

CURRICULUM VITAE

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EDUCATION: Ph.D. (Statistics), 1988, Pennsylvania State University
B.S. (Wildlife Resources, summa cum laude), 1982, University of Idaho

POSITIONS: **Carnegie Mellon University**, Pittsburgh, PA
Vice Provost for Faculty; 2015-
Departments of Statistics and Data Sciece & Computational Biology
1998-present, Professor; 1994-1997, Associate Professor
Yale University, New Haven, CT
1991-1994, Associate Professor; 1988-1991, Assistant Professor

SELECTED PROFESSIONAL ACTIVITIES & AWARDS:

Web of Science, Clarivate Analytics Cross-Fields Highly Cited Researcher, 2018
UPMC Professor of Statistics and Life Sciences, 2017
Penn State Eberly College of Science Outstanding Alumni Award, 2014
Janet L Norwood Award, outstanding achievement by a woman in Statistical Sciences, 2013
Medallian Lecture, 1999
Presidents' Award, Committee of Presidents of Statistical Societies 1997
Snedecor Award, for best biometrical paper, 1995-1997
NSF Young Investigator Award, 1992-1997
Distinguished Lecturer
Norman Breslow Lecture, 2019
Myra Samuels Lecture, 2017
Seaver Lecturer Mount Sinai School of Medicine, 2014
Donna J. Brogan Lecture, Emory University, 2014
Myrto Lefkopoulou Lecture, Harvard School of Public Health, 1998
Kansas State University, 1997
Goucher College, 1995
Purdue University's School of Science, 1994
Institute of Mathematical Statistics
Elected Fellow, 1997
Executive Secretary, 1996-1999
Program Chair, Spring Meetings, 1994
American Statistical Association

Elected Fellow, 1996
Associate Editor, Journal of the American Statistical Association, T&M 1994-1999, 2001-2005
Associate Editor, Journal of the American Statistical Association, CS&A 1999-2008
American Association for the Advancement of Science (AAAS)
Statistics Section chair 2017
International Statistical Institute
Elected member, 1995
International Biometrics Society
Associate Editor, Biometrics, 1997-
Best Abstract Award, 1992
Genetics Society
Associate Editor 2014 -2015
Regular BMRD Panelist for NIH, 2006-2009

Ph.D. Advisees:

Ron Yurko, Minshi Peng, Kevin Lin, Fuchen Liu,
Li Liu (2014), Corneliu Bodea (2015), Cong Lu (2016), Lingxue Zhu (2018),
Daniel Percival (2012), Drew Crossett (2012), Gaia Bellone (2012),
Diana Luca (2008), Hoa Nguyen (2005), Jung-Ying Tzeng (2003), Xiaohua Zhang (2002),
Bobby Jones (2001), Johnny Lam, Kevin Lynch (1997), and Chris Andrews (1997).

Advisory Boards:

Autism Sister Project, by Autism Science Foundation, 2015-
External Advisory Board, NIH Big Data, Purdue University, 2015-
FBI on DNA forensics, 1995
NRC/NAS on DNA forensics, 1994-95
Carnegie Commission Study on Early Childhood Development, 1994

Publications

Lindsay, B.G. and **Roeder, K.** A unified treatment of integer parameter models. *Journal of the American Statistical Association*, 82:758–764, 1987.

Roeder, K., Dennis, B., and Garton, E.O. Estimating density from variable circular plot census. *Journal of Wildlife Management*, 51:224–230, 1987.

Devlin, B., **Roeder, K.**, and Ellstrand, N.C. Fractional paternity assignment: Theoretical development and comparison to other methods. *Theoretical and Applied Genetics*, 76:369–380, 1988.

Roeder, K., Devlin, B., and Lindsay, B.G. Application of maximum likelihood methods to population genetic data for the estimation of individual fertilities. *Biometrics*, 45:363–380, 1989.

Devlin, B., Risch, N., and **Roeder, K.** No excess of homozygosity at loci used for DNA fingerprinting. *Science*, 249:1416–1420, Sep 1990.

Roeder, K. Density estimation with confidence sets exemplified by superclusters and voids in the galaxies. *Journal of the American Statistical Association*, 85:616–624, 1990.

Devlin, B., Risch, N., and **Roeder, K.** Estimation of allele frequencies for VNTR loci. *Am. J. Hum. Genet.*, 48:662–676, Apr 1991.

Devlin, B., Risch, N., and **Roeder, K.** Response. *Science*, 253:1039–1041, Aug 1991.

Lindsay, B.G. and **Roeder, K.** Residual diagnostics for mixture models. *Journal of the American Statistical Association*, 87:785–794, 1992.

Roeder, K. Discussion of 'Statistical issues concerning quasar absorption systems, by D. Tytler. In Feigelson, E.D. and Babu, G.J., editors, *Statistical Challenges in Astronomy*. Springer Verlag, New York, 1992.

Roeder, K. Semiparametric estimation of normal mixture densities. *Annals of Statistics*, 20:929–943, 1992.

Cox, D.R., Gleser, L., **Roeder, K.**, and Reid, N. Report on double blind refereeing. *Statistical Science*, 8:310–317, 1993.

Devlin, B., Risch, N., and **Roeder, K.** Forensic inference from DNA fingerprints. *Journal of the American Statistical Association*, 87:337–350, 1993.

Devlin, B., Risch, N., and **Roeder, K.** NRC report on DNA typing. *Science*, 260:1057–1059, May 1993.

Devlin, B., Risch, N., and **Roeder, K.** Statistical evaluation of DNA fingerprinting: a critique of the NRC's report. *Science*, 259:748–749, Feb 1993.

Devlin, B., Risch, N., and **Roeder, K.** Comments on the statistical aspects of the NRC's report on DNA typing. *J. Forensic Sci.*, 39:28–40, Jan 1994.

Roeder, K. A graphical technique for detecting the number of components in a normal mixture. *Journal of the American Statistical Association*, 89:487–495, 1994.

Roeder, K. DNA fingerprinting: A review of the controversy (with discussion). *Statistical Science*, 9:222–278, 1994.

Devlin, B., Fienberg, S., Resnick, D., and **Roeder, K.** Galton redux: Eugenics, intelligence, race, and society. *Journal of the American Statistical Association*, 90:1483–1488, 1995.

Devlin, B., Fienberg, S., Resnick, D., and **Roeder, K.** Wringing *The Bell Curve*: A cautionary tale about the realtionships among race, genes and IQ. *Chance*, 3:27–36, 1995.

Devlin, B. and **Roeder, K.** DNA profiling: Statistics and population genetics. In Faigman, D., Daye, D., Saks, M., and Sanders, J., editors, *Scientific Evidence Reference Manual*, 1995.

Lambert, D. and **Roeder, K.** Overdispersion diagnostics for generalized linear models. *Journal of the American Statistical Association*, 90:1225–1236, 1995.

Roeder, K. Discussion of accurate restoration of DNA sequences, by G. Churchill. In Gatsonis, C., Hodges, J.S., Kass, R.E., and Singpurwalla, N.D., editors, *Case Studies in Bayesian Statistics*, Springer Lecture Notes in Statistics. Springer, New York, 1995.

Devlin, B., Risch, N., and **Roeder, K.** Disequilibrium mapping: composite likelihood for pairwise disequilibrium. *Genomics*, 36:1–16, Aug 1996.

Roeder, K., Carroll, R.J., and Lindsay, B.G. A nonparametric maximum likelihood approach to case-control studies with errors in covariables. *Journal of the American Statistical Association*, 91:722–732, 1996.

Andrews, C., Devlin, B., Perlin, M., and **Roeder, K.** Binning clones by hybridization with complex probes: statistical refinement of an inner product mapping method. *Genomics*, 41:141–154, Apr 1997.

Crowley, E. M., **Roeder, K.**, and Bina, M. A statistical model for locating regulatory regions in genomic DNA. *J. Mol. Biol.*, 268:8–14, Apr 1997.

Daniels, M., Devlin, B., and **Roeder, K.** Of genes and IQ. In Devlin, B., Fienberg, S.E., Resnick, D., and **Roeder, K.**, editors, *Intelligence, Genes and Success: Scientists Respond to The Bell Curve*. Springer-Verlag, New York, 1997.

Devlin, B., Daniels, M., and **Roeder, K.** The heritability of IQ. *Nature*, 388:468–471, Jul 1997.

Devlin, B., Fienberg, S.E., Resnick, D., and Roeder, K. editors. *Intelligence, Genes and Success: Scientists Respond to The Bell Curve*. Springer-Verlag, 1997.

Devlin, B., Kadane, J.B., and **Roeder, K.** Discussion of 'Bayesian analysis of DNA profiling data in forensic identification applications,' by L.A. Foreman et al. *Journal of the Royal Statistical Society B*, 160:429–69, 1997.

Lindsay, B.G. and **Roeder, K.** Moment-based oscillation properties of mixture models. *Annals of Statistics*, 25:378–386, 1997.

Mueller, P. and **Roeder, K.** A Bayesian semiparametric model for case-control studies with errors in variables. *Biometrika*, 84:523–538, 1997.

Roeder, K. DNA fingerprinting. In *Statistical Encyclopedia*, pages 200–206. Wiley, New York, update volume edition, 1997.

Roeder, K. and Wasserman, L. Discussion of 'On Bayesian analysis of mixtures with unknown number of components,' by S. Richardson and P.J. Green. *Journal of the Royal Statistical Society A*, 59:782, 1997.

Roeder, K. and Wasserman, L. Practical Bayesian density estimation using mixtures of normals. *Journal of the American Statistical Association*, 92:894–902, 1997.

Roeder, K., Escobar, M., Kadane, J., and Balazs, I. Measuring heterogeneity in forensic databases using hierarchical Bayes models. *Biometrika*, 85(269-287), 1998.

Carroll, R. J., **Roeder, K.**, and Wasserman, L. Flexible parametric measurement error models. *Biometrics*, 55:44–54, Mar 1999.

Devlin, B. and **Roeder, K.** Genomic control for association studies. *Biometrics*, 55:997–1004, Dec 1999.

Roeder, K., Lynch, K., and Nagin, D. Modeling uncertainty in latent class membership: A case study in criminology. *Journal of the American Statistical Association*, 94:766–776, 1999.

Bacanu, S. A., Devlin, B., and **Roeder, K.** The power of genomic control. *Am. J. Hum. Genet.*, 66:1933–1944, Jun 2000.

Devlin, B., **Roeder, K.**, , and Wasserman, L. Genomic control for association studies: a semiparametric test to detect excess-haplotype sharing. *Biostatistics*, 1(4):369–87, Dec 2000.

Lam, J. C., **Roeder, K.**, and Devlin, B. Haplotype fine mapping by evolutionary trees. *Am. J. Hum. Genet.*, 66:659–673, Feb 2000.

Devlin, B., Fienberg, S.E., Resnick, D.P., and **Roeder, K.** Intelligence and success: Is it all in the genes? In Fish, J.M., editor, *Race and Intelligence: Separating Science from Myth*. Lawrence Erlbaum Associates, Mahwah, New Jersey, 2001.

Devlin, B., **Roeder, K.**, and Bacanu, S. A. Unbiased methods for population-based association studies. *Genet. Epidemiol.*, 21:273–284, Dec 2001.

Devlin, B., **Roeder, K.**, Otto, C., Tiobech, S., and Byerley, W. Genome-wide distribution of linkage disequilibrium in the population of Palau and its implications for gene flow in Remote Oceania. *Hum. Genet.*, 108:521–528, Jun 2001.

Devlin, B., **Roeder, K.**, and Wasserman, L. Genomic control, a new approach to genetic-based association studies. *Theor Popul Biol*, 60:155–166, Nov 2001.

