Ian Dunham

List of Publications by Year
in descending order

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129 papers	44,293 citations	28736 57 h-index	18944 123 g-index
144 all docs	144 docs citations	144 times ranked	63010 citing authors

#	Article	IF	Citations
1	Integrative analysis of 3604 GWAS reveals multiple novel cell type-specific regulatory associations. Genome Biology, 2022, 23, 13.	3.8	19
2	Immune disease variants modulate gene expression in regulatory CD4+ TÂcells. Cell Genomics, 2022, 2, 100117.	3.0	20
3	CACHE (Critical Assessment of Computational Hit-finding Experiments): A publicâ€“private partnership benchmarking initiative to enable the development of computational methods for hit-finding. Nature Reviews Chemistry, 2022, 6, 287-295.	13.8	22
4	Whole-exome sequencing identifies rare genetic variants associated with human plasma metabolites. American Journal of Human Genetics, 2022, 109, 1038-1054.	2.6	17
5	Open Targets Genetics: systematic identification of trait-associated genes using large-scale genetics and functional genomics. Nucleic Acids Research, 2021, 49, D1311-D1320.	6.5	295
6	Open Targets Platform: supporting systematic drugâ€“target identification and prioritisation. Nucleic Acids Research, 2021, 49, D1302-D1310.	6.5	265
7	The PROTACtable genome. Nature Reviews Drug Discovery, 2021, 20, 789-797.	21.5	112
8	Mapping the human genetic architecture of COVID-19. Nature, 2021, 600, 472-477.	13.7	640
9	A proteome-wide genetic investigation identifies several SARS-CoV-2-exploited host targets of clinical relevance. ELife, 2021, 10, .	2.8	23
10	An open approach to systematically prioritize causal variants and genes at all published human GWAS trait-associated loci. Nature Genetics, 2021, 53, 1527-1533.	9.4	208
11	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. Science, 2020, 370, .	6.0	508
12	Mining a GWAS of Severe Covid-19. New England Journal of Medicine, 2020, 383, 2588-2589.	13.9	20
13	The open targets post-GWAS analysis pipeline. Bioinformatics, 2020, 36, 2936-2937.	1.8	24
14	GARFIELD classifies disease-relevant genomic features through integration of functional annotations with association signals. Nature Genetics, 2019, 51, 343-353.	9.4	147
15	eFORGE v2.0: updated analysis of cell type-specific signal in epigenomic data. Bioinformatics, 2019, 35, 4767-4769.	1.8	84
16	Applications of machine learning in drug discovery and development. Nature Reviews Drug Discovery, 2019, 18, 463-477.	21.5	1,358
17	Open Targets Platform: new developments and updates two years on. Nucleic Acids Research, 2019, 47, D1056-D1065.	6.5	364
18	Designing an intuitive web application for drug discovery scientists. Drug Discovery Today, 2018, 23, 1169-1174.	3.2	9

