

## BIOGRAPHICAL SKETCH

NAME: Zhao, Jing Hua / 赵京华		POSITION TITLE: Genetic Analyst / Senior Research Associate	
EDUCATION/TRAINING <i>(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)</i>			
INSTITUTION AND LOCATION	DEGREE <i>(if applicable)</i>	YEAR(s)	FIELD OF STUDY
Shandong (Medical) University	Bachelor	1980-1985	Public Health
Fudan (Shanghai Medical) University	Master	1985-1988	Medical Statistics
King's College London	PhD	1996-2002 (part-time)	Statistical Genetics

My master courses include Linear Algebra/Design of Experiment/Medical Statistics/Multivariate Analysis/Epidemiology at Fudan, and Mathematical Statistics/Optimization Methods/Numerical Methods at Shanghai Jiaotong Universities.

### A. Positions and employment

1988.9-1994.8	Research associate, Division of Sampling Survey, Center for Health Statistics Information, Ministry of Health
1994.8-1996.5	Visiting scientist, Department of Environmental Science, School of Public Health & Channing Laboratory, Medical School, Harvard University
1996.5-2002.8	PostDoc & Lecturer (2001.3-2002.8), Section of Genetic Epidemiology and Biostatistics, Division of Psychological Medicine, Institute of Psychiatry, King's College London
2002.9-2005.9	Statistician, Social and Genetic Epidemiology, Department of Epidemiology and Public Health, University College London
2005.9-2018.7	Investigator scientist in Genetics, MRC Epidemiology Unit
2018.8-	Genetic Analyst / Senior Research Associate, Cardiovascular Epidemiology Unit, Department of Public Health and Primary Care, University of Cambridge

### B. Research interests

My work relates to methods and applications in epidemiology/public health with a recent focus on proteogenomics. Following earlier efforts on familial aggregation, segregation analysis, candidate genes and genomewide association studies (GWASs), my work is capitalised on the meta-analysis at the Cardiovascular Epidemiology Unit (CEU) and within the SCALLOP consortium using the Olink inflammation as well as mass spectrometry panels measured for the INTERVAL samples. I have led analysis contributed to collaborative projects such as the Host Genetics Initiative, the SCALLOP-Seq(ence) consortium and other ongoing projects. I have also been reaching out for analysis of various types of omics data such as single cell proteomics through the Bioconductor project. I have actively promoted reproducible research through distribution of software on CRAN (<https://cran.r-project.org>) and GitHub (<https://github.com>) and through web-based materials from my personal page, <https://jinghuazhao.github.io/> and CEU page, <https://cambridge-ceu.github.io/>.

At the Ministry of Health, I worked on a World Bank project for integrated regional health information systems and compiled *Practical Guides to Statistical Packages* with colleagues. My technical toolset includes Fortran, C/C++, SAS/Stata/R, Bayesian computation, Windows/Linux systems and web technologies; I developed one of the earliest R packages for genetic data analysis and most recently pQTLtools. I have interests in numerical analysis including signal processing and optimization and followed the development of expert systems/artificial intelligence, computational statistics, and machine learning, in particular implementations in Lisp, R and Python.

### C. Key publications

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**Zhao JH**, et al. Mapping pQTLs of circulating inflammatory proteins identifies drivers of immune-mediated disease risk and novel therapeutic targets. *Nat Immunol* 2023, **24**(9):1540-1551, 10.1038/s41590-023-01588-w, <https://www.nature.com/articles/s41590-023-01588-w>.

COVID-19 Host Genetics Initiative. Mapping the human genetic architecture of COVID-19. *Nature* **600**:472–477 (2021); Pathak, G.A. et al. A first update on mapping the human genetic architecture of COVID-19. *Nature* **608**:E1-E10 (2022); The Host Genetics Initiative. A second update on mapping the human genetic architecture of COVID-19. *Nature* **621**:E7–E26 (2023).