Jones, B., Nagin, D., and **Roeder, K.** A SAS procedure based on mixture model for estimating developmental trajectories. *Sociological Methods and Research*, 29(3):374–393, 2001.

Lockwood, J. R., **Roeder, K.**, and Devlin, B. A Bayesian hierarchical model for allele frequencies. *Genet. Epidemiol.*, 20:17–33, Jan 2001.

Seltman, H., **Roeder, K.**, and Devlin, B. Transmission/disequilibrium test meets measured haplotype analysis: family-based association analysis guided by evolution of haplotypes. *Am. J. Hum. Genet.*, 68:1250–1263, May 2001.

Bacanu, S. A., Devlin, B., and **Roeder, K.** Association studies for quantitative traits in structured populations. *Genet. Epidemiol.*, 22:78–93, Jan 2002.

Devlin, B., Bacanu, S. A., **Roeder, K.**, Reimherr, F., Wender, P., Galke, B., Novasad, D., Chu, A., TCuenco, K., Tiobek, S., Otto, C., and Byerley, W. Genome-wide multipoint linkage analyses of multiplex schizophrenia pedigrees from the oceanic nation of Palau. *Mol. Psychiatry*, 7:689–694, 2002.

- Devlin, B., Jones, B. L., Bacanu, S. A., and **Roeder, K.** Mixture models for linkage analysis of affected sibling pairs and covariates. *Genet. Epidemiol.*, 22:52–65, Jan 2002.
- Devlin, B., Jones, B.L., Bacanu, S-A., and **Roeder, K.** Mixture and linear models for linkage analysis with covariates. *Genetic Epidemiology*, 23:449–455, 2002.
- Devlin, B., Jones, B.L., Bacanu, S-A., and **Roeder, K.** Reply to olson: Mixture models for linkage analysis of affected sibling pairs and covariates. *Genetic Epidemiology*, 23:449–455, 2002.
- Devlin, B., **Roeder, K.**, and Bacanu, S-A. Unbiased methods for population-based association studies. *Genet Epidemiology*, 21:273–284, 2002.
- Devlin, B., **Roeder, K.**, and Wasserman, L. Statistical genetics: False discovery or missed discovery? *Heredity*, 91(6):537–538, December 2003.
- Devlin, B., **Roeder, K.**, and Wasserman, L. Analysis of multilocus models of association. *Genet. Epidemiol.*, 25:36–47, Jul 2003.
- Devlin, B., **Roeder, K.**, and Wasserman, L. False discovery or missed discovery? *Heredity (Edinb)*, 91:537–538, Dec 2003.
- Seltman, H., **Roeder, K.**, and Devlin, B. Evolutionary-based association analysis using haplotype data. *Genet. Epidemiol.*, 25:48–58, Jul 2003.
- Tzeng, J-Y., Byerley, W., Devlin, B., **Roeder, K.**, and Wasserman, L. Outlier detection and false discovery rates for whole-genome DNA matching. *Journal of the American Statistical Association*, 98:236–247, 2003.
- Tzeng, J. Y., Devlin, B., Wasserman, L., and **Roeder, K.** On the identification of disease mutations by the analysis of haplotype similarity and goodness of fit. *Am. J. Hum. Genet.*, 72:891–902, Apr 2003.
- Wang, G. Q., DiPietro, M., **Roeder, K.**, Heng, C. K., Bunker, C. H., Hamman, R. F., and Kamboh, M. I. Cladistic analysis of human apolipoprotein a4 polymorphisms in relation to quantitative plasma lipid risk factors of coronary heart disease. *Ann. Hum. Genet.*, 67:107–124, Mar 2003.
- Zhang, X., **Roeder, K.**, Wallstrom, G., and Devlin, B. Integration of association statistics over genomic regions using Bayesian adaptive regression splines. *Hum. Genomics*, 1:20–29, Nov 2003.
- Devlin, B., Bacanu, S. A., and **Roeder, K.** Genomic Control to the extreme. *Nat. Genet.*, 36:1129–1130, Nov 2004.
- Devlin, B. and **Roeder, K.** Avoiding stratification in association studies. In *Encyclopedia of Genetics, Genomics, Proteomics and Bioinformatics*. Wiley, New York, 2005.
- Klei, L., Bacanu, S. A., Myles-Worsley, M., Galke, B., Xie, W., Tiobech, J., Otto, C., **Roeder, K.**, Devlin, B., and Byerley, W. Linkage analysis of a completely ascertained sample of familial schizophrenics and bipolars from Palau, Micronesia. *Hum. Genet.*, 117:349–356, Aug 2005.

Rinaldo, A., Bacanu, S. A., Devlin, B., Sonpar, V., Wasserman, L., and **Roeder, K.** Characterization of multilocus linkage disequilibrium. *Genet. Epidemiol.*, 28:193–206, Apr 2005.

Roeder, K., Bacanu, S. A., Sonpar, V., Zhang, X., and Devlin, B. Analysis of single-locus tests to detect gene/disease associations. *Genet. Epidemiol.*, 28:207–219, Apr 2005.

Genovese, C., **Roeder, K.**, and Wasserman, L. False discovery control with p-value weighting. *Biometrika*, 93:509–524, 2006.

Steffens, M., Lamina, C., Illig, T., Bettecken, T., Vogler, R., Entz, P., Suk, E. K., Toliat, M. R., Klopp, N., Caliebe, A., Konig, I. R., Kohler, K., Ludemann, J., Diaz Lacava, A., Fimmers, R., Lichtner, P., Ziegler, A., Wolf, A., Krawczak, M., Nürnberg, P., Hampe, J., Schreiber, S., Meitinger, T., Wichmann, H. E., **Roeder, K.**, Wienker, T. F., and Baur, M. P. SNP-based analysis of genetic substructure in the German population. *Hum. Hered.*, 62:20–29, 2006.

Roeder, K., Bacanu, S. A., Wasserman, L., and Devlin, B. Using linkage genome scans to improve power of association in genome scans. *Am. J. Hum. Genet.*, 78:243–252, Feb 2006.

Devlin, B., Klei, L., Myles-Worsley, M., Tiobech, J., Otto, C., Byerley, W., and **Roeder, K.** Genetic liability to schizophrenia in Oceanic Palau: a search in the affected and maternal generation. *Hum. Genet.*, 121:675–684, Jul 2007.

Klei, L. and **Roeder, K.** Testing for association based on excess allele sharing in a sample of related cases and controls. *Hum. Genet.*, 121:549–557, Jun 2007.

Roeder, K., Devlin, B., and Wasserman, L. Improving power in genome-wide association studies: weights tip the scale. *Genet. Epidemiol.*, 31:741–747, Nov 2007.

Klei, L., Luca, D., Devlin, B., and **Roeder, K.** Pleiotropy and principal components of heritability combine to increase power for association analysis. *Genet. Epidemiol.*, 32:9–19, Jan 2008.

Luca, D., Ringquist, S., Klei, L., Lee, A. B., Gieger, C., Wichmann, H. E., Schreiber, S., Krawczak, M., Lu, Y., Styche, A., Devlin, B., **Roeder, K.**, and Trucco, M. On the use of general control samples for genome-wide association studies: genetic matching highlights causal variants. *Am. J. Hum. Genet.*, 82:453–463, Feb 2008.

Silverberg, Mark S, Cho, Judy H, Rioux, John D, McGovern, Dermot P B, Wu, Jing, Annese, Vito, Achkar, Jean-Paul, Goyette, Philippe, Scott, Regan, Xu, Wei, Barmada, M Michael, Klei, Lambertus, Daly, Mark J, Abraham, Clara, Bayless, Theodore M, Bossa, Fabrizio, Griffiths, Anne M, Ippoliti, Andrew F, Lahaie, Raymond G, Latiano, Anna, Paré, Pierre, Proctor, Deborah D, Regueiro, Miguel D, Steinhart, A Hillary, Targan, Stephan R, Schumm, L Philip, Kistner, Emily O, Lee, Annette T, Gregersen, Peter K, Rotter, Jerome I, Brant, Steven R, Taylor, Kent D, **Roeder, Kathryn**, and Duerr, Richard H. Ulcerative colitis-risk loci on chromosomes 1p36 and 12q15 found by genome-wide association study. *Nat Genet*, 41(2):216–20, Feb 2009.

Roeder, K. and Luca, D. Searching for disease susceptibility variants in structured populations. *Genomics*, 93:1–4, Jan 2009.

Roeder, Kathryn, and Wasserman, Larry. Genome-wide significance levels and weighted hypothesis testing. *Stat Sci*, 24(4):398–413, Nov 2009.

Wasserman, L. and **Roeder, K.** High dimensional variable selection. *Ann Stat*, 37:2178–2201, Jan 2009.

Yerges, L. M., Klei, L., Cauley, J. A., **Roeder, K.**, Kammerer, C. M., Moffett, S. P., Ensrud, K. E., Nestlerode, C. S., Marshall, L. M., Hoffman, A. R., Lewis, C., Lang, T. F., Barrett-Connor, E., Ferrell, R. E., Orwoll, E. S., and Zmuda, J. M. High-density association study of 383 candidate genes for volumetric BMD at the femoral neck and lumbar spine among older men. *J. Bone Miner. Res.*, 24:2039–2049, Dec 2009.

Anney, R., Klei, L., Pinto, D., Regan, R., Conroy, J., Magalhaes, T. R., Correia, C., Abrahams, B. S., Sykes, N., Pagnamenta, A. T., Almeida, J., Bacchelli, E., Bailey, A. J., Baird, G., Battaglia, A., Berney, T., Bolshakova, N., Bolte, S., Bolton, P. F., Bourgeron, T., Brennan, S., Brian, J., Carson, A. R., Casallo, G., Casey, J., Chu, S. H., Cochrane, L., Corsello, C., Crawford, E. L., Crossett, A., Dawson, G., Jonge, M., Delorme, R., Drmic, I., Duketis, E., Duque, F., Estes, A., Farrar, P., Fernandez, B. A., Folstein, S. E., Fombonne, E., Freitag, C. M., Gilbert, J., Gillberg, C., Glessner, J. T., Goldberg, J., Green, J., Guter, S. J., Hakonarson, H., Heron, E. A., Hill, M., Holt, R., Howe, J. L., Hughes, G., Hus, V., Iglizzi, R., Kim, C., Klauck, S. M., Kolevzon, A., Korvatska, O., Kustanovich, V., Lajonchere, C. M., Lamb, J. A., Laskawiec, M., Leboyer, M., Le Couteur, A., Leventhal, B. L., Lionel, A. C., Liu, X. Q., Lord, C., Lotspeich, L., Lund, S. C., Maestrini, E., Mahoney, W., Mantoulan, C., Marshall, C. R., McConachie, H., McDougale, C. J., McGrath, J., McMahon, W. M., Melhem, N. M., Merikangas, A., Migita, O., Minshew, N. J., Mirza, G. K., Munson, J., Nelson, S. F., Noakes, C., Noor, A., Nygren, G., Oliveira, G., Papanikolaou, K., Parr, J. R., Parrini, B., Paton, T., Pickles, A., Piven, J., Posey, D. J., Poustka, A., Poustka, F., Prasad, A., Ragoussis, J., Renshaw, K., Rickaby, J., Roberts, W., **Roeder, K.**, Roge, B., Rutter, M. L., Bierut, L. J., Rice, J. P., Salt, J., Sansom, K., Sato, D., Segurado, R., Senman, L., Shah, N., Sheffield, V. C., Soorya, L., Sousa, I., Stoppioni, V., Strawbridge, C., Tancredi, R., Tansey, K., Thiruvahindrapduram, B., Thompson, A. P., Thomson, S., Tryfon, A., Tsiantis, J., Van Engeland, H., Vincent, J. B., Volkmar, F., Wallace, S., Wang, K., Wang, Z., Wassink, T. H., Wing, K., Wittmeyer, K., Wood, S., Yaspan, B. L., Zurawiecki, D., Zwaigenbaum, L., Betancur, C., Buxbaum, J. D., Cantor, R. M., Cook, E. H., Coon, H., Cuccaro, M. L., Gallagher, L., Geschwind, D. H., Gill, M., Haines, J. L., Miller, J., Monaco, A. P., Nurnberger, J. I., Paterson, A. D., Pericak-Vance, M. A., Schellenberg, G. D., Scherer, S. W., Sutcliffe, J. S., Szatmari, P., Vicente, A. M., Vieland, V. J., Wijsman, E. M., Devlin, B., Ennis, S., and Hallmayer, J. A genome-wide scan for common alleles affecting risk for autism. *Hum. Mol. Genet.*, 19:4072–4082, Oct 2010.

