

# Peter Humburg

## List of Publications by Year in descending order

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Version: 2024-02-01

35  
papers

5,609  
citations

279701

23  
h-index

377752

34  
g-index

37  
all docs

37  
docs citations

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. <i>Pain</i> , 2023, 164, 14-26. | 2.0 | 10        |
| 2  | 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.   | 3.0 | 6         |
| 3  | 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.  | 1.6 | 22        |
| 4  | The Emotional Dysregulation Questionnaire: Development and comparative analysis. <i>Psychology and Psychotherapy: Theory, Research and Practice</i> , 2021, 94, 426-463.   | 1.3 | 6         |
| 5  | Effectiveness of Computer-Based Auditory Training for Adult Cochlear Implant Users: A Randomized Crossover Study. <i>Trends in Hearing</i> , 2021, 25, 233121652110259.  | 0.7 | 8         |
| 6  | Dealing With Deaths in Clinical Trials and Meta-Analyses. <i>Respiratory Care</i> , 2021, 66, 1503-1503.   | 0.8 | 0         |
| 7  | Cluster Analyses Reveals Subgroups of Children With Suspected Auditory Processing Disorders. <i>Frontiers in Psychology</i> , 2019, 10, 2481.  | 1.1 | 15        |
| 8  | AltHapAlignR: improved accuracy of RNA-seq analyses through the use of alternative haplotypes. <i>Bioinformatics</i> , 2018, 34, 2401-2408.  | 1.8 | 27        |
| 9  | NOX1 loss-of-function genetic variants in patients with inflammatory bowel disease. <i>Mucosal Immunology</i> , 2018, 11, 562-574.   | 2.7 | 71        |
| 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.  | 2.5 | 178       |
| 11 | Synergistic cooperation and crosstalk between <i>MYD88L265P</i> and mutations that dysregulate CD79B and surface IgM. <i>Journal of Experimental Medicine</i> , 2017, 214, 2759-2776.  | 4.2 | 38        |
| 12 | High resolution HLA haplotyping by imputation for a British population bioresource. <i>Human Immunology</i> , 2017, 78, 242-251.   | 1.2 | 31        |
| 13 | Characterisation of the global transcriptional response to heat shock and the impact of individual genetic variation. <i>Genome Medicine</i> , 2016, 8, 87.  | 3.6 | 4         |
| 14 | IgD attenuates the IgM-induced anergy response in transitional and mature B cells. <i>Nature Communications</i> , 2016, 7, 13381.  | 5.8 | 68        |
| 15 | Genomic landscape of the individual host response and outcomes in sepsis: a prospective cohort study. <i>Lancet Respiratory Medicine</i> , 2016, 4, 259-271.   | 5.2 | 536       |
| 16 | Genomic modulators of gene expression in human neutrophils. <i>Nature Communications</i> , 2015, 6, 7545.  | 5.8 | 120       |
| 17 | Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. <i>Nature Genetics</i> , 2015, 47, 717-726.  | 9.4 | 310       |
| 18 | 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.  | 1.4 | 100       |

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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.                 | 2.6  | 56        |
| 20 | Genomic mapping of the MHC transactivator CIITA using an integrated ChIP-seq and genetical genomics approach. <i>Genome Biology</i> , 2014, 15, 494.                                    | 3.8  | 32        |
| 21 | Choice of transcripts and software has a large effect on variant annotation. <i>Genome Medicine</i> , 2014, 6, 26.  | 3.6  | 158       |
| 22 | Whole-genome sequencing of bladder cancers reveals somatic CDKN1A mutations and clinicopathological associations with mutation burden. <i>Nature Communications</i> , 2014, 5, 3756.    | 5.8  | 81        |
| 23 | 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.              | 1.4  | 222       |
| 24 | Innate Immune Activity Conditions the Effect of Regulatory Variants upon Monocyte Gene Expression. <i>Science</i> , 2014, 343, 1246949.   | 6.0  | 706       |
| 25 | Integrating mapping-, assembly- and haplotype-based approaches for calling variants in clinical sequencing applications. <i>Nature Genetics</i> , 2014, 46, 912-918.                    | 9.4  | 937       |
| 26 | Erythrocytosis associated with a novel missense mutation in the BPGM gene. <i>Haematologica</i> , 2014, 99, e201-e204.  | 1.7  | 35        |
| 27 | 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.                  | 9.4  | 181       |
| 28 | Mosaic PPM1D mutations are associated with predisposition to breast and ovarian cancer. <i>Nature</i> , 2013, 493, 406-410.   | 13.7 | 218       |
| 29 | Germline mutations affecting the proofreading domains of POLE and POLD1 predispose to colorectal adenomas and carcinomas. <i>Nature Genetics</i> , 2013, 45, 136-144.                   | 9.4  | 851       |
| 30 | Congenital myasthenic syndromes due to mutations in <i>ALG2</i> and <i>ALG14</i> . <i>Brain</i> , 2013, 136, 944-956.   | 3.7  | 117       |
| 31 | A Fine-Scale Chimpanzee Genetic Map from Population Sequencing. <i>Science</i> , 2012, 336, 193-198.  | 6.0  | 273       |
| 32 | Extensive characterization of NF- $\kappa$ B binding uncovers non-canonical motifs and advances the interpretation of genetic functional traits. <i>Genome Biology</i> , 2011, 12, R70. | 13.9 | 137       |
| 33 | ChIPseqR: analysis of ChIP-seq experiments. <i>BMC Bioinformatics</i> , 2011, 12, 39.   | 1.2  | 19        |
| 34 | Parameter estimation for robust HMM analysis of ChIP-chip data. <i>BMC Bioinformatics</i> , 2008, 9, 343.   | 1.2  | 21        |
| 35 | Validation and functional annotation of expression-based clusters based on gene ontology. <i>BMC Bioinformatics</i> , 2006, 7, 380.   | 1.2  | 14        |