Bibliography

Note: Numbers in square brackets denote the chapter in which an entry is cited.

Abell, N. S., M. K. DeGorter, M. J. Gloudemans, et al. 2022. Multiple Causal Variants Underlie Genetic Associations in Humans. *Science* **375**:1247–1254. [8]

Abud, E. M., R. N. Ramirez, E. S. Martinez, et al. 2017. iPSC-Derived Human Microglia-Like Cells to Study Neurological Diseases. *Neuron* **94**:278–293. [7]

Adams, M. J., W. D. Hill, D. M. Howard, et al. 2020. Factors Associated with Sharing E-Mail Information and Mental Health Survey Participation in Large Population Cohorts. *Int. J. Epidemiol.* **49**:410–421. [2]

Ahn, K., N. Gotay, T. M. Andersen, et al. 2014. High Rate of Disease-Related Copy Number Variations in Childhood Onset Schizophrenia. *Mol. Psychiatry* **19**:568–572. [3]

Aibar, S., C. B. González-Blas, T. Moerman, et al. 2017. Scenic: Single-Cell Regulatory Network Inference and Clustering. *Nat. Methods* **14**:1083–1086. [11]

Aittokallio, J., A. Kauko, F. Vaura, et al. 2022. Polygenic Risk Scores for Predicting Adverse Outcomes after Coronary Revascularization. *Am. J. Cardiol.* **167**:9–14. [13]

Alareeki, A., B. Lashewicz, and L. Shipton. 2019. "Get Your Child in Order": Illustrations of Courtesy Stigma from Fathers Raising Both Autistic and Non-Autistic Children. *Disabil. Stud. Q.* **39**: [14]

Alasoo, K., J. Rodrigues, S. Mukhopadhyay, et al. 2018. Shared Genetic Effects on Chromatin and Gene Expression Indicate a Role for Enhancer Priming in Immune Response. *Nat. Genet.* **50**:424–431. [10]

Alkelai, A., L. Greenbaum, A. R. Docherty, et al. 2022. The Benefit of Diagnostic Whole Genome Sequencing in Schizophrenia and Other Psychotic Disorders. *Mol. Psychiatry* **27**:1435–1447. [13]

Alver, M., V. Mancini, K. Lall, et al. 2022. Contribution of Schizophrenia Polygenic Burden to Longitudinal Phenotypic Variance in 22q11.2 Deletion Syndrome. *Mol. Psychiatry* **27**:4191–4200. [13]

Amar, M., A. B. Pramod, N. K. Yu, et al. 2021. Autism-Linked Cullin3 Germline Haploinsufficiency Impacts Cytoskeletal Dynamics and Cortical Neurogenesis through RhoA Signaling. *Mol. Psychiatry* **26**:3586–3613. [5]

Amiri, A., G. Coppola, S. Scuderi, et al. 2018. Transcriptome and Epigenome Landscape of Human Cortical Development Modeled in Organoids. *Science* **362**:eaat6720. [5]

Anderson, K., and J. C. Austin. 2012. Effects of a Documentary Film on Public Stigma Related to Mental Illness Among Genetic Counselors. *J. Genet. Counsel.* **21**:573–581. [15]

Anderson, N. C., P. F. Chen, K. Meganathan, et al. 2021. Balancing Serendipity and Reproducibility: Pluripotent Stem Cells as Experimental Systems for Intellectual and Developmental Disorders. *Stem Cell Rep.* **16**:1446–1457. [5, 6]

Andlauer, T. F. M., J. Link, D. Martin, et al. 2020. Treatment- and Population-Specific Genetic Risk Factors for Anti-Drug Antibodies against Interferon-Beta: A GWAS. *BMC Med.* **18**:298. [2]

Anzalone, A. V., P. B. Randolph, J. R. Davis, et al. 2019. Search-and-Replace Genome Editing without Double-Strand Breaks or Donor DNA. *Nature* **576**:149–157. [7]

Appelbaum, P. S., and S. Benston. 2017. Anticipating the Ethical Challenges of Psychiatric Genetic Testing. *Curr. Psychiatry Rep.* **19**:39. [14]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Aragam, K. G., A. Dobbyn, R. Judy, et al. 2020. Limitations of Contemporary Guidelines for Managing Patients at High Genetic Risk of Coronary Artery Disease. *J. Am. Coll. Cardiol.* **75**:2769–2780. [13]

Araki, Y., I. Hong, T. R. Gamache, et al. 2020. SynGAP Isoforms Differentially Regulate Synaptic Plasticity and Dendritic Development. *eLife* **9**:e56273. [5]

Arango, C., C. M. Diaz-Caneja, P. D. McGorry, et al. 2018. Preventive Strategies for Mental Health. *Lancet Psychiatry* **5**:591–604. [13]

Araújo, D. S., and H. E. Wheeler. 2022. Genetic and Environmental Variation Impact Transferability of Polygenic Risk Scores. *Cell Rep. Med.* **3**:100687. [12]

Arnberg, F. K., R. Gudmundsdóttir, A. Butwicka, et al. 2015. Psychiatric Disorders and Suicide Attempts in Swedish Survivors of the 2004 Southeast Asia Tsunami: A 5 Year Matched Cohort Study. *Lancet Psychiatry* **2**:817–824. [4]

Arnett, D. K., R. S. Blumenthal, M. A. Albert, et al. 2019. 2019 ACC/AHA Guideline on the Primary Prevention of Cardiovascular Disease: Executive Summary: A Report of the American College of Cardiology/American Heart Association Task Force on Clinical Practice Guidelines. *J. Am. Coll. Cardiol.* **74**:1376–1414. [13]

Aschard, H., V. Guillemot, B. Vilhjalmsson, et al. 2017. Covariate Selection for Association Screening in Multiphenotype Genetic Studies. *Nat. Genet.* **49**:1789–1795. [2]

Ashburn, T. T., and K. B. Thor. 2004. Drug Repositioning: Identifying and Developing New Uses for Existing Drugs. *Nat. Rev. Drug Discov.* **3**:673–683. [6]

Attardo, A., J. E. Fitzgerald, and M. J. Schnitzer. 2015. Impermanence of Dendritic Spines in Live Adult CA1 Hippocampus. *Nature* **523** 592–596. [5]

Austin, J. C. 2015. The Effect of Genetic Test-Based Risk Information on Behavioral Outcomes: A Critical Examination of Failed Trials and a Call to Action. *Am. J. Med. Genet. A* **167**:2913–2915. [15]

———. 2019. Evidence-Based Genetic Counseling for Psychiatric Disorders: A Road Map. *Cold Spring Harb. Perspect. Med.* **10**:a036608. [15]

Austin, J. C., and W. G. Honer. 2004. The Potential Impact of Genetic Counseling for Mental Illness. *Clin. Genet.* **67**:134–142. [15]

———. 2008. Psychiatric Genetic Counselling for Parents of Individuals Affected with Psychotic Disorders: A Pilot Study. *Early. Interv. Psychiatry* **2**:80–89. [15]

Austin, J. C., C. G. S. Palmer, B. Rosen-Sheidley, et al. 2008. Psychiatric Disorders in Clinical Genetics II: Individualizing Recurrence Risks. *J. Genet. Counsel.* **17**:18–29. [15]

Austin, J. C., A. Semaka, and G. Hadjipavlou. 2014. Conceptualizing Genetic Counseling as Psychotherapy in the Era of Genomic Medicine. *J. Genet. Counsel.* **23**:903–909. [15]

Austin, J. C., G. N. Smith, and W. G. Honer. 2006. The Genomic Era and Perceptions of Psychotic Disorders: Genetic Risk Estimation, Associations with Reproductive Decisions and Views About Predictive Testing. *Am. J. Med. Genet. B Neuropsychiatr. Genet.* **141B**:926–928. [15]

Auton, A., G. R. Abecasis, D. M. Altshuler, et al. 2015. A Global Reference for Human Genetic Variation. *Nature* **526**:68–74. [2]

Auwerx, C., M. Lepamets, M. C. Sadler, et al. 2022. The Individual and Global Impact of Copy-Number Variants on Complex Human Traits. *Am. J. Hum. Genet.* **109**:647–668. [12]

Badini, I., J. R. I. Coleman, S. P. Hagenaars, et al. 2022. Depression with Atypical Neurovegetative Symptoms Shares Genetic Predisposition with Immuno-Metabolic Traits and Alcohol Consumption. *Psychol. Med.* **52**:726–736. [2]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Baglioni, C., G. Battagliese, B. Feige, et al. 2011. Insomnia as a Predictor of Depression: A Meta-Analytic Evaluation of Longitudinal Epidemiological Studies. *J. Affect. Disord.* **135**:10–19. [15]

Ballouz, S., and J. Gillis. 2017. Strength of Functional Signature Correlates with Effect Size in Autism. *Genome Med.* **9**:64. [7]

Baselmans, B. M. L., L. Yengo, W. van Rheenen, and N. R. Wray. 2021. Risk in Relatives, Heritability, Snp-Based Heritability, and Genetic Correlations in Psychiatric Disorders: A Review. *Biol. Psychiatry* **89**:11–19. [9]

Bashford, A., and P. Levine. 2010. The Oxford Handbook of the History of Eugenics. New York: Oxford Univ. Press. [14]

Bauer, M. S., and J. Kirchner. 2020. Implementation Science: What Is It and Why Should I Care? *Psychiatry Res.* **283**:112376. [13]

Bear, M. F., K. M. Huber, and S. T. Warren. 2004. The mGluR Theory of Fragile X Mental Retardation. *Trends Neurosci.* **27**:370–377. [5]

Beauchamp, M. R., R. E. Rhodes, C. Kreutzer, and J. L. Rupert. 2011. Experiential versus Genetic Accounts of Inactivity: Implications for Inactive Individuals' Self-Efficacy Beliefs and Intentions to Exercise. *Behav. Med.* **37**:8–14. [14]

Bélanger, S. A., and J. Caron. 2018. Evaluation of the Child with Global Developmental Delay and Intellectual Disability. *Paediatr. Child Health* **23**:403–419. [12]

Ben-David, E., and S. Shifman. 2013. Combined Analysis of Exome Sequencing Points toward a Major Role for Transcription Regulation during Brain Development in Autism. *Mol. Psychiatry* **18**:1054–1056. [11]

Bennett, C. F., B. F. Baker, N. Pham, E. Swayze, and R. S. Geary. 2017. Pharmacology of Antisense Drugs. *Annu. Rev. Pharmacol. Toxicol.* **57**:81–105. [6]

Ben-Shalom, R., C. M. Keeshen, K. N. Berrios, et al. 2017. Opposing Effects on Nav1.2 Function Underlie Differences between SCN2A Variants Observed in Individuals with Autism Spectrum Disorder or Infantile Seizures. *Biol. Psychiatry* **82**:224–232. [7]

Bentley, A. R., S. L. Callier, and C. N. Rotimi. 2020. Evaluating the Promise of Inclusion of African Ancestry Populations in Genomics. *NPJ Genom. Med.* **5**:5. [2]

Berendzen, K. M., R. Sharma, M. A. Mandujano, et al. 2023. Oxytocin Receptor Is Not Required for Social Attachment in Prairie Voles. *Neuron*, in press. [5]

Bergen, S. E., A. Ploner, D. Howrigan, et al. 2019. Joint Contributions of Rare Copy Number Variants and Common SNPs to Risk for Schizophrenia. *Am. J. Psychiatry* **176**:29–35. [13]

Berry-Kravis, E., V. Des Portes, R. Hagerman, et al. 2016. Mavoglurant in Fragile X Syndrome: Results of Two Randomized, Double-Blind, Placebo-Controlled Trials. *Sci. Transl. Med.* **8**:321. [5, 6]

Bershteyn, M., T. J. Nowakowski, A. A. Pollen, et al. 2017. Human iPSC-Derived Cerebral Organoids Model Cellular Features of Lissencephaly and Reveal Prolonged Mitosis of Outer Radial Glia. *Cell Stem Cell* **20**:435–449. [5]

Bhaduri, A., M. G. Andrews, W. Mancia Leon, et al. 2020. Cell Stress in Cortical Organoids Impairs Molecular Subtype Specification. *Nature* **578**:142–148. [5]

Bhakar, A. L., G. Dolen, and M. F. Bear. 2012. The Pathophysiology of Fragile X (and What It Teaches Us About Synapses). *Annu. Rev. Neurosci.* **35**:417–443. [6]

Biesecker, B. B. 2001. Goals of Genetic Counseling. *Clin. Genet.* **60**:323–330. [15]

Bigdeli, T. B., S. Ripke, R. E. Peterson, et al. 2017. Genetic Effects Influencing Risk for Major Depressive Disorder in China and Europe. *Transl. Psychiatry* **7**:e1074. [2]

Birey, F., J. Andersen, C. D. Makinson, et al. 2017. Assembly of Functionally Integrated Human Forebrain Spheroids. *Nature* **545**:54–59. [5, 7]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Birey, F., M. Y. Li, A. Gordon, et al. 2022. Dissecting the Molecular Basis of Human Interneuron Migration in Forebrain Assembloids from Timothy Syndrome. *Cell Stem Cell* **29**:248–264. [7]

Biroli, P., T. J. Galama, S. von Hinke, et al. 2022. The Economics and Econometrics of Gene–Environment Interplay. *arXiv* 00729. [4]

Bishop, S. L., A. Thurm, E. Robinson, and S. J. Sanders. 2021. *Preprint*: Prevalence of Returnable Genetic Results Based on Recognizable Phenotypes among Children with Autism Spectrum Disorder. *medRxiv* 2021.2005.2028.21257736. [3]

Bloss, C. S., N. J. Schork, and E. J. Topol. 2011. Effect of Direct-to-Consumer Genomewide Profiling to Assess Disease Risk. *N. Engl. J. Med.* **364**:524–534. [15]

Blout Zawatsky, C. L., N. Shah, K. Machini, et al. 2021. Returning Actionable Genomic Results in a Research Biobank: Analytic Validity, Clinical Implementation, and Resource Utilization. *Am. J. Hum. Genet.* **108**:2224–2237. [13]

Bodnar, L. M., and K. L. Wisner. 2005. Nutrition and Depression: Implications for Improving Mental Health Among Childbearing-Aged Women. *Biol. Psychiatry* **1**:679–685. [15]

Boeschoten, R. E., A. M. J. Braamse, A. T. F. Beekman, et al. 2017. Prevalence of Depression and Anxiety in Multiple Sclerosis: A Systematic Review and Meta-Analysis. *J. Neurologic. Sci.* **372**:331–341. [2]

Bonanno, S., R. Giossi, R. Zanin, et al. 2022. Amifampridine Safety and Efficacy in Spinal Muscular Atrophy Ambulatory Patients: A Randomized, Placebo-Controlled, Crossover Phase 2 Trial. *J. Neurol.* **269**:5858–5867. [5]

Booke, S., J. Austin, L. Calderwood, and M. Campion. 2020. Genetic Counselors' Attitudes toward and Practice Related to Psychiatric Genetic Counseling. *J. Genet. Counsel.* **29**:25–34. [15]

Borle, K., E. Morris, A. Inglis, and J. Austin. 2018. Risk Communication in Genetic Counseling: Exploring Uptake and Perception of Recurrence Numbers, and Their Impact on Patient Outcomes. *Clin. Genet.* **94**:239–245. [15]

Botkin, J. R., J. W. Belmont, J. S. Berg, et al. 2015. Points to Consider: Ethical, Legal, and Psychosocial Implications of Genetic Testing in Children and Adolescents. *Am. J. Hum. Genet.* **97**:6–21. [15]

Boyd Ritsher, J., and J. C. Phelan. 2005. Internalized Stigma Predicts Erosion of Morale among Psychiatric Outpatients. *Psychiatry Res.* **129**:257–265. [15]

Boyle, E. A., Y. I. Li, and J. K. Pritchard. 2017. An Expanded View of Complex Traits: From Polygenic to Omnigenic. *Cell* **169**:1177–1186. [9]

BRAIN Initiative Cell Census Network. 2021. A Multimodal Cell Census and Atlas of the Mammalian Primary Motor Cortex. *Nature* **598**:86–102. [8]

BrainSeq Consortium. 2015. Neurogenomics to Drive Novel Target Discovery for Neuropsychiatric Disorders. *Neuron* **88**:1078–1083. [10]

Brainstorm Consortium, V. Anttila, B. Bulik-Sullivan, et al. 2018. Analysis of Shared Heritability in Common Disorders of the Brain. *Science* **360**:eaap8757. [1, 2]

Breen, M. S., T. Rusielewicz, H. N. Bader, et al. 2021. Modeling Gene X Environment Interactions in PTSD Using Glucocorticoid-Induced Transcriptomics in Human Neurons. *bioRxiv* 433391. [7]

Brennand, K., J. N. Savas, Y. Kim, et al. 2015. Phenotypic Differences in hiPSC NPCs Derived from Patients with Schizophrenia. *Mol. Psychiatry* **20**:361–368. [7]

Brennand, K. J., A. Simone, J. Jou, et al. 2011. Modelling Schizophrenia Using Human Induced Pluripotent Stem Cells. *Nature* **473**:221–225. [7]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Bristow, G. C., D. M. Thomson, R. L. Openshaw, et al. 2020. 16p11 Duplication Disrupts Hippocampal-Orbitofrontal-Amygdala Connectivity, Revealing a Neural Circuit Endophenotype for Schizophrenia. *Cell Rep.* **31**:107536. [7]

Brown, R. C., E. C. Berenz, S. H. Aggen, et al. 2014. Trauma Exposure and Axis I Psychopathology: A Cotwin Control Analysis in Norwegian Young Adults. *Psychol. Trauma* **6**:652–660. [4]

Brownstein, C. A., E. Douard, J. Mollon, et al. 2022. Similar Rates of Deleterious Copy Number Variants in Early-Onset Psychosis and Autism Spectrum Disorder. *Am. J. Psychiatry* **179**:853–861. [12]

Brunner, C., M. Grillet, A. Sans-Dublanc, et al. 2020. A Platform for Brain-Wide Volumetric Functional Ultrasound Imaging and Analysis of Circuit Dynamics in Awake Mice. *Neuron* **108**:861–875. [8]

Brunner, C., M. Grillet, A. Urban, et al. 2021. Whole-Brain Functional Ultrasound Imaging in Awake Head-Fixed Mice. *Nat. Protoc.* **16**:3547–3571. [8]

Brunner, D., P. Kabitzke, D. He, et al. 2015. Comprehensive Analysis of the 16p11.2 Deletion and Null Cntnap2 Mouse Models of Autism Spectrum Disorder. *PLOS ONE* **10**:e0134572. [7]

Bryois, J., D. Calini, W. Macnair, et al. 2022. Cell-Type-Specific *cis*-eQTLs in Eight Human Brain Cell Types Identify Novel Risk Genes for Psychiatric and Neurological Disorders. *Nat. Neurosci.* **25**:1104–1112. [10, 11]

Bryois, J., M. E. Garrett, L. Song, et al. 2018. Evaluation of Chromatin Accessibility in Prefrontal Cortex of Individuals with Schizophrenia. *Nat. Commun.* **9**:3121. [10]

Butcher, L. M., and R. Plomin. 2008. The Nature of Nurture: A Genomewide Association Scan for Family Chaos. *Behav. Genet.* **38**:361–371. [2]

Butler, M. G., D. Moreno-De-Luca, and A. M. Persico. 2022. Actionable Genomics in Clinical Practice: Paradigmatic Case Reports of Clinical and Therapeutic Strategies Based Upon Genetic Testing. *Genes* **13**:323. [12]

Buxbaum, J. D., D. J. Cutler, M. J. Daly, et al. 2020. Not All Autism Genes Are Created Equal: A Response to Myers et al. *Am. J. Hum. Genet.* **107**:1000–1003. [6]

Byrne, L., and A. E. Toland. 2021. Polygenic Risk Scores in Prostate Cancer Risk Assessment and Screening. *Urol. Clin. North Am.* **48**:387–399. [13]

Bzdok, D., G. Varoquaux, and E. W. Steyerberg. 2021. Prediction, Not Association, Paves the Road to Precision Medicine. *JAMA Psychiatry* **78**:127–128. [13]

Cadwell, C. R., A. Palasantza, X. Jiang, et al. 2016. Electrophysiological, Transcriptomic and Morphologic Profiling of Single Neurons Using Patch-Seq. *Nat. Biotechnol.* **34**:199–203. [11]

Cai, N., K. W. Choi, and E. I. Fried. 2020a. Reviewing the Genetics of Heterogeneity in Depression: Operationalizations, Manifestations and Etiologies. *Hum. Mol. Genet.* **29**:R10–R18. [2]

Cai, N., J. A. Revez, M. J. Adams, et al. 2020b. Minimal Phenotyping Yields Genome-Wide Association Signals of Low Specificity for Major Depression. *Nat. Genet.* **52**:437–447. [2]

Cai, Z., S. Li, D. Matuskey, N. Nabulsi, and Y. Huang. 2019. PET Imaging of Synaptic Density: A New Tool for Investigation of Neuropsychiatric Diseases. *Neurosci. Lett.* **691**:44–50. [8]

Cakir, B., Y. Xiang, Y. Tanaka, et al. 2019. Engineering of Human Brain Organoids with a Functional Vascular-Like System. *Nat. Methods* **16**:1169–1175. [7]

Calderon, D., A. Bhaskar, D. A. Knowles, et al. 2017. Inferring Relevant Cell Types for Complex Traits by Using Single-Cell Gene Expression. *Am. J. Hum. Genet.* **101**:686–699. [11]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Califf, R. M. 2018. Biomarker Definitions and Their Applications. *Exp. Biol. Med.* **243**:213–221. [5]

Camp, J. G., F. Badsha, M. Florio, et al. 2015. Human Cerebral Organoids Recapitulate Gene Expression Programs of Fetal Neocortex Development. *PNAS* **112**:15672–15677. [5]

Campos, A. I., A. Mulcahy, J. G. Thorp, et al. 2021. Understanding Genetic Risk Factors for Common Side Effects of Antidepressant Medications. *Commun. Med.* **1**:45. [14]

Cantor-Graae, E., C. B. Pedersen, T. F. McNeil, and P. B. Mortensen. 2003. Migration as a Risk Factor for Schizophrenia: A Danish Population-Based Cohort Study. *Br. J. Psychiatry* **182**:117–122. [4]

Cantor-Graae, E., and J.-P. Selten. 2005. Schizophrenia and Migration: A Meta-Analysis and Review. *Am. J. Psychiatry* **162**:12–24. [4]

Cao, Z., H. Yang, Y. Ye, et al. 2021. Polygenic Risk Score, Healthy Lifestyles, and Risk of Incident Depression. *Transl. Psychiatry* **11**:189. [13]

Carlyle, B. C., R. R. Kitchen, J. E. Kanyo, et al. 2017. A Multiregional Proteomic Survey of the Postnatal Human Brain. *Nat. Neurosci.* **20**:1787–1795. [11]

Carrion, P., A. Semaka, R. Batallones, et al. 2022. Reflections of Parents of Children with 22q11.2 Deletion Syndrome on the Experience of Receiving Psychiatric Genetic Counseling: Awareness to Act. *J. Genet. Couns.* **31**:140–152. [12]

Carver, T., S. Hartley, A. Lee, et al. 2021. Canrisk Tool-a Web Interface for the Prediction of Breast and Ovarian Cancer Risk and the Likelihood of Carrying Genetic Pathogenic Variants. *Cancer Epidemiol. Biomarkers Prev.* **30**:469–473. [13]

Casale, F. P., D. Horta, B. Rakitsch, and O. Stegle. 2017. Joint Genetic Analysis Using Variant Sets Reveals Polygenic Gene-Context Interactions. *PLoS genetics* **13**:e1006693. [2]

Caspi, A., R. M. Houts, D. W. Belsky, et al. 2014. The P Factor: One General Psychopathology Factor in the Structure of Psychiatric Disorders? *Clin. Psychol. Sci.* **2**:119–137. [2]

Caswell-Jin, J. L., T. Gupta, E. Hall, et al. 2018. Racial/Ethnic Differences in Multiple-Gene Sequencing Results for Hereditary Cancer Risk. *Genet. Med.* **20**:234–239. [3]

Cearns, M., A. T. Amare, K. O. Schubert, et al. 2022. Using Polygenic Scores and Clinical Data for Bipolar Disorder Patient Stratification and Lithium Response Prediction: Machine Learning Approach. *Br. J. Psychiatry* **Feb. 28**:1–10. [13]

Cederquist, G. Y., J. Tchieu, S. J. Callahan, et al. 2020. A Multiplex Human Pluripotent Stem Cell Platform Defines Molecular and Functional Subclasses of Autism-Related Genes. *Cell Stem Cell* **27**:35–49. [7]

Centers for Disease Control and Prevention. 2022. Facts About Suicide. https://www.cdc.gov/suicide/facts/index.html. [14]

Chailangkarn, T., C. Noree, and A. R. Muotri. 2018. The Contribution of GTF2I Haploinsufficiency to Williams Syndrome. *Mol. Cell Probes* **40**:45–51. [5]

Chang, J., S. R. Gilman, A. H. Chiang, S. J. Sanders, and D. Vitkup. 2015. Genotype to Phenotype Relationships in Autism Spectrum Disorders. *Nat. Neurosci.* **18**:191–198. [5]

Chang, X., L. A. Lima, Y. Liu, et al. 2018. Common and Rare Genetic Risk Factors Converge in Protein Interaction Networks Underlying Schizophrenia. *Front. Genet.* **9**:434. [7]

Chanouha, N., D. L. Cragun, V. Y. Pan, J. C. Austin, and C. Hoell. 2022. Healthcare Decision Makers' Perspectives on the Creation of New Genetic Counselor Positions in North America: Exploring the Case for Psychiatric Genetic Counseling. *J. Genet. Counsel.* **31**:1– 12. [12, 15]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Charney, A. W., E. A. Stahl, E. K. Green, et al. 2018. Contribution of Rare Copy Number Variants to Bipolar Disorder Risk Is Limited to Schizoaffective Cases. *Biol. Psychiatry* **86**:110–119. [3]

Charvet, C. J. 2020. Closing the Gap from Transcription to the Structural Connectome Enhances the Study of Connections in the Human Brain. *Dev. Dynamics* **249**:1047–1061. [8]

Charvet, C. J., and B. L. Finlay. 2018. Comparing Adult Hippocampal Neurogenesis across Species: Translating Time to Predict the Tempo in Humans. *Front. Neurosci.* **12**:706. [8]

Charvet, C. J., K. Ofori, C. Baucum, et al. 2022. Tracing Modification to Cortical Circuits in Human and Nonhuman Primates from High-Resolution Tractography, Transcription, and Temporal Dimensions. *The Journal of Neuroscience* **42**:3749–3767. [8]

Chau, K. K., P. Zhang, J. Urresti, et al. 2021. Full-Length Isoform Transcriptome of the Developing Human Brain Provides Further Insights into Autism. *Cell Rep*. **36**:109631. [5]

Chawner, S., J. L. Doherty, R. J. L. Anney, et al. 2021. A Genetics-First Approach to Dissecting the Heterogeneity of Autism: Phenotypic Comparison of Autism Risk Copy Number Variants. *Am. J. Psychiatry* **178**:77–86. [1]

Chen, P. J., J. A. Hussmann, J. Yan, et al. 2021. Enhanced Prime Editing Systems by Manipulating Cellular Determinants of Editing Outcomes. *Cell* **184**:5635–5652. [6]

Chen, S., R. Fragoza, L. Klei, et al. 2018. An Interactome Perturbation Framework Prioritizes Damaging Missense Mutations for Developmental Disorders. *Nat. Genet.* **50**:1032–1040. [11]

Chen, X., S. Ravindra Kumar, C. D. Adams, et al. 2022. Engineered Aavs for Non-Invasive Gene Delivery to Rodent and Non-Human Primate Nervous Systems. *Neuron* **110**:2242–2257. [6]

Cheung, R., K. D. Insigne, D. Yao, et al. 2019. A Multiplexed Assay for Exon Recognition Reveals That an Unappreciated Fraction of Rare Genetic Variants Cause Large-Effect Splicing Disruptions. *Mol. Cell* **73**:183–194. [8]