Crossett, A., Kent, B. P., Klei, L., Ringquist, S., Trucco, M., **Roeder, K.**, and Devlin, B. Using ancestry matching to combine family-based and unrelated samples for genome-wide association studies. *Stat Med*, 29:2932–2945, Dec 2010.

Lee, A. B., Luca, D., Klei, L., Devlin, B., and **Roeder, K.** Discovering genetic ancestry using spectral graph theory. *Genet. Epidemiol.*, 34:51–59, Jan 2010.

Lee, A. B., Luca, D., and **Roeder, K.** A spectral graph approach to discovering genetic ancestry. *Ann Appl Stat*, 4:179–202, 2010.

Liu, Han, **Roeder, Kathryn**, and Wasserman, Larry. Stability approach to regularization selection (stars) for high dimensional graphical models. In Lafferty, J.D., Williams, C.K.I., Shawe-Taylor, J., Zemel, R.S., and Culotta, A., editors, *Advances in Neural Information Processing Systems 23*, pages 1432–1440. Curran Associates, Inc., 2010.

McGovern, D. P., Gardet, A., Torkvist, L., Goyette, P., Essers, J., Taylor, K. D., Neale, B. M., Ong, R. T., Lagace, C., Li, C., Green, T., Stevens, C. R., Beauchamp, C., Fleshner, P. R., Carlson, M., D’Amato, M., Halfvarson, J., Hibberd, M. L., Lordal, M., Padyukov, L., Andriulli, A., Colombo, E., Latiano, A., Palmieri, O., Bernard, E. J., Deslandres, C., Hommes, D. W., Jong, D. J., Stokkers, P. C., Weersma, R. K., Sharma, Y., Silverberg, M. S., Cho, J. H., Wu, J., **Roeder, K.**, Brant, S. R., Schumm, L. P., Duerr, R. H., Dubinsky, M. C., Glazer, N. L., Haritunians, T., Ippoliti, A., Melmed, G. Y., Siscovick, D. S., Vasiliauskas, E. A., Targan, S. R., Annese, V., Wijmenga, C., Pettersson, S., Rotter, J. I., Xavier, R. J., Daly, M. J., Rioux, J. D., and Seielstad, M. Genome-wide association identifies multiple ulcerative colitis susceptibility loci. *Nat. Genet.*, 42:332–337, Apr 2010.

Pinto, Dalila, Pagnamenta, Alistair T, Klei, Lambertus, Anney, Richard, Merico, Daniele, Regan, Regina, Conroy, Judith, Magalhaes, Tiago R, Correia, Catarina, Abrahams, Brett S, Almeida, Joana, Bacchelli, Elena, Bader, Gary D, Bailey, Anthony J, Baird, Gillian, Battaglia, Agatino, Berney, Tom, Bolshakova, Nadia, Bölte, Sven, Bolton, Patrick F, Bourgeron, Thomas, Brennan, Sean, Brian, Jessica, Bryson, Susan E, Carson, Andrew R, Casallo, Guillermo, Casey, Jillian, Chung, Brian H Y, Cochrane, Lynne, Corsello, Christina, Crawford, Emily L, Crossett, Andrew, Cytrynbaum, Cheryl, Dawson, Geraldine, Jonge, Maretha, Delorme, Richard, Drmic, Irene, Duketis, Eftichia, Duque, Frederico, Estes, Annette, Farrar, Penny, Fernandez, Bridget A, Folstein, Susan E, Fombonne, Eric, Freitag, Christine M, Gilbert, John, Gillberg, Christopher, Glessner, Joseph T, Goldberg, Jeremy, Green, Andrew, Green, Jonathan, Guter, Stephen J, Hakonarson, Hakon, Heron, Elizabeth A, Hill, Matthew, Holt, Richard, Howe, Jennifer L, Hughes, Gillian, Hus, Vanessa, Iglizzi, Roberta, Kim, Cecilia, Klauck, Sabine M, Klevzon, Alexander, Korvatska, Olena, Kustanovich, Vlad, Lajonchere, Clara M, Lamb, Janine A, Laskawiec, Magdalena, Leboyer, Marion, Le Couteur, Ann, Leventhal, Bennett L, Lionel, Anath C, Liu, Xiao-Qing, Lord, Catherine, Lotspeich, Linda, Lund, Sabata C, Maestrini, Elena, Mahoney, William, Mantoulan, Carine, Marshall, Christian R, McConachie, Helen, McDougle, Christopher J, McGrath, Jane, McMahon, William M, Merikangas, Alison, Migita, Ohsuke, Minshew, Nancy J, Mirza, Ghazala K, Munson, Jeff, Nelson, Stanley F, Noakes, Carolyn, Noor, Abdul, Nygren, Gudrun, Oliveira, Guiomar, Papanikolaou, Katerina, Parr, Jeremy R, Parrini, Barbara, Paton, Tara, Pickles, Andrew, Pilorge, Marion, Piven, Joseph, Ponting, Chris P, Posey, David J, Poustka, Annemarie, Poustka, Fritz, Prasad, Aparna, Ragousis, Jiannis, Renshaw, Katy, Rickaby, Jessica, Roberts, Wendy, **Roeder, Kathryn**, Roge, Bernadette, Rutter, Michael L, Bierut, Laura J, Rice, John P, Salt, Jeff, Sansom, Katherine, Sato, Daisuke, Segurado, Ricardo, Sequeira, Ana F, Senman, Lili, Shah, Naisha, Sheffield, Val C, Soorya, Latha, Sousa, Inês, Stein, Olaf, Sykes, Nuala, Stoppioni, Vera, Strawbridge, Christina, Tancredi, Raffaella, Tansey, Katherine, Thiruvahindrapduram, Bhooma, Thompson, Ann P, Thomson, Susanne, Tryfon, Ana, Tsiantis, John, Van Engeland, Herman, Vincent, John B, Volkmar, Fred, Wallace, Simon, Wang, Kai, Wang, Zhouzhi, Wassink, Thomas H, Webber, Caleb, Weksberg, Rosanna, Wing, Kirsty, Wittmeyer, Kerstin, Wood, Shawn, Wu, Jing, Yaspan, Brian L, Zurawiecki, Danielle, Zwaigenbaum, Lonnie, Buxbaum, Joseph D, Cantor,

Rita M, Cook, Edwin H, Coon, Hilary, Cuccaro, Michael L, Devlin, Bernie, Ennis, Sean, Gallagher, Louise, Geschwind, Daniel H, Gill, Michael, Haines, Jonathan L, Hallmayer, Joachim, Miller, Judith, Monaco, Anthony P, Nurnberger, John I, Paterson, Andrew D, Pericak-Vance, Margaret A, Schellenberg, Gerard D, Szatmari, Peter, Vicente, Astrid M, Vieland, Veronica J, Wijsman, Ellen M, Scherer, Stephen W, Sutcliffe, James S, and Betancur, Catalina. Functional impact of global rare copy number variation in autism spectrum disorders. *Nature*, 466(7304):368–72, Jul 2010.

Wu, J., Devlin, B., Ringquist, S., Trucco, M., and **Roeder, K.** Screen and clean: a tool for identifying interactions in genome-wide association studies. *Genet. Epidemiol.*, 34:275–285, Apr 2010.

Yerges, L. M., Klei, L., Cauley, J. A., **Roeder, K.**, Kammerer, C. M., Ensrud, K. E., Nestlerode, C. S., Lewis, C., Lang, T. F., Barrett-Connor, E., Moffett, S. P., Hoffman, A. R., Ferrell, R. E., Orwoll, E. S., and Zmuda, J. M. Candidate gene analysis of femoral neck trabecular and cortical volumetric bone mineral density in older men. *J. Bone Miner. Res.*, 25:330–338, Feb 2010.

Chu, S. H., **Roeder, K.**, Ferrell, R. E., Devlin, B., DeMichele-Sweet, M. A., Kamboh, M. I., Lopez, O. L., and Sweet, R. A. TOMM40 poly-T repeat lengths, age of onset and psychosis risk in Alzheimer disease. *Neurobiol. Aging*, 32:1–9, Dec 2011.

Devlin, B., Melhem, N., and **Roeder, K.** Do common variants play a role in risk for autism? Evidence and theoretical musings. *Brain Res.*, 1380:78–84, Mar 2011.

Melhem, Nadine, Middleton, Frank, McFadden, Kathryn, Klei, Lambertus, Faraone, Stephen V, Vinogradov, Sophia, Tiobech, Josepha, Yano, Victor, Kuartei, Stevenson, **Roeder, Kathryn**, Byerley, William, Devlin, Bernie, and Myles-Worsley, Marina. Copy number variants for schizophrenia and related psychotic disorders in oceanic palau: risk and transmission in extended pedigrees. *Biol Psychiatry*, 70(12):1115–21, Dec 2011.

Neale, B. M., Rivas, M. A., Voight, B. F., Altshuler, D., Devlin, B., Orho-Melander, M., Kathiresan, S., Purcell, S. M., **Roeder, K.**, and Daly, M. J. Testing for an unusual distribution of rare variants. *PLoS Genet.*, 7:e1001322, Mar 2011.

Percival, D., **Roeder, K.**, Rosenfeld, R., and Wasserman, L. Structured, sparse regression with application to HIV drug resistance. *Ann Appl Stat*, 5:628–644, Jun 2011.

Sanders, S. J., Ercan-Sencicek, A. G., Hus, V., Luo, R., Murtha, M. T., Moreno-De-Luca, D., Chu, S. H., Moreau, M. P., Gupta, A. R., Thomson, S. A., Mason, C. E., Bilguvar, K., Celestino-Soper, P. B., Choi, M., Crawford, E. L., Davis, L., Wright, N. R., Dhodapkar, R. M., DiCola, M., DiLullo, N. M., Fernandez, T. V., Fielding-Singh, V., Fishman, D. O., Frahm, S., Garagaloyan, R., Goh, G. S., Kammela, S., Klei, L., Lowe, J. K., Lund, S. C., McGrew, A. D., Meyer, K. A., Moffat, W. J., Murdoch, J. D., O’Roak, B. J., Ober, G. T., Pottenger, R. S., Raubeson, M. J., Song, Y., Wang, Q., Yaspan, B. L., Yu, T. W., Yurkiewicz, I. R., Beaudet, A. L., Cantor, R. M., Curland, M., Grice, D. E., Gunel, M., Lifton, R. P., Mane, S. M., Martin, D. M., Shaw, C. A., Sheldon, M., Tischfield, J. A., Walsh, C. A., Morrow, E. M., Ledbetter, D. H., Fombonne, E., Lord, C., Martin, C. L., Brooks, A. I., Sutcliffe, J. S., Cook, E. H.,

Geschwind, D., **Roeder, K.**, Devlin, B., and State, M. W. Multiple recurrent de novo CNVs, including duplications of the 7q11.23 Williams syndrome region, are strongly associated with autism. *Neuron*, 70:863–885, Jun 2011.

