

## **GWAS of persistent ADHD – Aug 2022 release**

The file 'persistent.sumstats.gz' contains summary statistics from GWAS of persistent ADHD (1,473 persistent ADHD cases vs 38,303 controls). Please note that the same controls are used for all the ADHD subtypes GWAS.

### **Citation for studies using these data:**

Veera M. Rajagopal, Jinjie Duan, Laura Vilar-Ribó, Jakob Grove, Tetyana Zayats, J. Antoni Ramos-Quiroga, F. Kyle Satterstrom, María Soler Artigas, Jonas Bybjerg-Grauholm, Marie Bækvad-Hansen, Thomas D. Als, Anders Rosengren, Mark J. Daly, Benjamin M. Neale, Merete Nordentoft, Thomas Werge, Ole Mors, David M. Hougaard, Preben B. Mortensen, Marta Ribasés, Anders D. Børglum, Ditte Demontis. **Differences in the genetic architecture of common and rare variants in childhood, persistent and late-diagnosed attention-deficit hyperactivity disorder.** Nature Genetics (Aug 2022). <https://doi.org/10.1038/s41588-022-01143-7>

### **Disclaimer**

These data are provided “as is”, and without warranty, for scientific and educational use only. If you download these data, you acknowledge that these data will be used only for non-commercial research purposes; that the investigator is in compliance with all applicable state, local, and federal laws or regulations and institutional policies regarding human subjects and genetics research; that secondary distribution of the data without registration by secondary parties is prohibited; and that the investigator will cite the publication in any communications or publications arising directly or indirectly from these data.

### **File description**

The file is a tab-delimited compressed (using gzip) text file containing 10 columns. The column description is as follows.

1. SNP = RSIDs of the SNPs; SNPs without RSIDs are named in the format 'CHR:BP:A1\_A2'
2. CHR = chromosome number
3. BP = Base pair position (hg19 build)
4. A1 = Effect allele
5. A2 = Reference allele
6. BETA = log of odds ratio
7. SE = standard error
8. P = P value
9. N = SNP specific sample size

### **Data Use Agreement**

1. Investigators acknowledge that these data are provided on an “as-is” basis, without warranty of any type, expressed or implied, including but not limited to any warranty as to their performance, merchantability, or fitness for any particular purpose;
2. Investigators will use these results for scientific research and educational use only.
3. The downloaded results can be shared among collaborators but the reposting or public distribution of the result file is prohibited;
4. Investigators certify that they are in compliance with all applicable local, state, and federal laws or regulations and institutional policies regarding human subjects and genetics research;
5. Investigators will cite the appropriate publication in any communications or publications arising directly or indirectly from these data;
6. Investigators will never attempt to identify any participant who contributed to these data;
7. Investigators may not use these data to develop any type of risk or predictive test for an unborn individual;
8. For any risk or predictive test for a child or adult, investigators must acknowledge that this is an experimental use of these data and that essentially all psychiatric disorders have important non-genetic etiological components;

9. When these data are made available prior to publication, investigators agree to respect and not compete with the scientific priorities of the iPSYCH team according to the Fort Lauderdale principles (<https://www.sanger.ac.uk/wp-content/uploads/fortlauderdalereport.pdf>)

Experience has taught us that the appropriate use of these data requires considerable attention to detail, prior experience, and technical skill. Errors are easy to make. If investigators use these data, any and all consequences are entirely their responsibility.

For inquiries about accessing this data, please contact Veera Rajagopal ([veera@biomed.au.dk](mailto:veera@biomed.au.dk)) or Ditte Demontis ([ditte@biomed.au.dk](mailto:ditte@biomed.au.dk))