Choi, K. W., C. Y. Chen, R. J. Ursano, et al. 2019. Prospective Study of Polygenic Risk, Protective Factors, and Incident Depression Following Combat Deployment in US Army Soldiers. *Psychol. Med.* **50**:737–745. [13]

Choi, K. W., M. B. Stein, K. M. Nishimi, et al. 2020a. An Exposure-Wide and Mendelian Randomization Approach to Identifying Modifiable Factors for the Prevention of Depression. *Am. J. Psychiatry* **177**:944–954. [13]

Choi, K. W., A. B. Zheutlin, R. A. Karlson, et al. 2020b. Physical Activity Offsets Genetic Risk for Incident Depression Assessed via Electronic Health Records in a Biobank Cohort Study. *Depress. Anxiety* **37**:106–114. [13]

Choi, S. W., T. S. Mak, and P. F. O'Reilly. 2020c. Tutorial: A Guide to Performing Polygenic Risk Score Analyses. *Nat. Protoc.* **15**:2759–2772. [13]

Clarke, M. C., A. Tanskanen, M. O. Huttunen, and M. Cannon. 2013. Sudden Death of Father or Sibling in Early Childhood Increases Risk for Psychotic Disorder. *Schizophr. Res.* **143**:363–366. [4]

Cleynen, I., W. Engchuan, M. S. Hestand, et al. 2021. Genetic Contributors to Risk of Schizophrenia in the Presence of a 22q11.2 Deletion. *Mol. Psychiatry* **26**:4496–4510. [13]

Clifton, N. E., E. Rees, P. A. Holmans, et al. 2020. Genetic Association of FMRP Targets with Psychiatric Disorders. *Mol. Psychiatry* **26**:2977–2990. [11]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Coffee and Caffeine Genetics Consortium, M. C. Cornelis, E. M. Byrne, et al. 2015. Genome-Wide Meta-Analysis Identifies Six Novel Loci Associated with Habitual Coffee Consumptions. *Mol. Psychiatry* **20**:647–656. [4]

Colasante, G., G. Lignani, S. Brusco, et al. 2020. dCas9-Based Scn1a Gene Activation Restores Inhibitory Interneuron Excitability and Attenuates Seizures in Dravet Syndrome Mice. *Mol. Ther.* **28**:235–253. [5]

Coleman, J. R. I., W. J. Peyrot, K. L. Purves, et al. 2020. Genome-Wide Gene–Environment Analyses of Major Depressive Disorder and Reported Lifetime Traumatic Experiences in UK Biobank. *Mol. Psychiatry* **25**:1430–1446. [4]

Collado-Torres, L., E. E. Burke, A. Peterson, et al. 2019. Regional Heterogeneity in Gene Expression, Regulation, and Coherence in the Frontal Cortex and Hippocampus across Development and Schizophrenia. *Neuron* **103**:203–216. [11]

Collins, R. E., A. J. Wright, and T. M. Marteau. 2010. Impact of Communicating Personalized Genetic Risk Information on Perceived Control over the Risk: A Systematic Review. *Genet. Med.* **13**:273–277. [15]

Colloca, L., and A. J. Barsky. 2020. Placebo and Nocebo Effects. *N. Engl. J. Med.* **382**:554–561. [14]

Converge Consortium. 2015. Sparse Whole-Genome Sequencing Identifies Two Loci for Major Depressive Disorder. *Nature* **523**:588–591. [2, 7]

Conway, C. C., M. K. Forbes, S. C. South, and HiTOP Consortium. 2022. A Hierarchical Taxonomy of Psychopathology (HiTOP) Primer for Mental Health Researchers. *Clin. Psychol. Sci.* **10**:236–258. [2]

Cook, N. R. 2018. Quantifying the Added Value of New Biomarkers: How and How Not. *Diagn. Progn. Res.* **2**:14. [13]

Corominas, R., X. Yang, G. N. Lin, et al. 2014. Protein Interaction Network of Alternatively Spliced Isoforms from Brain Links Genetic Risk Factors for Autism. *Nat. Commun.* **5**:3650. [11]

Corrigan, P. W., and A. C. Watson. 2002. The Paradox of Self-Stigma and Mental Illness. *Clin. Psychol.* **9**:35–53. [15]

Corvin, A., and P. F. Sullivan. 2016. What Next in Schizophrenia Genetics for the Psychiatric Genomics Consortium? *Schizophr. Bull.* **42**:538–541. [5]

Costain, G., M. J. Esplen, B. Toner, K. A. Hodgkinson, and A. S. Bassett. 2012. Evaluating Genetic Counseling for Family Members of Individuals with Schizophrenia in the Molecular Age. *Schizophr. Bull.* **40**:88–99. [15]

Costain, G., M. J. Esplen, B. Toner, et al. 2014. Evaluating Genetic Counseling for Individuals with Schizophrenia in the Molecular Age. *Schizophr. Bull.* **40**:78–87. [15]

Costello, E. J., A. Erkanli, W. Copeland, and A. Angold. 2010. Association of Family Income Supplements in Adolescence with Development of Psychiatric and Substance Use Disorders in Adulthood among an American Indian Population. *JAMA* **303**:1954–1960. [4]

Cox, N. J. 2017. Comments on Pritchard Paper. *J. Psychiatry Brain Sci.* **2**:S5. [9]

Cross-Disorder Group of the Psychiatric Genomics Consortium. 2019. Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. *Cell* **179**:1469–1482. [1, 7, 11]

Cross-Disorder Group of the Psychiatric Genomics Consortium, C. Lee, S. Ripke, et al. 2013. Genetic Relationship between Five Psychiatric Disorders Estimated from Genome-Wide SNPs. *Nat. Genet.* **45**:984–994. [9]

Cruceanu, C., L. Dony, A. C. Krontira, et al. 2021. Cell-Type-Specific Impact of Glucocorticoid Receptor Activation on the Developing Brain: A Cerebral Organoid Study. *Am. J. Psychiatry* **179**:21010095. [7]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Cuomo, A. S. E., D. D. Seaton, D. J. McCarthy, et al. 2020. Single-Cell RNA-Sequencing of Differentiating iPS Cells Reveals Dynamic Genetic Effects on Gene Expression. *Nat. Commun.* **11**:810. [7]

Curran, G. M., M. Bauer, B. Mittman, J. M. Pyne, and C. Stetler. 2012. Effectiveness-Implementation Hybrid Designs: Combining Elements of Clinical Effectiveness and Implementation Research to Enhance Public Health Impact. *Med. Care* **50**:217–226. [13]

Curtis, D. 2018. Polygenic Risk Score for Schizophrenia Is More Strongly Associated with Ancestry Than with Schizophrenia. *Psychiatr. Genet.* **28**:85–89. [2]

Dagani, J., G. Signorini, O. Nielssen, et al. 2017. Meta-Analysis of the Interval between the Onset and Management of Bipolar Disorder. *Can. J. Psychiatry* **62**:247–258. [13]

Daghlas, I., J. M. Lane, R. Saxena, and C. Vetter. 2021. Genetically Proxied Diurnal Preference, Sleep Timing, and Risk of Major Depressive Disorder. *JAMA Psychiatry* **78**:903–910. [4]

D'Agostino, R. S., R. Vasan, M. Pencina, et al. 2008. General Cardiovascular Risk Profile for Use in Primary Care: The Framingham Heart Study. *Circulation* **117**:743–753. [13]

Dahl, A., V. Guillemot, J. Mefford, H. Aschard, and N. Zaitlen. 2019. Adjusting for Principal Components of Molecular Phenotypes Induces Replicating False Positives. *Genetics* **211**:1179–1189. [2]

Dahl, A., K. Nguyen, N. Cai, et al. 2020. A Robust Method Uncovers Significant Context-Specific Heritability in Diverse Complex Traits. *Am. J. Hum. Genet.* **106**:71–91. [2]

Dai, J., J. Aoto, and T. C. Südhof. 2019. Alternative Splicing of Presynaptic Neurexins Differentially Controls Postsynaptic NMDA and AMPA Receptor Responses. *Neuron* **102**:993–1008. [5]

Daily, J. L., K. Nash, U. Jinwal, et al. 2011. Adeno-Associated Virus-Mediated Rescue of the Cognitive Defects in a Mouse Model for Angelman Syndrome. *PLOS ONE* **6**:e27221. [6]

Damask, A., P. G. Steg, G. G. Schwartz, et al. 2020. Patients with High Genome-Wide Polygenic Risk Scores for Coronary Artery Disease May Receive Greater Clinical Benefit from Alirocumab Treatment in the Odyssey Outcomes Trial. *Circulation* **141**:624–636. [13]

Dana, K., J. Finik, S. Koenig, et al. 2019. Prenatal Exposure to Famine and Risk for Development of Psychopathology in Adulthood: A Meta-Analysis. *J. Psychiatry Psychiatr. Disord.* **3**:227–240. [4]

D'Angelo, D., S. Lebon, Q. Chen, et al. 2016. Defining the Effect of the 16p11.2 Duplication on Cognition, Behavior, and Medical Comorbidities. *JAMA Psychiatry* **73**:20–30. [5]

Darnell, R. B. 2013. RNA Protein Interaction in Neurons. *Annu. Rev. Neurosci.* **36**:243–270. [11]

Dar-Nimrod, I., B. Y. Cheung, M. B. Ruby, and S. J. Heine. 2014. Can Merely Learning About Obesity Genes Affect Eating Behavior? *Appetite* **81**:269–276. [14]

Dar-Nimrod, I., M. Zuckerman, and P. R. Duberstein. 2012. The Effects of Learning About One's Own Genetic Susceptibility to Alcoholism: A Randomized Experiment. *Genet. Med.* **15**:132–138. [15]

Daskalakis, N. P., H. Cohen, G. Cai, J. D. Buxbaum, and R. Yehuda. 2014. Expression Profiling Associates Blood and Brain Glucocorticoid Receptor Signaling with Trauma-Related Individual Differences in Both Sexes. *PNAS* **111**:13529–13534. [7]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Davey Smith, G., and G. Hemani. 2014. Mendelian Randomization: Genetic Anchors for Causal Inference in Epidemiological Studies. *Hum. Mol. Genet.* **23**:R89–98. [2]

Daviaud, N., R. H. Friedel, and H. Zou. 2018. Vascularization and Engraftment of Transplanted Human Cerebral Organoids in Mouse Cortex. *eNeuro* **5**:0219–182018. [5]

Davidson, B. L., G. Gao, E. Berry-Kravis, et al. 2022. Gene-Based Therapeutics for Rare Genetic Neurodevelopmental Psychiatric Disorders. *Mol. Ther.* **30**:2416–2428. [6]

Davidsson, M., G. Wang, P. Aldrin-Kirk, et al. 2019. A Systematic Capsid Evolution Approach Performed *in Vivo* for the Design of AAV Vectors with Tailored Properties and Tropism. *PNAS* **116**:27053–27062. [6]

Davies, N. M., D. Gunnell, K. H. Thomas, et al. 2013. Physicians' Prescribing Preferences Were a Potential Instrument for Patients' Actual Prescriptions of Antidepressants. *J. Clin. Epidemiol.* **66**:1386–1396. [4]

Davies, R. W., A. M. Fiksinski, E. J. Breetvelt, et al. 2020. Using Common Genetic Variation to Examine Phenotypic Expression and Risk Prediction in 22q11.2 Deletion Syndrome. *Nat. Med.* **26**:1912–1918. [5, 12, 13]

Defelipe, J. 2011. The Evolution of the Brain, the Human Nature of Cortical Circuits, and Intellectual Creativity. *Front. Neuroanat.* **5**:29. [7]

de Klein, N., E. A. Tsai, M. Vochteloo, et al. 2023. Brain Expression Quantitative Trait Locus and Network Analyses Reveal Downstream Effects and Putative Drivers for Brain-Related Diseases. *Nat. Genet.* **55**:377–388. [10]

de la Torre-Ubieta, L., J. L. Stein, H. Won, et al. 2018. The Dynamic Landscape of Open Chromatin during Human Cortical Neurogenesis. *Cell* **172**:289–304. [10]

de la Torre-Ubieta, L., H. Won, J. L. Stein, and D. H. Geschwind. 2016. Advancing the Understanding of Autism Disease Mechanisms through Genetics. *Nat. Med.* **22**:345–361. [7]

de Leeuw, C., N. Y. A. Sey, D. Posthuma, and H. Won. 2020. *Preprint*: A Response to Yurko et al.: H-MAGMA, Inheriting a Shaky Statistical Foundation, Yields Excess False Positives. *bioRxiv* 310722 [10]

DeLisi, L. E., and H. Bertisch. 2006. A Preliminary Comparison of the Hopes of Researchers, Clinicians, and Families for the Future Ethical Use of Genetic Findings on Schizophrenia. *Am. J. Med. Genet. B Neuropsychiatr. Genet.* **141B**:110–115. [15]

Demange, P. A., M. Malanchini, T. T. Mallard, et al. 2021. Investigating the Genetic Architecture of Noncognitive Skills Using GWAS-by-Subtraction. *Nat. Genet.* **53**:35–44. [2]

Demontis, D., R. K. Walters, J. Martin, et al. 2019. Discovery of the First Genome-Wide Significant Risk Loci for Attention Deficit/Hyperactivity Disorder. *Nat. Genet.* **51**:63–75. [2, 3]

Demro, C., B. A. Mueller, J. S. Kent, et al. 2021. The Psychosis Human Connectome Project: An Overview. *Neuroimage* **241**:118439. [8]

Deng, C., S. Whalen, M. Steyert, et al. 2023. *Preprint*: Massively Parallel Characterization of Psychiatric Disorder-Associated and Cell-Type-Specific Regulatory Elements in the Developing Human Cortex. *bioRxiv* 2023.2002.2015.528663. [10]

De Rubeis, S., X. He, A. P. Goldberg, et al. 2014. Synaptic, Transcriptional and Chromatin Genes Disrupted in Autism. *Nature* **515**:209–215. [3, 5, 7, 11]

Deverman, B. E., P. L. Pravdo, B. P. Simpson, et al. 2016. Cre-Dependent Selection Yields AAV Variants for Widespread Gene Transfer to the Adult Brain. *Nat. Biotechnol.* **34**:204–209. [6]

Devlin, B., N. Melhem, and K. Roeder. 2011. Do Common Variants Play a Role in Risk for Autism? Evidence and Theoretical Musings. *Brain Res.* **1380**:78–84. [3]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Dezonne, R. S., R. C. Sartore, J. M. Nascimento, et al. 2017. Derivation of Functional Human Astrocytes from Cerebral Organoids. *Sci. Rep.* **7**:45091. [7]

Diefenbach, M. A., and H. Leventhal. 2010. The Common-Sense Model of Illness Representation: Theoretical and Practical Considerations. *J. Soc. Distress Homeless* **5**:11–38. [15]

Dillon, A., J. Austin, K. McGhee, and M. Watson. 2022. The Impact of a "Psychiatric Genetics for Genetic Counselors" Workshop on Genetic Counselor Attendees: An Exploratory Study. *Am. J. Med. Genet. B Neuropsychiatr. Genet.* **189**:108–115. [12, 15]

Ding, Y., K. Hou, K. S. Burch, et al. 2022. Large Uncertainty in Individual Polygenic Risk Score Estimation Impacts PRS-Based Risk Stratification. *Nat. Genet.* **54**:30–39. [13]

Dixit, A., O. Parnas, B. Li, et al. 2016. Perturb-Seq: Dissecting Molecular Circuits with Scalable Single-Cell RNA Profiling of Pooled Genetic Screens. *Cell* **167**:1853–1866. [7]

Doan, R. N., E. T. Lim, S. De Rubeis, et al. 2019. Recessive Gene Disruptions in Autism Spectrum Disorder. *Nat. Genet.* **51**:1092–1098. [3]

Dobrindt, K., H. Zhang, D. Das, et al. 2021. Publicly Available hiPSC Lines with Extreme Polygenic Risk Scores for Modeling Schizophrenia. *Complex Psychiatry* **6**:68–82. [8, 9]

Dölen, G., E. Osterweil, B. S. Rao, et al. 2007. Correction of Fragile X Syndrome in Mice. *Neuron* **56**:955–962. [5]

Domingue, B. W., L. Duncan, A. Harrati, and D. W. Belsky. 2021a. Short-Term Mental Health Sequelae of Bereavement Predict Long-Term Physical Health Decline in Older Adults: U.S. Health and Retirement Study Analysis. *J. Gerontol. B Psychol. Sci. Soc. Sci.* **76**:1231–1240. [4]

Domingue, B. W., K. Kanopka, S. Trejo, M. Rhemtulla, and E. M. Tucker-Drob. 2021b. *Preprint*: Ubiquitous Bias & False Discovery Due to Model Misspecification in Analysis of Statistical Interactions: The Role of the Outcome's Distribution and Metric Properties. *PsyArXiv* 1–21. [4]

Dominguez, A. A., W. A. Lim, and L. S. Qi. 2016. Beyond Editing: Repurposing CRISPR-Cas9 for Precision Genome Regulation and Interrogation. *Nat. Rev. Mol. Cell Biol.* **17**:5–15. [5]

Donsante, A., D. G. Miller, Y. Li, et al. 2007. AAV Vector Integration Sites in Mouse Hepatocellular Carcinoma. *Science* **317**:477. [6]

Douard, E., A. Zeribi, C. Schramm, et al. 2021. Effect Sizes of Deletions and Duplications on Autism Risk across the Genome. *Am. J. Psychiatry* **178**:87–98. [1]

Doyle Jr., J. J. 2008. Child Protection and Adult Crime: Using Investigator Assignment to Estimate Causal Effects of Foster Care. *J. Polit. Econ.* **116**:746–770. [4]

Dworkin, J. D., K. A. Linn, E. G. Teich, et al. 2020. The Extent and Drivers of Gender Imbalance in Neuroscience Reference Lists. *Nat. Neurosci.* **23**:918–926. [15]

Eichler, F., C. Duncan, P. L. Musolino, et al. 2017. Hematopoietic Stem-Cell Gene Therapy for Cerebral Adrenoleukodystrophy. *N. Engl. J. Med.* **377**:1630–1638. [6]

Eichmüller, O. L., N. S. Corsini, Á. Vértesy, et al. 2022. Amplification of Human Interneuron Progenitors Promotes Brain Tumors and Neurological Defects. *Science* **375**:eabf5546. [5]

Eisman, A. B., A. M. Kilbourne, A. R. Dopp, L. Saldana, and D. Eisenberg. 2020. Economic Evaluation in Implementation Science: Making the Business Case for Implementation Strategies. *Psychiatry Res.* **283**:112433. [13]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Ellenbroek, B., and J. Youn. 2016. Rodent Models in Neuroscience Research: Is It a Rat Race? *Dis. Model Mech.* **9**:1079–1087. [5]

Elliott, J., B. Bodinier, T. A. Bond, et al. 2020. Predictive Accuracy of a Polygenic Risk Score-Enhanced Prediction Model vs a Clinical Risk Score for Coronary Artery Disease. *JAMA* **323**:636–645. [13]

Ellison, S. M., A. Liao, S. Wood, et al. 2019. Pre-Clinical Safety and Efficacy of Lentiviral Vector-Mediated *ex Vivo* Stem Cell Gene Therapy for the Treatment of Mucopolysaccharidosis IIIA. *Mol. Ther. Methods Clin. Dev.* **13**:399–413. [6]

Engle, S. J., L. Blaha, and R. J. Kleiman. 2018. Best Practices for Translational Disease Modeling Using Human iPSC-Derived Neurons. *Neuron* **100**:783–797. [6]

Erickson, J. A., L. Kuzmich, K. E. Ormond, et al. 2014. Genetic Testing of Children for Predisposition to Mood Disorders: Anticipating the Clinical Issues. *J. Genet. Counsel.* **23**:566–577. [15]

Escamilla, C. O., I. Filonova, A. K. Walker, et al. 2017. *Kctd13* Deletion Reduces Synaptic Transmission via Increased RhoA. *Nature* **551**:227–231. [5]

Etherton, M. R., C. A. Blaiss, C. M. Powell, and T. C. Sudhof. 2009. Mouse Neurexin-1α Deletion Causes Correlated Electrophysiological and Behavioral Changes Consistent with Cognitive Impairments. *PNAS* **106**:17998–18003. [7]

Faden, J., and L. Citrome. 2020. Intravenous Brexanolone for Postpartum Depression: What It Is, How Well Does It Work, and Will It Be Used? *Ther. Adv. Psychopharmacol.* **10**:2045125320968658. [5]

Fagiolini, A., and D. J. Kupfer. 2003. Is Treatment-Resistant Depression a Unique Subtype of Depression? *Biol. Psychiatry* **53**:640–648. [2]

Fahed, A. C., A. A. Philippakis, and A. V. Khera. 2022. The Potential of Polygenic Scores to Improve Cost and Efficiency of Clinical Trials. *Nat. Commun.* **13**:2922. [13]

Fahed, A. C., M. Wang, J. R. Homburger, et al. 2020. Polygenic Background Modifies Penetrance of Monogenic Variants for Tier 1 Genomic Conditions. *Nat. Commun.* **11**:3635. [9, 13]

Falconer, D. S. 1965. The Inheritance of Liability to Certain Diseases, Estimated from the Incidence among Relatives. *Ann. Hum. Health* **29**:51–76. [9]

Fallesen, P., N. Emanuel, and C. Wildeman. 2014. Cumulative Risks of Foster Care Placement for Danish Children. *PLOS ONE* **9**:e109207. [4]

Fanelli, G., K. Domschke, A. Minelli, et al. 2022. A Meta-Analysis of Polygenic Risk Scores for Mood Disorders, Neuroticism, and Schizophrenia in Antidepressant Response. *Eur. Neuropsychopharmacol.* **55**:86–95. [13]

Farrell, M. S., T. Werge, P. Sklar, et al. 2015. Evaluating Historical Candidate Genes for Schizophrenia. *Mol. Psychiatry* **20**:555–562. [7]

Fatumo, S., T. Chikowore, M. Ayub, A. R. Martin, and K. Kuchenbaecker. 2022. A Roadmap to Increase Diversity in Genomic Studies. *Nat. Med.* **28**:243–250. [3]

Feinberg, I. 1982. Schizophrenia: Caused by a Fault in Programmed Synaptic Elimination during Adolescence? *J. Psychiatr. Res.* **17**:319–334. [11]

Fergusson, D., S. Doucette, K. C. Glass, et al. 2005. Association between Suicide Attempts and Selective Serotonin Reuptake Inhibitors: Systematic Review of Randomised Controlled Trials. *BMJ* **330**:396. [4]

Fernandes, G., P. K. Mishra, M. S. Nawaz, et al. 2021. Correction of Amygdalar Dysfunction in a Rat Model of Fragile X Syndrome. *Cell Rep.* **37**:109805. [5]

Ferrat, L. A., K. Vehik, S. A. Sharp, et al. 2020. A Combined Risk Score Enhances Prediction of Type 1 Diabetes among Susceptible Children. *Nat. Med.* **26**:1247–1255. [13]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Finkel, R. S., E. Mercuri, B. T. Darras, et al. 2017. Nusinersen versus Sham Control in Infantile-Onset Spinal Muscular Atrophy. *N. Engl. J. Med.* **377**:1723–1732. [5, 6]

Finn, C. T., and J. W. Smoller. 2006. Genetic Counseling in Psychiatry. *Harv. Rev. Psychiatry* **14**:109–121. [15]

Finn, C. T., M. A. Wilcox, B. R. Korf, et al. 2005. Psychiatric Genetics: A Survey of Psychiatrists' Knowledge, Opinions, and Practice Patterns. *J. Clin. Psychiatry* **66**:821–830. [15]

Finucane, B. M., D. H. Ledbetter, and J. A. Vorstman. 2021. Diagnostic Genetic Testing for Neurodevelopmental Psychiatric Disorders: Closing the Gap between Recommendation and Clinical Implementation. *Curr. Opin. Genet. Dev.* **68**:1–8. [12]

Finucane, B. M., S. M. Myers, C. L. Martin, and D. H. Ledbetter. 2020. Long Overdue: Including Adults with Brain Disorders in Precision Health Initiatives. *Curr. Opin. Genet. Dev.* **65**:47–52. [1, 12]

Finucane, B. M., M. T. Oetjens, A. Johns, et al. 2022. Medical Manifestations and Health Care Utilization among Adult Mycode Participants with Neurodevelopmental Psychiatric Copy Number Variants. *Genet. Med.* **24**:703–711. [12]

Finucane, H. K., B. Bulik-Sullivan, A. Gusev, et al. 2015. Partitioning Heritability by Functional Annotation Using Genome-Wide Association Summary Statistics. *Nat. Genet.* **47**:1228–1235. [11]

Finucane, H. K., Y. A. Reshef, V. Anttila, et al. 2018. Heritability Enrichment of Specifically Expressed Genes Identifies Disease-Relevant Tissues and Cell Types. *Nat. Genet.* **50**:621–629. [11]

Fitzjohn, S. M., M. J. Palmer, J. E. May, et al. 2001. A Characterisation of Long-Term Depression Induced by Metabotropic Glutamate Receptor Activation in the Rat Hippocampus *in vitro*. *J. Physiol.* **537**:421–430. [5]

Flaherty, E., S. Zhu, N. Barretto, et al. 2019. Neuronal Impact of Patient-Specific Aberrant NRXN1α Splicing. *Nat. Genet.* **51**:1679–1690. [7, 11]

Flint, J., and K. S. Kendler. 2014. The Genetics of Major Depression. *Neuron* **81**:484–503. [7]

Folkersen, L., O. Pain, A. Ingason, et al. 2020. Impute.Me: An Open-Source, Non-Profit Tool for Using Data from Direct-to-Consumer Genetic Testing to Calculate and Interpret Polygenic Risk Scores. *Front. Genet.* **11**:578. [13, 15]

Forrest, M. P., H. Zhang, W. Moy, et al. 2017. Open Chromatin Profiling in hiPSC-Derived Neurons Prioritizes Functional Noncoding Psychiatric Risk Variants and Highlights Neurodevelopmental Loci. *Cell Stem Cell* **21**:305–318. [7]

Foust, K. D., E. Nurre, C. L. Montgomery, et al. 2009. Intravascular AAV9 Preferentially Targets Neonatal Neurons and Adult Astrocytes. *Nat. Biotechnol.* **27**:59–65. [6]

Frances, A. J. 2013. Last Plea to DSM 5: Save Grief from the Drug Companies: Let Us Respect the Dignity of Love and Loss. *Psychology Today* Jan. 3, 2013. [4]

Franklin, J. C., J. D. Ribeiro, K. R. Fox, et al. 2017. Risk Factors for Suicidal Thoughts and Behaviors: A Meta-Analysis of 50 Years of Research. *Psychol. Bull.* **143**:187–232. [14]

Franz, D. N., J. Leonard, C. Tudor, et al. 2006. Rapamycin Causes Regression of Astrocytomas in Tuberous Sclerosis Complex. *Ann. Neurol.* **59**:490–498. [6]

French, J. A., J. A. Lawson, Z. Yapici, et al. 2016. Adjunctive Everolimus Therapy for Treatment-Resistant Focal-Onset Seizures Associated with Tuberous Sclerosis (Exist-3): A Phase 3, Randomised, Double-Blind, Placebo-Controlled Study. *Lancet* **388**:2153–2163. [6]

Fried, E. I. 2015. Problematic Assumptions Have Slowed Down Depression Research: Why Symptoms, Not Syndromes Are the Way Forward. *Front. Psychol.* **6**:309. [2]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Fried, E. I. 2017. The 52 Symptoms of Major Depression: Lack of Content Overlap among Seven Common Depression Scales. *J. Affect. Disord.* **208**:191–197. [2]

Frisell, T. 2021. Invited Commentary: Sibling-Comparison Designs, Are They Worth the Effort? *Am. J. Epidemiol.* **190**:738–741. [4]