Zmuda, J. M., Yerges-Armstrong, L. M., Moffett, S. P., Klei, L., Kammerer, C. M., **Roeder, K.**, Cauley, J. A., Kuipers, A., Ensrud, K. E., Nestlerode, C. S., Hoffman, A. R., Lewis, C. E., Lang, T. F., Barrett-Connor, E., Ferrell, R. E., and Orwoll, E. S. Genetic analysis of vertebral trabecular bone density and cross-sectional area in older men. *Osteoporos Int*, 22:1079–1090, Apr 2011.

Achkar, J-P, Klei, L, Bakker, P I W, Bellone, G, Rebert, N, Scott, R, Lu, Y, Regueiro, M, Brzezinski, A, Kamboh, M I, Focchi, C, Devlin, B, Trucco, M, Ringquist, S, **Roeder, K**, and Duerr, R H. Amino acid position 11 of hla-dr1 is a major determinant of chromosome 6p association with ulcerative colitis. *Genes Immun*, 13(3):245–52, Apr 2012.

Anney, Richard, Klei, Lambertus, Pinto, Dalila, Almeida, Joana, Bacchelli, Elena, Baird, Gillian, Bolshakova, Nadia, Bölte, Sven, Bolton, Patrick F, Bourgeron, Thomas, Brennan, Sean, Brian, Jessica, Casey, Jillian, Conroy, Judith, Correia, Catarina, Corsello, Christina, Crawford, Emily L, Jonge, Maretha, Delorme, Richard, Duketis, Eftichia, Duque, Frederico, Estes, Annette, Farrar, Penny, Fernandez, Bridget A, Folstein, Susan E, Fombonne, Eric, Gilbert, John, Gillberg, Christopher, Glessner, Joseph T, Green, Andrew, Green, Jonathan, Guter, Stephen J, Heron, Elizabeth A, Holt, Richard, Howe, Jennifer L, Hughes, Gillian, Hus, Vanessa, Iglizzi, Roberta, Jacob, Suma, Kenny, Graham P, Kim, Cecilia, Kolevzon, Alexander, Kustanovich, Vlad, Lajonchere, Clara M, Lamb, Janine A, Law-Smith, Miriam, Leboyer, Marion, Le Couteur, Ann, Leventhal, Bennett L, Liu, Xiao-Qing, Lombard, Frances, Lord, Catherine, Lotspeich, Linda, Lund, Sabata C, Magalhaes, Tiago R, Mantoulan, Carine, McDougle, Christopher J, Melhem, Nadine M, Merikangas, Alison, Minshew, Nancy J, Mirza, Ghazala K, Munson, Jeff, Noakes, Carolyn, Nygren, Gudrun, Papanikolaou, Katerina, Pagnamenta, Alistair T, Parrini, Barbara, Paton, Tara, Pickles, Andrew, Posey, David J, Poustka, Fritz, Ragoussis, Jiannis, Regan, Regina, Roberts, Wendy, **Roeder, Kathryn**, Roge, Bernadette, Rutter, Michael L, Schlitt, Sabine, Shah, Naisha, Sheffield, Val C, Soorya, Latha, Sousa, Inês, Stoppioni, Vera, Sykes, Nuala, Tancredi, Raffaella, Thompson, Ann P, Thomson, Susanne, Tryfon, Ana, Tsiantis, John, Van Engeland, Herman, Vincent, John B, Volkmar, Fred, Vorstman, J A S, Wallace, Simon, Wing, Kirsty, Wittemeyer, Kerstin, Wood, Shawn, Zurawiecki, Danielle, Zwaigenbaum, Lonnie, Bailey, Anthony J, Battaglia, Agatino, Cantor, Rita M, Coon, Hilary, Cuccaro, Michael L, Dawson, Geraldine, Ennis, Sean, Freitag, Christine M, Geschwind, Daniel H, Haines, Jonathan L, Klauck, Sabine M, McMahon, William M, Maestrini, Elena, Miller, Judith, Monaco, Anthony P, Nelson, Stanley F, Nurnberger, John I, Oliveira, Guiomar, Parr, Jeremy R, Pericak-Vance, Margaret A, Piven, Joseph, Schellenberg, Gerard D, Scherer, Stephen W, Vicente, Astrid M, Wassink, Thomas H, Wijsman, Ellen M, Betancur, Catalina, Buxbaum, Joseph D, Cook, Edwin H, Gallagher, Louise, Gill, Michael, Hallmayer, Joachim, Paterson, Andrew D, Sutcliffe, James S, Szatmari, Peter, Vieland, Veronica J, Hakonarson, Hakon, and Devlin, Bernie. Individual common variants exert weak effects on the risk for autism spectrum disorderspi. *Hum Mol Genet*, 21(21):4781–92, Nov 2012.

Brehm, John M, Acosta-Pérez, Edna, Klei, Lambertus, **Roeder, Kathryn**, , Barmada, Michael, Boutaoui, Nadia, Forno, Erick, Kelly, Roxanne, Paul, Kathryn, Sylvia, Jody, Liton-

jua, Augusto A, Cabana, Michael, Alvarez, María, Colón-Semidey, Angel, Canino, Glorisa, and Celedón, Juan C. Vitamin d insufficiency and severe asthma exacerbations in puerto rican children. *Am J Respir Crit Care Med*, 186(2):140–6, Jul 2012.

Brehm, John M, Acosta-Pérez, Edna, Klei, Lambertus, **Roeder, Kathryn**, , Barmada, Michael M, Boutaoui, Nadia, Forno, Erick, Cloutier, Michelle M, Datta, Soma, Kelly, Roxanne, Paul, Kathryn, Sylvia, Jody, Calvert, Deanna, Thornton-Thompson, Sherell, Wakefield, Dorothy, Litonjua, Augusto A, Alvarez, María, Colón-Semidey, Angel, Canino, Glorisa, and Celedón, Juan C. African ancestry and lung function in puerto rican children. *J Allergy Clin Immunol*, 129(6):1484–90.e6, Jun 2012.

Buxbaum, Joseph D, Daly, Mark J, Devlin, Bernie, Lehner, Thomas, **Roeder, Kathryn**, , State, Matthew W, and Autism Sequencing Consortium, . The autism sequencing consortium: large-scale, high-throughput sequencing in autism spectrum disorders. *Neuron*, 76(6):1052–6, Dec 2012.

Ionita-Laza, Iuliana, Makarov, Vlad, ARRA Autism Sequencing Consortium, and Buxbaum, Joseph D. Scan-statistic approach identifies clusters of rare disease variants in *lrp2*, a gene linked and associated with autism spectrum disorders, in three datasets. *Am J Hum Genet*, 90(6):1002–13, Jun 2012.

Klei, Lambertus, Sanders, Stephan J, Murtha, Michael T, Hus, Vanessa, Lowe, Jennifer K, Willsey, A Jeremy, Moreno-De-Luca, Daniel, Yu, Timothy W, Fombonne, Eric, Geschwind, Daniel, Grice, Dorothy E, Ledbetter, David H, Lord, Catherine, Mane, Shrikant M, Lese Martin, Christa, Martin, Donna M, Morrow, Eric M, Walsh, Christopher A, Melhem, Nadine M, Chaste, Pauline, Sutcliffe, James S, State, Matthew W, Cook, Edwin H, **Roeder, Kathryn**, and Devlin, Bernie. Common genetic variants, acting additively, are a major source of risk for autism. *Mol Autism*, 3(1):9, Oct 2012.

Mechanic, Leah E, Chen, Huann-Sheng, Amos, Christopher I, Chatterjee, Nilanjan, Cox, Nancy J, Divi, Rao L, Fan, Ruzong, Harris, Emily L, Jacobs, Kevin, Kraft, Peter, Leal, Suzanne M, McAllister, Kimberly, Moore, Jason H, Paltoo, Dina N, Province, Michael A, Ramos, Erin M, Ritchie, Marylyn D, **Roeder, Kathryn**, Schaid, Daniel J, Stephens, Matthew, Thomas, Duncan C, Weinberg, Clarice R, Witte, John S, Zhang, Shunpu, Zöllner, Sebastian, Feuer, Eric J, and Gillanders, Elizabeth M. Next generation analytic tools for large scale genetic epidemiology studies of complex diseases. *Genet Epidemiol*, 36(1):22–35, Jan 2012.

Neale, Benjamin M, Kou, Yan, Liu, Li, Ma’ayan, Avi, Samocha, Kaitlin E, Sabo, Aniko, Lin, Chiao-Feng, Stevens, Christine, Wang, Li-San, Makarov, Vladimir, Polak, Paz, Yoon, Seungtae, Maguire, Jared, Crawford, Emily L, Campbell, Nicholas G, Geller, Evan T, Valladares, Otto, Schafer, Chad, Liu, Han, Zhao, Tuo, Cai, Guiqing, Lihm, Jayon, Dannenfels, Ruth, Jabado, Omar, Peralta, Zuleyma, Nagaswamy, Uma, Muzny, Donna, Reid, Jeffrey G, Newsham, Irene, Wu, Yuanqing, Lewis, Lora, Han, Yi, Voight, Benjamin F, Lim, Elaine, Rossin, Elizabeth, Kirby, Andrew, Flannick, Jason, Fromer, Menachem, Shakir, Khalid, Fennell, Tim, Garimella, Kiran, Banks, Eric, Poplin, Ryan, Gabriel, Stacey, DePristo, Mark, Wimbish, Jack R, Boone, Braden E, Levy, Shawn E, Betancur, Catalina, Sunyaev, Shamil, Boerwinkle, Eric, Buxbaum, Joseph D, Cook, Edwin H, Devlin, Bernie, Gibbs, Richard A, **Roeder, Kathryn**, Schellenberg,

Gerard D, Sutcliffe, James S, and Daly, Mark J. Patterns and rates of exonic de novo mutations in autism spectrum disorders. *Nature*, 485(7397):242–5, May 2012.

Sanders, Stephan J, Murtha, Michael T, Gupta, Abha R, Murdoch, John D, Raubeson, Melanie J, Willsey, A Jeremy, Ercan-Sencicek, A Gulhan, DiLullo, Nicholas M, Parikshak, Neelroop N, Stein, Jason L, Walker, Michael F, Ober, Gordon T, Teran, Nicole A, Song, Youeun, El-Fishawy, Paul, Murtha, Ryan C, Choi, Murim, Overton, John D, Bjornson, Robert D, Carriero, Nicholas J, Meyer, Kyle A, Bilguvar, Kaya, Mane, Shrikant M, Sestan, Nenad, Lifton, Richard P, Günel, Murat, **Roeder, Kathryn**, Geschwind, Daniel H, Devlin, Bernie, and State, Matthew W. De novo mutations revealed by whole-exome sequencing are strongly associated with autism. *Nature*, 485(7397):237–41, May 2012.