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19	Transcription Factor Activities Enhance Markers of Drug Sensitivity in Cancer. Cancer Research, 2018, 78, 769-780.	0.4	161
20	Ten simple rules for delivering live distance training in bioinformatics across the globe using webinars. PLoS Computational Biology, 2018, 14, e1006419.	1.5	19
21	The COSMIC Cancer Gene Census: describing genetic dysfunction across all human cancers. Nature Reviews Cancer, 2018, 18, 696-705.	12.8	1,059
22	Uncovering new disease indications for G-protein coupled receptors and their endogenous ligands. BMC Bioinformatics, 2018, 19, 345.	1.2	10
23	Human genes: Time to follow the roads less traveled?. PLoS Biology, 2018, 16, e3000034.	2.6	9
24	Open Targets: a platform for therapeutic target identification and validation. Nucleic Acids Research, 2017, 45, D985-D994.	6.5	355
25	Uncovering novel repositioning opportunities using the Open Targets platform. Drug Discovery Today, 2017, 22, 1800-1807.	3.2	16
26	Literature evidence in open targets - a target validation platform. Journal of Biomedical Semantics, 2017, 8, 20.	0.9	16
27	In silico prediction of novel therapeutic targets using geneâ€“disease association data. Journal of Translational Medicine, 2017, 15, 182.	1.8	85
28	Ensembl regulation resources. Database: the Journal of Biological Databases and Curation, 2016, 2016, bav119.	1.4	45
29	eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. Cell Reports, 2016, 17, 2137-2150.	2.9	102
30	Linking rare and common disease: mapping clinical disease-phenotypes to ontologies in therapeutic target validation. Journal of Biomedical Semantics, 2016, 7, 8.	0.9	28
31	Where Next for Genetics and Genomics?. PLoS Biology, 2015, 13, e1002216.	2.6	9
32	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	13.7	1,014
33	Using human genetics to make new medicines. Nature Reviews Genetics, 2015, 16, 561-562.	7.7	25
34	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	9.4	365
35	Defining functional DNA elements in the human genome. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6131-6138.	3.3	635
36	Quantitative Genetics of CTCF Binding Reveal Local Sequence Effects and Different Modes of X-Chromosome Association. PLoS Genetics, 2014, 10, e1004798.	1.5	55

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37	Functional annotation of noncoding sequence variants. Nature Methods, 2014, 11, 294-296.	9.0	493
38	Integrative annotation of chromatin elements from ENCODE data. Nucleic Acids Research, 2013, 41, 827-841.	6.5	490
39	Genome-wide meta-analysis identifies new susceptibility loci for migraine. Nature Genetics, 2013, 45, 912-917.	9.4	338
40	High-resolution analysis of cis -acting regulatory networks at the Î±-globin locus. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120361.	1.8	12
41	MiR-25 Regulates Wwp2 and Fbxw7 and Promotes Reprogramming of Mouse Fibroblast Cells to iPSCs. PLoS ONE, 2012, 7, e40938.	1.1	65
42	Ensembl 2012. Nucleic Acids Research, 2012, 40, D84-D90.	6.5	840
43	Ensembl 2013. Nucleic Acids Research, 2012, 41, D48-D55.	6.5	856
44	Large-Scale Identification of MicroRNA Targets in Murine Dgcr8-Deficient Embryonic Stem Cell Lines. PLoS ONE, 2012, 7, e41762.	1.1	8
45	Hes6 is required for actin cytoskeletal organization in differentiating C2C12 myoblasts. Experimental Cell Research, 2011, 317, 1590-1602.	1.2	13
46	Ensembl 2011. Nucleic Acids Research, 2011, 39, D800-D806.	6.5	630
47	Systematic analysis of off-target effects in an RNAi screen reveals microRNAs affecting sensitivity to TRAIL-induced apoptosis. BMC Genomics, 2010, 11, 175.	1.2	41
48	High-throughput analysis of candidate imprinted genes and allele-specific gene expression in the human term placenta. BMC Genetics, 2010, 11, 25.	2.7	64
49	Complex Exon-Intron Marking by Histone Modifications Is Not Determined Solely by Nucleosome Distribution. PLoS ONE, 2010, 5, e12339.	1.1	64
50	Cell-type-specific long-range looping interactions identify distant regulatory elements of the CFTR gene. Nucleic Acids Research, 2010, 38, 4325-4336.	6.5	94
51	Ensembl's 10th year. Nucleic Acids Research, 2010, 38, D557-D562.	6.5	251
52	ATR-X Syndrome Protein Targets Tandem Repeats and Influences Allele-Specific Expression in a Size-Dependent Manner. Cell, 2010, 143, 367-378.	13.5	365
53	Evidence That Replication-Associated Mutation Alone Does Not Explain Between-Chromosome Differences In Substitution Rates. Genome Biology and Evolution, 2009, 1, 13-22.	1.1	16
54	Functional diversity for REST (NRSF) is defined by in vivo binding affinity hierarchies at the DNA sequence level. Genome Research, 2009, 19, 994-1005.	2.4	73

