Peter Humburg

List of Publications by Year
in descending order

35 papers	5,609 citations	279487 23 h-index	377514 34 g-index
37 all docs	37 docs citations	37 times ranked	15745 citing authors

#	Article	IF	Citations
1	Integrating mapping-, assembly- and haplotype-based approaches for calling variants in clinical sequencing applications. Nature Genetics, 2014, 46, 912-918.	9.4	937
2	Germline mutations affecting the proofreading domains of POLE and POLD1 predispose to colorectal adenomas and carcinomas. Nature Genetics, 2013, 45, 136-144.	9.4	851
3	Innate Immune Activity Conditions the Effect of Regulatory Variants upon Monocyte Gene Expression. Science, 2014, 343, 1246949.	6.0	706
4	Genomic landscape of the individual host response and outcomes in sepsis: a prospective cohort study. Lancet Respiratory Medicine,the, 2016, 4, 259-271.	5.2	536
5	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. Nature Genetics, 2015, 47, 717-726.	9.4	310
6	A Fine-Scale Chimpanzee Genetic Map from Population Sequencing. Science, 2012, 336, 193-198.	6.0	273
7	Clinical whole-genome sequencing in severe early-onset epilepsy reveals new genes and improves molecular diagnosis. Human Molecular Genetics, 2014, 23, 3200-3211.	1.4	222
8	Mosaic PPM1D mutations are associated with predisposition to breast and ovarian cancer. Nature, 2013, 493, 406-410.	13.7	218
9	Mutations in TCF12, encoding a basic helix-loop-helix partner of TWIST1, are a frequent cause of coronal craniosynostosis. Nature Genetics, 2013, 45, 304-307.	9.4	181
10	Shared and Distinct Aspects of the Sepsis Transcriptomic Response to Fecal Peritonitis and Pneumonia. American Journal of Respiratory and Critical Care Medicine, 2017, 196, 328-339.	2.5	178
11	Choice of transcripts and software has a large effect on variant annotation. Genome Medicine, 2014, 6, 26.	3.6	158
12	Extensive characterization of NF-ÎºB binding uncovers non-canonical motifs and advances the interpretation of genetic functional traits. Genome Biology, 2011, 12, R70.	13.9	137
13	Genomic modulators of gene expression in human neutrophils. Nature Communications, 2015, 6, 7545.	5.8	120
14	Congenital myasthenic syndromes due to mutations inALG2andALG14. Brain, 2013, 136, 944-956.	3.7	117
15	Application of whole genome and RNA sequencing to investigate the genomic landscape of common variable immunodeficiency disorders. Clinical Immunology, 2015, 160, 301-314.	1.4	100
16	Whole-genome sequencing of bladder cancers reveals somatic CDKN1A mutations and clinicopathological associations with mutation burden. Nature Communications, 2014, 5, 3756.	5.8	81
17	NOX1 loss-of-function genetic variants in patients with inflammatory bowel disease. Mucosal Immunology, 2018, 11, 562-574.	2.7	71
18	IgD attenuates the IgM-induced anergy response in transitional and mature B cells. Nature Communications, 2016, 7, 13381.	5.8	68

#	Article	IF	Citations
19	Gain-of-Function Mutations in ZIC1 Are Associated with Coronal Craniosynostosis and Learning Disability. American Journal of Human Genetics, 2015, 97, 378-388.	2.6	56
20	Synergistic cooperation and crosstalk between MYD88L265P and mutations that dysregulate CD79B and surface IgM. Journal of Experimental Medicine, 2017, 214, 2759-2776.	4.2	38
21	Erythrocytosis associated with a novel missense mutation in the BPGM gene. Haematologica, 2014, 99, e201-e204.	1.7	35
22	Genomic mapping of the MHC transactivator CIITA using an integrated ChIP-seq and genetical genomics approach. Genome Biology, 2014, 15, 494.	3.8	32
23	High resolution HLA haplotyping by imputation for a British population bioresource. Human Immunology, 2017, 78, 242-251.	1.2	31
24	AltHapAlignR: improved accuracy of RNA-seq analyses through the use of alternative haplotypes. Bioinformatics, 2018, 34, 2401-2408.	1.8	27
25	Free play predicts self-regulation years later: Longitudinal evidence from a large Australian sample of toddlers and preschoolers. Early Childhood Research Quarterly, 2022, 59, 148-161.	1.6	22
26	Parameter estimation for robust HMM analysis of ChIP-chip data. BMC Bioinformatics, 2008, 9, 343.	1.2	21
27	ChIPseqR: analysis of ChIP-seq experiments. BMC Bioinformatics, 2011, 12, 39.	1.2	19
28	Cluster Analyses Reveals Subgroups of Children With Suspected Auditory Processing Disorders. Frontiers in Psychology, 2019, 10, 2481.	1.1	15
29	Validation and functional annotation of expression-based clusters based on gene ontology. BMC Bioinformatics, 2006, 7, 380.	1.2	14
30	Cortical function and sensorimotor plasticity are prognostic factors associated with future low back pain after an acute episode: the Understanding persistent Pain Where it ResiDes prospective cohort study. Pain, 2023, 164, 14-26.	2.0	10
31	Effectiveness of Computer-Based Auditory Training for Adult Cochlear Implant Users: A Randomized Crossover Study. Trends in Hearing, 2021, 25, 233121652110259.	0.7	8
32	The Emotional Dysregulation Questionnaire: Development and comparative analysis. Psychology and Psychotherapy: Theory, Research and Practice, 2021, 94, 426-463.	1.3	6
33	Identifying individual-based injury patterns in multi-trauma road users by using an association rule mining method. Accident Analysis and Prevention, 2022, 164, 106479.	3.0	6
34	Characterisation of the global transcriptional response to heat shock and the impact of individual genetic variation. Genome Medicine, 2016, 8, 87.	3.6	4
35	Dealing With Deaths in Clinical Trials and Meta-Analyses. Respiratory Care, 2021, 66, 1503-1503.	0.8	0