Fromer, M., A. J. Pocklington, D. H. Kavanagh, et al. 2014. *De Novo* Mutations in Schizophrenia Implicate Synaptic Networks. *Nature* **506**:179–184. [7, 11]

Fromer, M., P. Roussos, S. K. Sieberts, et al. 2016. Gene Expression Elucidates Functional Impact of Polygenic Risk for Schizophrenia. *Nat. Neurosci.* **19**:1442–1453. [3, 8, 11]

Fry, A., T. J. Littlejohns, C. Sudlow, et al. 2017. Comparison of Sociodemographic and Health-Related Characteristics of UK Biobank Participants with Those of the General Population. *Am. J. Epidemiol.* **186**:1026–1034. [2]

Fu, J. M., F. K. Satterstrom, M. Peng, et al. 2022. Rare Coding Variation Provides Insight into the Genetic Architecture and Phenotypic Context of Autism. *Nat. Genet.* **54**:1320–1331. [3, 5, 6]

Fulco, C. P., J. Nasser, T. R. Jones, et al. 2019. Activity-by-Contact Model of Enhancer-Promoter Regulation from Thousands of CRISPR Perturbations. *Nat. Genet.* **51**:1664–1669. [7, 8, 10]

Fumagalli, F., V. Calbi, M. G. Natali Sora, et al. 2022. Lentiviral Haematopoietic Stem-Cell Gene Therapy for Early-Onset Metachromatic Leukodystrophy: Long-Term Results from a Non-Randomised, Open-Label, Phase 1/2 Trial and Expanded Access. *Lancet* **399**:372–383. [6]

Fusar-Poli, P., S. Borgwardt, A. Bechdolf, et al. 2013. The Psychosis High-Risk State: A Comprehensive State-of-the-Art Review. *JAMA Psychiatry* **70**:107–120. [13]

Gadalla, K. K., M. E. Bailey, R. C. Spike, et al. 2013. Improved Survival and Reduced Phenotypic Severity Following AAV9/MECP2 Gene Transfer to Neonatal and Juvenile Male Mecp2 Knockout Mice. *Mol. Ther.* **21**:18–30. [6]

Gallois, A., J. Mefford, A. Ko, et al. 2019. A Comprehensive Study of Metabolite Genetics Reveals Strong Pleiotropy and Heterogeneity across Time and Context. *Nat. Commun.* **10**:4788. [2]

Gandal, M. J., J. R. Haney, N. N. Parikshak, et al. 2018a. Shared Molecular Neuropathology across Major Psychiatric Disorders Parallels Polygenic Overlap. *Science* **359**:693–697. [2, 11]

Gandal, M. J., V. Leppa, H. Won, N. N. Parikshak, and D. H. Geschwind. 2016. The Road to Precision Psychiatry: Translating Genetics into Disease Mechanisms. *Nat. Neurosci.* **19**:1397–1407. [11]

Gandal, M. J., P. Zhang, E. Hadjimichael, et al. 2018b. Transcriptome-Wide Isoform-Level Dysregulation in ASD, Schizophrenia, and Bipolar Disorder. *Science* **362**:eaat8127. [10, 11]

Ganesalingam, J., and R. Bowser. 2010. The Application of Biomarkers in Clinical Trials for Motor Neuron Disease. *Biomark. Med.* **4**:281–297. [5]

Gariepy, G., H. Honkaniemi, and A. Quesnel-Vallee. 2016. Social Support and Protection from Depression: Systematic Review of Current Findings in Western Countries. *Br. J. Psychiatry* **209**:284–293. [13]

Garrido, M. M., H. G. Prigerson, S. Neupane, et al. 2017. Mental Illness and Mental Healthcare Receipt among Hospitalized Veterans with Serious Physical Illnesses. *J. Palliat. Med.* **20**:247–252. [2]

Garrido-Martín, D., B. Borsari, M. Calvo, F. Reverter, and R. Guigó. 2021. Identification and Analysis of Splicing Quantitative Trait Loci across Multiple Tissues in the Human Genome. *Nat. Commun.* **12**:727. [11]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Gasperini, M., A. J. Hill, J. L. McFaline-Figueroa, et al. 2019. A Genome-Wide Framework for Mapping Gene Regulation via Cellular Genetic Screens. *Cell* **176**:1516. [7, 8]

Gaugler, T., L. Klei, S. J. Sanders, et al. 2014. Most Genetic Risk for Autism Resides with Common Variation. *Nat. Genet.* **46**:881–885. [6]

Gaynes, B. N., D. Warden, M. H. Trivedi, et al. 2009. What Did Star*D Teach Us? Results from a Large-Scale, Practical, Clinical Trial for Patients with Depression. *Psychiatr. Serv.* **60**:1439–1445. [13]

GBD 2016 Disease and Injury Incidence and Prevalence Collaborators. 2017. Global, Regional, and National Incidence, Prevalence, and Years Lived with Disability for 328 Diseases and Injuries for 195 Countries, 1990–2016: A Systematic Analysis for the Global Burden of Disease Study 2016. *Lancet* **390**:1211–1259. [7]

Ge, T., A. Patki, V. Srinivasasainagendra, et al. 2021. Development and Validation of a Trans-Ancestry Polygenic Risk Score for Type 2 Diabetes in Diverse Populations. *Genome Med.* **14**:70. [13]

Geller, E., J. Gockley, D. Emera, et al. 2019. *Preprint*: Massively Parallel Disruption of Enhancers Active during Human Corticogenesis. *bioRxiv* 852673. [7, 8]

Gentner, B., F. Tucci, S. Galimberti, et al. 2021. Hematopoietic Stem- and Progenitor-Cell Gene Therapy for Hurler Syndrome. *N. Engl. J. Med.* **385**:1929–1940. [6]

Germain, P. L., and G. Testa. 2017. Taming Human Genetic Variability: Transcriptomic Meta-Analysis Guides the Experimental Design and Interpretation of iPSC-Based Disease Modeling. *Stem Cell Rep.* **8**:1784–1796. [6]

Gerrard, S., A. Inglis, E. Morris, and J. Austin. 2020. Relationships between Patient- and Session-Related Variables and Outcomes of Psychiatric Genetic Counseling. *Eur. J. Hum. Genet.* **28**:907–914. [12, 15]

Gershon, E. S., and N. Alliey-Rodriguez. 2013. New Ethical Issues for Genetic Counseling in Common Mental Disorders. *Am. J. Psychiatry* **170**:968–976. [15]

Giannakopoulou, O., K. Lin, X. Meng, et al. 2021. The Genetic Architecture of Depression in Individuals of East Asian Ancestry: A Genome-Wide Association Study. *JAMA Psychiatry* **78**:1258–1269. [2, 3]

Gidaro, T., and L. Servais. 2019. Nusinersen Treatment of Spinal Muscular Atrophy: Current Knowledge and Existing Gaps. *Dev. Med. Child Neurol.* **61**:19–24. [5]

Gilman, S. R., J. Chang, B. Xu, et al. 2012. Diverse Types of Genetic Variation Converge on Functional Gene Networks Involved in Schizophrenia. *Nat. Neurosci.* **15**:1723–1728. [11]

Girdhar, K., G. E. Hoffman, Y. Jiang, et al. 2018. Cell-Specific Histone Modification Maps in the Human Frontal Lobe Link Schizophrenia Risk to the Neuronal Epigenome. *Nat. Neurosci.* **21**:1126–1136. [11]

Glessner, J. T., K. Wang, G. Cai, et al. 2009. Autism Genome-Wide Copy Number Variation Reveals Ubiquitin and Neuronal Genes. *Nature* **459**:569–573. [11]

Golan, D., E. S. Lander, and S. Rosset. 2014. Measuring Missing Heritability: Inferring the Contribution of Common Variants. *PNAS* **111**:E5272–E5281. [4]

Golzio, C., J. Willer, M. E. Talkowski, et al. 2012. *KCTD13* Is a Major Driver of Mirrored Neuroanatomical Phenotypes of the 16p11.2 Copy Number Variant. *Nature* **485**:363–367. [5]

Gong, S., M. Doughty, C. R. Harbaugh, et al. 2007. Targeting Cre Recombinase to Specific Neuron Populations with Bacterial Artificial Chromosome Constructs. *J. Neurosci.* **27**:9817–9823. [7]

Goodman, R. 1997. The Strengths and Difficulties Questionnaire: A Research Note. *J. Child Psychol. Psychiatry* **38**:581–586. [2]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Goorden, S. M., G. M. van Woerden, L. van der Weerd, J. P. Cheadle, and Y. Elgersma. 2007. Cognitive Deficits in Tsc1$^{+/-}$ Mice in the Absence of Cerebral Lesions and Seizures. *Ann. Neurol.* **62**:648–655. [7]

Gorzynski, J. E., S. D. Goenka, K. Shafin, et al. 2022. Ultrarapid Nanopore Genome Sequencing in a Critical Care Setting. *N. Engl. J. Med.* **386**:700–702. [1]

Govek, E. E., M. E. Hatten, and L. Van Aelst. 2011. The Role of Rho GTPase Proteins in CNS Neuronal Migration. *Dev. Neurobiol.* **71**:528–553. [5]

Grabb, M. C., and W. Z. Potter. 2022. Central Nervous System Trial Failures: Using the Fragile X Syndrome-mGluR5 Drug Target to Highlight the Complexities of Translating Preclinical Discoveries into Human Trials. *J. Clin. Psychopharmacol.* **42**:234–237. [5]

Graham, D. B., and R. J. Xavier. 2020. Pathway Paradigms Revealed from the Genetics of Inflammatory Bowel Disease. *Nature* **578**:527–539. [9]

Grasby, K. L., N. Jahanshad, J. N. Painter, et al. 2020. The Genetic Architecture of the Human Cerebral Cortex. *Science* **367**:eaay6690. [8]

Gray, S. J., V. Matagne, L. Bachaboina, et al. 2011. Preclinical Differences of Intravascular AAV9 Delivery to Neurons and Glia: A Comparative Study of Adult Mice and Nonhuman Primates. *Mol. Ther.* **19**:1058–1069. [6]

Green, R. C., J. S. Roberts, L. A. Cupples, et al. 2009. Disclosure of APOE Genotype for Risk of Alzheimer's Disease. *N. Engl. J. Med.* **361**:245–254. [14, 15]

Gregory, G., K. Das Gupta, B. Meiser, et al. 2022. Polygenic Risk in Familial Breast Cancer: Changing the Dynamics of Communicating Genetic Risk. *J. Genet. Couns.* **31**:120–129. [13]

Griesemer, D., J. R. Xue, S. K. Reilly, et al. 2021. Genome-Wide Functional Screen of 3'UTR Variants Uncovers Causal Variants for Human Disease and Evolution. *Cell* **184**:5247–5260. [8]

Grob, R. 2019. Qualitative Research on Expanded Prenatal and Newborn Screening: Robust but Marginalized. *Hastings Cent. Rep.* **49**:S72–S81. [14]

Groenendyk, J. W., P. Greenland, and S. S. Khan. 2022. Incremental Value of Polygenic Risk Scores in Primary Prevention of Coronary Heart Disease: A Review. *JAMA Intern. Med.* **182**:1082–1088. [13]

Grotzinger, A. D., T. T. Mallard, W. A. Akingbuwa, et al. 2022. Genetic Architecture of 11 Major Psychiatric Disorders at Biobehavioral, Functional Genomic and Molecular Genetic Levels of Analysis. *Nat. Genet.* **54**:548–559. [2]

Grotzinger, A. D., M. Rhemtulla, R. de Vlaming, et al. 2019. Genomic Structural Equation Modelling Provides Insights into the Multivariate Genetic Architecture of Complex Traits. *Nat. Hum. Behav.* **3**:513–525. [2]

Grove, J., S. Ripke, T. D. Als, et al. 2019. Identification of Common Genetic Risk Variants for Autism Spectrum Disorder. *Nat. Genet.* **51**:431–444. [3, 7, 11]

GTEx Consortium. 2017. Genetic Effects on Gene Expression across Human Tissues. *Nature* **550**:204–213. [3]

———. 2020. The GTEx Consortium Atlas of Genetic Regulatory Effects across Human Tissues. *Science* **369**:1318–1330. [3, 8, 10, 11]

Gudmundsson, S., M. Singer-Berk, N. A. Watts, et al. 2022. Variant Interpretation Using Population Databases: Lessons from Gnomad. *Hum. Mutat.* **43**:1012–1030. [3]

Gulinello, M., H. A. Mitchell, Q. Chang, et al. 2019. Rigor and Reproducibility in Rodent Behavioral Research. *Neurobiol. Learn. Mem.* **165**:106780. [5]

Gulsuner, S., T. Walsh, A. C. Watts, et al. 2013. Spatial and Temporal Mapping of *de Novo* Mutations in Schizophrenia to a Fetal Prefrontal Cortical Network. *Cell* **154**:518–529. [7, 11]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Gunnell, D., J. Saperia, and D. Ashby. 2005. Selective Serotonin Reuptake Inhibitors (SSRIs) and Suicide in Adults: Meta-Analysis of Drug Company Data from Placebo Controlled, Randomised Controlled Trials Submitted to the MHRA's Safety Review. *BMJ* **330**:385. [4]

Gupta, A., G. de Bruyn, S. Tousseyn, et al. 2020. Epilepsy and Neurodevelopmental Comorbidities in Tuberous Sclerosis Complex: A Natural History Study. *Pediatr. Neurol.* **106**:10–16. [5]

Guy, J., J. Gan, J. Selfridge, S. Cobb, and A. Bird. 2007. Reversal of Neurological Defects in a Mouse Model of Rett Syndrome. *Science* **315**:1143–1147. [5]

Haaker, J., S. Maren, M. Andreatta, et al. 2019. Making Translation Work: Harmonizing Cross-Species Methodology in the Behavioural Neuroscience of Pavlovian Fear Conditioning. *Neurosci. Biobehav. Rev.* **107**:329–345. [2]

Hamilton, J. G., and M. E. Robson. 2019. Psychosocial Effects of Multigene Panel Testing in the Context of Cancer Genomics. *Hastings Cent. Rep.* **49**:S44–S52. [14]

Han, S. K., D. Kim, H. Lee, I. Kim, and S. Kim. 2018. Divergence of Noncoding Regulatory Elements Explains Gene-Phenotype Differences between Human and Mouse Orthologous Genes. *Mol. Biol. Evol.* **35**:1653–1667. [8]

Haney, J. R., B. Wamsley, G. T. Chen, et al. 2020. *Preprint*: Broad Transcriptomic Dysregulation across the Cerebral Cortex in ASD. *bioRxiv* 423129. [11]

Hannon, E., H. Spiers, J. Viana, et al. 2016. Methylation QTLs in the Developing Brain and Their Enrichment in Schizophrenia Risk Loci. *Nat. Neurosci.* **19**:48–54. [11]

Hansen, B. T., K. M. Sønderskov, I. Hageman, P. T. Dinesen, and S. D. Østergaard. 2017. Daylight Savings Time Transitions and the Incidence Rate of Unipolar Depressive Episodes. *Epidemiology* **28**:346–353. [4]

Hansen, D. V., J. H. Lui, P. R. Parker, and A. R. Kriegstein. 2010. Neurogenic Radial Glia in the Outer Subventricular Zone of Human Neocortex. *Nature* **464**:554–561. [7]

Harrington, R., M. Rutter, and E. Fombonne. 1996. Developmental Pathways in Depression: Multiple Meanings, Antecedents, and Endpoints. *Dev. Psychopathol.* **8**:601–616. [2]

Hartl, C. L., G. Ramaswami, W. G. Pembroke, et al. 2021. Coexpression Network Architecture Reveals the Brain-Wide and Multiregional Basis of Disease Susceptibility. *Nat. Neurosci.* **24**:1313–1323. [11]

Harvey, S. B., S. Øverland, S. L. Hatch, et al. 2018. Exercise and the Prevention of Depression: Results of the Hunt Cohort Study. *Am. J. Psychiatry* **175**:28–36. [15]

Hawrylycz, M. J., E. S. Lein, A. L. Guillozet-Bongaarts, et al. 2012. An Anatomically Comprehensive Atlas of the Adult Human Brain Transcriptome. *Nature* **489**:391–399. [5, 11]

He, X., S. J. Sanders, L. Liu, et al. 2013. Integrated Model of *de Novo* and Inherited Genetic Variants Yields Greater Power to Identify Risk Genes. *PLOS Genet.* **9**:e1003671. [5]

Hebebrand, J., A. Scherag, B. G. Schimmelmann, and A. Hinney. 2010. Child and Adolescent Psychiatric Genetics. *Eur. Child Adolesc. Psychiatry* **19**:259–279. [6]

Herculano-Houzel, S., B. Mota, and R. Lent. 2006. Cellular Scaling Rules for Rodent Brains. *PNAS* **103**:12138–12143. [7]

Hernandez, L. M., M. Kim, G. D. Hoftman, et al. 2021. Transcriptomic Insight into the Polygenic Mechanisms Underlying Psychiatric Disorders. *Biol. Psychiatry* **89**:54–64. [11]

Herzeg, A., G. Almeida-Porada, R. A. Charo, et al. 2022. Prenatal Somatic Cell Gene Therapies: Charting a Path toward Clinical Applications (Proc. of the Cersi-FDA Meeting). *J. Clin. Pharmacol.* **62(Suppl 1)**:S36–S52. [5]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Hess, J. L., D. S. Tylee, M. Mattheisen, et al. 2021. A Polygenic Resilience Score Moderates the Genetic Risk for Schizophrenia. *Mol. Psychiatry* **26**:800–815. [7]

Hikishima, K., M. M. Quallo, Y. Komaki, et al. 2011. Population-Averaged Standard Template Brain Atlas for the Common Marmoset (*Callithrix jacchus*). *Neuroimage* **54**:2741–2749. [5]

Hill, R. S., and C. A. Walsh. 2005. Molecular Insights into Human Brain Evolution. *Nature* **437**:64–67. [7]

Hill, S. F., and M. H. Meisler. 2021. Antisense Oligonucleotide Therapy for Neurodevelopmental Disorders. *Dev. Neurosci.* **43**:247–252. [5]

Hill, W. D., S. P. Hagenaars, R. E. Marioni, et al. 2016. Molecular Genetic Contributions to Social Deprivation and Household Income in UK Biobank. *Curr. Biol.* **26**:3083–3089. [2]

Hilton, I. B., A. M. D'Ippolito, C. M. Vockley, et al. 2015. Epigenome Editing by a CRISPR-Cas9-Based Acetyltransferase Activates Genes from Promoters and Enhancers. *Nat. Biotechnol.* **33**:510–517. [7]

Hinderer, C., N. Katz, E. L. Buza, et al. 2018. Severe Toxicity in Nonhuman Primates and Piglets Following High-Dose Intravenous Administration of an Adeno-Associated Virus Vector Expressing Human Smn. *Hum. Gene Ther.* **29**:285–298. [6]

Hindy, G., K. G. Aragam, K. Ng, et al. 2020. Genome-Wide Polygenic Score, Clinical Risk Factors, and Long-Term Trajectories of Coronary Artery Disease. *Arterioscler. Thromb. Vasc. Biol.* **40**:2738–2746. [13]

Hinshaw, S. P., and A. Stier. 2008. Stigma as Related to Mental Disorders. *Clin. Psychol.* **4**:367. [15]

Hippman, C., A. Ringrose, A. Inglis, et al. 2016. A Pilot Randomized Clinical Trial Evaluating the Impact of Genetic Counseling for Serious Mental Illnesses. *J. Clin. Psychiatry* **77**:e190–e198. [15]

Hirschfeld, R. M. 2000. History and Evolution of the Monoamine Hypothesis of Depression. *J. Clin. Psychiatry* **61 Suppl 6**:4–6. [7]

Ho, S. M., B. J. Hartley, E. Flaherty, et al. 2017. Evaluating Synthetic Activation and Repression of Neuropsychiatric-Related Genes in hiPSC-Derived NPCs, Neurons, and Astrocytes. *Stem Cell Rep.* **9**:615–628. [7]

Hodge, R. D., T. E. Bakken, J. A. Miller, et al. 2019. Conserved Cell Types with Divergent Features in Human versus Mouse Cortex. *Nature* **573**:61–68. [7]

Hodgkinson, K. A., J. Murphy, S. O'Neill, L. Brzustowicz, and A. S. Bassett. 2001. Genetic Counselling for Schizophrenia in the Era of Molecular Genetics. *Can. J. Psychiatry* **46**:123–130. [15]

Hoek, H. W., A. S. Brown, and E. Susser. 1998. The Dutch Famine and Schizophrenia Spectrum Disorders. *Soc. Psychiatry Psychiatr. Epidemiol.* **33**:373–379. [4]

Hoffman, G. E., B. J. Hartley, E. Flaherty, et al. 2017. Transcriptional Signatures of Schizophrenia in hiPSC-Derived NPCs and Neurons Are Concordant with Post-Mortem Adult Brains. *Nat. Commun.* **8**:2225. [7]

Hoffman, G. E., N. Schrode, E. Flaherty, and K. J. Brennand. 2019. New Considerations for hiPSC-Based Models of Neuropsychiatric Disorders. *Mol. Psychiatry* **24**:49–66. [5]

Hoge, S. K., and P. S. Appelbaum. 2012. Ethics and Neuropsychiatric Genetics: A Review of Major Issues. *Int. J. Neuropsychopharmacol.* **15**:1547–1557. [14]

Holloway, A., and H. E. Watson. 2002. Role of Self-Efficacy and Behaviour Change. *Int. J. Nurs. Pract.* **8**:106–115. [15]

Holm, I. A., P. B. Agrawal, O. Ceyhan-Birsoy, et al. 2018. The BabySeq Project: Implementing Genomic Sequencing in Newborns. *BMC Pediatr.* **18**:225. [14]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Hook, V., K. J. Brennand, Y. Kim, et al. 2014. Human iPSC Neurons Display Activity-Dependent Neurotransmitter Secretion: Aberrant Catecholamine Levels in Schizophrenia Neurons. *Stem Cell Rep.* **3**:531–538. [7]

Hoop, J. G., L. W. Roberts, K. A. G. Hammond, and N. J. Cox. 2008. Psychiatrists' Attitudes, Knowledge, and Experience Regarding Genetics: A Preliminary Study. *Genet. Med.* **10**:439. [15]

Hoop, J. G., and G. Salva. 2010. The Current State of Genetics Training in Psychiatric Residency: Views of 235 US Educators and Trainees. *Acad. Psychiatry* **34**:109–114. [15]

Hordeaux, J., C. Hinderer, T. Goode, et al. 2018. Toxicology Study of Intra-Cisterna Magna Adeno-Associated Virus 9 Expressing Human Alpha-L-Iduronidase in Rhesus Macaques. *Mol. Ther. Methods Clin. Dev.* **10**:79–88. [6]

Horev, G., J. Ellegood, J. P. Lerch, et al. 2011. Dosage-Dependent Phenotypes in Models of 16p11.2 Lesions Found in Autism. *PNAS* **108**:17076–17081. [7]

Horváth, S., and K. Mirnics. 2015. Schizophrenia as a Disorder of Molecular Pathways. *Biol. Psychiatry* **77**:22–28. [11]

Hoskovec, J. M., R. L. Bennett, M. E. Carey, et al. 2018. Projecting the Supply and Demand for Certified Genetic Counselors: A Workforce Study. *J. Genet. Counsel.* **27**:16–20. [15]

Hou, L., M. D. Antion, D. Hu, et al. 2006. Dynamic Translational and Proteasomal Regulation of Fragile X Mental Retardation Protein Controls mGluR-Dependent Long-Term Depression. *Neuron* **51**:441–454. [5]

Hou, L., U. Heilbronner, F. Degenhardt, et al. 2016. Genetic Variants Associated with Response to Lithium Treatment in Bipolar Disorder: A Genome-Wide Association Study. *Lancet* **387**:1085–1093. [7]

Howard, D. M., M. J. Adams, T. K. Clarke, et al. 2019. Genome-Wide Meta-Analysis of Depression Identifies 102 Independent Variants and Highlights the Importance of the Prefrontal Brain Regions. *Nat. Neurosci.* **22**:343–352. [3, 7]

Howard, D. M., L. Folkersen, J. R. I. Coleman, et al. 2020. Genetic Stratification of Depression in UK Biobank. *Transl. Psychiatry* **10**:163. [2]

Howe, J. R., M. F. Bear, P. Golshani, et al. 2018. The Mouse as a Model for Neuropsychiatric Drug Development. *Curr. Biol.* **28**:R909–R914. [5, 6]

Hsu, P. D., E. S. Lander, and F. Zhang. 2014. Development and Applications of CRISPR-Cas9 for Genome Engineering. *Cell* **157**:1262–1278. [7]

Hu, B., H. Won, W. Mah, et al. 2021. Neuronal and Glial 3D Chromatin Architecture Informs the Cellular Etiology of Brain Disorders. *Nat. Commun.* **12**:3968. [10]

Hua, Y., K. Sahashi, G. Hung, et al. 2010. Antisense Correction of SMN2 Splicing in the CNS Rescues Necrosis in a Type III SMA Mouse Model. *Genes Dev.* **24**:1634–1644. [5]

Hua, Y., T. A. Vickers, B. F. Baker, C. F. Bennett, and A. R. Krainer. 2007. Enhancement of SMN2 Exon 7 Inclusion by Antisense Oligonucleotides Targeting the Exon. *PLOS Biol.* **5**:e73. [5]

Huan, T., J. Rong, C. Liu, et al. 2015. Genome-Wide Identification of microRNA Expression Quantitative Trait Loci. *Nat. Commun.* **6**:6601. [8]

Huang, S., K. Chaudhary, and L. X. Garmire. 2017. More Is Better: Recent Progress in Multi-Omics Data Integration Methods. *Front. Genet.* **8**:84. [11]

Huber, K. M., S. M. Gallagher, S. T. Warren, and M. F. Bear. 2002. Altered Synaptic Plasticity in a Mouse Model of Fragile X Mental Retardation. *PNAS* **99**:7746–7750. [5]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Hurson, A. N., P. Pal Choudhury, C. Gao, et al. 2022. Prospective Evaluation of a Breast-Cancer Risk Model Integrating Classical Risk Factors and Polygenic Risk in 15 Cohorts from Six Countries. *Int. J. Epidemiol.* **50**:1897–1911. [13]

Hyde, C. L., M. W. Nagle, C. Tian, et al. 2016. Identification of 15 Genetic Loci Associated with Risk of Major Depression in Individuals of European Descent. *Nat. Genet.* **48**:1031–1036. [2, 7]

Hyman, S. E. 2012. Revolution Stalled. *Sci. Transl. Med.* **4**:155cm111. [7]

Iakoucheva, L. M., A. R. Muotri, and J. Sebat. 2019. Getting to the Cores of Autism. *Cell* **178**:1287–1298. [1]

Iglewicz, A., K. Seay, S. D. Zetumer, and S. Zisook. 2013. The Removal of the Bereavement Exclusion in the DSM-5: Exploring the Evidence. *Curr. Psychiatry Rep.* **15**:413. [4]

Inglis, A., D. Koehn, B. McGillivray, S. E. Stewart, and J. Austin. 2015. Evaluating a Unique, Specialist Psychiatric Genetic Counseling Clinic: Uptake and Impact. *Clin. Genet.* **87**:218–224. [15]

Inoue, F., A. Kreimer, T. Ashuach, N. Ahituv, and N. Yosef. 2019. Identification and Massively Parallel Characterization of Regulatory Elements Driving Neural Induction. *Cell Stem Cell* **25**:713–727. [7]

International Common Disease Alliance. 2020. Recommendations and White Paper. https://drive.google.com/file/d/16SVJ5lbneN9hB9E03PZMhpescAN527HO/view. (accessed Jan. 18, 2023). [8]

International Consortium on Lithium Genetics, A. T. Amare, K. O. Schubert, et al. 2018. Association of Polygenic Score for Schizophrenia and HLA Antigen and Inflammation Genes with Response to Lithium in Bipolar Affective Disorder: A Genome-Wide Association Study. *JAMA Psychiatry* **75**:65–74. [13]

