2016, 17, 2101-2111.	6.4	54
20	Chromatin activation as a unifying principle underlying pathogenic mechanisms in multiple myeloma. Genome Research, 2020, 30, 1217-1227.	5.5	35
21	Clonal dynamics monitoring during clinical evolution in chronic lymphocytic leukaemia. Scientific Reports, 2019, 9, 975.	3.3	8