Peter Humburg

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3990916/publications.pdf

Version: 2024-02-01

35 papers 5,609 citations

279798 23 h-index 377865 34 g-index

37 all docs

 $\begin{array}{c} 37 \\ \text{docs citations} \end{array}$

37 times ranked

15745 citing authors

#	Article	IF	CITATIONS
1	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.	4.2	10
2	Identifying individual-based injury patterns in multi-trauma road users by using an association rule mining method. Accident Analysis and Prevention, 2022, 164, 106479.	5.7	6
3	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.	2.7	22
4	The Emotional Dysregulation Questionnaire: Development and comparative analysis. Psychology and Psychotherapy: Theory, Research and Practice, 2021, 94, 426-463.	2.5	6
5	Effectiveness of Computer-Based Auditory Training for Adult Cochlear Implant Users: A Randomized Crossover Study. Trends in Hearing, 2021, 25, 233121652110259.	1.3	8
6	Dealing With Deaths in Clinical Trials and Meta-Analyses. Respiratory Care, 2021, 66, 1503-1503.	1.6	0
7	Cluster Analyses Reveals Subgroups of Children With Suspected Auditory Processing Disorders. Frontiers in Psychology, 2019, 10, 2481.	2.1	15
8	AltHapAlignR: improved accuracy of RNA-seq analyses through the use of alternative haplotypes. Bioinformatics, 2018, 34, 2401-2408.	4.1	27
9	NOX1 loss-of-function genetic variants in patients with inflammatory bowel disease. Mucosal Immunology, 2018, 11, 562-574.	6.0	71
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.	5.6	178
11	Synergistic cooperation and crosstalk between <i>MYD88L265P</i> and mutations that dysregulate CD79B and surface IgM. Journal of Experimental Medicine, 2017, 214, 2759-2776.	8.5	38
12	High resolution HLA haplotyping by imputation for a British population bioresource. Human Immunology, 2017, 78, 242-251.	2.4	31
13	Characterisation of the global transcriptional response to heat shock and the impact of individual genetic variation. Genome Medicine, 2016, 8, 87.	8.2	4
14	IgD attenuates the IgM-induced anergy response in transitional and mature B cells. Nature Communications, 2016, 7, 13381.	12.8	68
15	Genomic landscape of the individual host response and outcomes in sepsis: a prospective cohort study. Lancet Respiratory Medicine, the, 2016, 4, 259-271.	10.7	536
16	Genomic modulators of gene expression in human neutrophils. Nature Communications, 2015, 6, 7545.	12.8	120
17	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. Nature Genetics, 2015, 47, 717-726.	21.4	310
18	Application of whole genome and RNA sequencing to investigate the genomic landscape of common variable immunodeficiency disorders. Clinical Immunology, 2015, 160, 301-314.	3.2	100

#	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.	6.2	56
20	Genomic mapping of the MHC transactivator CIITA using an integrated ChIP-seq and genetical genomics approach. Genome Biology, 2014, 15, 494.	8.8	32
21	Choice of transcripts and software has a large effect on variant annotation. Genome Medicine, 2014, 6, 26.	8.2	158
22	Whole-genome sequencing of bladder cancers reveals somatic CDKN1A mutations and clinicopathological associations with mutation burden. Nature Communications, 2014, 5, 3756.	12.8	81
23	Clinical whole-genome sequencing in severe early-onset epilepsy reveals new genes and improves molecular diagnosis. Human Molecular Genetics, 2014, 23, 3200-3211.	2.9	222
24	Innate Immune Activity Conditions the Effect of Regulatory Variants upon Monocyte Gene Expression. Science, 2014, 343, 1246949.	12.6	706
25	Integrating mapping-, assembly- and haplotype-based approaches for calling variants in clinical sequencing applications. Nature Genetics, 2014, 46, 912-918.	21.4	937
26	Erythrocytosis associated with a novel missense mutation in the BPGM gene. Haematologica, 2014, 99, e201-e204.	3.5	35
27	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.	21.4	181
28	Mosaic PPM1D mutations are associated with predisposition to breast and ovarian cancer. Nature, 2013, 493, 406-410.	27.8	218
29	Germline mutations affecting the proofreading domains of POLE and POLD1 predispose to colorectal adenomas and carcinomas. Nature Genetics, 2013, 45, 136-144.	21.4	851
30	Congenital myasthenic syndromes due to mutations in <i>ALG2</i> and <i>ALG14</i> Brain, 2013, 136, 944-956.	7.6	117
31	A Fine-Scale Chimpanzee Genetic Map from Population Sequencing. Science, 2012, 336, 193-198.	12.6	273
32	Extensive characterization of NF- \hat{l}^2 B binding uncovers non-canonical motifs and advances the interpretation of genetic functional traits. Genome Biology, 2011, 12, R70.	9.6	137
33	ChIPseqR: analysis of ChIP-seq experiments. BMC Bioinformatics, 2011, 12, 39.	2.6	19
34	Parameter estimation for robust HMM analysis of ChIP-chip data. BMC Bioinformatics, 2008, 9, 343.	2.6	21
35	Validation and functional annotation of expression-based clusters based on gene ontology. BMC Bioinformatics, 2006, 7, 380.	2.6	14