**Zhao JH**, Luan JA, Congdon P. Bayesian linear mixed model of polygenic effects. *J Stat Soft.* 2018, **85**(6):1-27. doi: 10.18637/jss.v085.i06

**Zhao JH**, Luan JA. Mixed modeling with whole genome data. *J Prob Stat.* 2012. doi: 10.1155/2012.485174.

Xue F, Li S, Luan J, Yuan Z, Luben RN, Khaw K-T, Wareham NJ, Loos RJF, **Zhao JH**. A latent variable partial least squares path modeling approach to regional association and polygenic effect with applications to a human obesity study. *PLoS ONE* 2012, **7**(2): e31927

Loos RJ, et al. Common variants near MC4R are associated with fat mass, weight and risk of obesity. *Nat Genet* 2008; **40**(6):768-75

**Zhao JH**. gap: genetic analysis package. *J Stat Soft* 2007, **23** (8):1-18. doi: 10.18637/jss.v023.i08.

**Zhao JH**, Brunner EJ, Kumari M, Singh-Manoux A, Hawe E, Talmud PJ, Marmot MG, Humphries SE. APOE polymorphism, socioeconomic status and cognitive function in later mid-life: The Whitehall II longitudinal study. *Soc Psychiatr and Psychiatr Epidemiol* 2005, **40**:557-563

**Zhao JH**, D Curtis, PC Sham. Model-free and permutation tests for allelic associations. *Hum Hered* 2000, **50**(2), 133-139.

#### D. Peer-reviewed publications (in chronological order)

1. **Zhao JH**. Computer software for secondary analysis of statistical data. *Chin J Health Stat* 1990, **7**:9-10.
2. **Zhao JH**. Some perspectives of SAS/STAT 6.03 on personal computers. *Chin J Health Stat* 1990, **7**:49-51.
3. Li NH, **Zhao JH**. Principal component analysis of factors affecting diabetes of the old people. *Chin J Gerontol* 1991, **11**(6): 333-334.
4. **Zhao JH**. Computer data processing for survey of total health expenditure. in Du, LX et al. eds. *The Survey of Total Health Expenditure*. Also in *The Survey of Total Health Expenditure* edited by Center for Health Statistics Information, 1993.
5. **Zhao JH**. A quick method to produce frequency table using Foxbase+. *J China Computer Users Group*. 1993 Supplement.
6. **Zhao JH**. A BASIC program for debugging Fortran code. *China Computers* 1991 Jan, and also in *Digest of Personal Computer Applications*, Kehai Hi-tech Co.
7. **Zhao JH**. A simple method to identify your type of personal computer. *China Computers* 1991 Jun.
8. **Zhao JH**, Tan Q. Trend analysis of fertility data in Shandong province. *Chin J Health Stat* 1994, **11** (supplement).