Whitcomb, David C, Larusch, Jessica, Krasinskas, Alyssa M, Klei, Lambertus, Smith, Jill P, Brand, Randall E, Neoptolemos, John P, Lerch, Markus M, Tector, Matt, Sandhu, Bimaljit S, Guda, Nalini M, Orlichenko, Lidiya, Alzheimer’s Disease Genetics Consortium, , Albert, Marilyn S, Albin, Roger L, Apostolova, Liana G, Arnold, Steven E, Baldwin, Clinton T, Barber, Robert, Barnes, Lisa L, Beach, Thomas G, Beecham, Gary W, Beekly, Duane, Bennett, David A, Bigio, Eileen H, Bird, Thomas D, Blacker, Deborah, Boxer, Adam, Burke, James R, Buxbaum, Joseph D, Cairns, Nigel J, Cantwell, Laura B, Cao, Chuanhai, Carney, Regina M, Carroll, Steven L, Chui, Helena C, Clark, David G, Cribbs, David H, Crocco, Elizabeth A, Cruchaga, Carlos, Decarli, Charles, Demirci, F Yesim, Dick, Malcolm, Dickson, Dennis W, Duara, Ranjan, Ertekin-Taner, Nilufer, Faber, Kelley M, Fallon, Kenneth B, Farlow, Martin R, Ferris, Steven, Foroud, Tatiana M, Frosch, Matthew P, Galasko, Douglas R, Ganguli, Mary, Gearing, Marla, Geschwind, Daniel H, Ghetti, Bernardino, Gilbert, John R, Gilman, Sid, Glass, Jonathan D, Goate, Alison M, Graff-Radford, Neill R, Green, Robert C, Growdon, John H, Hakonarson, Hakon, Hamilton-Nelson, Kara L, Hamilton, Ronald L, Harrell, Lindy E, Head, Elizabeth, Honig, Lawrence S, Hulette, Christine M, Hyman, Bradley T, Jicha, Gregory A, Jin, Lee-Way, Jun, Gyungah, Kamboh, M Ilyas, Karydas, Anna, Kaye, Jeffrey A, Kim, Ronald, Koo, Edward H, Kowall, Neil W, Kramer, Joel H, Kramer, Patricia, Kukull, Walter A, Laferla, Frank M, Lah, James J, Leverenz, James B, Levey, Allan I, Li, Ge, Lin, Chiao-Feng, Lieberman, Andrew P, Lopez, Oscar L, Lunetta, Kathryn L, Lyketsos, Constantine G, Mack, Wendy J, Marson, Daniel C, Martin, Eden R, Martiniuk, Frank, Mash, Deborah C, Masliah, Eliezer, McKee, Ann C, Mesulam, Marsel, Miller, Bruce L, Miller, Carol A, Miller, Joshua W, Montine, Thomas J, Morris, John C, Murrell, Jill R, Naj, Adam C, Olichney, John M, Parisi, Joseph E, Peskind, Elaine, Petersen, Ronald C, Pierce, Aimee, Poon, Wayne W, Potter, Huntington, Quinn, Joseph F, Raj, Ashok, Raskind, Murray, Reiman, Eric M, Reisberg, Barry, Reitz, Christiane, Ringman, John M, Roberson, Erik D, Rosen, Howard J, Rosenberg, Roger N, Sano, Mary, Saykin, Andrew J, Schneider, Julie A, Schneider, Lon S, Seeley, William W, Smith, Amanda G, Sonnen, Joshua A, Spina, Salvatore, Stern, Robert A, Tanzi, Rudolph E, Trojanowski, John Q, Troncoso, Juan C, Tsuang, Debby W, Valladares, Otto, Van Deerlin, Viviana M, Van Eldik, Linda J, Vardarajan, Badri N, Vinters, Harry V, Vonsattel, Jean Paul, Wang, Li-San, Weintraub, Sandra, Welsh-Bohmer, Kathleen A, Williamson, Jennifer, Woltjer, Randall L, Wright, Clinton B, Younkin, Steven G, Yu, Chang-En, Yu, Lei, Alkaade, Samer, Amann, Stephen T, Anderson, Michelle A, Baillie, John, Banks, Peter A, Conwell, Darwin, Coté, Gregory A, Cotton, Peter B, Disario, James, Farrer, Lindsay A, Forsmark, Chris E, Johnstone, Marianne, Gardner, Timothy B, Gelrud, Andres, Greenhalf, William, Haines, Jonathan L, Hartman,

Douglas J, Hawes, Robert A, Lawrence, Christopher, Lewis, Michele, Mayerle, Julia, Mayeux, Richard, Melhem, Nadine M, Money, Mary E, Muniraj, Thiruvengadam, Papachristou, Georgios I, Pericak-Vance, Margaret A, Romagnuolo, Joseph, Schellenberg, Gerard D, Sherman, Stuart, Simon, Peter, Singh, Vijay P, Slivka, Adam, Stolz, Donna, Sutton, Robert, Weiss, Frank Ulrich, Wilcox, C Mel, Zarnescu, Narcis Octavian, Wisniewski, Stephen R, O’Connell, Michael R, Kienholz, Michelle L, **Roeder, Kathryn**, Barmada, M Michael, Yadav, Dhiraj, and Devlin, Bernie. Common genetic variants in the *cldn2* and *prss1-prss2* loci alter risk for alcohol-related and sporadic pancreatitis. *Nat Genet*, 44(12):1349–54, Nov 2012.

Zhao, Tuo, Liu, Han, **Roeder, Kathryn**, Lafferty, John, and Wasserman, Larry. Huge: High dimensional undirected graph estimation. *JMLR*, 13:1059–1062, Apr 2012.

Zhao, Tuo, **Roeder, Kathryn**, and Liu, Han. Smooth-projected neighborhood pursuit for high-dimensional nonparanormal graph estimation. In Bartlett, P., Pereira, F.C.N., Burges, C.J.C., Bottou, L., and Weinberger, K.Q., editors, *Advances in Neural Information Processing Systems 25*, pages 162–170. 2012.

Cross-Disorder Group of the Psychiatric Genomics Consortium, , Lee, S Hong, Ripke, Stephan, Neale, Benjamin M, Faraone, Stephen V, Purcell, Shaun M, Perlis, Roy H, Mowry, Bryan J, Thapar, Anita, Goddard, Michael E, Witte, John S, Absher, Devin, Agartz, Ingrid, Akil, Huda, Amin, Farooq, Andreassen, Ole A, Anjorin, Adebayo, Anney, Richard, Anttila, Verner, Arking, Dan E, Asherson, Philip, Azevedo, Maria H, Backlund, Lena, Badner, Judith A, Bailey, Anthony J, Banaschewski, Tobias, Barchas, Jack D, Barnes, Michael R, Barrett, Thomas B, Bass, Nicholas, Battaglia, Agatino, Bauer, Michael, Bayés, Mònica, Bellivier, Frank, Bergen, Sarah E, Berrettini, Wade, Betancur, Catalina, Bettecken, Thomas, Biederman, Joseph, Binder, Elisabeth B, Black, Donald W, Blackwood, Douglas H R, Bloss, Cinnamon S, Boehnke, Michael, Boomsma, Dorret I, Breen, Jerome, Breuer, René, Bruggeman, Richard, Cormican, Paul, Bucola, Nancy G, Buitelaar, Jan K, Bunney, William E, Buxbaum, Joseph D, Byerley, William F, Byrne, Enda M, Caesar, Sian, Cahn, Wiepke, Cantor, Rita M, Casas, Miguel, Chakravarti, Aravinda, Chambert, Kimberly, Choudhury, Khalid, Cichon, Sven, Cloninger, C Robert, Collier, David A, Cook, Edwin H, Coon, Hilary, Cormand, Bru, Corvin, Aiden, Coryell, William H, Craig, David W, Craig, Ian W, Crosbie, Jennifer, Cuccaro, Michael L, Curtis, David, Czamara, Darina, Datta, Susmita, Dawson, Geraldine, Day, Richard, De Geus, Eco J, Degenhardt, Franziska, Djurovic, Srdjan, Donohoe, Gary J, Doyle, Alysa E, Duan, Jubao, Dudbridge, Frank, Duketis, Eftichia, Ebstein, Richard P, Edenberg, Howard J, Elia, Josephine, Ennis, Sean, Etain, Bruno, Fanous, Ayman, Farmer, Anne E, Ferrier, I Nicol, Flickinger, Matthew, Fombonne, Eric, Foroud, Tatiana, Frank, Josef, Franke, Barbara, Fraser, Christine, Freedman, Robert, Freimer, Nelson B, Freitag, Christine M, Friedl, Marion, Frisén, Louise, Gallagher, Louise, Gejman, Pablo V, Georgieva, Lyudmila, Gershon, Elliot S, Geschwind, Daniel H, Giegling, Ina, Gill, Michael, Gordon, Scott D, Gordon-Smith, Katherine, Green, Elaine K, Greenwood, Tiffany A, Grice, Dorothy E, Gross, Magdalena, Grozeva, Detelina, Guan, Weihua, Gurling, Hugh, De Haan, Lieuwe, Haines, Jonathan L, Hakonarson, Hakon, Hallmayer, Joachim, Hamilton, Steven P, Hamshere, Marian L, Hansen, Thomas F, Hartmann, Annette M, Hautzinger, Martin, Heath, Andrew C, Henders, Anjali K, Herms, Stefan, Hickie, Ian B, Hipolito, Maria, Hoefels, Susanne, Holmans, Peter A, Holsboer, Florian, Hoogendijk, Witte J, Hottenga, Jouke-Jan, Hultman, Christina M, Hus, Vanessa, Ingason, Andrés, Ising, Marcus, Jamain, Stéphane, Jones, Edward G, Jones, Ian, Jones, Lisa, Tzeng, Jung-Ying, Kähler, Anna K, Kahn, René S,