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55	DNA methylation-histone modification relationships across the desmin locus in human primary cells. BMC Molecular Biology, 2009, 10, 51.	3.0	18
56	Mosaic 22q13 deletions: evidence for concurrent mosaic segmental isodisomy and gene conversion. European Journal of Human Genetics, 2009, 17, 426-433.	1.4	16
57	Novel genes in cell cycle control and lipid metabolism with dynamically regulated binding sites for sterol regulatory elementâ€binding proteinâ€ƒ1 and RNA polymeraseâ€ƒII in HepG2 cells detected by chromatin immunoprecipitation with microarray detection. FEBS Journal, 2009, 276, 1878-1890.	2.2	22
58	Applications of high-throughput sequencing to chromatin structure and function in mammals. F1000 Biology Reports, 2009, 1, 32.	4.0	0
59	Epigenetic Marking Prepares the Human HOXA Cluster for Activation During Differentiation of Pluripotent Cells. Stem Cells, 2008, 26, 1174-1185.	1.4	36
60	Conservation of the H19 noncoding RNA and H19-IGF2 imprinting mechanism in therians. Nature Genetics, 2008, 40, 971-976.	9.4	169
61	A systematic library for comprehensive overexpression screens in Saccharomyces cerevisiae. Nature Methods, 2008, 5, 239-241.	9.0	187
62	Finishing the finished human chromosome 22 sequence. Genome Biology, 2008, 9, R78.	13.9	20
63	Epigenomics at the tipping point. Pharmacogenomics, 2008, 9, 1781-1783.	0.6	3
64	The Evolution of the DLK1-DIO3 Imprinted Domain in Mammals. PLoS Biology, 2008, 6, e135.	2.6	162
65	Systematic evaluation of variability in ChIP-chip experiments using predefined DNA targets. Genome Research, 2008, 18, 393-403.	2.4	117
66	The role of the polycomb complex in silencing Î±-globin gene expression in nonerythroid cells. Blood, 2008, 112, 3889-3899.	0.6	51
67	The landscape of histone modifications across 1% of the human genome in five human cell lines. Genome Research, 2007, 17, 691-707.	2.4	353
68	Butyrate mediates decrease of histone acetylation centered on transcription start sites and down-regulation of associated genes. Genome Research, 2007, 17, 708-719.	2.4	130
69	hORFeome v3.1: A resource of human open reading frames representing over 10,000 human genes. Genomics, 2007, 89, 307-315.	1.3	248
70	Tissue-specific histone modification and transcription factor binding in Î± globin gene expression. Blood, 2007, 110, 4503-4510.	0.6	69
71	Sequencing and association analysis of the type 1 diabetes â€“ linked region on chromosome 10p12-q11. BMC Genetics, 2007, 8, 24.	2.7	10
72	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	13.7	4,709