International Schizophrenia Consortium, S. M. Purcell, N. R. Wray, et al. 2009. Common Polygenic Variation Contributes to Risk of Schizophrenia and Bipolar Disorder. *Nature* **460**:748–752. [7]

Iossifov, I., B. J. O'Roak, S. J. Sanders, et al. 2014. The Contribution of *de Novo* Coding Mutations to Autism Spectrum Disorder. *Nature* **515**:216–221. [11]

Iossifov, I., M. Ronemus, D. Levy, et al. 2012. *De Novo* Gene Disruptions in Children on the Autistic Spectrum. *Neuron* **74**:285–299. [7, 11]

Iwanami, A., J. Yamane, H. Katoh, et al. 2005. Establishment of Graded Spinal Cord Injury Model in a Nonhuman Primate: The Common Marmoset. *J. Neurosci. Res.* **80**:172–181. [5]

Jacquemont, S., G. Huguet, M. Klein, et al. 2022. Genes to Mental Health (G2MH): A Framework to Map the Combined Effects of Rare and Common Variants on Dimensions of Cognition and Psychopathology. *Am. J. Psychiatry* **179**:189–203. [5]

Jaffe, A. E., Y. Gao, A. Deep-Soboslay, et al. 2016. Mapping DNA Methylation across Development, Genotype and Schizophrenia in the Human Frontal Cortex. *Nat. Neurosci.* **19**:40–47. [11]

Jaffe, A. E., D. J. Hoeppner, T. Saito, et al. 2020. Profiling Gene Expression in the Human Dentate Gyrus Granule Cell Layer Reveals Insights into Schizophrenia and Its Genetic Risk. *Nat. Neurosci.* **23**:510–519. [11]

Jaffe, A. E., R. E. Straub, J. H. Shin, et al. 2018. Developmental and Genetic Regulation of the Human Cortex Transcriptome Illuminate Schizophrenia Pathogenesis. *Nat. Neurosci.* **21**:1117–1125. [11]

Janssens, A. C. J. W. 2019. Proprietary Algorithms for Polygenic Risk: Protecting Scientific Innovation or Hiding the Lack of It? *Genes* **10**:448–447. [15]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Javierre, B. M., O. S. Burren, S. P. Wilder, et al. 2016. Lineage-Specific Genome Architecture Links Enhancers and Non-Coding Disease Variants to Target Gene Promoters. *Cell* **167**:1369–1384. [10]

Jehuda, R. B., Y. Shemer, and B. Ofer. 2018. Genome Editing in Induced Pluripotent Stem Cells Using CRISPR/Cas9. *Stem Cell Rev. Rep.* **14**:323–336. [5]

Jerber, J., D. D. Seaton, A. S. E. Cuomo, et al. 2021. Population-Scale Single-Cell RNA-Seq Profiling across Dopaminergic Neuron Differentiation. *Nat. Genet.* **53**:304–312. [7, 8]

Jermy, B. S., S. P. Hagenaars, K. P. Glanville, et al. 2022. Using Major Depression Polygenic Risk Scores to Explore the Depressive Symptom Continuum. *Psychol. Med.* **52**:149–158. [2]

Jia, P., X. Chen, A. H. Fanous, and Z. Zhao. 2018. Convergent Roles of *de Novo* Mutations and Common Variants in Schizophrenia in Tissue-Specific and Spatiotemporal Co-Expression Network. *Transl. Psychiatry* **8**:105. [7]

Jin, X., S. K. Simmons, A. Guo, et al. 2020. *In Vivo* Perturb-Seq Reveals Neuronal and Glial Abnormalities Associated with Autism Risk Genes. *Science* **370**:eaaz6063. [7, 10]

Johnston, J., and L. J. Matthews. 2022. Polygenic Embryo Testing: Understated Ethics, Unclear Utility. *Nat. Med.* **28**:446–448. [14]

Jonas, K. G., T. Lencz, K. Li, et al. 2019. Schizophrenia Polygenic Risk Score and 20-Year Course of Illness in Psychotic Disorders. *Transl. Psychiatry* **9**:300. [13]

Jørgensen, K. T., M. Bøg, M. Kabra, et al. 2021. Predicting Time to Relapse in Patients with Schizophrenia According to Patients' Relapse History: A Historical Cohort Study Using Real-World Data in Sweden. *BMC Psychiatry* **21**:634. [4]

Juanatey, A., L. Blanco-Garcia, and N. Tellez. 2018. Ocrelizumab: Its Efficacy and Safety in Multiple Sclerosis. *Rev. Neurol.* **66**:423–433. [5]

Judson, M. C., C. Shyng, J. M. Simon, et al. 2021. Dual-Isoform hUBE3A Gene Transfer Improves Behavioral and Seizure Outcomes in Angelman Syndrome Model Mice. *JCI Insight* **6**:e144712. [5]

Kadoshima, T., H. Sakaguchi, T. Nakano, et al. 2013. Self-Organization of Axial Polarity, inside-out Layer Pattern, and Species-Specific Progenitor Dynamics in Human Es Cell-Derived Neocortex. *PNAS* **110**:20284–20289. [7]

Kahn-Greene, E. T., D. B. Killgore, G. H. Kamimori, T. J. Balkin, and W. D. S. Killgore. 2007. The Effects of Sleep Deprivation on Symptoms of Psychopathology in Healthy Adults. *Sleep Med.* **8**:215–221. [4]

Kalb, F. M., V. Vincent, T. Herzog, and J. Austin. 2017. Genetic Counseling for Alcohol Addiction: Assessing Perceptions and Potential Utility in Individuals with Lived Experience and Their Family Members. *J. Genet. Counsel.* **26**:963–970. [15]

Kalman, J. L., L. M. Olde Loohuis, A. Vreeker, et al. 2021. Characterisation of Age and Polarity at Onset in Bipolar Disorder. *Br. J. Psychiatry* **219**:659–669. [2]

Kang, H. J., Y. I. Kawasawa, F. Cheng, et al. 2011a. Spatio-Temporal Transcriptome of the Human Brain. *Nature* **478**:483–489. [8, 10, 11]

Kaplanis, J., K. E. Samocha, L. Wiel, et al. 2020. Evidence for 28 Genetic Disorders Discovered by Combining Healthcare and Research Data. *Nature* **586**:757–762. [3]

Karamihalev, S., C. Flachskamm, N. Eren, M. Kimura, and A. Chen. 2019. Social Context and Dominance Status Contribute to Sleep Patterns and Quality in Groups of Freely-Moving Mice. *Sci. Rep.* **9**:15190. [8]

Karayiorgou, M., M. A. Morris, B. Morrow, et al. 1995. Schizophrenia Susceptibility Associated with Interstitial Deletions of Chromosome 22q11. *PNAS* **92**:7612–7616. [7]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Karczewski, K. J., L. C. Francioli, G. Tiao, et al. 2020. The Mutational Constraint Spectrum Quantified from Variation in 141,456 Humans. *Nature* **581**:434–443. [3, 5]

Katayama, Y., M. Nishiyama, H. Shoji, et al. 2016. CHD8 Haploinsufficiency Results in Autistic-Like Phenotypes in Mice. *Nature* **537**:675–679. [7]

Ke, S., J. Lai, T. Sun, et al. 2015. Healthy Young Minds: The Effects of a 1-Hour Classroom Workshop on Mental Illness Stigma in High School Students. *Comm. Ment. Health J.* **51**:329–337. [12]

Keinath, M. C., D. E. Prior, and T. W. Prior. 2021. Spinal Muscular Atrophy: Mutations, Testing, and Clinical Relevance. *Appl. Clin. Genet.* **14**:11–25. [5]

Keller, M. C. 2014. Gene × Environment Interaction Studies Have Not Properly Controlled for Potential Confounders: The Problem and the (Simple) Solution. *Biol. Psychiatry* **75**:18–24. [4]

Kelley, K. W., H. Nakao-Inoue, A. V. Molofsky, and M. C. Oldham. 2018. Variation among Intact Tissue Samples Reveals the Core Transcriptional Features of Human CNS Cell Classes. *Nat. Neurosci.* **21**:1171–1184. [11]

Kelley, K. W., and S. P. Pașca. 2022. Human Brain Organogenesis: Toward a Cellular Understanding of Development and Disease. *Cell* **185**:42–61. [5]

Kendall, K. M., E. Rees, M. Bracher-Smith, et al. 2019. Association of Rare Copy Number Variants with Risk of Depression. *JAMA Psychiatry* **76**:818–825. [3]

Kendler, K. S. 2021. The Prehistory of Psychiatric Genetics: 1780-1910. *Am. J. Psychiatry* **178**:490–508. [1]

Kendler, K. S., C. M. Bulik, J. Silberg, et al. 2000. Childhood Sexual Abuse and Adult Psychiatric and Substance Use Disorders in Women: An Epidemiological and Cotwin Control Analysis. *Arch. Gen. Psychiatry* **57**:953. [4]

Kendler, K. S., L. M. Karkowski, and C. A. Prescott. 1999. Causal Relationship between Stressful Life Events and the Onset of Major Depression. *Am. J. Psychiatry* **156**:837–841. [4]

Kendler, K. S., J. Myers, and S. Zisook. 2008. Does Bereavement-Related Major Depression Differ from Major Depression Associated with Other Stressful Life Events? *Am. J. Psychiatry* **165**:1449–1455. [4]

Kendler, K. S., H. Ohlsson, J. Sundquist, and K. Sundquist. 2021. The Rearing Environment and the Risk for Alcohol Use Disorder: A Swedish National High-Risk Home-Reared V. Adopted Co-Sibling Control Study. *Psychol. Med.* **51**:2370–2377. [4]

Kendler, K. S., and K. F. Schaffner. 2011. The Dopamine Hypothesis of Schizophrenia: An Historical and Philosophical Analysis. *Philos. Psychiatr. Psychol.* **18**:41–63 [7]

Kerin, M., and J. Marchini. 2020. Inferring Gene-by-Environment Interactions with a Bayesian Whole-Genome Regression Model. *Am. J. Hum. Genet.* **107**:698–713. [2]

Kessler, R. C., W. T. Chiu, O. Demler, K. R. Merikangas, and E. E. Walters. 2005. Prevalence, Severity, and Comorbidity of 12-Month DSM-IV Disorders in the National Comorbidity Survey Replication. *Arch. Gen. Psychiatry* **62**:617–627. [2]

Khan, A., M. C. Turchin, A. Patki, et al. 2022. Genome-Wide Polygenic Score to Predict Chronic Kidney Disease across Ancestries. *Nat. Med.* **28**:1412–1420. [13]

Khan, T. A., O. Revah, A. Gordon, et al. 2020. Neuronal Defects in a Human Cellular Model of 22q11.2 Deletion Syndrome. *Nat. Med.* **26**:1888–1898. [3, 7]

Khera, A. V., M. Chaffin, K. G. Aragam, et al. 2018. Genome-Wide Polygenic Scores for Common Diseases Identify Individuals with Risk Equivalent to Monogenic Mutations. *Nat. Genet.* **50**:1219–1224. [13]

Khera, A. V., C. A. Emdin, and S. Kathiresan. 2017. Genetic Risk, Lifestyle, and Coronary Artery Disease. *N. Engl. J. Med.* **376**:1194–1195. [13]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Kiiskinen, T., N. J. Mars, T. Palviainen, et al. 2020. Genomic Prediction of Alcohol-Related Morbidity and Mortality. *Transl. Psychiatry* **10**:23. [13]

Kilpinen, H., A. Goncalves, A. Leha, et al. 2017. Common Genetic Variation Drives Molecular Heterogeneity in Human iPSCs. *Nature* **546**:370–375. [8]

Kim, J., C. Hu, C. Moufawad El Achkar, et al. 2019. Patient-Customized Oligonucleotide Therapy for a Rare Genetic Disease. *N. Engl. J. Med.* **381**:1644–1652. [5, 6]

Kim, M., J. R. Haney, P. Zhang, et al. 2021a. Brain Gene Co-Expression Networks Link Complement Signaling with Convergent Synaptic Pathology in Schizophrenia. *Nat. Neurosci.* **24**:799–809. [11]

Kim, S. S., K. Jagadeesh, K. K. Dey, et al. 2021b. *Preprint*: Leveraging Single-Cell ATAC-Seq to Identify Disease-Critical Fetal and Adult Brain Cell Types. *bioRxiv* 445067. [11]

Kim-Hellmuth, S., F. Aguet, M. Oliva, et al. 2020. Cell Type-Specific Genetic Regulation of Gene Expression across Human Tissues. *Science* **369**:eaaz8528. [10]

Kinge, J. M., S. Øverland, M. Flatø, et al. 2021. Parental Income and Mental Disorders in Children and Adolescents: Prospective Register-Based Study. *Int. J. Epidemiol.* **50**:1615–1627. [4]

Kious, B. M., A. R. Docherty, J. R. Botkin, et al. 2021. Ethical and Public Health Implications of Genetic Testing for Suicide Risk: Family and Survivor Perspectives. *Genet. Med.* **23**:289–297. [14]

Kishi, N., K. Sato, E. Sasaki, and H. Okano. 2014. Common Marmoset as a New Model Animal for Neuroscience Research and Genome Editing Technology. *Dev. Growth Differ.* **56**:53–62. [5]

Kita, Y., H. Nishibe, Y. Wang, et al. 2021. Cellular-Resolution Gene Expression Profiling in the Neonatal Marmoset Brain Reveals Dynamic Species- and Region-Specific Differences. *PNAS* **118**:e2020125118. [5]

Kleiman, R. J., and M. D. Ehlers. 2016. Data Gaps Limit the Translational Potential of Preclinical Research. *Sci. Transl. Med.* **8**:320. [6]

Knevel, R., S. le Cessie, C. C. Terao, et al. 2020. Using Genetics to Prioritize Diagnoses for Rheumatology Outpatients with Inflammatory Arthritis. *Sci. Transl. Med.* **12**:eaay1548. [13]

Koblan, L. W., M. R. Erdos, L. B. Gordon, et al. 2021. Base Editor Treats Progeria in Mice. *Nature* **589**:608–614. [6]

Koene, L. M., E. Niggl, I. Wallaard, et al. 2021. Identifying the Temporal Electrophysiological and Molecular Changes That Contribute to TSC-Associated Epileptogenesis. *JCI Insight* **6**:e150120. [5]

Kolberg, L., N. Kerimov, H. Peterson, and K. Alasoo. 2020. Co-Expression Analysis Reveals Interpretable Gene Modules Controlled by Trans-Acting Genetic Variants. *eLife* **9**:e58705. [11]

Konermann, S., P. Lotfy, N. J. Brideau, et al. 2018. Transcriptome Engineering with RNA-Targeting Type VI-D CRISPR Effectors. *Cell* **173**:665–676. [7]

Kong, A., G. Thorleifsson, M. L. Frigge, et al. 2018. The Nature of Nurture: Effects of Parental Genotypes. *Science* **359**:424–428. [2]

Konjarski, M., G. Murray, V. V. Lee, and M. L. Jackson. 2018. Reciprocal Relationships between Daily Sleep and Mood: A Systematic Review of Naturalistic Prospective Studies. *Sleep Med. Rev.* **42**:47–58. [4]

Koopmans, F., P. van Nierop, M. Andres-Alonso, et al. 2019. SynGO: An Evidence-Based, Expert-Curated Knowledge Base for the Synapse. *Neuron* **103**:217–234. [8, 11]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Krebs, M. D., G. E. Themudo, M. E. Benros, et al. 2021. Associations between Patterns in Comorbid Diagnostic Trajectories of Individuals with Schizophrenia and Etiological Factors. *Nat. Commun.* **12**:6617. [2]

Krey, J. F., S. P. Paşca, A. Shcheglovitov, et al. 2013. Timothy Syndrome Is Associated with Activity-Dependent Dendritic Retraction in Rodent and Human Neurons. *Nat. Neurosci.* **16**:201–209. [5]

Krieg, A. M. 2006. Therapeutic Potential of Toll-Like Receptor 9 Activation. *Nat. Rev. Drug Discov.* **5**:471–484. [6]

Krishnan, A., R. Zhang, V. Yao, et al. 2016. Genome-Wide Prediction and Functional Characterization of the Genetic Basis of Autism Spectrum Disorder. *Nat. Neurosci.* **19**:1454–1462. [11]

Krueger, D. A., M. M. Care, K. Holland, et al. 2010. Everolimus for Subependymal Giant-Cell Astrocytomas in Tuberous Sclerosis. *N. Engl. J. Med.* **363**:1801–1811. [6]

Krueger, D. A., A. Sadhwani, A. W. Byars, et al. 2017. Everolimus for Treatment of Tuberous Sclerosis Complex-Assocaited Neuropsychiatric Disorders. *Ann. Clin. Transl. Neurol.* **4**:877–887. [6]

Ksinan, A. J., R. L. Smith, P. B. Barr, and A. T. Vazsonyi. 2022. The Associations of Polygenic Scores for Risky Behaviors and Parenting Behaviors with Adolescent Externalizing Problems. *Behav. Genet.* **52**:26–37. [13]

Kuchenbaecker, K. B., L. McGuffog, D. Barrowdale, et al. 2017. Evaluation of Polygenic Risk Scores for Breast and Ovarian Cancer Risk Prediction in BRCA1 and BRCA2 Mutation Carriers. *J. Natl. Cancer Inst.* **109**: [12]

Kuleshov, M. V., M. R. Jones, A. D. Rouillard, et al. 2016. Enrichr: A Comprehensive Gene Set Enrichment Analysis Web Server 2016 Update. *Nucleic Acids Res.* **44**:W90–W97. [11]

Kullo, I. J., H. Jouni, E. E. Austin, et al. 2016. Incorporating a Genetic Risk Score into Coronary Heart Disease Risk Estimates: Effect on Low-Density Lipoprotein Cholesterol Levels (the MI-Genes Clinical Trial). *Circulation* **133**:1181–1188. [13]

Kumar, M., L. Atwoli, R. A. Burgess, et al. 2022. What Should Equity in Global Health Research Look Like? *Lancet* **400**:145–147. [2]

Kumar, P. 1968. Genetic Counselling in Family Planning. *Antiseptic* **65**:831–834. [15]

Kuzmin, D. A., M. V. Shutova, N. R. Johnston, et al. 2021. The Clinical Landscape for AAV Gene Therapies. *Nat. Rev. Drug Discov.* **20**:173–174. [5]

Laegsgaard, M. M., A. S. Kristensen, and O. Mors. 2009. Potential Consumers' Attitudes toward Psychiatric Genetic Research and Testing and Factors Influencing Their Intentions to Test. *Genet. Test. Mol. Biomarkers* **13**:57–65. [14]

Lake, B. B., S. Chen, B. C. Sos, et al. 2018. Integrative Single-Cell Analysis of Transcriptional and Epigenetic States in the Human Adult Brain. *Nat. Biotechnol.* **36**:70–80. [11]

Lakhan, S. E., and K. F. Vieira. 2008. Nutritional Therapies for Mental Disorders. *Nutr. J.* **7**:2. [15]

Lam, M., C. Y. Chen, Z. Li, et al. 2019. Comparative Genetic Architectures of Schizophrenia in East Asian and European Populations. *Nat. Genet.* **51**:1670–1678. [2, 3]

Lamb, J., E. D. Crawford, D. Peck, et al. 2006. The Connectivity Map: Using Gene-Expression Signatures to Connect Small Molecules, Genes, and Disease. *Science* **313**:1929–1935. [8]

Lancaster, M. A., M. Renner, C. A. Martin, et al. 2013. Cerebral Organoids Model Human Brain Development and Microcephaly. *Nature* **501**:373–379. [5]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Landes, S. J., S. A. McBain, and G. M. Curran. 2019. An Introduction to Effectiveness-Implementation Hybrid Designs. *Psychiatry Res.* **280**:112513. [13]

Landi, I., D. A. Kaji, L. Cotter, et al. 2021. Prognostic Value of Polygenic Risk Scores for Adults with Psychosis. *Nat. Med.* **27**:1576–1581. [13]

Langfelder, P., and S. Horvath. 2008. WGCNA: An R Package for Weighted Correlation Network Analysis. *BMC Bioinformat.* **9**:559. [11]

Lázaro-Muñoz, G., S. Pereira, S. Carmi, and T. Lencz. 2021. Screening Embryos for Polygenic Conditions and Traits: Ethical Considerations for an Emerging Technology. *Genet. Med.* **23**:432–434. [13]

Leach, E., E. Morris, H. J. White, et al. 2016. How Do Physicians Decide to Refer Their Patients for Psychiatric Genetic Counseling? A Qualitative Study of Physicians' Practice. *J. Genet. Counsel.* **25**:1235–1242. [15]

Leader, L. D., M. O'Connell, and A. VandenBerg. 2019. Brexanolone for Postpartum Depression: Clinical Evidence and Practical Considerations. *Pharmacotherapy* **39**:1105–1112. [5]

Lebowitz, M. S., and W.-K. Ahn. 2017. Testing Positive for a Genetic Predisposition to Depression Magnifies Retrospective Memory for Depressive Symptoms. *J. Consult. Clin. Psychol.* **85**:1052–1063. [15]

Lebowitz, M. S., and W.-K. Ahn. 2018. Blue Genes? Understanding and Mitigating Negative Consequences of Personalized Information About Genetic Risk for Depression. *J. Genet. Couns.* **27**:204–216. [14]

Lebowitz, M. S., W.-K. Ahn, and S. Nolen-Hoeksema. 2013. Fixable or Fate? Perceptions of the Biology of Depression. *J. Consult. Clin. Psychol.* **81**:518–527. [14]

Lebowitz, M. S., and P. S. Appelbaum. 2019. Biomedical Explanations of Psychopathology and Their Implications for Attitudes and Beliefs About Mental Disorders. *Annu. Rev. Clin. Psychol.* **15**:555–577. [14]

Lebowitz, M. S., P. S. Appelbaum, L. B. Dixon, R. R. Girgis, and M. M. Wall. 2021. Experimentally Exploring the Potential Behavioral Effects of Personalized Genetic Information About Marijuana and Schizophrenia Risk. *J. Psychiatr. Res.* **140**:316–322. [14]

Lee, A., N. Mavaddat, A. N. Wilcox, et al. 2019a. BOADICEA: A Comprehensive Breast Cancer Risk Prediction Model Incorporating Genetic and Nongenetic Risk Factors. *Genet. Med.* **21**:1708–1718. [13]

Lee, J.-M., K. Correia, J. Loupe, et al. 2019b. CAG Repeat Not Polyglutamine Length Determines Timing of Huntington's Disease Onset. *Cell* **178**:887–900. [9]

Lee, P. H., V. Anttila, H. Won, et al. 2019c. Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. *Cell* **179**:1469–1482. [2]

Lee, P. H., V. Anttila, H. Won, et al. 2019d. *Preprint*: Genome Wide Meta-Analysis Identifies Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. *bioRxiv* 528117. [7]

Lee, P. H., Y. A. Feng, and J. W. Smoller. 2021. Pleiotropy and Cross-Disorder Genetics Among Psychiatric Disorders. *Biol. Psychiatry* **89**:20–31. [1, 13]

Lee, Y. H., T. Thaweethai, Y.-C. A. Feng, et al. 2022. *Preprint*: Impact of Selection Bias on Polygenic Risk Score Estimates in Healthcare Settings. *medRxiv* 22277710. [2]

Leiserson, M. D. M., J. V. Eldridge, S. Ramachandran, and B. J. Raphael. 2013. Network Analysis of GWAS Data. *Curr. Opin. Genet. Dev.* **23**:602–610. [11]

Lek, M., K. J. Karczewski, E. V. Minikel, et al. 2016. Analysis of Protein-Coding Genetic Variation in 60,706 Humans. *Nature* **536**:285–291. [3]

Lencz, T., D. Backenroth, E. Granot-Hershkovitz, et al. 2021. Utility of Polygenic Embryo Screening for Disease Depends on the Selection Strategy. *eLife* **10**:e64716. [13]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Leonard, H., S. Cobb, and J. Downs. 2017. Clinical and Biological Progress over 50 Years in Rett Syndrome. *Nat. Rev. Neurol.* **13**:37–51. [6]

Levey, D. F., J. Gerlernter, R. Polimanti, et al. 2020. Reproducible Genetic Risk Loci for Anxiety: Results from ~200,000 Participants in the Million Veteran Program. *Am. J. Psychiatry* **177**:223–232. [3]

Levey, D. F., M. B. Stein, F. R. Wendt, et al. 2021. Bi-Ancestral Depression GWAS in the Million Veteran Program and Meta-Analysis in >1.2 Million Individuals Highlight New Therapeutic Directions. *Nat. Neurosci.* **24**:954–963. [7]

Lewis, A. C. F., R. C. Green, and J. L. Vassy. 2021. Polygenic Risk Scores in the Clinic: Translating Risk into Action. *HGG Adv.* **2**:100047. [13]

Lewis, A. C. F., E. F. Perez, A. E. R. Prince, et al. 2022. Patient and Provider Perspectives on Polygenic Risk Scores: Implications for Clinical Reporting and Utilization. *Genome Med.* **14**:114. [12]

Lewis, C. M., and E. Vassos. 2022. Polygenic Scores in Psychiatry: On the Road from Discovery to Implementation. *Am. J. Psychiatry* **179**:800–806. [12]

Li, J., Z. Ma, M. Shi, et al. 2015. Identification of Human Neuronal Protein Complexes Reveals Biochemical Activities and Convergent Mechanisms of Action in Autism Spectrum Disorders. *Cell Syst.* **1**:361–374. [11]

Li, J. H., C. A. Mazur, T. Berisa, and J. K. Pickrell. 2021a. Low-Pass Sequencing Increases the Power of GWAS and Decreases Measurement Error of Polygenic Risk Scores Compared to Genotyping Arrays. *Genome Res.* **31**:529–537. [2]

Li, L., K.-L. Huang, Y. Gao, et al. 2021b. An Atlas of Alternative Polyadenylation Quantitative Trait Loci Contributing to Complex Trait and Disease Heritability. *Nat. Genet.* **53**:994–1005. [8]

Li, M., N. Jancovski, P. Jafar-Nejad, et al. 2021c. Antisense Oligonucleotide Therapy Reduces Seizures and Extends Life Span in an SCN2A Gain-of-Function Epilepsy Model. *J. Clin. Invest.* **131**:e152079. [5]

Li, M., G. Santpere, Y. Imamura Kawasawa, et al. 2018. Integrative Functional Genomic Analysis of Human Brain Development and Neuropsychiatric Risks. *Science* **362**:eaat7615. [5, 10, 11]

Li, Q. S., C. Tian, D. Hinds, and 23andMe Research Team. 2020. Genome-Wide Association Studies of Antidepressant Class Response and Treatment-Resistant Depression. *Transl. Psychiatry* **10**:360. [13]

Li, S. X., R. L. Milne, T. Nguyen-Dumont, et al. 2021d. Prospective Evaluation of the Addition of Polygenic Risk Scores to Breast Cancer Risk Models. *JNCI Cancer Spectr.* **5**:pkab021. [13]

Li, Y. I., B. van de Geijn, A. Raj, et al. 2016. RNA Splicing Is a Primary Link between Genetic Variation and Disease. *Science* **352**:600–604. [10, 11]

Liang, H., J. Olsen, W. Yuan, et al. 2016. Early Life Bereavement and Schizophrenia: A Nationwide Cohort Study in Denmark and Sweden. *Medicine* **95**:e2434. [4]

Liang, L., S. Fazel Darbandi, S. Pochareddy, et al. 2021. Developmental Dynamics of Voltage-Gated Sodium Channel Isoform Expression in the Human and Mouse Brain. *Genome Med.* **13**:135. [5]

Liang, X. H., H. Sun, W. Shen, et al. 2017. Antisense Oligonucleotides Targeting Translation Inhibitory Elements in 5' UTRs Can Selectively Increase Protein Levels. *Nucleic Acids Res.* **45**:9528–9546. [5]

