

Peter Humburg

List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

5,609
citations

279798

23
h-index

377865

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. <i>Nature Genetics</i> , 2014, 46, 912-918.	21.4	937
2	Germline mutations affecting the proofreading domains of POLE and POLD1 predispose to colorectal adenomas and carcinomas. <i>Nature Genetics</i> , 2013, 45, 136-144.	21.4	851
3	Innate Immune Activity Conditions the Effect of Regulatory Variants upon Monocyte Gene Expression. <i>Science</i> , 2014, 343, 1246949.	12.6	706
4	Genomic landscape of the individual host response and outcomes in sepsis: a prospective cohort study. <i>Lancet Respiratory Medicine</i> , 2016, 4, 259-271.	10.7	536
5	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. <i>Nature Genetics</i> , 2015, 47, 717-726.	21.4	310
6	A Fine-Scale Chimpanzee Genetic Map from Population Sequencing. <i>Science</i> , 2012, 336, 193-198.	12.6	273
7	Clinical whole-genome sequencing in severe early-onset epilepsy reveals new genes and improves molecular diagnosis. <i>Human Molecular Genetics</i> , 2014, 23, 3200-3211.	2.9	222
8	Mosaic PPM1D mutations are associated with predisposition to breast and ovarian cancer. <i>Nature</i> , 2013, 493, 406-410.	27.8	218
9	Mutations in TCF12, encoding a basic helix-loop-helix partner of TWIST1, are a frequent cause of coronal craniosynostosis. <i>Nature Genetics</i> , 2013, 45, 304-307.	21.4	181
10	Shared and Distinct Aspects of the Sepsis Transcriptomic Response to Fecal Peritonitis and Pneumonia. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017, 196, 328-339.	5.6	178
11	Choice of transcripts and software has a large effect on variant annotation. <i>Genome Medicine</i> , 2014, 6, 26.	8.2	158
12	Extensive characterization of NF- κ B binding uncovers non-canonical motifs and advances the interpretation of genetic functional traits. <i>Genome Biology</i> , 2011, 12, R70.	9.6	137
13	Genomic modulators of gene expression in human neutrophils. <i>Nature Communications</i> , 2015, 6, 7545.	12.8	120
14	Congenital myasthenic syndromes due to mutations in <i>ALG2</i> and <i>ALG14</i> . <i>Brain</i> , 2013, 136, 944-956.	7.6	117
15	Application of whole genome and RNA sequencing to investigate the genomic landscape of common variable immunodeficiency disorders. <i>Clinical Immunology</i> , 2015, 160, 301-314.	3.2	100
16	Whole-genome sequencing of bladder cancers reveals somatic CDKN1A mutations and clinicopathological associations with mutation burden. <i>Nature Communications</i> , 2014, 5, 3756.	12.8	81
17	NOX1 loss-of-function genetic variants in patients with inflammatory bowel disease. <i>Mucosal Immunology</i> , 2018, 11, 562-574.	6.0	71
18	IgD attenuates the IgM-induced energy response in transitional and mature B cells. <i>Nature Communications</i> , 2016, 7, 13381.	12.8	68

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19	Gain-of-Function Mutations in ZIC1 Are Associated with Coronal Craniosynostosis and Learning Disability. <i>American Journal of Human Genetics</i> , 2015, 97, 378-388.	6.2	56
20	Synergistic cooperation and crosstalk between MYD88L265P and mutations that dysregulate CD79B and surface IgM. <i>Journal of Experimental Medicine</i> , 2017, 214, 2759-2776.	8.5	38
21	Erythrocytosis associated with a novel missense mutation in the BPGM gene. <i>Haematologica</i> , 2014, 99, e201-e204.	3.5	35
22	Genomic mapping of the MHC transactivator CIITA using an integrated ChIP-seq and genetical genomics approach. <i>Genome Biology</i> , 2014, 15, 494.	8.8	32
23	High resolution HLA haplotyping by imputation for a British population bioresource. <i>Human Immunology</i> , 2017, 78, 242-251.	2.4	31
24	AltHapAlignR: improved accuracy of RNA-seq analyses through the use of alternative haplotypes. <i>Bioinformatics</i> , 2018, 34, 2401-2408.	4.1	27
25	Free play predicts self-regulation years later: Longitudinal evidence from a large Australian sample of toddlers and preschoolers. <i>Early Childhood Research Quarterly</i> , 2022, 59, 148-161.	2.7	22
26	Parameter estimation for robust HMM analysis of ChIP-chip data. <i>BMC Bioinformatics</i> , 2008, 9, 343.	2.6	21
27	ChIPseqR: analysis of ChIP-seq experiments. <i>BMC Bioinformatics</i> , 2011, 12, 39.	2.6	19
28	Cluster Analyses Reveals Subgroups of Children With Suspected Auditory Processing Disorders. <i>Frontiers in Psychology</i> , 2019, 10, 2481.	2.1	15
29	Validation and functional annotation of expression-based clusters based on gene ontology. <i>BMC Bioinformatics</i> , 2006, 7, 380.	2.6	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. <i>Pain</i> , 2023, 164, 14-26.	4.2	10
31	Effectiveness of Computer-Based Auditory Training for Adult Cochlear Implant Users: A Randomized Crossover Study. <i>Trends in Hearing</i> , 2021, 25, 233121652110259.	1.3	8
32	The Emotional Dysregulation Questionnaire: Development and comparative analysis. <i>Psychology and Psychotherapy: Theory, Research and Practice</i> , 2021, 94, 426-463.	2.5	6
33	Identifying individual-based injury patterns in multi-trauma road users by using an association rule mining method. <i>Accident Analysis and Prevention</i> , 2022, 164, 106479.	5.7	6
34	Characterisation of the global transcriptional response to heat shock and the impact of individual genetic variation. <i>Genome Medicine</i> , 2016, 8, 87.	8.2	4
35	Dealing With Deaths in Clinical Trials and Meta-Analyses. <i>Respiratory Care</i> , 2021, 66, 1503-1503.	1.6	0