Kandaswamy, Radhika, Keller, Matthew C, Kennedy, James L, Kenny, Elaine, Kent, Lindsey, Kim, Yunjung, Kirov, George K, Klauck, Sabine M, Klei, Lambertus, Knowles, James A, Kohli, Martin A, Koller, Daniel L, Konte, Bettina, Korszun, Ania, Krabbendam, Lydia, Krasucki, Robert, Kuntsi, Jonna, Kwan, Phoenix, Landén, Mikael, Långström, Niklas, Lathrop, Mark, Lawrence, Jacob, Lawson, William B, Leboyer, Marion, Ledbetter, David H, Lee, Phil H, Lencz, Todd, Lesch, Klaus-Peter, Levinson, Douglas F, Lewis, Cathryn M, Li, Jun, Lichtenstein, Paul, Lieberman, Jeffrey A, Lin, Dan-Yu, Linszen, Don H, Liu, Chunyu, Lohoff, Falk W, Loo, Sandra K, Lord, Catherine, Lowe, Jennifer K, Lucae, Susanne, MacIntyre, Donald J, Madden, Pamela A F, Maestrini, Elena, Magnusson, Patrik K E, Mahon, Pamela B, Maier, Wolfgang, Malhotra, Anil K, Mane, Shrikant M, Martin, Christa L, Martin, Nicholas G, Mattheisen, Manuel, Matthews, Keith, Mattingsdal, Morten, McCarroll, Steven A, McGhee, Kevin A, McGough, James J, McGrath, Patrick J, McGuffin, Peter, McInnis, Melvin G, McIntosh, Andrew, McKinney, Rebecca, McLean, Alan W, McMahan, Francis J, McMahan, William M, McQuillin, Andrew, Medeiros, Helena, Medland, Sarah E, Meier, Sandra, Melle, Ingrid, Meng, Fan, Meyer, Jobst, Middeldorp, Christel M, Middleton, Lefkos, Milanova, Vihra, Miranda, Ana, Monaco, Anthony P, Montgomery, Grant W, Moran, Jennifer L, Moreno-De-Luca, Daniel, Morken, Gunnar, Morris, Derek W, Morrow, Eric M, Moskvina, Valentina, Muglia, Pierandrea, Mühleisen, Thomas W, Muir, Walter J, Müller-Myhsok, Bertram, Murtha, Michael, Myers, Richard M, Myin-Germeys, Inez, Neale, Michael C, Nelson, Stan F, Nievergelt, Caroline M, Nikolov, Ivan, Ningaonkar, Vishwajit, Nolen, Willem A, Nöthen, Markus M, Nurnberger, John I, Nwulia, Evaristus A, Nyholt, Dale R, O'Dushlaine, Colm, Oades, Robert D, Olincy, Ann, Oliveira, Guiomar, Olsen, Line, Ophoff, Roel A, Osby, Urban, Owen, Michael J, Palotie, Aarno, Parr, Jeremy R, Paterson, Andrew D, Pato, Carlos N, Pato, Michele T, Penninx, Brenda W, Pergadia, Michele L, Pericak-Vance, Margaret A, Pickard, Benjamin S, Pimm, Jonathan, Piven, Joseph, Posthuma, Danielle, Potash, James B, Poustka, Fritz, Propping, Peter, Puri, Vinay, Queded, Digby J, Quinn, Emma M, Ramos-Quiroga, Josep Antoni, Rasmussen, Henrik B, Raychaudhuri, Soumya, Rehnström, Karola, Reif, Andreas, Ribasés, Marta, Rice, John P, Rietschel, Marcella, **Roeder, Kathryn**, Roeyers, Herbert, Rossin, Lizzy, Rothenberger, Aribert, Rouleau, Guy, Ruderfer, Douglas, Rujescu, Dan, Sanders, Alan R, Sanders, Stephan J, Santangelo, Susan L, Sergeant, Joseph A, Schachar, Russell, Schalling, Martin, Schatzberg, Alan F, Scheftner, William A, Schellenberg, Gerard D, Scherer, Stephen W, Schork, Nicholas J, Schulze, Thomas G, Schumacher, Johannes, Schwarz, Markus, Scolnick, Edward, Scott, Laura J, Shi, Jianxin, Shilling, Paul D, Shyn, Stanley I, Silverman, Jeremy M, Slager, Susan L, Smalley, Susan L, Smit, Johannes H, Smith, Erin N, Sonuga-Barke, Edmund J S, St Clair, David, State, Matthew, Steffens, Michael, Steinhausen, Hans-Christoph, Strauss, John S, Strohmaier, Jana, Stroup, T Scott, Sutcliffe, James S, Szatmari, Peter, Szelinger, Szaboels, Thirumalai, Srinivasa, Thompson, Robert C, Todorov, Alexandre A, Tozzi, Federica, Treutlein, Jens, Uhr, Manfred, Oord, Edwin J C G, Van Grootheest, Gerard, Van Os, Jim, Vicente, Astrid M, Vieland, Veronica J, Vincent, John B, Visscher, Peter M, Walsh, Christopher A, Wassink, Thomas H, Watson, Stanley J, Weissman, Myrna M, Werge, Thomas, Wienker, Thomas F, Wijsman, Ellen M, Willemsen, Gonneke, Williams, Nigel, Willsey, A Jeremy, Witt, Stephanie H, Xu, Wei, Young, Allan H, Yu, Timothy W, Zammit, Stanley, Zandi, Peter P, Zhang, Peng, Zitman, Frans G, Zöllner, Sebastian, International Inflammatory Bowel Disease Genetics Consortium (IIBDGC), , Devlin, Bernie, Kelsoe, John R, Sklar, Pamela, Daly, Mark J, O'Donovan, Michael C, Craddock, Nicholas, Sullivan, Patrick F, Smoller, Jordan W, Kendler, Kenneth S,

and Wray, Naomi R. Genetic relationship between five psychiatric disorders estimated from genome-wide snps. *Nat Genet*, 45(9):984–94, Sep 2013.

Crossett, A., A.B., Lee, L., Klei, B., Devlin, and **Roeder, K**. Refining genetically inferred relationships using treelet covariance smoothing. *Annals of Applied Statistics*, 7:669–690, 2013.

Hamilton, P J, Campbell, N G, Sharma, S, Erreger, K, Herborg Hansen, F, Saunders, C, Belovich, A N, NIH ARRA Autism Sequencing Consortium, , Sahai, M A, Cook, E H, Gether, U, McHaourab, H S, Matthies, H J G, Sutcliffe, J S, and Galli, A. De novo mutation in the dopamine transporter gene associates dopamine dysfunction with autism spectrum disorder. *Mol Psychiatry*, 18(12):1315–23, Dec 2013.

He, Xin, Sanders, Stephan J, Liu, Li, De Rubeis, Silvia, Lim, Elaine T, Sutcliffe, James S, Schellenberg, Gerard D, Gibbs, Richard A, Daly, Mark J, Buxbaum, Joseph D, State, Matthew W, Devlin, Bernie, and **Roeder, Kathryn**. Integrated model of de novo and inherited genetic variants yields greater power to identify risk genes. *PLoS Genet*, 9(8):e1003671, 2013.

Lim, Elaine T, Raychaudhuri, Soumya, Sanders, Stephan J, Stevens, Christine, Sabo, Aniko, MacArthur, Daniel G, Neale, Benjamin M, Kirby, Andrew, Ruderfer, Douglas M, Fromer, Menachem, Lek, Monkol, Liu, Li, Flannick, Jason, Ripke, Stephan, Nagaswamy, Uma, Muzny, Donna, Reid, Jeffrey G, Hawes, Alicia, Newsham, Irene, Wu, Yuanqing, Lewis, Lora, Dinh, Huyen, Gross, Shannon, Wang, Li-San, Lin, Chiao-Feng, Valladares, Otto, Gabriel, Stacey B, dePristo, Mark, Altshuler, David M, Purcell, Shaun M, NHLBI Exome Sequencing Project, , State, Matthew W, Boerwinkle, Eric, Buxbaum, Joseph D, Cook, Edwin H, Gibbs, Richard A, Schellenberg, Gerard D, Sutcliffe, James S, Devlin, Bernie, **Roeder, Kathryn**, and Daly, Mark J. Rare complete knockouts in humans: population distribution and significant role in autism spectrum disorders. *Neuron*, 77(2):235–42, Jan 2013.

Liu, Li, Sabo, Aniko, Neale, Benjamin M, Nagaswamy, Uma, Stevens, Christine, Lim, Elaine, Bodea, Corneliu A, Muzny, Donna, Reid, Jeffrey G, Banks, Eric, Coon, Hillary, Depristo, Mark, Dinh, Huyen, Fennel, Tim, Flannick, Jason, Gabriel, Stacey, Garimella, Kiran, Gross, Shannon, Hawes, Alicia, Lewis, Lora, Makarov, Vladimir, Maguire, Jared, Newsham, Irene, Poplin, Ryan, Ripke, Stephan, Shakir, Khalid, Samocha, Kaitlin E, Wu, Yuanqing, Boerwinkle, Eric, Buxbaum, Joseph D, Cook, Edwin H, Devlin, Bernie, Schellenberg, Gerard D, Sutcliffe, James S, Daly, Mark J, Gibbs, Richard A, and **Roeder, Kathryn**. Analysis of rare, exonic variation amongst subjects with autism spectrum disorders and population controls. *PLoS Genet*, 9(4):e1003443, Apr 2013.

Ringquist, Steven, Bellone, Gaia, Lu, Ying, **Roeder, Kathryn**, and Trucco, Massimo. Clustering and alignment of polymorphic sequences for hla-drb1 genotyping. *PLoS One*, 8(3):e59835, 2013.

Schafer, Chad M, Campbell, Nicholas G, Cai, Guiqing, Yu, Fei, Makarov, Vladimir, Yoon, Seungtai, Daly, Mark J, Gibbs, Richard A, Schellenberg, Gerard D, Devlin, Bernie, Sutcliffe, James S, Buxbaum, Joseph D, and **Roeder, Kathryn**. Whole exome sequencing reveals minimal differences between cell line and whole blood derived dna. *Genomics*, Jun 2013.

Willsey, A Jeremy, Sanders, Stephan J, Li, Mingfeng, Dong, Shan, Tebbenkamp, Andrew T, Muhle, Rebecca A, Reilly, Steven K, Lin, Leon, Fertuzinhos, Sofia, Miller, Jeremy A, Murtha,

Michael T, Bichsel, Candace, Niu, Wei, Cotney, Justin, Ercan-Sencicek, A Gulhan, Gockley, Jake, Gupta, Abha R, Han, Wenqi, He, Xin, Hoffman, Ellen J, Klei, Lambertus, Lei, Jing, Liu, Wenzhong, Liu, Li, Lu, Cong, Xu, Xuming, Zhu, Ying, Mane, Shrikant M, Lein, Ed S, Wei, Liping, Noonan, James P, **Roeder, Kathryn**, Devlin, Bernie, Sestan, Nenad, and State, Matthew W. Coexpression networks implicate human midfetal deep cortical projection neurons in the pathogenesis of autism. *Cell*, 155(5):997–1007, Nov 2013.

Zhao, Tuo, **Roeder, Kathryn**, and Liu, Han. Positive semidefinite rank-based correlation matrix estimation with application to semiparametric graph estimation. *Journal of Computational and Graphical Statistics*, (DOI: 10.1080/10618600.2013.858633), 2013.

Blumenthal, Ian, Ragavendran, Ashok, Erdin, Serkan, Klei, Lambertus, Sugathan, Aarathi, Guide, Jolene R, Manavalan, Poornima, Zhou, Julian Q, Wheeler, Vanessa C, Levin, Joshua Z, Ernst, Carl, **Roeder, Kathryn**, Devlin, Bernie, Gusella, James F, and Talkowski, Michael E. Transcriptional consequences of 16p11.2 deletion and duplication in mouse cortex and multiplex autism families. *Am J Hum Genet*, 94(6):870–83, Jun 2014.

Cicek, A Ercument, **Roeder, Kathryn**, and Ozsoyoglu, Gultekin. Mira: mutual information-based reporter algorithm for metabolic networks. *Bioinformatics*, 30(12):i175–84, Jun 2014.

De Rubeis, Silvia, He, Xin, Goldberg, Arthur P, Poultney, Christopher S, Samocha, Kaitlin, Ercument Cicek, A, Kou, Yan, Liu, Li, Fromer, Menachem, Walker, Susan, Singh, Tarjinder, Klei, Lambertus, Kosmicki, Jack, Fu, Shih-Chen, Aleksic, Branko, Biscaldi, Monica, Bolton, Patrick F, Brownfeld, Jessica M, Cai, Jinlu, Campbell, Nicholas G, Carracedo, Angel, Chahrouh, Maria H, Chiocchetti, Andreas G, Coon, Hilary, Crawford, Emily L, Crooks, Lucy, Curran, Sarah R, Dawson, Geraldine, Duketis, Eftichia, Fernandez, Bridget A, Gallagher, Louise, Geller, Evan, Guter, Stephen J, Sean Hill, R, Ionita-Laza, Iuliana, Jimenez Gonzalez, Patricia, Kilpinen, Helena, Klauck, Sabine M, Kolevzon, Alexander, Lee, Irene, Lei, Jing, Lehtimäki, Terho, Lin, Chiao-Feng, Ma’ayan, Avi, Marshall, Christian R, McInnes, Alison L, Neale, Benjamin, Owen, Michael J, Ozaki, Norio, Parellada, Mara, Parr, Jeremy R, Purcell, Shaun, Puura, Kaija, Rajagopalan, Deepthi, Rehnström, Karola, Reichenberg, Abraham, Sabo, Aniko, Sachse, Michael, Sanders, Stephan J, Schafer, Chad, Schulte-Rüther, Martin, Skuse, David, Stevens, Christine, Szatmari, Peter, Tammimies, Kristiina, Valladares, Otto, Voran, Annette, Wang, Li-San, Weiss, Lauren A, Jeremy Willsey, A, Yu, Timothy W, Yuen, Ryan K C, The DDD Study, , Homozygosity Mapping Collaborative for Autism, , UK10K Consortium, , The Autism Sequencing Consortium, , Cook, Edwin H, Freitag, Christine M, Gill, Michael, Hultman, Christina M, Lehner, Thomas, Palotie, Aarno, Schellenberg, Gerard D, Sklar, Pamela, State, Matthew W, Sutcliffe, James S, Walsh, Christopher A, Scherer, Stephen W, Zwick, Michael E, Barrett, Jeffrey C, Cutler, David J and **Roeder, Kathryn**, Devlin, Bernie, Daly, Mark J, and Buxbaum, Joseph D. Synaptic, transcriptional and chromatin genes disrupted in autism. *Nature*, 515(7526):209–215, Nov 2014.