Lichtenstein, P., B. H. Yip, C. Björk, et al. 2009. Common Genetic Determinants of Schizophrenia and Bipolar Disorder in Swedish Families: A Population-Based Study. *Lancet Psychiatry* **373**:234–239. [4]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Liebers, D. T., M. Pirooznia, A. Ganna, S. Bipolar Genome, and F. S. Goes. 2021. Discriminating Bipolar Depression from Major Depressive Disorder with Polygenic Risk Scores. *Psychol. Med.* **51**:1451–1458. [13]

Lim, E. T., S. Raychaudhuri, S. J. Sanders, et al. 2013. Rare Complete Knockouts in Humans: Population Distribution and Significant Role in Autism Spectrum Disorders. *Neuron* **77**:235–242. [3]

Lin, G. N., R. Corominas, I. Lemmens, et al. 2015. Spatiotemporal 16p11.2 Protein Network Implicates Cortical Late Mid-Fetal Brain Development and KCTD13-Cul3-RhoA Pathway in Psychiatric Diseases. *Neuron* **85**:742–754. [5]

Lin, K., X. Zhong, L. Li, et al. 2020. AAV9-Retro Mediates Efficient Transduction with Axon Terminal Absorption and Blood-Brain Barrier Transportation. *Mol. Brain* **13**:138. [6]

Lineweaver, T. T., M. W. Bondi, D. Galasko, and D. P. Salmon. 2014. Effect of Knowledge of APOE Genotype on Subjective and Objective Memory Performance in Healthy Older Adults. *Am. J. Psychiatry* **171**:201–208. [14, 15]

Liu, L., J. Lei, S. J. Sanders, et al. 2014. Dawn: A Framework to Identify Autism Genes and Subnetworks Using Gene Expression and Genetics. *Mol. Autism* **5**:22. [11]

Liu, P., M. Chen, Y. Liu, L. S. Qi, and S. Ding. 2018a. CRISPR-Based Chromatin Remodeling of the Endogenous Oct4 or Sox2 Locus Enables Reprogramming to Pluripotency. *Cell Stem Cell* **22**:252–261. [7]

Liu, X. S., H. Wu, M. Krzisch, et al. 2018b. Rescue of Fragile X Syndrome Neurons by DNA Methylation Editing of the Fmr1 Gene. *Cell* **172**:979–992. [7]

Liu, Y., C. Yu, T. P. Daley, et al. 2018c. CRISPR Activation Screens Systematically Identify Factors That Drive Neuronal Fate and Reprogramming. *Cell Stem Cell* **23**:758–771. [7]

Livingston, J. D., and J. E. Boyd. 2010. Correlates and Consequences of Internalized Stigma for People Living with Mental Illness: A Systematic Review and Meta-Analysis. *Soc. Sci. Med.* **71**:2150–2161. [15]

Loh, K. H., P. S. Stawski, A. S. Draycott, et al. 2016. Proteomic Analysis of Unbounded Cellular Compartments: Synaptic Clefts. *Cell* **166**:1295–1307. [11]

Loh, P. R., G. Bhatia, A. Gusev, et al. 2015. Contrasting Genetic Architectures of Schizophrenia and Other Complex Diseases Using Fast Variance-Components Analysis. *Nat. Genet.* **47**:1385–1392. [3]

Loohuis, L. M., J. A. Vorstman, A. P. Ori, et al. 2015. Genome-Wide Burden of Deleterious Coding Variants Increased in Schizophrenia. *Nat. Commun.* **6**:7501. [7]

Lourida, I., E. Hannon, T. J. Littlejohns, et al. 2019. Association of Lifestyle and Genetic Risk with Incidence of Dementia. *JAMA* **322**:430–437. [13]

Lowther, C., G. Costain, D. A. Baribeau, and A. S. Bassett. 2017. Genomic Disorders in Psychiatry: What Does the Clinician Need to Know? *Curr. Psychiatry Rep.* **19**:82. [13]

Lu, C., X. Shi, A. Allen, et al. 2019. Overexpression of $NEUROG_2$ and $NEUROG_1$ in Human Embryonic Stem Cells Produces a Network of Excitatory and Inhibitory Neurons. *FASEB J.* **33**:5287–5299. [7]

Lukashchuk, V., K. E. Lewis, I. Coldicott, A. J. Grierson, and M. Azzouz. 2016. AAV9-Mediated Central Nervous System-Targeted Gene Delivery via Cisterna magna Route in Mice. *Mol. Ther. Methods Clin. Dev.* **3**:15055. [6]

Lund, C., M. De Silva, S. Plagerson, et al. 2011. Poverty and Mental Disorders: Breaking the Cycle in Low-Income and Middle-Income Countries. *Lancet Psychiatry* **378**:1502–1514. [4]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Luningham, J. M., A. M. Hendriks, E. Krapohl, et al. 2020. Harmonizing Behavioral Outcomes across Studies, Raters, and Countries: Application to the Genetic Analysis of Aggression in the Action Consortium. *J. Child Psychol. Psychiatry* **61**:807–817. [2]

Luningham, J. M., D. B. McArtor, A. M. Hendriks, et al. 2019. Data Integration Methods for Phenotype Harmonization in Multi-Cohort Genome-Wide Association Studies with Behavioral Outcomes. *Front. Genet.* **10**:1227. [2]

Luo, C., M. A. Lancaster, R. Castanon, et al. 2016. Cerebral Organoids Recapitulate Epigenomic Signatures of the Human Fetal Brain. *Cell Rep.* **17**:3369–3384. [5]

Luo, C., H. Liu, F. Xie, et al. 2022. Single Nucleus Multi-Omics Identifies Human Cortical Cell Regulatory Genome Diversity. *Cell Genom.* **2**: [11]

Luo, Y., K. M. de Lange, L. Jostins, et al. 2017. Exploring the Genetic Architecture of Inflammatory Bowel Disease by Whole-Genome Sequencing Identifies Association at ADCY7. *Nat. Genet.* **49**:186–192. [2]

Luoni, M., S. Giannelli, M. T. Indrigo, et al. 2020. Whole Brain Delivery of an Instability-Prone *Mecp2* Transgene Improves Behavioral and Molecular Pathological Defects in Mouse Models of Rett Syndrome. *eLife* **9**:e52629. [5]

Lyus, V. L. 2007. The Importance of Genetic Counseling for Individuals with Schizophrenia and Their Relatives: Potential Clients' Opinions and Experiences. *Am. J. Med. Genet. B Neuropsychiatr. Genet.* **144B**:1014–1021. [15]

Ma, S., M. Skarica, Q. Li, et al. 2022. Molecular and Cellular Evolution of the Primate Dorsolateral Prefrontal Cortex. *Science* **377**:eabo7257. [5]

Ma, S., B. Zhang, L. M. LaFave, et al. 2020. Chromatin Potential Identified by Shared Single-Cell Profiling of RNA and Chromatin. *Cell* **183**:1103–1116. [10]

MacDonald, M. L., M. Garver, J. Newman, et al. 2020. Synaptic Proteome Alterations in the Primary Auditory Cortex of Individuals with Schizophrenia. *JAMA Psychiatry* **77**:86–95. [11]

Madisen, L., T. Mao, H. Koch, et al. 2012. A Toolbox of Cre-Dependent Optogenetic Transgenic Mice for Light-Induced Activation and Silencing. *Nat. Neurosci.* **15**:793–802. [7]

Magnus, P., C. Birke, K. Vejrup, et al. 2016. Cohort Profile Update: The Norwegian Mother and Child Cohort Study (MoBa). *Int. J. Epidemiol.* **45**:382–388. [2]

Mah, W., and H. Won. 2020. The Three-Dimensional Landscape of the Genome in Human Brain Tissue Unveils Regulatory Mechanisms Leading to Schizophrenia Risk. *Schizophr. Res.* **217**:17–25. [8, 10]

Mahjani, B., S. De Rubeis, C. Gustavsson Mahjani, et al. 2021. Prevalence and Phenotypic Impact of Rare Potentially Damaging Variants in Autism Spectrum Disorder. *Mol. Autism* **12**:65. [6]

Maier, R., G. Moser, G. B. Chen, et al. 2015. Joint Analysis of Psychiatric Disorders Increases Accuracy of Risk Prediction for Schizophrenia, Bipolar Disorder, and Major Depressive Disorder. *Am. J. Hum. Genet.* **96**:283–294. [2]

Major Depressive Disorder Working Group of the Psychiatric GWAS Consortium. 2013. A Mega-Analysis of Genome-Wide Association Studies for Major Depressive Disorder. *Mol. Psychiatry* **18**:497–511. [7]

Maltzberg, B. 1936. Migration and Mental Disease among Negroes in New York State. *Am. J. Biol. Anthropol.* **21**:107–113. [4]

Maltzberg, B. 1962. NIVARD

Mancini, M., A. Karakuzu, J. Cohen-Adad, et al. 2020. An Interactive Meta-Analysis of MRI Biomarkers of Myelin. *eLife* **9**:e61523. [5]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Manickam, K., M. R. McClain, L. A. Demmer, et al. 2021. Exome and Genome Sequencing for Pediatric Patients with Congenital Anomalies or Intellectual Disability: an Evidence-Based Clinical Guideline of the American College of Medical Genetics and Genomics. *Genet. Med.* **23**:2029–2037. [6, 12]

Mansfield, K. 2003. Marmoset Models Commonly Used in Biomedical Research. *Comp. Med.* **53**:383–392. [5]

Mansour, A. A., J. T. Gonçalves, C. W. Bloyd, et al. 2018. An *in Vivo* Model of Functional and Vascularized Human Brain Organoids. *Nat. Biotechnol.* **36**:432–441. [5, 7]

Marbach, D., D. Lamparter, G. Quon, et al. 2016. Tissue-Specific Regulatory Circuits Reveal Variable Modular Perturbations across Complex Diseases. *Nat. Methods* **13**:366–370. [11]

Marchetto, M. C., C. Carromeu, A. Acab, et al. 2010. A Model for Neural Development and Treatment of Rett Syndrome Using Human Induced Pluripotent Stem Cells. *Cell* **143**:527–539. [7]

Marek, S., B. Tervo-Clemmens, F. J. Calabro, et al. 2022. Reproducible Brain-Wide Association Studies Require Thousands of Individuals. *Nature* **603**:654–660. [8]

Mariani, J., G. Coppola, P. Zhang, et al. 2015. FOXG1-Dependent Dysregulation of GABA/Glutamate Neuron Differentiation in Autism Spectrum Disorders. *Cell* **162**:375–390. [5, 7]

Mariani, J., M. V. Simonini, D. Palejev, et al. 2012. Modeling Human Cortical Development *in vitro* Using Induced Pluripotent Stem Cells. *PNAS* **109**:12770–12775. [7]

Marouli, E., M. Graff, C. Medina-Gomez, et al. 2017. Rare and Low-Frequency Coding Variants Alter Human Adult Height. *Nature* **542**:186–190. [2]

Marro, S. G., S. Chanda, N. Yang, et al. 2019. Neuroligin-4 Regulates Excitatory Synaptic Transmission in Human Neurons. *Neuron* **103**:617–626. [7]

Mars, N., S. Kerminen, Y. A. Feng, et al. 2022. Genome-Wide Risk Prediction of Common Diseases across Ancestries in One Million People. *Cell Genom.* **2**:None. [13]

Mars, N., J. T. Koskela, P. Ripatti, et al. 2020. Polygenic and Clinical Risk Scores and Their Impact on Age at Onset and Prediction of Cardiometabolic Diseases and Common Cancers. *Nat. Med.* **26**:549–557. [13]

Marshall, C. R., D. P. Howrigan, D. Merico, et al. 2017. Contribution of Copy Number Variants to Schizophrenia from a Genome-Wide Study of 41,321 Subjects. *Nat. Genet.* **49**:27–35. [3, 7, 11]

Marshall, C. R., A. Noor, J. B. Vincent, et al. 2008. Structural Variation of Chromosomes in Autism Spectrum Disorder. *Am. J. Hum. Genet.* **82**:477–488. [5]

Marshall, J. J., and J. O. Mason. 2019. Mouse vs Man: Organoid Models of Brain Development & Disease. *Brain Res.* **1724**:146427. [5]

Marteau, T., D. French, and S. Griffin. 2010. Effects of Communicating DNA-Based Disease Risk Estimates on Risk-Reducing Behaviours. *Cochrane Database Syst. Rev.* **Oct 6**:CD007275. [15]

Martin, A. R., E. G. Atkinson, S. B. Chapman, et al. 2021. Low-Coverage Sequencing Cost-Effectively Detects Known and Novel Variation in Underrepresented Populations. *Am. J. Hum. Genet.* **108**:656–668. [2]

Martin, A. R., M. J. Daly, E. B. Robinson, S. E. Hyman, and B. M. Neale. 2019a. Predicting Polygenic Risk of Psychiatric Disorders. *Biol. Psychiatry* **86**:97–109. [13, 14]

Martin, A. R., C. R. Gignoux, R. K. Walters, et al. 2017. Human Demographic History Impacts Genetic Risk Prediction across Diverse Populations. *Am. J. Hum. Genet.* **100**:635–649. [2]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Martin, A. R., M. Kanai, Y. Kamatani, et al. 2019b. Clinical Use of Current Polygenic Risk Scores May Exacerbate Health Disparities. *Nat. Genet.* **51**:584–591. [2, 3, 8, 13]

Martin, A. R., R. E. Stroud 2nd, T. Abebe, et al. 2022. Increasing Diversity in Genomics Requires Investment in Equitable Partnerships and Capacity Building. *Nat. Genet.* **54**:740–745. [2]

Martin, J., K. Tilling, L. Hubbard, et al. 2016. Association of Genetic Risk for Schizophrenia with Nonparticipation over Time in a Population-Based Cohort Study. *Am. J. Epidemiol.* **183**:1149–1158. [2]

Martin-Brevet, S., B. Rodríguez-Herreros, J. A. Nielsen, et al. 2018. Quantifying the Effects of 16p11.2 Copy Number Variants on Brain Structure: A Multisite Genetic-First Study. *Biol. Psychiatry* **84**:253–264. [5]

Marton, R. M., Y. Miura, S. A. Sloan, et al. 2019. Differentiation and Maturation of Oligodendrocytes in Human Three-Dimensional Neural Cultures. *Nat. Neurosci.* **22**:484–491. [7]

Mashiko, H., A. C. Yoshida, S. S. Kikuchi, et al. 2012. Comparative Anatomy of Marmoset and Mouse Cortex from Genomic Expression. *J. Neurosci.* **32**:5039–5053. [5]

Matharu, N., S. Rattanasopha, S. Tamura, et al. 2019. CRISPR-Mediated Activation of a Promoter or Enhancer Rescues Obesity Caused by Haploinsufficiency. *Science* **363**:eaau0629. [6]

Matoba, N., D. Liang, H. Sun, et al. 2020. Common Genetic Risk Variants Identified in the Spark Cohort Support Ddhd2 as a Candidate Risk Gene for Autism. *Transl. Psychiatry* **10**:265. [8]

Matzner, U., E. Herbst, K. K. Hedayati, et al. 2005. Enzyme Replacement Improves Nervous System Pathology and Function in a Mouse Model for Metachromatic Leukodystrophy. *Hum. Mol. Genet.* **14**:1139–1152. [6]

McAfee, J. C., J. L. Bell, O. Krupa, et al. 2022a. Focus on Your Locus with a Massively Parallel Reporter Assay. *J. Neurodev. Disord.* **14**:50. [10]

McAfee, J. C., S. Lee, J. Lee, et al. 2022b. *Preprint*: Systematic Investigation of Allelic Regulatory Activity of Schizophrenia-Associated Common Variants. *medRxiv* 22279954. [8, 10]

McAllister, M., G. Dunn, and C. Todd. 2010. Empowerment: Qualitative Underpinning of a New Clinical Genetics-Specific Patient-Reported Outcome. *Eur. J. Hum. Genet.* **19**:125–130. [15]

McCarthy, M. I. 2017. Painting a New Picture of Personalised Medicine for Diabetes. *Diabetologia* **60**:793–799. [9]

McCarthy, S. E., V. Makarov, G. Kirov, et al. 2009. Microduplications of 16p11.2 Are Associated with Schizophrenia. *Nat. Genet.* **41**:1223–1227. [5]

McGillivray, P., D. Clarke, W. Meyerson, et al. 2018. Network Analysis as a Grand Unifier in Biomedical Data Science. *Annu. Rev. Biomed. Data Sci.* **1**:153–180. [11]

McGinty, E. E., and M. D. Eisenberg. 2022. Mental Health Treatment Gap: The Implementation Problem as a Research Problem. *JAMA Psychiatry* **79**:746–747. [13]

McIntyre, R. S., M. Berk, E. Brietzke, et al. 2020. Bipolar Disorders. *Lancet* **396**:1841–1856. [13]

McPhie, D. L., R. Nehme, C. Ravichandran, et al. 2018. Oligodendrocyte Differentiation of Induced Pluripotent Stem Cells Derived from Subjects with Schizophrenias Implicate Abnormalities in Development. *Transl. Psychiatry* **8**:230. [7]

Meehan, A. J., S. J. Lewis, S. Fazel, et al. 2022. Clinical Prediction Models in Psychiatry: A Systematic Review of Two Decades of Progress and Challenges. *Mol. Psychiatry* **27**:2700–2708. [13]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Meerman, J. J., S. E. Ter Hark, J. G. E. Janzing, and M. J. H. Coenen. 2022. The Potential of Polygenic Risk Scores to Predict Antidepressant Treatment Response in Major Depression: A Systematic Review. *J. Affect. Disord.* **304**:1–11. [13]

Mega, J. L., N. O. Stitziel, J. G. Smith, et al. 2015. Genetic Risk, Coronary Heart Disease Events, and the Clinical Benefit of Statin Therapy: an Analysis of Primary and Secondary Prevention Trials. *Lancet* **385**:2264–2271. [13]

Meikle, L., K. Pollizzi, A. Egnor, et al. 2008. Response of a Neuronal Model of Tuberous Sclerosis to Mammalian Target of Rapamycin (mTOR) Inhibitors: Effects on mTORC1 and Akt Signaling Lead to Improved Survival and Function. *J. Neurosci.* **28**:5422–5432. [6]

Meiser, B., N. A. Kasparian, P. B. Mitchell, et al. 2008. Attitudes to Genetic Testing in Families with Multiple Cases of Bipolar Disorder. *Genet. Test.* **12**:233–243. [15]

Meiser, B., P. B. Mitchell, N. A. Kasparian, et al. 2007. Attitudes Towards Childbearing, Causal Attributions for Bipolar Disorder and Psychological Distress: A Study of Families with Multiple Cases of Bipolar Disorder. *Psychol. Med.* **37**:1601–1611. [14]

Meiser, B., P. B. Mitchell, H. McGirr, M. Van Herten, and P. R. Schofield. 2005. Implications of Genetic Risk Information in Families with a High Density of Bipolar Disorder: an Exploratory Study. *Soc. Sci. Med.* **60**:109–118. [15]

Melby, M. K., L. C. Loh, J. Evert, et al. 2016. Beyond Medical "Missions" to Impact-Driven Short-Term Experiences in Global Health (STEGHs): Ethical Principles to Optimize Community Benefit and Learner Experience. *Acad. Med.* **91**:633–638. [2]

Meng, L., A. J. Ward, S. Chun, et al. 2015. Towards a Therapy for Angelman Syndrome by Targeting a Long Non-Coding RNA. *Nature* **518**:409–412. [6]

Merikangas, K. R., W. Wicki, and J. Angst. 1994. Heterogeneity of Depression. Classification of Depressive Subtypes by Longitudinal Course. *Br. J. Psychiatry* **164**:342–348. [2]

Mertens, J., Q. W. Wang, Y. Kim, et al. 2015. Differential Responses to Lithium in Hyperexcitable Neurons from Patients with Bipolar Disorder. *Nature* **527**:95–99. [7]

Meseck, E. K., G. Guibinga, S. Wang, et al. 2022. Intrathecal sc-AAV9-CB-GFP: Systemic Distribution Predominates Following Single-Dose Administration in Cynomolgus Macaques. *Toxicol. Pathol.* **50**:415–431. [6]

Messina, S., and M. Sframeli. 2020. New Treatments in Spinal Muscular Atrophy: Positive Results and New Challenges. *J. Clin. Med.* **9**:2222. [5]

Meyer, J. E. 1988. The Fate of the Mentally Ill in Germany during the Third Reich. *Psychol. Med.* **18**:575–581. [14]

Micali, N., E. Simonoff, and J. Treasure. 2007. Risk of Major Adverse Perinatal Outcomes in Women with Eating Disorders. *BMC Psychiatry* **190**:255–259. [4]

Michael, J. E., C. M. Bulik, S. J. Hart, L. Doyle, and J. Austin. 2020. Perceptions of Genetic Risk, Testing, and Counseling among Individuals with Eating Disorders. *Int. J. Eat. Disord.* **53**:1496–1505. [15]

Mikl, M., D. Eletto, M. Nijim, et al. 2022. A Massively Parallel Reporter Assay Reveals Focused and Broadly Encoded RNA Localization Signals in Neurons. *Nucleic Acids Res.* **50**:10643–10664. [8]

Milaneschi, Y., F. Lamers, M. Berk, and B. Penninx. 2020. Depression Heterogeneity and Its Biological Underpinnings: Toward Immunometabolic Depression. *Biol. Psychiatry* **88**:369–380. [2]

Milaneschi, Y., F. Lamers, W. J. Peyrot, et al. 2016. Polygenic Dissection of Major Depression Clinical Heterogeneity. *Mol. Psychiatry* **21**:516–522. [2]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Milaneschi, Y., F. Lamers, W. J. Peyrot, et al. 2017. Genetic Association of Major Depression with Atypical Features and Obesity-Related Immunometabolic Dysregulations. *JAMA Psychiatry* **74**:1214–1225. [2]

Milazzo, C., E. J. Mientjes, I. Wallaard, et al. 2021. Antisense Oligonucleotide Treatment Rescues *UBE3A* Expression and Multiple Phenotypes of an Angelman Syndrome Mouse Model. *JCI Insight* **6**:e145991. [5, 7]

Miller, D. T., M. P. Adam, S. Aradhya, et al. 2010. Consensus Statement: Chromosomal Microarray Is a First-Tier Clinical Diagnostic Test for Individuals with Developmental Disabilities or Congenital Anomalies. *Am. J. Hum. Genet.* **86**:749–764. [12]

Miller, J. A., S.-L. Ding, S. M. Sunkin, et al. 2014. Transcriptional Landscape of the Prenatal Human Brain. *Nature* **508**:199–206. [11]

Milosavljevic, F., N. Bukvic, Z. Pavlovic, et al. 2021. Association of CYP2C19 and CYP2D6 Poor and Intermediate Metabolizer Status with Antidepressant and Antipsychotic Exposure: A Systematic Review and Meta-Analysis. *JAMA Psychiatry* **78**:270–280. [13]

Mimitou, E. P., A. Cheng, A. Montalbano, et al. 2019. Multiplexed Detection of Proteins, Transcriptomes, Clonotypes and CRISPR Perturbations in Single Cells. *Nat. Methods* **16**:409–412. [7]

Mitchell, J. M., J. Nemesh, S. Ghosh, et al. 2020. *Preprint*: Mapping Genetic Effects on Cellular Phenotypes with "Cell Villages" *BioRxiv* 174383 [7, 8]

Modi, M. E., and M. Sahin. 2017. Translational Use of Event-Related Potentials to Assess Circuit Integrity in ASD. *Nat. Rev. Neurol.* **13**:160–170. [5]

Moldovan, R., K. McGhee, D. A. Coviello, et al. 2019. Psychiatric Genetic Counseling: A Mapping Exercise. *Am. J. Med. Genet. B Neuropsychiatr. Genet.* **180**:523–532. [15]

Moldovan, R., S. Pintea, and J. Austin. 2017. The Efficacy of Genetic Counseling for Psychiatric Disorders: A Meta-Analysis. *J. Genet. Counsel.* **26**:1341–1347. [15]

Monteys, A. M., A. A. Hundley, P. T. Ranum, et al. 2021. Regulated Control of Gene Therapies by Drug-Induced Splicing. *Nature* **596**:291–295. [6]

Moore, R., F. P. Casale, M. J. Bonder, et al. 2019. A Linear Mixed-Model Approach to Study Multivariate Gene–Environment Interactions. *Nat. Genet.* **51**:180–186. [2]

Moreno-De-Luca, D., M. E. Ross, and D. A. Ross. 2018. Leveraging the Power of Genetics to Bring Precision Medicine to Psychiatry: Too Little of a Good Thing? *Biol. Psychiatry* **83**:e45–e46. [15]

Morris, E., R. Batallones, J. Ryan, et al. 2021. Psychiatric Genetic Counseling for Serious Mental Illness: Impact on Psychopathology and Psychotropic Medication Adherence. *Psychiatry Res.* **296**:113663. [12, 15]

Morris, E., M. O'Donovan, A. Virani, and J. Austin. 2022. An Ethical Analysis of Divergent Clinical Approaches to the Application of Genetic Testing for Autism and Schizophrenia. *Hum. Genet.* **141**:1069–1084. [12, 15]

Mosley, J. D., D. K. Gupta, J. Tan, et al. 2020. Predictive Accuracy of a Polygenic Risk Score Compared with a Clinical Risk Score for Incident Coronary Heart Disease. *JAMA* **323**:627–635. [13]

Mostafavi, H., A. Harpak, I. Agarwal, et al. 2020. Variable Prediction Accuracy of Polygenic Scores within an Ancestry Group. *eLife* **9**:e48376. [13]

Mostafavi, H., J. P. Spence, S. Naqvi, and J. K. Pritchard. 2022. *Preprint*: Limited Overlap of eQTLs and GWAS Hits Due to Systematic Differences in Discovery. *bioRxiv* 491045. [10]

Mueller, C., J. D. Berry, D. M. McKenna-Yasek, et al. 2020. SOD1 Suppression with Adeno-Associated Virus and MicroRNA in Familial Als. *N. Engl. J. Med.* **383**:151–158. [6]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Mukai, J., E. Cannavo, G. W. Crabtree, et al. 2019. Recapitulation and Reversal of Schizophrenia-Related Phenotypes in Setd1a-Deficient Mice. *Neuron* **104**:471–487. [7]

Mullins, N., A. J. Forstner, K. S. O'Connell, et al. 2021. Genome-Wide Association Study of over 40,000 Bipolar Disorder Cases Provides New Insights into the Underlying Biology. *Nat. Genet.* **53**:817–829. [3]

Mullins, N., J. Kang, A. I. Campos, et al. 2022. Dissecting the Shared Genetic Architecture of Suicide Attempt, Psychiatric Disorders, and Known Risk Factors. *Biol. Psychiatry* **91**:313–327. [14]

Mulvey, B., and J. D. Dougherty. 2021. Transcriptional-Regulatory Convergence across Functional Mdd Risk Variants Identified by Massively Parallel Reporter Assays. *Transl. Psychiatry* **11**:403. [7]

Mumbach, M. R., A. T. Satpathy, E. A. Boyle, et al. 2017. Enhancer Connectome in Primary Human Cells Identifies Target Genes of Disease-Associated DNA Elements. *Nat. Genet.* **49**:1602–1612. [10]

Muñoz-Castañeda, R., B. Zingg, K. S. Matho, et al. 2021. Cellular Anatomy of the Mouse Primary Motor Cortex. *Nature* **598**:159–166. [11]

Muntoni, F., and M. J. Wood. 2011. Targeting RNA to Treat Neuromuscular Disease. *Nat. Rev. Drug Discov.* **10**:621–637. [5]

Murphy, L. E., T. M. Fonseka, C. A. Bousman, and D. J. Muller. 2022. Gene-Drug Pairings for Antidepressants and Antipsychotics: Level of Evidence and Clinical Application. *Mol. Psychiatry* **27**:593–605. [13]

Murray, G. K., T. Lin, J. Austin, et al. 2021. Could Polygenic Risk Scores Be Useful in Psychiatry? A Review. *JAMA Psychiatry* **78**:210–219. [13, 14]

Musliner, K. L., E. Agerbo, B. J. Vilhjálmsson, et al. 2021. Polygenic Liability and Recurrence of Depression in Patients with First-Onset Depression Treated in Hospital-Based Settings. *JAMA Psychiatry* **78**:792–795. [13]