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73	The evolution of imprinting: chromosomal mapping of orthologues of mammalian imprinted domains in monotreme and marsupial mammals. BMC Evolutionary Biology, 2007, 7, 157.	3.2	38
74	The portability of tagSNPs across populations: A worldwide survey. Genome Research, 2006, 16, 323-330.	2.4	82
75	Identifying gene regulatory elements by genomic microarray mapping of DNaseI hypersensitive sites. Genome Research, 2006, 16, 1310-1319.	2.4	34
76	Binding sites for metabolic disease related transcription factors inferred at base pair resolution by chromatin immunoprecipitation and genomic microarrays. Human Molecular Genetics, 2005, 14, 3435-3447.	1.4	71
77	Replication Timing of Human Chromosome 6. Cell Cycle, 2005, 4, 172-176.	1.3	66
78	Investigating chromosome organization with genomic microarrays. Chromosome Research, 2005, 13, 249-257.	1.0	8
79	Evidence for Widespread Reticulate Evolution within Human Duplicons. American Journal of Human Genetics, 2005, 77, 824-840.	2.6	33
80	Complete MHC Haplotype Sequencing for Common Disease Gene Mapping. Genome Research, 2004, 14, 1176-1187.	2.4	260
81	Novel microsatellite markers and single nucleotide polymorphisms refine the tylosis with oesophageal cancer (TOC) minimal region on 17q25 to 42.5ï¿½kb: sequencing does not identify the causative gene. Human Genetics, 2004, 114, 534-540.	1.8	41
82	A genome annotation-driven approach to cloning the human ORFeome. Genome Biology, 2004, 5, R84.	13.9	38
83	Replication timing of the human genome. Human Molecular Genetics, 2004, 13, 191-202.	1.4	295
84	The Characteristics of Human Genes: Analysis of Human Chromosome 22. Comparative and Functional Genomics, 2003, 4, 635-646.	2.0	2
85	Reevaluating Human Gene Annotation: A Second-Generation Analysis of Chromosome 22. Genome Research, 2003, 13, 27-36.	2.4	73
86	DNA Rescue by the Vectorette Method. , 2003, , 393-399.		1
87	Human genome sequences: enigmatic variations. Mutagenesis, 2002, 17, 457-461.	1.0	1
88	A full-coverage, high-resolution human chromosome 22 genomic microarray for clinical and research applications. Human Molecular Genetics, 2002, 11, 3221-3229.	1.4	129
89	An Anthropoid-Specific Locus of Orphan C to U RNA-Editing Enzymes on Chromosome 22. Genomics, 2002, 79, 285-296.	1.3	655
90	The human homologue of unc-93 maps to chromosome 6q27 - characterisation and analysis in sporadic epithelial ovarian cancer. BMC Genetics, 2002, 3, 20.	2.7	21

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91	Physical and transcript map of the region between D6S264 and D6S149 on chromosome 6q27, the minimal region of allele loss in sporadic epithelial ovarian cancer. Oncogene, 2002, 21, 387-399.	2.6	26
92	A first-generation linkage disequilibrium map of human chromosome 22. Nature, 2002, 418, 544-548.	13.7	376
93	Initial sequencing and analysis of the human genome. Nature, 2001, 409, 860-921.	13.7	21,074
94	A Sequence-Based Integrated Map of Chromosome 22. Genome Research, 2001, 11, 1290-1295.	2.4	17
95	A SNP Resource for Human Chromosome 22: Extracting Dense Clusters of SNPs From the Genomic Sequence. Genome Research, 2001, 11, 170-178.	2.4	69
96	The Gene Guessing Game. Yeast, 2000, 1, 218-224.	0.8	12
97	A systematic, high-resolution linkage of the cytogenetic and physical maps of the human genome. Nature Genetics, 2000, 24, 339-340.	9.4	52
98	Genomics â€“ the new rock and roll?. Trends in Genetics, 2000, 16, 456-461.	2.9	9
99	DNA Rescue by the Vectorette Method. , 2000, , 667-673.		0
100	An Integrated Map of Human 6q22.3â€“q24 Including a 3-Mb High-Resolution BAC/PAC Contig Encompassing a QTL for Fetal Hemoglobin. Genomics, 2000, 64, 264-276.	1.3	12
101	The Extent of Linkage Disequilibrium in Four Populations with Distinct Demographic Histories. American Journal of Human Genetics, 2000, 67, 1544-1554.	2.6	192
102	Mechanism of spreading of the highly related neurofibromatosis type 1 (NF1) pseudogenes on chromosomes 2, 14 and 22. European Journal of Human Genetics, 2000, 8, 209-214.	1.4	37
103	The Gene Guessing Game. Yeast, 2000, 1, 218-224.	0.8	1
104	Psoriasis Upregulated Phorbolin-1 Shares Structural but not Functional Similarity to the mRNA-Editing Protein Apobec-1. Journal of Investigative Dermatology, 1999, 113, 162-169.	0.3	51
105	A molecular cytogenetic clone resource for chromosome 22. Chromosome Research, 1999, 7, 571-573.	1.0	5
106	Comparative analyses of the Dominant megacolon-SOX10 genomic interval in mouse and human. Mammalian Genome, 1999, 10, 744-749.	1.0	15
107	Mutations in a gene encoding a novel protein tyrosine phosphatase cause progressive myoclonus epilepsy. Nature Genetics, 1998, 20, 171-174.	9.4	499
108	Data disclosure in the Human Genome Project. Trends in Molecular Medicine, 1998, 4, 335.	2.6	1