Dong, Shan, Walker, Michael F, Carriero, Nicholas J, DiCola, Michael, Willsey, A Jeremy, Ye, Adam Y, Waqar, Zainulabedin, Gonzalez, Luis E, Overton, John D, Frahm, Stephanie, Keaney, John F, Teran, Nicole A, Dea, Jeanselle, Mandell, Jeffrey D, Hus Bal, Vanessa, Sullivan, Catherine A, DiLullo, Nicholas M, Khalil, Rehab O, Gockley, Jake, Yuksel, Zafer, Sertel, Sinem M, Ercan-Sencicek, A Gulhan, Gupta, Abha R, Mane, Shrikant M, Sheldon, Michael,

Brooks, Andrew I, **Roeder, Kathryn**, Devlin, Bernie, State, Matthew W, Wei, Liping, and Sanders, Stephan J. De novo insertions and deletions of predominantly paternal origin are associated with autism spectrum disorder. *Cell Rep*, 9(1):16–23, Oct 2014.

Gaugler, Trent, Klei, Lambertus, Sanders, Stephan J, Bodea, Corneliu A, Goldberg, Arthur P, Lee, Ann B, Mahajan, Milind, Manaa, Dina, Pawitan, Yudi, Reichert, Jennifer, Ripke, Stephan, Sandin, Sven, Sklar, Pamela, Svantesson, Oscar, Reichenberg, Abraham, Hultman, Christina M, Devlin, Bernie, **Roeder, Kathryn**, and Buxbaum, Joseph D. Most genetic risk for autism resides with common variation. *Nat Genet*, 46(8):881–5, Aug 2014.

Liu, Li, Lei, Jing, Sanders, Stephan J, Willsey, Arthur Jeremy, Kou, Yan, Cicek, Abdullah Ercument, Klei, Lambertus, Lu, Cong, He, Xin, Li, Mingfeng, Muhle, Rebecca A, Ma'ayan, Avi, Noonan, James P, Sestan, Nenad, McFadden, Kathryn A, State, Matthew W, Buxbaum, Joseph D, Devlin, Bernie, and **Roeder, Kathryn**. Dawn: a framework to identify autism genes and subnetworks using gene expression and genetics. *Mol Autism*, 5(1):22, 2014.

Melhem, Nadine M, Lu, Cong, Dresbold, Cara, Middleton, Frank A, Klei, Lambertus, Wood, Shawn, Faraone, Stephen V, Vinogradov, Sophia, Tiobech, Josepha, Yano, Victor, **Roeder, Kathryn**, Byerley, William, Myles-Worsley, Marina, and Devlin, Bernie. Characterizing runs of homozygosity and their impact on risk for psychosis in a population isolate. *Am J Med Genet B Neuropsychiatr Genet*, 165B(6):521–30, Sep 2014.

Samocha, Kaitlin E, Robinson, Elise B, Sanders, Stephan J, Stevens, Christine, Sabo, Aniko, McGrath, Lauren M, Kosmicki, Jack A, Rehnström, Karola, Mallick, Swapam, Kirby, Andrew, Wall, Dennis P, MacArthur, Daniel G, Gabriel, Stacey B, DePristo, Mark, Purcell, Shaun M, Palotie, Aarno, Boerwinkle, Eric, Buxbaum, Joseph D, Cook, Edwin H, Gibbs, Richard A, Schellenberg, Gerard D, Sutcliffe, James S, Devlin, Bernie, **Roeder, Kathryn**, Neale, Benjamin M, and Daly, Mark J. A framework for the interpretation of de novo mutation in human disease. *Nat Genet*, 46(9):944–50, Sep 2014.

Cicek, A Ercument, **Roeder, Kathryn**, and Ozsoyoglu, Gultekin. Mira: mutual information-based reporter algorithm for metabolic networks. *Bioinformatics*, 31(7):1160, Apr 2015.

Cotney, Justin, Muhle, Rebecca A, Sanders, Stephan J, Liu, Li, Willsey, A Jeremy, Niu, Wei, Liu, Wenzhong, Klei, Lambertus, Lei, Jing, Yin, Jun, Reilly, Steven K, Tebbenkamp, Andrew T, Bichsel, Candace, Pletikos, Mihovil, Sestan, Nenad, **Roeder, Kathryn**, State, Matthew W, Devlin, Bernie, and Noonan, James P. The autism-associated chromatin modifier *chd8* regulates other autism risk genes during human neurodevelopment. *Nat Commun*, 6:6404, 2015.

Liu, L, Lei, J, and **Roeder K**. Network assisted analysis to reveal the genetic basis of autism. *Ann Appl Stat*, 9:1571–1600, 2015.

Sanders, Stephan J, He, Xin, Willsey, A Jeremy, Ercan-Sencicek, A Gulhan, Samocha, Kaitlin E, Cicek, A Ercument, Murtha, Michael T, Bal, Vanessa H, Bishop, Somer L, Dong, Shan, Goldberg, Arthur P, Jinlu, Cai, Keaney, John F, Klei, Lambertus, Mandell, Jeffrey D, Moreno-De-Luca, Daniel, Poultney, Christopher S, Robinson, Elise B, Smith, Louw, Solli-Nowlan, Tor, Su, Mack Y, Teran, Nicole A, Walker, Michael F, Werling, Donna M, Beaudet,

Arthur L, Cantor, Rita M, Fombonne, Eric, Geschwind, Daniel H, Grice, Dorothy E, Lord, Catherine, Lowe, Jennifer K, Mane, Shrikant M, Martin, Donna M, Morrow, Eric M, Talkowski, Michael E, Sutcliffe, James S, Walsh, Christopher A, Yu, Timothy W, Autism Sequencing Consortium, , Ledbetter, David H, Martin, Christa Lese, Cook, Edwin H, Buxbaum, Joseph D, Daly, Mark J, Devlin, Bernie, **Roeder, Kathryn**, and State, Matthew W. Insights into autism spectrum disorder genomic architecture and biology from 71 risk loci. *Neuron*, 87(6):1215–33, Sep 2015.

Bodea, Corneliu A, Neale, Benjamin M, Ripke, Stephan, International IBD Genetics Consortium, , Daly, Mark J, Devlin, Bernie, and **Roeder, Kathryn**. A method to exploit the structure of genetic ancestry space to enhance case-control studies. *Am J Hum Genet*, 98(5):857–68, May 2016.

Fromer, Menachem, Roussos, Panos, Sieberts, Solveig K, Johnson, Jessica S, Kavanagh, David H, Perumal, Thanneer M, Ruderfer, Douglas M, Oh, Edwin C, Topol, Aaron, Shah, Hardik R, Klei, Lambertus L, Kramer, Robin, Pinto, Dalila, Gümüş, Zeynep H, Cicek, A Er-cument, Dang, Kristen K, Browne, Andrew, Lu, Cong, Xie, Lu, Readhead, Ben, Stahl, Eli A, Xiao, Jianqiu, Parvizi, Mahsa, Hamamsy, Tymor, Fullard, John F, Wang, Ying-Chih, Mahajan, Milind C, Derry, Jonathan M J, Dudley, Joel T, Hemby, Scott E, Logsdon, Benjamin A, Talbot, Konrad, Raj, Towfique, Bennett, David A, De Jager, Philip L, Zhu, Jun, Zhang, Bin, Sullivan, Patrick F, Chess, Andrew, Purcell, Shaun M, Shinobu, Leslie A, Mangravite, Lara M, Toyoshiba, Hiroyoshi, Gur, Raquel E, Hahn, Chang-Gyu, Lewis, David A, Haroutunian, Vahram, Peters, Mette A, Lipska, Barbara K, Buxbaum, Joseph D, Schadt, Eric E, Hirai, Keisuke, **Roeder, Kathryn**, Brennand, Kristen J, Katsanis, Nicholas, Domenici, Enrico, Devlin, Bernie, and Sklar, Pamela. Gene expression elucidates functional impact of polygenic risk for schizophrenia. *Nat Neurosci*, 19(11):1442–1453, Nov 2016.

Autism Spectrum Disorders Working Group of The Psychiatric Genomics Consortium. Meta-analysis of gwas of over 16,000 individuals with autism spectrum disorder highlights a novel locus at 10q24.32 and a significant overlap with schizophrenia. *Mol Autism*, 8:21, 2017.

Bodea, Corneliu A, Middleton, Frank A, Melhem, Nadine M, Klei, Lambertus, Song, Youeun, Tiobech, Josepha, Marumoto, Pearl, Yano, Victor, Faraone, Stephen V, **Roeder, Kathryn**, Myles-Worsley, Marina, Devlin, Bernie, and Byerley, William. Analysis of shared haplotypes amongst palauans maps loci for psychotic disorders to 4q28 and 5q23-q31. *Mol Neuropsychiatry*, 2(4):173–184, Feb 2017.

Chaste, Pauline, **Roeder, Kathryn**, and Devlin, Bernie. The yin and yang of autism genetics: How rare de novo and common variations affect liability. *Annu Rev Genomics Hum Genet*, 18:167–187, Aug 2017.

De Rubeis, Silvia, **Roeder, Kathryn**, and Bernie, Devlin. Neurodevelopmental mechanisms of pediatric psychiatric disorders: Animal and human studies. 2017.

Kosmicki, Jack A, Samocha, Kaitlin E, Howrigan, Daniel P, Sanders, Stephan J, Slowikowski, Kamil, Lek, Monkol, Karczewski, Konrad J, Cutler, David J, Devlin, Bernie, **Roeder, Kathryn**, Buxbaum, Joseph D, Neale, Benjamin M, MacArthur, Daniel G, Wall, Dennis P, Robinson, Elise B, and Daly, Mark J. Refining the role of de novo protein-truncating variants in neurodevelopmental disorders by using population reference samples. *Nat Genet*, Feb 2017.

Weiner, Daniel J, Wigdor, Emilie M, Ripke, Stephan, Walters, Raymond K, Kosmicki, Jack A, Grove, Jakob, Samocha, Kaitlin E, Goldstein, Jacqueline I, Okbay, Aysu, Bybjerg-Grauholm, Jonas, Werge, Thomas, Hougaard, David M, Taylor, Jacob, iPSYCH-Broad Autism Group, Psychiatric Genomics Consortium Autism Group, Skuse, David, Devlin, Bernie, Anney, Richard, Sanders, Stephan J, Bishop, Somer, Mortensen, Preben Bo, Børglum, Anders D, Smith, George Davey, Daly, Mark J, and Robinson, Elise B. Polygenic transmission disequilibrium confirms that common and rare variation act additively to create risk for autism spectrum disorders. *Nat Genet*, 49(7):978–985, Jul 2017.