Musliner, K. L., M. D. Krebs, C. Albiñana, et al. 2020. Polygenic Risk and Progression to Bipolar or Psychotic Disorders Among Individuals Diagnosed with Unipolar Depression in Early Life. *Am. J. Psychiatry* **177**:936–943. [13]

Myers, S. M., T. D. Challman, R. Bernier, et al. 2020a. Insufficient Evidence for "Autism-Specific" Genes. *Am. J. Hum. Genet.* **106**:587–595. [6]

Myers, S. M., T. D. Challman, C. L. Martin, and D. H. Ledbetter. 2020b. Response to Buxbaum et Al. *Am. J. Hum. Genet.* **107**:1004. [6]

Myint, L., R. Wang, L. Boukas, et al. 2020. A Screen of 1,049 Schizophrenia and 30 Alzheimer's-Associated Variants for Regulatory Potential. *Am. J. Med. Genet. B Neuropsychiatr. Genet.* **183**:61–73. [7, 8]

Nagahama, K., K. Sakoori, T. Watanabe, et al. 2020. Setd1a Insufficiency in Mice Attenuates Excitatory Synaptic Function and Recapitulates Schizophrenia-Related Behavioral Abnormalities. *Cell Rep.* **32**:108126. [7]

Nakamoto, M., V. Nalavadi, M. P. Epstein, et al. 2007. Fragile X Mental Retardation Protein Deficiency Leads to Excessive mGluR5-Dependent Internalization of AMPA Receptors. *PNAS* **104**:15537–15542. [5]

Namjou, B., M. Lape, E. Malolepsza, et al. 2022. Multiancestral Polygenic Risk Score for Pediatric Asthma. *J. Allergy Clin. Immunol.* **150**:1086–1109. [13]

Narcisa, V., M. Discenza, E. Vaccari, et al. 2013. Parental Interest in a Genetic Risk Assessment Test for Autism Spectrum Disorders. *Clin. Pediatr.* **52**:139–146. [14]

Natarajan, P., R. Young, N. O. Stitziel, et al. 2017. Polygenic Risk Score Identifies Subgroup with Higher Burden of Atherosclerosis and Greater Relative Benefit from Statin Therapy in the Primary Prevention Setting. *Circulation* **135**:2091–2101. [13]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Neale, B. M., Y. Kou, L. Liu, et al. 2012. Patterns and Rates of Exonic *de Novo* Mutations in Autism Spectrum Disorders. *Nature* **485**:242–245. [7]

Neavin, D., Q. Nguyen, M. S. Daniszewski, et al. 2021a. Single Cell eQTL Analysis Identifies Cell Type-Specific Genetic Control of Gene Expression in Fibroblasts and Reprogrammed Induced Pluripotent Stem Cells. *Genome Biol.* **22**:76. [7]

Neavin, D. R., A. M. Steinmann, H. S. Chiu, et al. 2021b. *Preprint*: Village in a Dish: A Model System for Population-Scale hiPSC Studies. *BioRxiv* 457030. [8]

Nehme, R., O. Pietiläine, M. Artomov, et al. 2021. *Preprint*: The 22q11.2 Region Regulates Presynaptic Gene-Products Linked to Schizophrenia. *bioRxiv* 461360. [7]

Nelson, A. D., A. M. Catalfio, J. M. Gupta, et al. 2022. *Preprint*: Physical and Functional Convergence of the Autism Risk Genes *Scn2a* and *Ank2* in Neocortical Pyramidal Cell Dendrites. *bioRxiv*2022.2005.2031.494205. [5]

Nelson, C. A., Z. A. Bhutta, N. B. Harris, A. Danese, and M. Samara. 2020. Adversity in Childhood Is Linked to Mental and Physical Health Throughout Life. *BMJ* **371**:m3048. [2]

Nelson, E. C., A. C. Heath, P. A. F. Madden, et al. 2002. Association between Self-Reported Childhood Sexual Abuse and Adverse Psychosocial Outcomes: Results from a Twin Study. *Arch. Gen. Psychiatry* **59**:139. [4]

Network Pathway Analysis Subgroup of Psychiatric Genomics Consortium. 2015. Psychiatric Genome-Wide Association Study Analyses Implicate Neuronal, Immune and Histone Pathways. *Nat. Neurosci.* **18**:199–209. [1, 11]

Ni, G., J. Zeng, J. A. Revez, et al. 2021. A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied across Multiple Cohorts. *Biol. Psychiatry* **90**:611–620. [13]

Nicholas, C. R., J. Chen, Y. Tang, et al. 2013. Functional Maturation of Hpsc-Derived Forebrain Interneurons Requires an Extended Timeline and Mimics Human Neural Development. *Cell Stem Cell* **12**:573–586. [7]

Niemi, M. E. K., H. C. Martin, D. L. Rice, et al. 2018. Common Genetic Variants Contribute to Risk of Rare Severe Neurodevelopmental Disorders. *Nature* **562**:268–271. [3, 9, 13]

Nonnenmacher, M., W. Wang, M. A. Child, et al. 2021. Rapid Evolution of Blood-Brain-Barrier-Penetrating AAV Capsids by RNA-Driven Biopanning. *Mol. Ther. Methods Clin. Dev.* **20**:366–378. [6]

Noor, A., L. Dupuis, K. Mittal, et al. 2015. 15q11.2 Duplication Encompassing Only the *UBE3A* Gene Is Associated with Developmental Delay and Neuropsychiatric Phenotypes. *Hum. Mutat.* **36**:689–693. [5]

Nott, A., I. R. Holtman, N. G. Coufal, et al. 2019. Brain Cell Type-Specific Enhancer-Promoter Interactome Maps and Disease-Risk Association. *Science* **366**:1134–1139. [10]

Nowakowski, T. J., A. Bhaduri, A. A. Pollen, et al. 2017. Spatiotemporal Gene Expression Trajectories Reveal Developmental Hierarchies of the Human Cortex. *Science* **358**:1318–1323. [11]

O'Brien, H. E., E. Hannon, M. J. Hill, et al. 2018. Expression Quantitative Trait Loci in the Developing Human Brain and Their Enrichment in Neuropsychiatric Disorders. *Genome Biol.* **19**:194. [11]

Ochoa, D., M. Karim, M. Ghoussaini, et al. 2022. Human Genetics Evidence Supports Two-Thirds of the 2021 FDA-Approved Drugs. *Nat. Rev. Drug Discov.* **21**:551. [8]

O'Connor, L. J., A. P. Schoech, F. Hormozdiari, et al. 2019. Extreme Polygenicity of Complex Traits Is Explained by Negative Selection. *Am. J. Hum. Genet.* **105**:456–476. [3]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Oetjens, M. T., M. A. Kelly, A. C. Sturm, C. L. Martin, and D. H. Ledbetter. 2019. Quantifying the Polygenic Contribution to Variable Expressivity in Eleven Rare Genetic Disorders. *Nat. Commun.* **10**:4897. [13]

Okano, H., K. Hikishima, A. Iriki, and E. Sasaki. 2012. The Common Marmoset as a Novel Animal Model System for Biomedical and Neuroscience Research Applications. *Semin. Fetal Neonatal Med.* **17**:336–340. [5]

Oldham, M. C., G. Konopka, K. Iwamoto, et al. 2008. Functional Organization of the Transcriptome in Human Brain. *Nat. Neurosci.* **11**:1271–1282. [11]

Olney, J. W., J. W. Newcomer, and N. B. Farber. 1999. NMDA Receptor Hypofunction Model of Schizophrenia. *J. Psychiatr. Res.* **33**:523–533. [11]

Onishi, K., S. S. Kikuchi, T. Abe, T. Tokuhara, and T. Shimogori. 2022. Molecular Cell Identities in the Mediodorsal Thalamus of Infant Mice and Marmoset. *J. Comp. Neurol.* **530**:963–977. [5]

Orlando, L. A., C. Voils, C. R. Horowitz, et al. 2019. Ignite Network: Response of Patients to Genomic Medicine Interventions. *Mol. Genet. Genomic Med.* **7**:e636. [13]

Ormond, K. E., M. Y. Laurino, K. Barlow-Stewart, et al. 2018. Genetic Counseling Globally: Where Are We Now? *Am. J. Med. Genet. B Neuropsychiatr. Genet.* **178**:98–107. [15]

O'Roak, B. J., H. A. Stessman, E. A. Boyle, et al. 2014. Recurrent *de Novo* Mutations Implicate Novel Genes Underlying Simplex Autism Risk. *Nat. Commun.* **5**:5595. [7]

O'Roak, B. J., L. Vives, W. Fu, et al. 2012a. Multiplex Targeted Sequencing Identifies Recurrently Mutated Genes in Autism Spectrum Disorders. *Science* **338**:1619–1622. [7]

O'Roak, B. J., L. Vives, S. Girirajan, et al. 2012b. Sporadic Autism Exomes Reveal a Highly Interconnected Protein Network of *de Novo* Mutations. *Nature* **485**:246–250. [11]

O'Sullivan, J. W., S. Raghavan, C. Marquez-Luna, et al. 2022. Polygenic Risk Scores for Cardiovascular Disease: A Scientific Statement from the American Heart Association. *Circulation* **146**:e93–e118. [13]

Overwater, I. E., A. B. Rietman, S. E. Mous, et al. 2019. A Randomized Controlled Trial with Everolimus for IQ and Autism in Tuberous Sclerosis Complex. *Neurology* **93**:e200–e209. [6]

Owen, M. J., H. J. Williams, and M. C. O'Donovan. 2009. Schizophrenia Genetics: Advancing on Two Fronts. *Curr. Opin. Genet. Dev.* **19**:266–270. [5]

Page, S. C., S. R. Sripathy, F. Farinelli, et al. 2022. Electrophysiological Measures from Human iPSC-Derived Neurons Are Associated with Schizophrenia Clinical Status and Predict Individual Cognitive Performance. *PNAS* **119**:e2109395119. [8]

Pain, O., F. Dudbridge, A. G. Cardno, et al. 2018. Genome-Wide Analysis of Adolescent Psychotic-Like Experiences Shows Genetic Overlap with Psychiatric Disorders. *Am. J. Med. Genet. B Neuropsychiatr. Genet.* **177**:416–425. [2]

Pain, O., A. C. Gillett, J. C. Austin, L. Folkersen, and C. M. Lewis. 2022a. A Tool for Translating Polygenic Scores onto the Absolute Scale Using Summary Statistics. *Eur. J. Hum. Genet.* **30**:339–348. [13]

Pain, O., K. Hodgson, V. Trubetskoy, et al. 2022b. Identifying the Common Genetic Basis of Antidepressant Response. *Biol. Psychiatry Glob. Open Sci.* **2**:115–126. [12, 14]

Pak, C., T. Danko, V. R. Mirabella, et al. 2021. Cross-Platform Validation of Neurotransmitter Release Impairments in Schizophrenia Patient-Derived NRXN1-Mutant Neurons. *PNAS* **118**:e2025598118. [1]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Pak, C., T. Danko, Y. Zhang, et al. 2015. Human Neuropsychiatric Disease Modeling Using Conditional Deletion Reveals Synaptic Transmission Defects Caused by Heterozygous Mutations in NRXN1. *Cell Stem Cell* **17**:316–328. [5, 7]

Palmer, D. S., D. P. Howrigan, S. B. Chapman, et al. 2022. Exome Sequencing in Bipolar Disorder Identifies AKAP11 as a Risk Gene Shared with Schizophrenia. *Nat. Genet.* **54**:541–547. [3, 7]

Palmer, M. J., A. J. Irving, G. R. Seabrook, D. E. Jane, and G. L. Collingridge. 1997. The Group I mGlu Receptor Agonist Dhpg Induces a Novel Form of LTD in the CA1 Region of the Hippocampus. *Neuropharmacol.* **36**:1517–1532. [5]

Pankevich, D. E., B. M. Altevogt, J. Dunlop, F. H. Gage, and S. E. Hyman. 2014. Improving and Accelerating Drug Development for Nervous System Disorders. *Neuron* **84**:546–553. [6]

Pardiñas, A. F., P. Holmans, A. J. Pocklington, et al. 2018. Common Schizophrenia Alleles Are Enriched in Mutation-Intolerant Genes and in Regions under Strong Background Selection. *Nat. Genet.* **50**:381–389. [7, 10]

Pardiñas, A. F., M. Nalmpanti, A. J. Pocklington, et al. 2019. Pharmacogenomic Variants and Drug Interactions Identified through the Genetic Analysis of Clozapine Metabolism. *Am. J. Psychiatry* **176**:477–486. [4]

Pardiñas, A. F., M. J. Owen, and J. T. R. Walters. 2021. Pharmacogenomics: A Road Ahead for Precision Medicine in Psychiatry. *Neuron* **109**:3914–3929. [13]

Parellada, M., Á. Andreu-Bernabeu, M. Burdeus, et al. 2023. In Search of Biomarkers to Guide Interventions in Autism Spectrum Disorder: A Systematic Review. *Am. J. Psychiatry* **180**:23–40. [5]

Parikshak, N. N., M. J. Gandal, and D. H. Geschwind. 2015. Systems Biology and Gene Networks in Neurodevelopmental and Neurodegenerative Disorders. *Nat. Rev. Genet.* **16**:441–458. [11]

Parikshak, N. N., R. Luo, A. Zhang, et al. 2013. Integrative Functional Genomic Analyses Implicate Specific Molecular Pathways and Circuits in Autism. *Cell* **155**:1008–1021. [3, 5, 11]

Parikshak, N. N., V. Swarup, T. G. Belgard, et al. 2016. Genome-Wide Changes in Incrna, Splicing, and Regional Gene Expression Patterns in Autism. *Nature* **540**:423–427. [11]

Park, C. Y., J. Zhou, A. K. Wong, et al. 2021. Genome-Wide Landscape of RNA-Binding Protein Target Site Dysregulation Reveals a Major Impact on Psychiatric Disorder Risk. *Nat. Genet.* **53**:166–173. [11]

Pasaniuc, B., and A. L. Price. 2017. Dissecting the Genetics of Complex Traits Using Summary Association Statistics. *Nat. Rev. Genet.* **18**:117–127. [9]

Paşca, A. M., S. A. Sloan, L. E. Clarke, et al. 2015. Functional Cortical Neurons and Astrocytes from Human Pluripotent Stem Cells in 3D Culture. *Nat. Methods* **12**:671–678. [7]

Paşca, S. P. 2019. Assembling Human Brain Organoids. *Science* **363**:126. [7]

Paşca, S. P., P. Arlotta, H. S. Bateup, et al. 2022. A Nomenclature Consensus for Nervous System Organoids and Assembloids. *Nature* **609**:907–910. [5]

Paşca, S. P., T. Portmann, I. Voineagu, et al. 2011. Using iPSC-Derived Neurons to Uncover Cellular Phenotypes Associated with Timothy Syndrome. *Nat. Med.* **17**:1657–1662. [7]

Patch, C., and A. Middleton. 2018. Genetic Counselling in the Era of Genomic Medicine. *Br. Med. Bull.* **126**:27–36. [12]

Paulsen, B., S. Velasco, A. J. Kedaigle, et al. 2022. Autism Genes Converge on Asynchronous Development of Shared Neuron Classes. *Nature* **602**:268–273. [7]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Pearce, M., L. Garcia, A. Abbas, et al. 2022. Association between Physical Activity and Risk of Depression: A Systematic Review and Meta-Analysis. *JAMA Psychiatry* **79**:550–559. [13]

Pearl, R. L., and M. S. Lebowitz. 2014. Beyond Personal Responsibility: Effects of Causal Attributions for Overweight and Obesity on Weight-Related Beliefs, Stigma, and Policy Support. *Psychol. Health* **29**:1176–1191. [14]

Peay, H. L., and J. C. Austin. 2011. How to Talk with Families About Genetics and Psychiatric Illness. New York: W. W. Norton. [15]

Peca, J., C. Feliciano, J. T. Ting, et al. 2011. Shank3 Mutant Mice Display Autistic-Like Behaviours and Striatal Dysfunction. *Nature* **472**:437–442. [7]

Peck, L., K. Borle, L. Folkersen, and J. Austin. 2022. Why Do People Seek out Polygenic Risk Scores for Complex Disorders, and How Do They Understand and React to Results? *Eur. J. Hum. Genet.* **30**:81–87. [12, 13, 15]

Penagarikano, O., B. S. Abrahams, E. I. Herman, et al. 2011. Absence of CNTNAP2 Leads to Epilepsy, Neuronal Migration Abnormalities, and Core Autism-Related Deficits. *Cell* **147**:235–246. [7]

Penner-Goeke, S., M. Bothe, N. Kappelmann, et al. 2022. *Preprint*: Assessment of Glucocorticoid-Induced Enhancer Activity of Esnp Regions Using Starr-Seq Reveals Novel Molecular Mechanisms in Psychiatric Disorders. *MedRxiv* 22275090. [8]

Pereira, S., K. A. Muñoz, B. J. Small, et al. 2022. Psychiatric Polygenic Risk Scores: Child and Adolescent Psychiatrists' Knowledge, Attitudes, and Experiences. *Am. J. Med. Genet. B Neuropsychiatr. Genet.* **189**:293–302. [12]

Perkins, D. O., L. Olde Loohuis, J. Barbee, et al. 2020. Polygenic Risk Score Contribution to Psychosis Prediction in a Target Population of Persons at Clinical High Risk. *Am. J. Psychiatry* **177**:155–163. [13]

Pers, T. H., J. M. Karjalainen, Y. Chan, et al. 2015. Biological Interpretation of Genome-Wide Association Studies Using Predicted Gene Functions. *Nat. Commun.* **6**:5890. [11]

Persons, J. B. 1986. The Advantages of Studying Psychological Phenomena Rather Than Psychiatric Diagnoses. *Am. Psychol.* **41**:1252–1260. [2]

Petersen, A. H., and T. Lange. 2020. What Is the Causal Interpretation of Sibling Comparison Designs? *Epidemiology* **31**:75–81. [4]

Peterson, R. E., N. Cai, A. W. Dahl, et al. 2018. Molecular Genetic Analysis Subdivided by Adversity Exposure Suggests Etiologic Heterogeneity in Major Depression. *Am. J. Psychiatry* **175**:545–554. [2]

Petrazzini, B. O., K. Chaudhary, C. Marquez-Luna, et al. 2022. Coronary Risk Estimation Based on Clinical Data in Electronic Health Records. *J. Am. Coll. Cardiol.* **79**:1155–1166. [13]

Peyrot, W. J., D. I. Boomsma, B. W. Penninx, and N. R. Wray. 2016. Disease and Polygenic Architecture: Avoid Trio Design and Appropriately Account for Unscreened Control Subjects for Common Disease. *Am. J. Hum. Genet.* **98**:382–391. [2]

Peyrot, W. J., and A. L. Price. 2021. Identifying Loci with Different Allele Frequencies among Cases of Eight Psychiatric Disorders Using CC-GWAS. *Nat. Genet.* **53**:445–454. [2]

Pino, M. G., K. A. Rich, and S. J. Kolb. 2021. Update on Biomarkers in Spinal Muscular Atrophy. *Biomark. Insights* **16**:11772719211035643. [5]

Pintacuda, G., Y.-H. H. Hsu, K. Tsafou, et al. 2021. *Preprint*: Interaction Studies of Risk Proteins in Human Induced Neurons Reveal Convergent Biology and Novel Mechanisms Underlying Autism Spectrum Disorders. *medRxiv* 21264575. [11]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Pinto, D., A. T. Pagnamenta, L. Klei, et al. 2010. Functional Impact of Global Rare Copy Number Variation in Autism Spectrum Disorders. *Nature* **466**:368–372. [11]

Plomin, R. 2014. Genotype-Environment Correlation in the Era of DNA. *Behav. Genet.* **44**:629–638. [2]

Polderman, T. J., B. Benyamin, C. A. de Leeuw, et al. 2015. Meta-Analysis of the Heritability of Human Traits Based on Fifty Years of Twin Studies. *Nat. Genet.* **47**:702–709. [7]

Polioudakis, D., L. de la Torre-Ubieta, J. Langerman, et al. 2019. A Single-Cell Transcriptomic Atlas of Human Neocortical Development during Mid-Gestation. *Neuron* **103**:785–801. [11]

Polygenic Risk Score Task Force of the Intl. Common Disease Alliance. 2021. Responsible Use of Polygenic Risk Scores in the Clinic: Potential Benefits, Risks and Gaps. *Nat. Med.* **27**:1876–1884. [13]

Popejoy, A. B., D. I. Ritter, K. Crooks, et al. 2018. The Clinical Imperative for Inclusivity: Race, Ethnicity, and Ancestry (REA) in Genomics. *Hum. Mutat.* **39**:1713–1720. [3]

Power, R. A., S. Kyaga, R. Uher, et al. 2013. Fecundity of Patients with Schizophrenia, Autism, Bipolar Disorder, Depression, Anorexia Nervosa, or Substance Abuse vs Their Unaffected Siblings. *JAMA Psychiatry* **70**:22–30. [3]

Pratt, B. M., and H. Won. 2022. Advances in Profiling Chromatin Architecture Shed Light on the Regulatory Dynamics Underlying Brain Disorders. *Semin. Cell Dev. Biol.* **121**:153–160. [10]

Privé, F., B. J. Vilhjálmsson, H. Aschard, and M. G. B. Blum. 2019. Making the Most of Clumping and Thresholding for Polygenic Scores. *Am. J. Hum. Genet.* **105**:1213–1221. [13]

Prohl, A. K., B. Scherrer, X. Tomas-Fernandez, et al. 2019. Reproducibility of Structural and Diffusion Tensor Imaging in the Tacern Multi-Center Study. *Front. Integr. Neurosci.* **13**:24. [5]

Psaty, B. M., C. J. O'Donnell, V. Gudnason, et al. 2009. Cohorts for Heart and Aging Research in Genomic Epidemiology (Charge) Consortium: Design of Prospective Meta-Analyses of Genome-Wide Association Studies from 5 Cohorts. *Circ. Cardiovasc. Genet.* **2**:73–80. [8]

PsychENCODE Consortium, S. Akbarian, C. Liu, et al. 2015. The Psychencode Project. *Nat. Neurosci.* **18**:1707–1712. [5, 8, 11]

Purcell, S. M., J. L. Moran, M. Fromer, et al. 2014. A Polygenic Burden of Rare Disruptive Mutations in Schizophrenia. *Nature* **506**:185–190. [7, 11]

Purves, K. L., J. R. I. Coleman, S. M. Meier, et al. 2020. A Major Role for Common Genetic Variation in Anxiety Disorders. *Mol. Psychiatry* **25**:3292–3303. [3]

Qi, L. S., M. H. Larson, L. A. Gilbert, et al. 2013. Repurposing CRISPR as an RNA-Guided Platform for Sequence-Specific Control of Gene Expression. *Cell* **152**:1173–1183. [5]

Qian, X., H. N. Nguyen, M. M. Song, et al. 2016. Brain-Region-Specific Organoids Using Mini-Bioreactors for Modeling Zikv Exposure. *Cell* **165**:1238–1254. [7]

Qiu, Y., T. Arbogast, S. M. Lorenzo, et al. 2019. Oligogenic Effects of 16p11.2 Copy-Number Variation on Craniofacial Development. *Cell Rep.* **28**:3320–3328. [5]

Quaid, K. A., S. R. Aschen, C. L. Smiley, and J. I. Nurnberger. 2001. Perceived Genetic Risks for Bipolar Disorder in a Patient Population: An Exploratory Study. *J. Genet. Counsel.* **10**:41–51. [15]

Quinn, V., B. Meiser, A. Wilde, et al. 2014. Preferences Regarding Targeted Education and Risk Assessment in People with a Family History of Major Depressive Disorder. *J. Genet. Counsel.* **23**:785–795. [15]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Rabani, M., L. Pieper, G. L. Chew, and A. F. Schier. 2017. A Massively Parallel Reporter Assay of 3'UTR Sequences Identifies *in Vivo* Rules for mRNA Degradation. *Mol. Cell* **68**:1083–1094. [8]

Rajarajan, P., T. Borrman, W. Liao, et al. 2018. Neuron-Specific Signatures in the Chromosomal Connectome Associated with Schizophrenia Risk. *Science* **362**:eaat4311. [7]

Rajkumar, A. P., B. Poonkuzhali, A. Kuruvilla, M. Jacob, and K. S. Jacob. 2013. Clinical Predictors of Serum Clozapine Levels in Patients with Treatment-Resistant Schizophrenia. *Int. Clin. Psychopharmacol.* **28**:50–56. [4]

Ramaswami, G., H. Won, M. J. Gandal, et al. 2020. Integrative Genomics Identifies a Convergent Molecular Subtype That Links Epigenomic with Transcriptomic Differences in Autism. *Nat. Commun.* **11**:4873. [11]

Raznahan, A., H. Won, D. C. Glahn, and S. Jacquemont. 2022. Convergence and Divergence of Rare Genetic Disorders on Brain Phenotypes: A Review. *JAMA Psychiatry* **79**:818–828. [1]

Readhead, B., B. J. Hartley, B. J. Eastwood, et al. 2018. Expression-Based Drug Screening of Neural Progenitor Cells from Individuals with Schizophrenia. *Nat. Commun.* **9**:4412. [7]

Rees, E., H. D. J. Creeth, H. G. Hwu, et al. 2021. Schizophrenia, Autism Spectrum Disorders and Developmental Disorders Share Specific Disruptive Coding Mutations. *Nat. Commun.* **12**:5353. [7]

Reid, N. J., D. G. Brockman, C. Elisabeth Leonard, R. Pelletier, and A. V. Khera. 2021. Concordance of a High Polygenic Score Among Relatives: Implications for Genetic Counseling and Cascade Screening. *Circ. Genom. Precis. Med.* **14**:e003262. [13]

Resta, R. G. 1997. The Historical Perspective: Sheldon Reed and 50 Years of Genetic Counseling. *J. Genet. Counsel.* **6**:375–377. [15]

———. 2006. Defining and Redefining the Scope and Goals of Genetic Counseling. *Am. J. Med. Genet. C Semin. Med. Genet.* **142**:269–275. [15]

Resta, R. G., B. B. Biesecker, R. L. Bennett, et al. 2006. A New Definition of Genetic Counseling: National Society of Genetic Counselors' Task Force Report. *J. Genet. Counsel.* **15**:77–83. [12, 15]

Reveley, A. 1985. Genetic Counselling for Schizophrenia. *Br. J. Psychiatry* **147**:107–112. [15]

Rimfeld, K., M. Malanchini, T. Spargo, et al. 2019. Twins Early Development Study: A Genetically Sensitive Investigation into Behavioral and Cognitive Development from Infancy to Emerging Adulthood. *Twin Res. Hum. Genet.* **22**:508–513. [2]

Rinaldi, C., and M. J. A. Wood. 2018. Antisense Oligonucleotides: The Next Frontier for Treatment of Neurological Disorders. *Nat. Rev. Neurol.* **14**:9–21. [5]

Ripke, S., C. O'Dushlaine, K. Chambert, et al. 2013. Genome-Wide Association Analysis Identifies 13 New Risk Loci for Schizophrenia. *Nat. Genet.* **45**:1150–1159. [9]

Ritchie, M. D., E. R. Holzinger, R. Li, S. A. Pendergrass, and D. Kim. 2015. Methods of Integrating Data to Uncover Genotype-Phenotype Interactions. *Nat. Rev. Genet.* **16**:85–97. [11]

Rizzardi, L. F., P. F. Hickey, V. Rodriguez DiBlasi, et al. 2019. Neuronal Brain-Region-Specific DNA Methylation and Chromatin Accessibility Are Associated with Neuropsychiatric Trait Heritability. *Nat. Neurosci.* **22**:307–316. [11]

Robins, C., Y. Liu, W. Fan, et al. 2021. Genetic Control of the Human Brain Proteome. *Am. J. Hum. Genet.* **108**:400–410. [11]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Robinson, E. B., K. E. Samocha, J. A. Kosmicki, et al. 2014. Autism Spectrum Disorder Severity Reflects the Average Contribution of *de Novo* and Familial Influences. *PNAS* **111**:15161–15165. [9]

