The genetic architecture of neuropsychiatric traits: mechanism, polygenicity, and genome function

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References

Brief Funct Genomics 2015, 14:352-357.
19. Cross-Disorder Group of the Psychiatric Genomics C: Identification of risk loci with shared 
F, Ripke S, Kelsoe JR, et al: Genetic pleiotropy between multiple sclerosis and schizophrenia 
22. Gamazon ER, Im HK, Liu C, Members of the Bipolar Disorder Genome Study Consortium, Nicolae 
DL, Cox NJ: The Convergence of eQTL Mapping, Heritability Estimation and Polygenic 
23. Davis LK, Yu D, Keenan CL, Gamazon ER, Konkashbaev AI, Derks EM, Neale BM, Yang J, Lee SH, 
Evans P, et al: Partitioning the heritability of Tourette syndrome and obsessive compulsive 
24. Torres JM, Gamazon ER, Parra EJ, Below JE, Valladares-Salgado A, Wacher N, Cruz M, Hanis CL, 
Cox NJ: Cross-tissue and tissue-specific eQTLs: partitioning the heritability of a complex trait. 
Hum Genet 2014.
Psychiatric Genomics Consortium, Patterson N, Daly MJ, Price AL, Neale BM: LD Score 
regression distinguishes confounding from polygenicity in genome-wide association studies. 
27. Shi H, Khichaev G, Pasaniuc B: Contrasting the genetic architecture of 30 complex traits from 
28. Krishna Kumar S, Feldman MW, Rehkopf DH, Tuljapurkar S: Limitations of GCTA as a solution to 
29. Gamazon ER, Park DS: SNP-based heritability estimation: measurement noise, population 
30. The GTEx Consortium: The GENotype-Tissue Expression (GTEx) pilot analysis: multi-tissue gene 
31. The GTEx Consortium: The GENotype-Tissue Expression (GTEx) project. Nat Genet 2013, 45:580- 
585.
32. Gamazon ER, Stranger BE: Genomics of alternative splicing: evolution, development and 
33. Gamazon ER: Alternative Splicing and Genome Evolution. Encyclopedia of Life Sciences (eLS) 
2016.
34. Gamazon ER, Pinto N, Konkashbaev A, Im HK, Diskin SJ, London WB, Maris JM, Dolan ME, Cox NJ, 
Cohn SL: Trans-population analysis of genetic mechanisms of ethnic disparities in 
35. Gamazon ER, Perera M: Genome-wide approaches in pharmacogenomics: heritability 
estimation and pharmacoethnicity as primary challenges. Pharmacogenomics 2012, 13:1101- 
1104.


50. WTCCC: Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. Nature 2007, 447:661-678.


205. !!! INVALID CITATION !!!


211. Purcell S, Neale B, Todd-Brown K, Thomas L, Ferreira MA, Bender D, Maller J, Sklar P, de Bakker PI, Daly MJ, Sham PC: PLINK: a tool set for whole-genome association and population-based linkage analyses. *Am J Hum Genet* 2007, 81:559-575.


301. Hinze-Selch D: Infection, treatment and immune response in patients with bipolar disorder versus patients with major depression, schizophrenia or healthy controls. Bipolar Disord 2002, 4 Suppl 1:81-83.


328. WTCCC: Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. Nature 2007, 447:661-678.


369. Materials and Methods are available in the supplementary material on Science Online.


376. Wen X: Robust Bayesian FDR Control with Bayes Factors.


514


542. Table of Pharmacogenomic Biomarkers in Drug Labels [http://www.fda.gov/Drugs/ScienceResearch/ResearchAreas/Pharmacogenetics/ucm083378.htm]


519


572. Cropp CD, Komori T, Shima JE, Urban TJ, Yee SW, More SS, Giacomini KM: Organic anion transporter 2 (SLC22A7) is a facilitative transporter of cGMP. 

Mol Pharm 2013, 10:650-663.


576. Daly AK: Using genome-wide association studies to identify genes important in serious adverse drug reactions. 

577. Daly AK: Pharmacogenomics of adverse drug reactions. 
Genome Med 2013, 5:5.

Cancer Res 2010, 70:8055-8065.


PloS One 2013, 8:e61980.

581. Thompson CH, Kahlig KM, George AL, Jr.: SCN1A splice variants exhibit divergent sensitivity to commonly used antiepileptic drugs. 
Epilepsia 2011, 52:1000-1009.

Mol Pharmacol 2012, 81:620-630.


584. Manolio TA: Genomewide association studies and assessment of the risk of disease. 


595. Sham PC, Purcell SM: Statistical power and significance testing in large-scale genetic studies. *Nat Rev Genet* 2014, 15:335-346.


List of Publications


54.


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