Zhu, Lingxue, Lei, Jing, Devlin, Bernie, and **Roeder, Kathryn**. Testing high-dimensional covariance matrices, with application to detecting schizophrenia risk genes. *Ann Appl Stat*, 11(3):1810–1831, Sep 2017.

An, Joon-Yong, Lin, Kevin, Zhu, Lingxue, Werling, Donna M, Dong, Shan, Brand, Harrison, Wang, Harold Z, Zhao, Xuefang, Schwartz, Grace B, Collins, Ryan L, Currall, Benjamin B, Dastmalchi, Claudia, Dea, Jeanselle, Duhn, Clif, Gilson, Michael C, Klei, Lambertus, Liang, Lindsay, Markenscoff-Papadimitriou, Eirene, Pochareddy, Sirisha, Ahituv, Nadav, Buxbaum, Joseph D, Coon, Hilary, Daly, Mark J, Kim, Young Shin, Marth, Gabor T, Neale, Benjamin M, Quinlan, Aaron R, Rubenstein, John L, Sestan, Nenad, State, Matthew W, Willsey, A Jeremy, Talkowski, Michael E, Devlin, Bernie, **Roeder, Kathryn**, and Sanders, Stephan J. Genome-wide de novo risk score implicates promoter variation in autism spectrum disorder. *Science*, 362(6420), 12 2018.

Chen, Siwei, Fragoza, Robert, Klei, Lambertus, Liu, Yuan, Wang, Jiebiao, **Roeder, Kathryn**, Devlin, Bernie, and Yu, Haiyuan. An interactome perturbation framework prioritizes damaging missense mutations for developmental disorders. *Nat Genet*, Jun 2018.

Dobbyn, Amanda, Huckins, Laura M, Boocock, James, Sloofman, Laura G, Glicksberg, Benjamin S, Giambartolomei, Claudia, Hoffman, Gabriel E, Perumal, Thanneer M, Girdhar, Kiran, Jiang, Yan, Raj, Towfique, Ruderfer, Douglas M, Kramer, Robin S, Pinto, Dalila, Common-Mind Consortium, Akbarian, Schahram, Roussos, Panos, Domenici, Enrico, Devlin, Bernie, Sklar, Pamela, Stahl, Eli A, and Sieberts, Solveig K. Landscape of conditional eqtl in dorsolateral prefrontal cortex and co-localization with schizophrenia gwas. *Am J Hum Genet*, 102(6):1169–1184, 06 2018.

Hauberg, Mads E, Fullard, John F, Zhu, Lingxue, Cohain, Ariella T, Giambartolomei, Claudia, Misir, Ruth, Reach, Sarah, Johnson, Jessica S, Wang, Minghui, Mattheisen, Manuel, Børglum, Anders Dupont, Zhang, Bin, Sieberts, Solveig K, Peters, Mette A, Domenici, Enrico, Schadt, Eric E, Devlin, Bernie, Sklar, Pamela, **Roeder, Kathryn**, Roussos, Panos, and CommonMind Consortium, . Differential activity of transcribed enhancers in the prefrontal cortex of 537 cases with schizophrenia and controls. *Mol Psychiatry*, May 2018.

Liu, Fuchen, Choi, David, Xie, Lu, and **Roeder, Kathryn**. Global spectral clustering in dynamic networks. *Proc Natl Acad Sci U S A*, 115(5):927–932, Jan 2018.

Werling, Donna M, Brand, Harrison, An, Joon-Yong, Stone, Matthew R, Zhu, Lingxue, Glessner, Joseph T, Collins, Ryan L, Dong, Shan, Layer, Ryan M, Markenscoff-Papadimitriou,

Eirene, Farrell, Andrew, Schwartz, Grace B, Wang, Harold Z, Currall, Benjamin B, Zhao, Xuefang, Dea, Jeanselle, Duhn, Clif, Erdman, Carolyn A, Gilson, Michael C, Yadav, Rachita, Handsaker, Robert E, Kashin, Seva, Klei, Lambertus, Mandell, Jeffrey D, Nowakowski, Tomasz J, Liu, Yuwen, Pochareddy, Sirisha, Smith, Louw, Walker, Michael F, Waterman, Matthew J, He, Xin, Kriegstein, Arnold R, Rubenstein, John L, Sestan, Nenad, McCarroll, Steven A, Neale, Benjamin M, Coon, Hilary, Willsey, A Jeremy, Buxbaum, Joseph D, Daly, Mark J, State, Matthew W, Quinlan, Aaron R, Marth, Gabor T, **Roeder, Kathryn**, Devlin, Bernie, Talkowski, Michael E, and Sanders, Stephan J. An analytical framework for whole-genome sequence association studies and its implications for autism spectrum disorder. *Nat Genet*, 50(5):727–736, May 2018.

Yip, Benjamin Hon Kei, Bai, Dan, Mahjani, Behrang, Klei, Lambertus, Pawitan, Yudi, Hultman, Christina M, Grice, Dorothy E, **Roeder, Kathryn**, Buxbaum, Joseph D, Devlin, Bernie, Reichenberg, Abraham, and Sandin, Sven. Heritable variation, with little or no maternal effect, accounts for recurrence risk to autism spectrum disorder in sweden. *Biol Psychiatry*, 83(7):589–597, Apr 2018.

Zhu, Lingxue, Lei, Jing, Devlin, Bernie, and **Roeder, Kathryn**. A unified statistical framework for single cell and bulk rna sequencing data. *Ann Appl Stat*, 12(1):609–632, Mar 2018.

Zhu, Lingxue, Lei, Jing, Klei, Lambertus, Devlin, Bernie, and **Roeder, Kathryn**. Semisoft clustering of single-cell data. *Proc Natl Acad Sci U S A*, Dec 2018.

Invited Presentations at Meetings:

- 1991 WNAR Meetings
- 1991 IMS Statistical Challenges in Astronomy meetings
- 1992 IBC Meetings
- 1992 ENAR Meetings
- 1992 ASA meetings
- 1992 IMS Likelihood meetings
- 1993 Bayesian Statistics in Science and Technology
- 1993 Hierarchical Bayes Conference
- 1994 IMS Meetings
- 1994 NRC/NAS Committee on DNA Fingerprinting.
- 1995 IMS Meetings
- 1995 Human Genetics Meetings
- 1996 Genome Mapping and Sequencing
- 1996 ASA, New Jersey Chapter meetings
- 1996 ASA, Joint statistical meetings
- 1996 Social Science and Statistics: in honor of Clifford Clogg.
- 1997 Canadian statistical meetings
- 1997 Human Genetics Meetings
- 1998 ENAR Meetings
- 1998 Ohio State, Cleveland Clinic & Case Western Reserve Minisymposium (featured speaker)
- 1998 ASA Meetings
- 1999 ENAR Meetings, IMS SIP

1999 JSM Meetings
2000 IMS/Bernoulli Society Meetings
2000 Association Analysis for Neurobehavioral Genetics
2000 Speaker for Atlanta Chapter of American Statistical Association
2001 Pennsylvania State University, Alumni Society Meetings.
2002 SNP2000 Consortium (international conference on genomics)
2002 DIMACS Conference on Haplotypes
2003 Genomics Bonn — Genetics of Complex Disease.
2003 UAB Short Course in Statistical Genetics
2004 Keil Workshop, Germany
2004 RECOMB Workshop
2004 UAB Short Course in Statistical Genetics
2004 Pymatuning Short Course in Statistical Genetics
2004 Biological Language Conference, CMU
2005 Joint Statistics Meetings
2005 Canadian Statistical Society Meetings, Presidential Invited Address
2005 UAB Short Course in Statistical Genetics
2005 American Society Human Genetics Meetings, Plenary Session
2005 American Society Human Genetics Meetings, Special Invited Session
2005 National Academy of Sciences, Session on Forensic Inference
2006 National Academy of Sciences invited speaker for the national meetings
2006 American Society Human Genetics Meetings, Special Invited Session
2007 Emerging Design and Analysis Issues in Genomic Studies in Population Sciences.
2007 Computational Biology Genomic Conferences at CMU.
2008 American Society Human Genetics Meetings, Special Invited Session
2008 GENEVA meeting on Genome-wide Association analysis. Featured Speaker
2008 Statistics in Biology, special conference, University of Iowa.
2009 JSM Special Invited Session.
2009 Gordon Conference on Genetics and Genomics.
2010 JSM Special Invited Session.
2010 NCI special invited speaker for the division
2010 NIH conference "Next Generation Tools for Genetic Studies of Complex Diseases"
2011 4th Paris Workshop on Genomics, invited speaker
2011 Special conference in honor of Brad Efron, Washington DC
2011 IPAM invited speaker, UCLA
2012 PQG Conference Sequencing and Complex Traits: beyond 1000 Genomes.
2013 COPSS Junior Researcher Panel: Building a Research Career.
2013 COPSS 50'th Anniversary Session: Reflections on Statistical Science.
2013 JSM invited speaker.
2013 Speaker at Janet L. Norwood Award Ceremony.
2014 Donna J Brogan Lecturer, Emery University.
2014 International Indian Statistical Association Plenary Speaker
2014 Seaver Distinguished Lecturer, Mount Sinai School of Medicine
2015 SFARI invited Webinar speaker for autism research
2015 JSM Invited speaker

2016 ENAR Invited speaker
2016 JSM Invited speaker
2016 Nature conference on Genetics of Common Disease, invited speaker
2016 Molecular Psychiatry Meetings, invited speaker
2016 Women in Statistics Conference
2017 ENAR Invited speaker
2017 Graybill conference, Keynote speaker
2017 JSM Invited speaker
2017 Nature Neuro Genetics conference, invited speaker
2018 Women in Data Science Invited speaker
2018 Pamela Sklar Symposium, Invited speaker
2018 New Aspects on Statistics, Financial Econometrics, and Data Science, invited speaker
2018 NCI SeqSPACE Webinar, Invited speaker
2019 BIRS workshop, Invited speaker
2019 ENAR, Invited speaker

Invited Presentations at Departments:

U. of Connecticut (1989)
Carnegie Mellon (1989,1992)
Rutgers (1991)
Harvard Biostatistics (1991)
U. of Chicago (1991, 1995)
U. of Indiana (1991)
U. of Georgia (1992)
North Carolina State (1992)
Stanford University (1993)
Bellcore (1993)
Harvard (1994)
Johns Hopkins, Biostat & Stat (1994)
U. Michigan, Biostat (1995)
Rice University (1996)
CMU Dept of Biology (2000)
Center of Disease Control (2000)
Pennsylvania State University (2001)
UCLA Genetics and Biostatistics (2003)
University of Chicago (2007)
Texas A&M University (2012)
Pennsylvania State University (2014),
University of Chicago (2015),
Purdue University (2017)
University of North Carolina (2018),
University of Michigan (2019),
AT&T Bell Labs. (1990,1992,1996)
Yale Math (1991)
Johns Hopkins, Biostat (1991)
U. of Chicago, School of Business (1991)
Northwestern (1991)
Purdue (1991,1994)
UCLA (1992)
U. of Pittsburgh (1992)
U. Victoria (1993)
Yale Law School (1994)
Duke (1994)
NIST (1995)
Univ of Texas (1996)
Kansas State University (1998)
Univ of Pittsburgh, Biostat (2000)
Cleveland Clinic (2001)
Harvard Statistics (2002)
N Carolina State Univ. (2005)
University of Toronto (2010)
Carnegie Mellon University, Lane Center (2013)
Stanford (2015),
Emery University (2017)
UC Berkeley (2017)
Johns Hopkins (2018)
University of Pittsburgh (2019)