Rodrigues, S. M., E. P. Bauer, C. R. Farb, G. E. Schafe, and J. E. LeDoux. 2002. The Group I Metabotropic Glutamate Receptor mGluR5 Is Required for Fear Memory Formation and Long-Term Potentiation in the Lateral Amygdala. *J. Neurosci.* **22**:5219–5229. [5]

Ronald, A., N. de Bode, and T. J. Polderman. 2021. Systematic Review: How the Attention-Deficit/Hyperactivity Disorder Polygenic Risk Score Adds to Our Understanding of ADHD and Associated Traits. *J. Am. Acad. Child Adolesc. Psychiatry* **60**:1234–1277. [2]

Ronald, A., H. Larsson, H. Anckarsater, and P. Lichtenstein. 2011. A Twin Study of Autism Symptoms in Sweden. *Mol. Psychiatry* **16**:1039–1047. [2]

Rosenberg, A. B., R. P. Patwardhan, J. Shendure, and G. Seelig. 2015. Learning the Sequence Determinants of Alternative Splicing from Millions of Random Sequences. *Cell* **163**:698–711. [8]

Rosenthal, D., I. Goldberg, B. Jacobsen, et al. 1974. Migration, Heredity, and Schizophrenia. *Psychiatry* **37**:321–339. [4]

Rotaru, D. C., G. M. van Woerden, I. Wallaard, and Y. Elgersma. 2018. Adult *Ube3a* Gene Reinstatement Restores the Electrophysiological Deficits of Prefrontal Cortex Layer 5 Neurons in a Mouse Model of Angelman Syndrome. *J. Neurosci.* **38**:8011–8030. [5]

Roussos, P., P. Katsel, K. L. Davis, L. J. Siever, and V. Haroutunian. 2012. A System-Level Transcriptomic Analysis of Schizophrenia Using Postmortem Brain Tissue Samples. *Arch. Gen. Psychiatry* **69**:1205–1213. [11]

Roussos, P., A. C. Mitchell, G. Voloudakis, et al. 2014. A Role for Noncoding Variation in Schizophrenia. *Cell Rep.* **9**:1417–1429. [7]

Ruan, Y., Y. F. Lin, Y. A. Feng, et al. 2022. Improving Polygenic Prediction in Ancestrally Diverse Populations. *Nat. Genet.* **54**:573–580. [13]

Ruderfer, D. M., A. W. Charney, B. Readhead, et al. 2016. Polygenic Overlap between Schizophrenia Risk and Antipsychotic Response: A Genomic Medicine Approach. *Lancet Psychiatry* **3**:350–357. [7]

Ruth, K. S., F. R. Day, J. Tyrrell, et al. 2020. Using Human Genetics to Understand the Disease Impacts of Testosterone in Men and Women. *Nat. Med.* **26**:252–258. [9]

Ruzzo, E. K., L. Perez-Cano, J. Y. Jung, et al. 2019. Inherited and *de Novo* Genetic Risk for Autism Impacts Shared Networks. *Cell* **178**:850–866. [7]

Ryan, J., A. Virani, and J. C. Austin. 2015. Ethical Issues Associated with Genetic Counseling in the Context of Adolescent Psychiatry. *Appl. Transl. Genom.* **5**:23–29. [12]

Sabo, A., D. Murdock, S. Dugan, et al. 2020. Community-Based Recruitment and Exome Sequencing Indicates High Diagnostic Yield in Adults with Intellectual Disability. *Mol. Genet. Genomic Med.* **8**:e1439. [12]

Saby, J. N., T. A. Benke, S. U. Peters, et al. 2021. Multisite Study of Evoked Potentials in Rett Syndrome. *Ann. Neurol.* **89**:790–802. [5]

Sahin, M., S. R. Jones, J. A. Sweeney, et al. 2018. Discovering Translational Biomarkers in Neurodevelopmental Disorders. *Nat. Rev. Drug Discov.* **18**:235–236. [5, 6]

Sahin, M., and M. Sur. 2015. Genes, Circuits, and Precision Therapies for Autism and Related Neurodevelopmental Disorders. *Science* **350**:aab3897. [6]

Sakai, Y., C. A. Shaw, B. C. Dawson, et al. 2011. Protein Interactome Reveals Converging Molecular Pathways among Autism Disorders. *Sci. Transl. Med.* **3**:86ra49. [11]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Sánchez Fernández, I., T. Loddenkemper, M. Gaínza-Lein, B. R. Sheidley, and A. Poduri. 2019. Diagnostic Yield of Genetic Tests in Epilepsy: A Meta-Analysis and Cost-Effectiveness Study. *Neurology* **92**:e418–428. [12]

Sanders, S. J., A. J. Campbell, J. R. Cottrell, et al. 2018. Progress in Understanding and Treating SCN2A-Mediated Disorders. *Trends Neurosci.* **41**:442–456. [3, 5]

Sanders, S. J., X. He, A. J. Willsey, et al. 2015. Insights into Autism Spectrum Disorder Genomic Architecture and Biology from 71 Risk Loci. *Neuron* **87**:1215–1233. [5–7, 11]

Sanders, S. J., M. T. Murtha, A. R. Gupta, et al. 2012. *De Novo* Mutations Revealed by Whole-Exome Sequencing Are Strongly Associated with Autism. *Nature* **485**:237–241. [7]

Sanders, S. J., B. M. Neale, H. Huang, et al. 2017. Whole Genome Sequencing in Psychiatric Disorders: The WGSPD Consortium. *Nat. Neurosci.* **20**:1661–1668. [3, 5]

Sanders, S. J., M. Sahin, J. Hostyk, et al. 2019. A Framework for the Investigation of Rare Genetic Disorders in Neuropsychiatry. *Nat. Med.* **25**:1477–1487. [6]

Sanderson, E., M. M. Glymour, M. V. Holmes, et al. 2022. Mendelian Randomization. *Nat. Rev. Meth. Primers* **2**:6. [4]

Sandweiss, A. J., V. L. Brandt, and H. Y. Zoghbi. 2020. Advances in Understanding of Rett Syndrome and MECP2 Duplication Syndrome: Prospects for Future Therapies. *Lancet Neurol.* **19**:689–698. [1]

Sanghani, H. R., A. Jagannath, T. Humberstone, et al. 2021. Patient Fibroblast Circadian Rhythms Predict Lithium Sensitivity in Bipolar Disorder. *Mol. Psychiatry* **26**:5252–5265. [8, 9]

Sanson, K. R., R. E. Hanna, M. Hegde, et al. 2018. Optimized Libraries for CRISPR-Cas9 Genetic Screens with Multiple Modalities. *Nat. Commun.* **9**:5416. [7]

Saragosa-Harris, N. M., N. Chaku, N. MacSweeney, et al. 2022. A Practical Guide for Researchers and Reviewers Using the ABCD Study and Other Large Longitudinal Datasets. *Dev. Cogn. Neurosci.* **55**:101115. [2]

Sariaslan, A., L. Arseneault, H. Larsson, P. Lichtenstein, and S. Fazel. 2020. Risk of Subjection to Violence and Perpetration of Violence in Persons with Psychiatric Disorders in Sweden. *JAMA Psychiatry* **77**:359–367. [4]

Sariaslan, A., A. Kääriälä, J. Pitkänen, et al. 2021a. Long-Term Health and Social Outcomes in Children and Adolescents Placed in out-of-Home Care. *JAMA Pediatr.* **176**:e214324. [4]

Sariaslan, A., J. Mikkonen, M. Aaltonen, et al. 2021b. No Causal Associations between Childhood Family Income and Subsequent Psychiatric Disorders, Substance Misuse and Violent Crime Arrests: A Nationwide Finnish Study of >650 000 Individuals and Their Siblings. *Int. J. Epidemiol.* **50**:1628–1638. [4]

Sasaki, E., H. Suemizu, A. Shimada, et al. 2009. Generation of Transgenic Non-Human Primates with Germline Transmission. *Nature* **459**:523–527. [5]

Satterstrom, F. K., J. A. Kosmicki, J. Wang, et al. 2020. Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. *Cell* **180**:568–584.e523. [3, 5–7, 11]

Satterstrom, F. K., R. K. Walters, T. Singh, et al. 2019. Autism Spectrum Disorder and Attention Deficit Hyperactivity Disorder Have a Similar Burden of Rare Protein-Truncating Variants. *Nat. Neurosci.* **22**:1961–1965. [3]

Savatt, J. M., and S. M. Myers. 2021. Genetic Testing in Neurodevelopmental Disorders. *Front. Pediatr.* **9**:526779. [12]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Sawiak, S. J., Y. Shiba, L. Oikonomidis, et al. 2018. Trajectories and Milestones of Cortical and Subcortical Development of the Marmoset Brain from Infancy to Adulthood. *Cerebral Cortex* **28**:4440–4453. [8]

Schaefer, G. B., N. J. Mendelsohn, and Professional Practice and Guidelines Committee. 2013. Clinical Genetics Evaluation in Identifying the Etiology of Autism Spectrum Disorders: 2013 Guideline Revisions. *Genet. Med.* **15**:399–407. [13]

Schaid, D. J., W. Chen, and N. B. Larson. 2018. From Genome-Wide Associations to Candidate Causal Variants by Statistical Fine-Mapping. *Nat. Rev. Genet.* **19**:491–504. [8]

Schizophrenia Working Group of the Psychiatric Genomics Consortium. 2014. Biological Insights from 108 Schizophrenia-Associated Genetic Loci. *Nature* **511**:421–427. [8]

Schmid, R. S., X. Deng, P. Panikker, et al. 2021. CRISPR/Cas9 Directed to the *Ube3a* Antisense Transcript Improves Angelman Syndrome Phenotype in Mice. *J. Clin. Invest.* **131**:e142574. [5]

Schork, A. J., H. Won, V. Appadurai, et al. 2019. A Genome-Wide Association Study of Shared Risk across Psychiatric Disorders Implicates Gene Regulation during Fetal Neurodevelopment. *Nat. Neurosci.* **22**:353–361. [2, 7, 11]

Schrode, N., S. M. Ho, K. Yamamuro, et al. 2019. Synergistic Effects of Common Schizophrenia Risk Variants. *Nat. Genet.* **51**:1475–1485. [7, 8]

Schulte, S., M. Gries, A. Christmann, and K.-H. Schäfer. 2021. Using Multielectrode Arrays to Investigate Neurodegenerative Effects of the Amyloid-Beta Peptide. *Bioelectron. Med.* **7**:15. [8]

Sebat, J., B. Lakshmi, D. Malhotra, et al. 2007. Strong Association of *de Novo* Copy Number Mutations with Autism. *Science* **316**:445–449. [3, 7]

Segura, À. G., A. Martinez-Pinteño, P. Gassó, et al. 2022. Metabolic Polygenic Risk Scores Effect on Antipsychotic-Induced Metabolic Dysregulation: A Longitudinal Study in a First Episode Psychosis Cohort. *Schizophr. Res.* **244**:101–110. [13]

Seibert, T. M., C. C. Fan, Y. Wang, et al. 2018. Polygenic Hazard Score to Guide Screening for Aggressive Prostate Cancer: Development and Validation in Large Scale Cohorts. *BMJ* **360**:j5757. [13]

Sekar, A., A. R. Bialas, H. de Rivera, et al. 2016. Schizophrenia Risk from Complex Variation of Complement Component 4. *Nature* **530**:177–183. [3, 5, 11]

Sellgren, C. M., J. Gracias, B. Watmuff, et al. 2019. Increased Synapse Elimination by Microglia in Schizophrenia Patient-Derived Models of Synaptic Pruning. *Nat. Neurosci.* **22**:374–385. [7]

Selten, J.-P., E. Cantor-Graae, J. Slaets, and R. S. Kahn. 2002. Ødegaard's Selection Hypothesis Revisited: Schizophrenia in Surinamese Immigrants to the Netherlands. *Am. J. Psychiatry* **159**:669–671. [4]

Selten, J.-P., J. P. J. Slaets, and R. S. Kahn. 1997. Schizophrenia in Surinamese and Dutch Antillean Immigrants to the Netherlands: Evidence of an Increased Incidence. *Psychol. Med.* **27**:807–811. [4]

Selzam, S., J. R. I. Coleman, A. Caspi, T. E. Moffitt, and R. Plomin. 2018. A Polygenic P Factor for Major Psychiatric Disorders. *Transl. Psychiatry* **8**:205. [2]

Selzam, S., S. J. Ritchie, J. B. Pingault, et al. 2019. Comparing Within- and between-Family Polygenic Score Prediction. *Am. J. Hum. Genet.* **105**:351–363. [2]

Semaka, A., and J. Austin. 2019. Patient Perspectives on the Process and Outcomes of Psychiatric Genetic Counseling: An Empowering Encounter. *J. Genet. Couns.* **28**:856–868. [12, 15]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Sey, N. Y. A., B. Hu, M. Iskhakova, et al. 2022. Chromatin Architecture in Addiction Circuitry Identifies Risk Genes and Potential Biological Mechanisms Underlying Cigarette Smoking and Alcohol Use Traits. *Mol. Psychiatry* **27**:3085–3094. [10]

Sey, N. Y. A., B. Hu, W. Mah, et al. 2020. A Computational Tool (H-MAGMA) for Improved Prediction of Brain-Disorder Risk Genes by Incorporating Brain Chromatin Interaction Profiles. *Nat. Neurosci.* **23**:583–593. [7, 8, 10]

Shah, J. L., J. Scott, P. D. McGorry, et al. 2020. Transdiagnostic Clinical Staging in Youth Mental Health: A First International Consensus Statement. *World Psychiatry* **19**:233–242. [8]

Shakoor, S., H. M. Zavos, C. M. Haworth, et al. 2016. Association between Stressful Life Events and Psychotic Experiences in Adolescence: Evidence for Gene–Environment Correlations. *Br. J. Psychiatry* **208**:532–538. [2]

Shao, Z., H. Noh, W. Bin Kim, et al. 2019. Dysregulated Protocadherin-Pathway Activity as an Intrinsic Defect in Induced Pluripotent Stem Cell-Derived Cortical Interneurons from Subjects with Schizophrenia. *Nat. Neurosci.* **22**:229–242. [7]

Shcheglovitov, A., O. Shcheglovitova, M. Yazawa, et al. 2013. SHANK3 and IGF1 Restore Synaptic Deficits in Neurons from 22q13 Deletion Syndrome Patients. *Nature* **503**:267–271. [7]

Shima, Y., K. Sugino, C. M. Hempel, et al. 2016. A Mammalian Enhancer Trap Resource for Discovering and Manipulating Neuronal Cell Types. *eLife* **5**:e13503. [7]

Shitamukai, A., D. Konno, and F. Matsuzaki. 2011. Oblique Radial Glial Divisions in the Developing Mouse Neocortex Induce Self-Renewing Progenitors Outside the Germinal Zone That Resemble Primate Outer Subventricular Zone Progenitors. *J. Neurosci.* **31**:3683–3695. [7]

Sieberts, S. K., T. M. Perumal, M. M. Carrasquillo, et al. 2020. Large eQTL Meta-Analysis Reveals Differing Patterns between Cerebral Cortical and Cerebellar Brain Regions. *Sci. Data* **7**:1–11. [3]

Sigström, R., K. Kowalec, L. Jonsson, et al. 2022. Association between Polygenic Risk Scores and Outcome of ECT. *Am. J. Psychiatry* **179**:844–852. [13]

Sigurdsson, T., K. L. Stark, M. Karayiorgou, J. A. Gogos, and J. A. Gordon. 2010. Impaired Hippocampal-Prefrontal Synchrony in a Genetic Mouse Model of Schizophrenia. *Nature* **464**:763–767. [7]

Silbereis, J. C., S. Pochareddy, Y. Zhu, M. Li, and N. Sestan. 2016. The Cellular and Molecular Landscapes of the Developing Human Central Nervous System. *Neuron* **89**:248–268. [11]

Silva-Santos, S., G. M. van Woerden, C. F. Bruinsma, et al. 2015. *Ube3a* Reinstatement Identifies Distinct Developmental Windows in a Murine Angelman Syndrome Model. *J. Clin. Invest.* **125**:2069–2076. [5]

Singh, T., M. I. Kurki, D. Curtis, et al. 2016. Rare Loss-of-Function Variants in Setd1a Are Associated with Schizophrenia and Developmental Disorders. *Nat. Neurosci.* **19**:571–577. [7]

Singh, T., T. Poterba, D. Curtis, et al. 2022. Rare Coding Variants in Ten Genes Confer Substantial Risk for Schizophrenia. *Nature* **604**:509–516. [1–3, 5, 7, 11]

Singh, T., and M. Rajput. 2006. Misdiagnosis of Bipolar Disorder. *Psychiatry* **3**:57–63. [13]

Sinnett, S. E., E. Boyle, C. Lyons, and S. J. Gray. 2021. Engineered microRNA-Based Regulatory Element Permits Safe High-Dose Minimecp2 Gene Therapy in Rett Mice. *Brain* **144**:3005–3019. [6]

Sinnett, S. E., and S. J. Gray. 2017. Recent Endeavors in MECP2 Gene Transfer for Gene Therapy of Rett Syndrome. *Discov. Med.* **24**:153–159. [6]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Sinnott-Armstrong, N., S. Naqvi, M. Rivas, and J. K. Pritchard. 2021. GWAS of Three Molecular Traits Highlights Core Genes and Pathways Alongside a Highly Polygenic Background. *eLife* **10**:e58615. [9]

Skene, N. G., J. Bryois, T. E. Bakken, et al. 2018. Genetic Identification of Brain Cell Types Underlying Schizophrenia. *Nat. Genet.* **50**:825–833. [7, 8, 11]

Slatkin, M. 2008. Exchangeable Models of Complex Inherited Diseases. *Genetics* **179**:2253–2261. [9]

Smoller, J. W., N. Craddock, K. Kendler, et al. 2013. Erratum: Identification of Risk Loci with Shared Effects on Five Major Psychiatric Disorders: A Genome-Wide Analysis. *Lancet* **381**:1371–1379. [2]

So, H. C., and P. C. Sham. 2017. Exploring the Predictive Power of Polygenic Scores Derived from Genome-Wide Association Studies: A Study of 10 Complex Traits. *Bioinformatics* **33**:886–892. [13]

Song, M., M. P. Pebworth, X. Yang, et al. 2020. Cell-Type-Specific 3D Epigenomes in the Developing Human Cortex. *Nature* **587**:644–649. [10]

Sperber, N. R., O. M. Dong, M. C. Roberts, et al. 2021. Strategies to Integrate Genomic Medicine into Clinical Care: Evidence from the Ignite Network. *J. Pers. Med.* **11**:647. [13]

Spiess, K., and H. Won. 2020. Regulatory Landscape in Brain Development and Disease. *Curr. Opin. Genet. Dev.* **65**:53–60. [10]

Spratt, P. W. E., R. Ben-Shalom, C. M. Keeshen, et al. 2019. The Autism-Associated Gene Scn2a Contributes to Dendritic Excitability and Synaptic Function in the Prefrontal Cortex. *Neuron* **103**:673–685. [5, 7]

Srivastava, S., J. A. Love-Nichols, K. A. Dies, et al. 2019. Meta-Analysis and Multidisciplinary Consensus Statement: Exome Sequencing Is a First-Tier Clinical Diagnostic Test for Individuals with Neurodevelopmental Disorders. *Genet. Med.* **21**:2413–2421. [6, 13]

Stahl, E. A., G. Breen, A. J. Forstner, et al. 2019. Genome-Wide Association Study Identifies 30 Loci Associated with Bipolar Disorder. *Nat. Genet.* **51**:793–803. [2]

Stancer, H. C., and D. K. Wagener. 1984. Genetic Counselling: Its Need in Psychiatry and the Directions It Gives for Future Research. *Can. J. Psychiatry* **29**:289–294. [15]

Stein, M. B., D. F. Levey, Z. Cheng, et al. 2021. Genome-Wide Association Analyses of Post-Traumatic Stress Disorder and Its Symptom Subdomains in the Million Veteran Program. *Nat. Genet.* **53**:174–184. [2]

Steinberg, S., S. Gudmundsdottir, G. Sveinbjornsson, et al. 2017. Truncating Mutations in Rbm12 Are Associated with Psychosis. *Nat. Genet.* **49**:1251–1254. [7]

Stern, S., S. Linker, K. C. Vadodaria, M. C. Marchetto, and F. H. Gage. 2018. Prediction of Response to Drug Therapy in Psychiatric Disorders. *Open Biol.* **8**:180031. [7]

Stevenson, A., D. Akena, R. E. Stroud, et al. 2019. Neuropsychiatric Genetics of African Populations-Psychosis (NeuroGAP-Psychosis): A Case-Control Study Protocol and GWAS in Ethiopia, Kenya, South Africa and Uganda. *BMJ Open* **9**:e025469. [2]

Steyerberg, E. W., A. J. Vickers, N. R. Cook, et al. 2010. Assessing the Performance of Prediction Models: A Framework for Traditional and Novel Measures. *Epidemiology* **21**:128–138. [13]

Stoker, T. B., K. E. R. Andresen, and R. A. Barker. 2021. Hydrocephalus Complicating Intrathecal Antisense Oligonucleotide Therapy for Huntington's Disease. *Mov. Disord.* **36**:263–264. [6]

Stoll, G., O. P. H. Pietilainen, B. Linder, et al. 2013. Deletion of TOP3beta, a Component of FMRP-Containing Mrnps, Contributes to Neurodevelopmental Disorders. *Nat. Neurosci.* **16**:1228–1237. [2]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Südhof, T. C. 2008. Neuroligins and Neurexins Link Synaptic Function to Cognitive Disease. *Nature* **455**:903–911. [5]

———. 2017a. Molecular Neuroscience in the 21st Century: A Personal Perspective. *Neuron* **96**:536–541. [7]

———. 2017b. Synaptic Neurexin Complexes: A Molecular Code for the Logic of Neural Circuits. *Cell* **171**:745–769. [5]

———. 2018. Towards an Understanding of Synapse Formation. *Neuron* **100**:276–293. [11]

Sugathan, A., M. Biagioli, C. Golzio, et al. 2014. CHD8 Regulates Neurodevelopmental Pathways Associated with Autism Spectrum Disorder in Neural Progenitors. *PNAS* **111**:E4468–E4477. [11]

Sullivan, P. F. 2005. The Genetics of Schizophrenia. *PLOS Med.* **2**:e212. [5]

———. 2013. Questions About DISC1 as a Genetic Risk Factor for Schizophrenia. *Mol. Psychiatry* **18**:1050–1052. [7]

Sullivan, P. F., A. Agrawal, C. M. Bulik, et al. 2018. Psychiatric Genomics: An Update and an Agenda. *Am. J. Psychiatry* **175**:15–27. [1]

Sullivan, P. F., and D. H. Geschwind. 2019. Defining the Genetic, Genomic, Cellular, and Diagnostic Architectures of Psychiatric Disorders. *Cell* **177**:162–183. [7, 11]

Sun, L., L. Pennells, S. Kaptoge, et al. 2021. Polygenic Risk Scores in Cardiovascular Risk Prediction: A Cohort Study and Modelling Analyses. *PLOS Med.* **18**:e1003498. [13]

Suvrathan, A., C. A. Hoeffer, H. Wong, E. Klann, and S. Chattarji. 2010. Characterization and Reversal of Synaptic Defects in the Amygdala in a Mouse Model of Fragile X Syndrome. *PNAS* **107**:11591–11596. [5]

Szklarczyk, D., A. L. Gable, K. C. Nastou, et al. 2021. The String Database in 2021: Customizable Protein-Protein Networks, and Functional Characterization of User-Uploaded Gene/Measurement Sets. *Nucleic Acids Res.* **49**:D605–D612. [11]

Takahashi, K., K. Tanabe, M. Ohnuki, et al. 2007. Induction of Pluripotent Stem Cells from Adult Human Fibroblasts by Defined Factors. *Cell* **131**:861–872. [7]

Takata, A., N. Matsumoto, and T. Kato. 2017. Genome-Wide Identification of Splicing QTLs in the Human Brain and Their Enrichment among Schizophrenia-Associated Loci. *Nat. Commun.* **8**:14519. [11]

Takata, A., B. Xu, I. Ionita-Laza, et al. 2014. Loss-of-Function Variants in Schizophrenia Risk and Setd1a as a Candidate Susceptibility Gene. *Neuron* **82**:773–780. [7]

Talkowski, M. E., J. A. Rosenfeld, I. Blumenthal, et al. 2012. Sequencing Chromosomal Abnormalities Reveals Neurodevelopmental Loci That Confer Risk across Diagnostic Boundaries. *Cell* **149**:525–537. [7]

Tamura, S., A. D. Nelson, P. W. E. Spratt, et al. 2022. *Preprint*: CRISPR Activation Rescues Abnormalities in *SCN2A* Haploinsufficiency-Associated Autism Spectrum Disorder. *bioRxiv* 486483. [5]

Taniguchi, H., M. He, P. Wu, et al. 2011. A Resource of Cre Driver Lines for Genetic Targeting of GABAergic Neurons in Cerebral Cortex. *Neuron* **71**:995–1013. [7]

Tansey, K. E., M. Guipponi, X. Hu, et al. 2013. Contribution of Common Genetic Variants to Antidepressant Response. *Biol. Psychiatry* **73**:679–682. [13]

Tansey, K. E., E. Rees, D. E. Linden, et al. 2016. Common Alleles Contribute to Schizophrenia in CNV Carriers. *Mol. Psychiatry* **21**:1153. [7]

Taylor, M. J., D. Freeman, S. Lundstrom, H. Larsson, and A. Ronald. 2022. Heritability of Psychotic Experiences in Adolescents and Interaction with Environmental Risk. *JAMA Psychiatry* **79**:889–897. [2]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Tewhey, R., D. Kotliar, D. S. Park, et al. 2016. Direct Identification of Hundreds of Expression-Modulating Variants Using a Multiplexed Reporter Assay. *Cell* **165**:1519–1529. [8]

Thakore, P. I., A. M. D'Ippolito, L. Song, et al. 2015. Highly Specific Epigenome Editing by CRISPR-Cas9 Repressors for Silencing of Distal Regulatory Elements. *Nat. Methods* **12**:1143–1149. [7]

Thomas, K. R., and M. R. Capecchi. 1987. Site-Directed Mutagenesis by Gene Targeting in Mouse Embryo-Derived Stem Cells. *Cell* **51**:503–512. [5]

Thompson, P. M., N. Jahanshad, L. Schmaal, et al. 2022. The Enhancing Neuroimaging Genetics through Meta-Analysis Consortium: 10 Years of Global Collaborations in Human Brain Mapping. *Hum. Brain Mapp.* **43**:15–22. [8]

Thomson, J. A., J. Itskovitz-Eldor, S. S. Shapiro, et al. 1998. Embryonic Stem Cell Lines Derived from Human Blastocysts. *Science* **282**:1145–1147. [7]

Thygesen, J. H., K. Wolfe, A. McQuillin, et al. 2018 Neurodevelopmental Risk Copy Number Variants in Adults with Intellectual Disabilities and Comorbid Psychiatric Disorders. *Br. J. Psychiatry* **212**:287–294. [12]

Tian, R., M. A. Gachechiladze, C. H. Ludwig, et al. 2019. CRISPR Interference-Based Platform for Multimodal Genetic Screens in Human iPSC-Derived Neurons. *Neuron* **104**:239–255. [7]

Till, S. M., A. Asiminas, A. D. Jackson, et al. 2015. Conserved Hippocampal Cellular Pathophysiology but Distinct Behavioural Deficits in a New Rat Model of FXS. *Hum. Mol. Genet.* **24**:5977–5984. [5]

Tillotson, R., J. Selfridge, M. V. Koerner, et al. 2017. Radically Truncated MeCP2 Rescues Rett Syndrome-Like Neurological Defects. *Nature* **550**:398–401. [6]