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109	Characterization of the human synaptogyrin gene family. Human Genetics, 1998, 103, 131-141.	1.8	54
110	Fine-Mapping, Genomic Organization, and Transcript Analysis of the Human Ubiquitin-Conjugating Enzyme Gene UBE2L3. Genomics, 1998, 51, 124-127.	1.3	21
111	The Organization of the Î³-Glutamyl Transferase Genes and Other Low Copy Repeats in Human Chromosomeâ€‰22q11. Genome Research, 1997, 7, 522-531.	2.4	53
112	Use of ACEDB as a Database for YAC Library Data Management. , 1996, 54, 253-280.		3
113	DNA Rescue by the Vectorette Method. , 1996, 65, 201-208.		0
114	Identification and characterization of NF1 -related loci on human chromosomes 22, 14 and 2. Human Genetics, 1996, 98, 7-11.	1.8	36
115	Characterization of a second human clathrin heavy chain polypeptide gene (CLH-22) from chromosome 22q11. Human Molecular Genetics, 1996, 5, 625-631.	1.4	54
116	Mapping human chromosomes. Current Opinion in Genetics and Development, 1995, 5, 328-334.	1.5	16
117	Characterization of a new member of the human /-adaptin gene family from chromosome 22q12, a candidate meningioma gene. Human Molecular Genetics, 1994, 3, 1393-1399.	1.4	103
118	Genetic mapping of 14 short tandem repeat polymorphisms on human chromosome 22. Human Genetics, 1994, 93, 688-90.	1.8	5
119	A YAC Contig Spanning the Ataxia-Telangiectasia Locus (Groups A and C) at 11q22-q23. Genomics, 1994, 24, 234-242.	1.3	8
120	Cloning of a novel, anonymous gene from a megabase-range YAC and cosmid contig in the neurofibromatosis type 2/meningioma region on human chromosome 22q12. Human Molecular Genetics, 1993, 2, 1361-1368.	1.4	26
121	Isolation of a putative transcriptional regulator from the region of 22q11 deleted in DiGeorge syndrome, Shprintzen syndrome and familial congenital heart disease. Human Molecular Genetics, 1993, 2, 2099-2107.	1.4	140
122	Possible role for COMT in psychosis associated with velo-cardio-facial syndrome. Lancet, The, 1992, 340, 1361-1362.	6.3	63
123	Identification of region-specific yeast artificial chromosomes using pools of Alu element-mediated polymerase chain reaction probes labeled via linear amplification. Genomics, 1992, 14, 931-938.	1.3	11
124	A random STS strategy for construction of YAC contigs spanning defined chromosomal regions. Genomics, 1992, 14, 256-262.	1.3	13
125	A panel of human chromosome 22-specific sequence tagged sites. Genomics, 1992, 14, 1098-1103.	1.3	7
126	Rapid generation of chromosome-specific alphoid DNA probes using the polymerase chain reaction. Human Genetics, 1992, 88, 457-462.	1.8	66

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127	Characterization of the class III region in different MHC haplotypes by pulsed-field gel electrophoresis. Immunogenetics, 1990, 32, 175-182.	1.2	24
128	An analysis of variation in the long-range genomic organization of the human major histocompatibility complex class II region by pulsed-field gel electrophoresis. Genomics, 1989, 5, 787-796.	1.3	48
129	FORGE: A tool to discover cell specific enrichments of GWAS associated SNPs in regulatory regions. F1000Research, 0, 4, 18.	0.8	16