Timshel, P. N., J. J. Thompson, and T. H. Pers. 2020. Genetic Mapping of Etiologic Brain Cell Types for Obesity. *eLife* **9**:e55851. [9]

Tomioka, I., T. Maeda, H. Shimada, et al. 2010. Generating Induced Pluripotent Stem Cells from Common Marmoset (*Callithrix jacchus*) Fetal Liver Cells Using Defined Factors, Including Lin28. *Genes Cells* **15**:959–969. [5]

Townsley, K. G., K. J. Brennand, and L. M. Huckins. 2020. Massively Parallel Techniques for Cataloguing the Regulome of the Human Brain. *Nat. Neurosci.* **23**:1509–1521. [7]

Townsley, K. G., A. Li, P. J. M. Deans, et al. 2022. *Preprint*: Convergent Impact of Schizophrenia Risk Genes. *bioRxiv* 486286. [7]

Toyonaga, T., A. Fesharaki-Zadeh, S. M. Strittmatter, R. E. Carson, and Z. Cai. 2022. PET Imaging of Synaptic Density: Challenges and Opportunities of Synaptic Vesicle Glycoprotein 2a PET in Small Animal Imaging. *Front. Neurosci.* **16**:787404. [8]

Tremblay, I., A. Janvier, and A. M. Laberge. 2018. Paediatricians Underuse Recommended Genetic Tests in Children with Global Developmental Delay. *Paediatr. Child Health* **23**:e156–e162. [12]

Tremblay, J., M. Haloui, R. Attaoua, et al. 2021. Polygenic Risk Scores Predict Diabetes Complications and Their Response to Intensive Blood Pressure and Glucose Control. *Diabetologia* **64**:2012–2025. [13]

Treutlein, B., O. Gokce, S. R. Quake, and T. C. Südhof. 2014. Cartography of Neurexin Alternative Splicing Mapped by Single-Molecule Long-Read mRNA Sequencing. *PNAS* **111**:E1291–E1299. [11]

Tromp, A., B. Mowry, and J. Giacomotto. 2021. Neurexins in Autism and Schizophrenia-a Review of Patient Mutations, Mouse Models and Potential Future Directions. *Mol. Psychiatry* **26**:747–760. [5]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Trubetskoy, V., A. F. Pardinas, T. Qi, et al. 2022. Mapping Genomic Loci Implicates Genes and Synaptic Biology in Schizophrenia. *Nature* **604**:502–508. [3, 7–9, 11–13]

Trujillo, C. A., R. Gao, P. D. Negraes, et al. 2019. Complex Oscillatory Waves Emerging from Cortical Organoids Model Early Human Brain Network Development. *Cell Stem Cell* **25**:558–569. [5]

Truong, T. K., A. Kenneson, A. R. Rosen, and R. H. Singh. 2021. Genetic Referral Patterns and Responses to Clinical Scenarios: A Survey of Primary Care Providers and Clinical Geneticists. *J. Prim. Care Comm. Health* **12**:21501327211046734. [12]

Tsai, P. T., C. Hull, Y. Chu, et al. 2012. Autistic-Like Behaviour and Cerebellar Dysfunction in Purkinje Cell Tsc1 Mutant Mice. *Nature* **488**:647–651. [6]

Tsai, P. T., S. Rudolph, C. Guo, et al. 2018. Sensitive Periods for Cerebellar-Mediated Autistic-Like Behaviors. *Cell Rep.* **25**:357–367. [5, 6]

Tsuda, Y., J. Saruwatari, and N. Yasui-Furukori. 2014. Meta-Analysis: The Effects of Smoking on the Disposition of Two Commonly Used Antipsychotic Agents, Olanzapine and Clozapine. *BMJ Open* **4**:e004216. [4]

Turissini, M., T. Mercer, J. Baenziger, et al. 2020. Developing Ethical and Sustainable Global Health Educational Exchanges for Clinical Trainees: Implementation and Lessons Learned from the 30-Year Academic Model Providing Access to Healthcare (AMPATH) Partnership. *Ann. Glob. Health* **86**:137. [2]

Turley, P., M. N. Meyer, N. Wang, et al. 2021. Problems with Using Polygenic Scores to Select Embryos. *N. Engl. J. Med.* **385**:78–86. [13, 14]

Turnwald, B. P., J. P. Goyer, D. Z. Boles, et al. 2019. Learning One's Genetic Risk Changes Physiology Independent of Actual Genetic Risk. *Nat. Hum. Behav.* **3**:48–56. [15]

Tyler, J., S. W. Choi, and M. Tewari. 2020. Real-Time, Personalized Medicine through Wearable Sensors and Dynamic Predictive Modeling: A New Paradigm for Clinical Medicine. *Curr. Opin. Syst. Biol.* **20**:17–25. [5]

Udler, M. S., M. I. McCarthy, J. C. Florez, and A. Mahajan. 2019. Genetic Risk Scores for Diabetes Diagnosis and Precision Medicine. *Endocr. Rev.* **40**:1500–1520. [9]

Uebbing, S., J. Gockley, S. K. Reilly, et al. 2021. Massively Parallel Discovery of Human-Specific Substitutions That Alter Enhancer Activity. *PNAS* **118**:e2007049118. [7, 8]

Uezu, A., D. J. Kanak, T. W. A. Bradshaw, et al. 2016. Identification of an Elaborate Complex Mediating Postsynaptic Inhibition. *Science* **353**:1123–1129. [11]

Uhlmann, W. R., J. L. Schuette, and B. Yashar, eds. 2010. A Guide to Genetic Counseling. Hoboken: John Wiley and Sons. [15]

Ure, K., H. Lu, W. Wang, et al. 2016. Restoration of Mecp2 Expression in GABAergic Neurons Is Sufficient to Rescue Multiple Disease Features in a Mouse Model of Rett Syndrome. *eLife* **5**:e14198. [5]

Urresti, J., P. Zhang, P. Moran-Losada, et al. 2021. Cortical Organoids Model Early Brain Development Disrupted by 16p11.2 Copy Number Variants in Autism. *Mol. Psychiatry* **26**:7560–7580. [5]

Valassina, N., S. Brusco, A. Salamone, et al. 2022. *Scn1a* Gene Reactivation after Symptom Onset Rescues Pathological Phenotypes in a Mouse Model of Dravet Syndrome. *Nat. Commun.* **13**:161. [5]

van Alten, S., B. W. Domingue, T. Galama, and A. T. Marees. 2022. *Preprint*: Reweighting the UK Biobank to Reflect Its Underlying Sampling Population Substantially Reduces Pervasive Selection Bias Due to Volunteering. *medRxiv* 22275048. [2]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Van den Adel, B., A. Inglis, and J. Austin. 2022. An Internship in Psychiatric Genetic Counseling: Impact on Genetic Counseling Graduates' Practice and Career Choices. *J. Genet. Counsel.* **31**:1071–1079. [15]

van der Wijst, M. G. P., D. H. de Vries, H. Brugge, H.-J. Westra, and L. Franke. 2018. An Integrative Approach for Building Personalized Gene Regulatory Networks for Precision Medicine. *Genome Med.* **10**:96. [11]

van Loo, H. M., P. de Jonge, J. W. Romeijn, R. C. Kessler, and R. A. Schoevers. 2012. Data-Driven Subtypes of Major Depressive Disorder: A Systematic Review. *BMC Med.* **10**:156. [2]

Van Nostrand, E. L., P. Freese, G. A. Pratt, et al. 2020. A Large-Scale Binding and Functional Map of Human RNA-Binding Proteins. *Nature* **583**:711–719. [11]

Van Os, J., D. J. Castle, N. Takei, G. Der, and R. M. Murray. 1996. Psychotic Illness in Ethnic Minorities: Clarification from the 1991 Census. *Psychol. Med.* **26**:203–208. [4]

Vassena, E., J. Deraeve, and W. H. Alexander. 2017. Predicting Motivation: Computational Models of Pfc Can Explain Neural Coding of Motivation and Effort-Based Decision-Making in Health and Disease. *J. Cogn. Neurosci.* **29**:1633–1645. [2]

Vatine, G. D., R. Barrile, M. J. Workman, et al. 2019. Human iPSC-Derived Blood-Brain Barrier Chips Enable Disease Modeling and Personalized Medicine Applications. *Cell Stem Cell* **24**:995–1005. [7]

Veach, P. M. C., D. M. Bartels, and B. S. LeRoy. 2007. Coming Full Circle: A Reciprocal-Engagement Model of Genetic Counseling Practice. *J. Genet. Counsel.* **16**:713–728. [15]

Velasco, S., A. J. Kedaigle, S. K. Simmons, et al. 2019. Individual Brain Organoids Reproducibly Form Cell Diversity of the Human Cerebral Cortex. *Nature* **570**:523–527. [5, 7]

Velmeshev, D., L. Schirmer, D. Jung, et al. 2019. Single-Cell Genomics Identifies Cell Type-Specific Molecular Changes in Autism. *Science* **364**:685–689. [5, 11]

Vickers, A. J., B. Van Calster, and E. W. Steyerberg. 2016. Net Benefit Approaches to the Evaluation of Prediction Models, Molecular Markers, and Diagnostic Tests. *BMJ* **352**:i6. [13]

Visscher, P. M., W. G. Hill, and N. R. Wray. 2008. Heritability in the Genomics Era: Concepts and Misconceptions. *Nat. Rev. Genet.* **9**:255–266. [7]

Vodopivec, M., S. Laporsek, J. Stare, and M. Vodopivec. 2021. The Effects of Unemployment on Health, Hospitalizations, and Mortality: Evidence from Administrative Data. *SSRN IZA Disc. Paper* **14318**:1–53. [4]

Voineagu, I., X. Wang, P. Johnston, et al. 2011. Transcriptomic Analysis of Autistic Brain Reveals Convergent Molecular Pathology. *Nature* **474**:380–384. [11]

Volpato, V., J. Smith, C. Sandor, et al. 2018. Reproducibility of Molecular Phenotypes after Long-Term Differentiation to Human iPSC-Derived Neurons: A Multi-Site Omics Study. *Stem Cell Rep.* **11**:897–911. [6]

Wainberg, M., G. R. Jacobs, M. di Forti, and S. J. Tripathy. 2021. Cannabis, Schizophrenia Genetic Risk, and Psychotic Experiences: A Cross-Sectional Study of 109,308 Participants from the UK Biobank. *Transl. Psychiatry* **11**:211. [13]

Wainger, B. J., E. Kiskinis, C. Mellin, et al. 2014. Intrinsic Membrane Hyperexcitability of Amyotrophic Lateral Sclerosis Patient-Derived Motor Neurons. *Cell Rep.* **7**:1–11. [5, 6]

Walker, R. L., G. Ramaswami, C. Hartl, et al. 2019. Genetic Control of Expression and Splicing in Developing Human Brain Informs Disease Mechanisms. *Cell* **179**:750–771.e722. [3, 10, 11]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Wang, B., A. M. Mezlini, F. Demir, et al. 2014. Similarity Network Fusion for Aggregating Data Types on a Genomic Scale. *Nat. Methods* **11**:333–337. [11]

Wang, B. S., R. Sarnaik, and J. Cang. 2010. Critical Period Plasticity Matches Binocular Orientation Preference in the Visual Cortex. *Neuron* **65**:246–256. [5]

Wang, D., S. Liu, J. Warrell, et al. 2018. Comprehensive Functional Genomic Resource and Integrative Model for the Human Brain. *Science* **362**:eaat8464. [3, 8, 10, 11]

Wang, D., P. W. L. Tai, and G. Gao. 2019. Adeno-Associated Virus Vector as a Platform for Gene Therapy Delivery. *Nat. Rev. Drug Discov.* **18**:358–378. [6]

Wang, X., and D. B. Goldstein. 2020. Enhancer Domains Predict Gene Pathogenicity and Inform Gene Discovery in Complex Disease. *Am. J. Hum. Genet.* **106**:215–233. [10]

Wang, X., J. W. Tsai, B. LaMonica, and A. R. Kriegstein. 2011. A New Subtype of Progenitor Cell in the Mouse Embryonic Neocortex. *Nat. Neurosci.* **14**:555–561. [7]

Wang, Y., K. Tsuo, M. Kanai, B. M. Neale, and A. R. Martin. 2022. Challenges and Opportunities for Developing More Generalizable Polygenic Risk Scores. *Annu. Rev. Biomed. Data Sci.* **5**:293–320. [13]

Ward, J., N. Graham, R. J. Strawbridge, et al. 2018. Polygenic Risk Scores for Major Depressive Disorder and Neuroticism as Predictors of Antidepressant Response: Meta-Analysis of Three Treatment Cohorts. *PLOS ONE* **13**:e0203896. [13, 14]

Warren, C. R., C. E. Jaquish, and C. A. Cowan. 2017. The Nextgen Genetic Association Studies Consortium: A Foray into *in Vitro* Population Genetics. *Cell Stem Cell* **20**:431–433. [8]

Watanabe, K., S. Stringer, O. Frei, et al. 2019a. A Global Overview of Pleiotropy and Genetic Architecture in Complex Traits. *Nat. Genet.* **51**:1339–1348. [7, 8]

Watanabe, K., E. Taskesen, A. van Bochoven, and D. Posthuma. 2017. Functional Mapping and Annotation of Genetic Associations with Fuma. *Nat. Commun.* **8**:1826. [11]

Watanabe, K., M. Umićević Mirkov, C. A. de Leeuw, M. P. van den Heuvel, and D. Posthuma. 2019b. Genetic Mapping of Cell Type Specificity for Complex Traits. *Nat. Commun.* **10**:3222. [10, 11]

Weiner, D. J., S. Gazal, E. B. Robinson, and L. J. O'Connor. 2022a. Partitioning Gene-Mediated Disease Heritability without eQTLs. *Am. J. Hum. Genet.* **109**:405–416. [3]

Weiner, D. J., E. Ling, S. Erdin, et al. 2022b. Statistical and Functional Convergence of Common and Rare Genetic Influences on Autism at Chromosome 16p. *Nat. Genet.* **54**:1630–1639. [3]

Weiner, D. J., E. M. Wigdor, S. Ripke, et al. 2017. Polygenic Transmission Disequilibrium Confirms That Common and Rare Variation Act Additively to Create Risk for Autism Spectrum Disorders. *Nat. Genet.* **49**:978–985. [7]

Weiss, L. A., Y. Shen, J. M. Korn, et al. 2008. Association between Microdeletion and Microduplication at 16p11.2 and Autism. *N. Engl. J. Med.* **358**:667–675. [5]

Weissbrod, O., M. Kanai, H. Shi, et al. 2022. Leveraging Fine-Mapping and Multipopulation Training Data to Improve Cross-Population Polygenic Risk Scores. *Nat. Genet.* **54**:450–458. [13]

Werling, D. M., H. Brand, J.-Y. An, et al. 2018. An Analytical Framework for Whole-Genome Sequence Association Studies and Its Implications for Autism Spectrum Disorder. *Nat. Genet.* **50**:727–736. [3]

Werling, D. M., S. Pochareddy, J. Choi, et al. 2020. Whole-Genome and RNA Sequencing Reveal Variation and Transcriptomic Coordination in the Developing Human Prefrontal Cortex. *Cell Rep.* **31**:107489. [3, 10, 11]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Werner-Lin, A., J. L. M. McCoyd, and B. A. Bernhardt. 2019. Actions and Uncertainty: How Prenatally Diagnosed Variants of Uncertain Significance Become Actionable. Looking for the Psychosocial Impacts of Genomic Information, Special Report. *Hastings Cent. Rep.* **49**:S61–S71. [14]

Whalen, S., and K. S. Pollard. 2019. Most Chromatin Interactions Are Not in Linkage Disequilibrium. *Genome Res.* **29**:334–343. [8]

Wheat, R., M. Vess, and P. Holte. 2022. Genetic Risk Information Influences Risk-Taking Behavior. *Soc. Cogn.* **40**:387–395. [14]

Wickstrom, J., C. Farmer, L. Green Snyder, et al. 2021. Patterns of Delay in Early Gross Motor and Expressive Language Milestone Attainment in Probands with Genetic Conditions versus Idiopathic ASD from Sfari Registries. *J. Child Psychol. Psychiatry* **62**:1297–1307. [3]

Wilhelm, K., B. Meiser, P. B. Mitchell, et al. 2009. Issues Concerning Feedback About Genetic Testing and Risk of Depression. *Br. J. Psychiatry* **194**:404–410. [14, 15]

Williams, M. S. 2019. Early Lessons from the Implementation of Genomic Medicine Programs. *Annu. Rev. Genomics Hum. Genet.* **20**:389–411. [13]

Williams, M. S., C. O. Taylor, N. A. Walton, et al. 2019. Genomic Information for Clinicians in the Electronic Health Record: Lessons Learned from the Clinical Genome Resource Project and the Electronic Medical Records and Genomics Network. *Front. Genet.* **10**:1059. [13]

Willsey, A. J., M. T. Morris, S. Wang, et al. 2018. The Psychiatric Cell Map Initiative: A Convergent Systems Biological Approach to Illuminating Key Molecular Pathways in Neuropsychiatric Disorders. *Cell* **174**:505–520. [11]

Willsey, A. J., S. J. Sanders, M. Li, et al. 2013. Coexpression Networks Implicate Human Midfetal Deep Cortical Projection Neurons in the Pathogenesis of Autism. *Cell* **155**:997–1007. [3, 5]

Willsey, H. R., C. R. T. Exner, Y. Xu, et al. 2021. Parallel *in Vivo* Analysis of Large-Effect Autism Genes Implicates Cortical Neurogenesis and Estrogen in Risk and Resilence. *Neuron* **109**:788–804. [7]

Windrem, M. S., M. Osipovitch, Z. Liu, et al. 2017. Human iPSC Glial Mouse Chimeras Reveal Glial Contributions to Schizophrenia. *Cell Stem Cell* **21**:195–208. [7]

Wingo, T. S., Y. Liu, E. S. Gerasimov, et al. 2021. Brain Proteome-Wide Association Study Implicates Novel Proteins in Depression Pathogenesis. *Nat. Neurosci.* **24**:810–817. [11]

Wolter, J. M., H. Mao, G. Fragola, et al. 2020. Cas9 Gene Therapy for Angelman Syndrome Traps *Ube3a-Ats* Long Non-Coding RNA. *Nature* **587**:281–284. [5, 6]

Won, H., L. de la Torre-Ubieta, J. L. Stein, et al. 2016. Chromosome Conformation Elucidates Regulatory Relationships in Developing Human Brain. *Nature* **538**:523–527. [10]

Wortmann, S. B., M. M. Oud, M. Alders, et al. 2022. How to Proceed after "Negative" Exome: A Review on Genetic Diagnostics, Limitations, Challenges, and Emerging New Multiomics Techniques. *J. Inherit. Metab. Dis.* **45**:663–681. [12]

Wray, N. R., T. Lin, J. Austin, et al. 2021. From Basic Science to Clinical Application of Polygenic Risk Scores: A Primer. *JAMA Psychiatry* **78**:101–109. [12, 13, 15]

Wray, N. R., and R. Maier. 2014. Genetic Basis of Complex Genetic Disease: The Contribution of Disease Heterogeneity to Missing Heritability. *Curr. Epidemiol. Rep.* **1**:220–227. [2, 9]

Wray, N. R., S. Ripke, M. Mattheisen, et al. 2018a. Genome-Wide Association Analyses Identify 44 Risk Variants and Refine the Genetic Architecture of Major Depression. *Nat. Genet.* **50**:668–681. [7, 15]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)

Wray, N. R., C. Wijmenga, P. F. Sullivan, J. Yang, and P. M. Visscher. 2018b. Common Disease Is More Complex Than Implied by the Core Gene Omnigenic Model. *Cell* **173**:1573–1580. [7, 9]

Wu, Y., Z. Zheng, P. M. Visscher, and J. Yang. 2017. Quantifying the Mapping Precision of Genome-Wide Association Studies Using Whole-Genome Sequencing Data. *Genome Biol.* **18**:86. [8]

Xiang, Y., Y. Tanaka, B. Cakir, et al. 2019. Hesc-Derived Thalamic Organoids Form Reciprocal Projections When Fused with Cortical Organoids. *Cell Stem Cell* **24**:487–497. [7]

Xu, M.-Q., W.-S. Sun, B.-X. Liu, et al. 2009. Prenatal Malnutrition and Adult Schizophrenia: Further Evidence from the 1959-1961 Chinese Famine. *Schizophr. Bull.* **35**:568–576. [4]

Xu, X., A. B. Wells, D. R. O'Brien, A. Nehorai, and J. D. Dougherty. 2014. Cell Type-Specific Expression Analysis to Identify Putative Cellular Mechanisms for Neurogenetic Disorders. *J. Neurosci.* **34**:1420–1431. [11]

Yamazaki, Y., C. Echigo, M. Saiki, et al. 2011. Tool-Use Learning by Common Marmosets (*Callithrix jacchus*). *Exp. Brain Res.* **213**:63–71. [5]

Yang, C., F. H. G. Farias, L. Ibanez, et al. 2021. Genomic Atlas of the Proteome from Brain, Csf and Plasma Prioritizes Proteins Implicated in Neurological Disorders. *Nat. Neurosci.* **24**:1302–1312. [3]

Yang, J., S. H. Lee, M. E. Goddard, and P. M. Visscher. 2011. Gcta: A Tool for Genome-Wide Complex Trait Analysis. *Am. J. Hum. Genet.* **88**:76–82. [2]

Yang, S., and X. Zhou. 2022. Pgs-Server: Accuracy, Robustness and Transferability of Polygenic Score Methods for Biobank Scale Studies. *Brief. Bioinform.* **23**:bbac039. [2]

Yengo, L., S. Vedantam, E. Marouli, et al. 2022. *Preprint*: A Saturated Map of Common Genetic Variants Associated with Human Height from 5.4 Million Individuals of Diverse Ancestries. *bioRxiv* 475305. [2]

Yeo, N. C., A. Chavez, A. Lance-Byrne, et al. 2018. An Enhanced CRISPR Repressor for Targeted Mammalian Gene Regulation. *Nat. Methods* **15**:611–616. [10]

Yi, F., T. Danko, S. C. Botelho, et al. 2016. Autism-Associated SHANK3 Haploinsufficiency Causes Ih Channelopathy in Human Neurons. *Science* **352**:aaf2669. [7]

Yilmaz, M., E. Yalcin, J. Presumey, et al. 2021. Overexpression of Schizophrenia Susceptibility Factor Human Complement C4A Promotes Excessive Synaptic Loss and Behavioral Changes in Mice. *Nat. Neurosci.* **24**:214–224. [1]

Yoshimizu, T., J. Q. Pan, A. E. Mungenast, et al. 2015. Functional Implications of a Psychiatric Risk Variant within CACNA1C in Induced Human Neurons. *Mol. Psychiatry* **20**:162–169. [7]

Yu, A. W., J. D. Peery, and H. Won. 2021. Limited Association between Schizophrenia Genetic Risk Factors and Transcriptomic Features. *Genes* **12**:1062. [10]

Yu, D. X., F. P. Di Giorgio, J. Yao, et al. 2014. Modeling Hippocampal Neurogenesis Using Human Pluripotent Stem Cells. *Stem Cell Rep.* **2**:295–310. [7]

Zaneva, M., C. Guzman-Holst, A. Reeves, and L. Bowes. 2022. The Impact of Monetary Poverty Alleviation Programs on Children's and Adolescents' Mental Health: A Systematic Review and Meta-Analysis across Low-, Middle-, and High-Income Countries. *J. Adolesc. Health* **71**:147–156. [4]

Zebrowski, A. M., D. E. Ellis, F. K. Barg, et al. 2019. Qualitative Study of System-Level Factors Related to Genomic Implementation. *Genet. Med.* **21**:1534–1540. [13]

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Zeier, Z., L. L. Carpenter, N. H. Kalin, et al. 2018. Clinical Implementation of Pharmacogenetic Decision Support Tools for Antidepressant Drug Prescribing. *Am. J. Psychiatry* **175**:873–886. [13]

Zeng, B., J. Bendl, R. Kosoy, et al. 2022. Multi-Ancestry eQTL Meta-Analysis of Human Brain Identifies Candidate Causal Variants for Brain-Related Traits. *Nat. Genet.* **54**:161–169. [8, 10]

Zeng, J., A. Xue, L. Jiang, et al. 2021. Widespread Signatures of Natural Selection across Human Complex Traits and Functional Genomic Categories. *Nat. Commun.* **12**:1164. [1, 9]

Zeng, L. H., L. Xu, D. H. Gutmann, and M. Wong. 2008. Rapamycin Prevents Epilepsy in a Mouse Model of Tuberous Sclerosis Complex. *Ann. Neurol.* **63**:444–453. [6]

Zerres, K., and S. Rudnik-Schöneborn. 1995. Natural History in Proximal Spinal Muscular Atrophy. Clinical Analysis of 445 Patients and Suggestions for a Modification of Existing Classifications. *Arch. Neurol.* **52**:518–523. [5]

Zhang, J. P., D. Robinson, J. Yu, et al. 2019. Schizophrenia Polygenic Risk Score as a Predictor of Antipsychotic Efficacy in First-Episode Psychosis. *Am. J. Psychiatry* **176**:21–28. [7, 13, 14]

Zhang, S., H. Zhang, M. P. Forrest, et al. 2021. *Preprint*: Multiple Genes in cis Mediate the Effects of a Single Chromatin Accessibility Variant on Aberrant Synaptic Development and Function in Human Neurons. *bioRxiv* 472229. [7]

Zhang, T., L. Xu, X. Tang, et al. 2020a. Real-World Effectiveness of Antipsychotic Treatment in Psychosis Prevention in a 3-Year Cohort of 517 Individuals at Clinical High Risk from the Sharp (Shanghai at Risk for Psychosis). *Aust. N. Z. J. Psychiatry* **54**:696–706. [13]

Zhang, Y., H. T. Yang, K. Kadash-Edmondson, et al. 2020b. Regional Variation of Splicing QTLs in Human Brain. *Am. J. Hum. Genet.* **107**:196. [3]

Zhang, Z., S. G. Marro, Y. Zhang, et al. 2018. The Fragile X Mutation Impairs Homeostatic Plasticity in Human Neurons by Blocking Synaptic Retinoic Acid Signaling. *Sci. Transl. Med.* **10**:eaar4338. [7]

Zheutlin, A. B., J. Dennis, R. Karlsson Linner, et al. 2019. Penetrance and Pleiotropy of Polygenic Risk Scores for Schizophrenia in 106,160 Patients across Four Health Care Systems. *Am. J. Psychiatry* **176**:846–855. [1, 7, 13]

Zhu, H., L. Shang, and X. Zhou. 2020. A Review of Statistical Methods for Identifying Trait-Relevant Tissues and Cell Types. *Front. Genet.* **11**:587887. [9]

Zhu, Y., A. M. M. Sousa, T. Gao, et al. 2018. Spatiotemporal Transcriptomic Divergence across Human and Macaque Brain Development. *Science* **362**:eaat8077. [8]

Zierhut, H. A., K. M. Shannon, D. L. Cragun, and S. A. Cohen. 2016. Elucidating Genetic Counseling Outcomes from the Perspective of Genetic Counselors. *J. Genet. Counsel.* **25**:993–1001. [15]

Zoghbi, H. Y. 2003. Postnatal Neurodevelopmental Disorders: Meeting at the Synapse? *Science* **302**:826–830. [11]

Zolkowska, K., E. Cantor-Graae, and T. F. McNeil. 2001. Increased Rates of Psychosis among Immigrants to Sweden: Is Migration a Risk Factor for Psychosis? *Psychol. Med.* **31**:669–678. [4]

Zylka, M. J. 2020. Prenatal Treatment Path for Angelman Syndrome and Other Neurodevelopmental Disorders. *Autism Res.* **13**:11–17. [5]

From "Exploring and Exploiting Genetic Risk for Psychiatric Disorders," edited by Joshua A. Gordon and Elisabeth B. Binder. Strüngmann Forum Reports, vol. 31, Julia R. Lupp, series editor. Cambridge, MA: MIT Press. ISBN 9780262547383 (paperback) 9780262377423 (pdf)