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9. **Zhao JH**, Wang CY. Internet and health statistics. *Med Info Proc Res* (Chinese). 1996. **4**(1):35-38
10. Xu X, **JH Zhao**. Ecogenetics I. *J Environ Health* 1996, **1**:43-46.
11. **Zhao JH**, Niu T. Ecogenetics II. *J Environ Health* 1996, **3**:139-144.
12. **Zhao JH**, Niu T. Ecogenetics III. *J Environ Health* 1996, **4**:189-190.
13. Sham PC, **JH Zhao**, D. Curtis. Optimal weighting scheme for affected sib-pair analysis of sibship data. *Ann Hum Genet* 1997, **61**:61-69.
14. Li T, K Xu, H Deng, G Cai, J Liu, X Liu, RA Wang, XY Xiang, **JH Zhao**, RM Murray, PC Sham, DA Collier. Association analysis of the dopamine D4 gene exon III VNTR and heroin abuse in Chinese subjects. *Mol Psychiatr* 1997, **2**:413-416.
15. Li T, HP Vallada, X Liu, T Xie, XD Tang, **JH Zhao**, MC O'Donovan, RM Murray, PC Sham, DA Collier. Analysis of CAG/CTG repeat size in Chinese subjects with schizophrenia and bipolar affective disorder using the repeat expansion detection method. *Biol Psychiatr* 1998, **44**(11):1160-5.
16. Arranz MJ, J Munro, MJ Owen, G Spurlock, PC Sham, **J Zhao**, G Kirov, DA Collier, RW Kerwin. Evidence for association between polymorphisms in the promoter and coding regions of the 5-HT<sub>2A</sub> receptor gene and response to clozapine. *Mol Psychiatr* 1998, **3**:61-66.
17. Niu T, X Xu, J Rogus, Y Zhou, C Chen, J Yang, Z Fang, C Schmitz, **J Zhao**, VS Rao, K Lindpainter. Angiotensinogen gene and hypertension in Chinese. *J Clin Invest* 1998, **101**(1): 188-194.
18. **Zhao JH**, PC Sham. A method for calculating probability convolution using ternary numbers with application in the determination of twin zygosity. *Comp Stat Data Anal* 1998, **28**(2): 225-232.
19. Vallada H, D Curtis, P Sham, H Kunugi, **J Zhao**, R Murray, P McGuffin et al. A transmission disequilibrium and linkage analysis of D22S278 marker alleles in 574 families: further support for a susceptibility locus for schizophrenia at 22q12. *Schizophr Res* 1998, **32**:115-121.
20. Wright P, E Dawson, PT Donaldson, JA Underhill, PC Sham, **JH Zhao**, M Gill, S Nanko, MJ Owen, P McGuffin, RM Murray. A transmission/disequilibrium study of the DRB1\*04 gene locus on chromosome 6p21.3 with schizophrenia. *Schizophr Res* 1998, **32**:75-80.
21. Ohadi M, MRA Laloz, P Sham, **J Zhao**, AM Dearlove, C Shiach, S Kinsey, M Rhodes, DM Layton. Localization of a Gene for Familial Hemophagocytic Lymphohistiocytosis at Chromosome 9q21.3-22 by Homozygosity Mapping. *Am J Hum Genet* 1999, **64**(1):165-171.
22. Abusaad I, D Mackay, **J Zhao**, P Stanford, DA Collier, IP Everall. Stereological estimation of the total number of neurons in the murine hippocampus using the optical disector. *Am J Med Genet (Neuropsychiatric Genet)* 1998, **81**(6):483, *The J Comparat Neurol* 1999, **408**:560-566.
23. **Zhao JH**, PC Sham, D Curtis. Letter to the Editor: A program for the Monte Carlo evaluation of significance of the extended TDT (ETDT). *Am J Hum Genet* 1999, **64**(5):1484-1485.
24. Curtis D, **JH Zhao**, PC Sham. Comparison of GENEHUNTER and MFLINK for analysis of COGA linkage data. *Genet Epidemiol* 1999, **17** (suppl 1):115-120.
25. **Zhao JH**, D Curtis, PC Sham. Model-free and permutation tests for allelic associations. *Hum Hered* 2000, **50**(2):133-139.
26. Li T, ZH Zhu, XH Liu, X Hu, **JH Zhao**, PC Sham, DA Collier. Association analysis of polymorphisms in the DRD4 gene and heroin in Chinese subjects. *Am J Med Genet* 2000, **96**:616-621.
27. Sham PC, MW Lin, **JH Zhao**, D Curtis. Power comparison of parametric and nonparametric linkage tests in small pedigrees. *Am J Hum Genet* 2000, **66**(5):1661-1668.
28. Sham PC, **JH Zhao**, D Curtis. The effect of marker polymorphism on the power to detect linkage disequilibrium due to single or multiple ancestral mutations. *Ann Hum Genet* 2000, **64**, 161-169.
29. Aitchison KJ, JG Frank, LC Quattrochi, A Sapone, **JH Zhao**, H Zaher, G Elizondo, C Bryant, JM, DA Collier, AJ Makoff, RW Kerwin. Identification of novel polymorphisms in the 5' flanking region of CYP1A2, characterization of interethnic variability, and investigation of their functional significance. *Pharmacogenet*, 2000, **10**:695-704.

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30. Aitchison KJ, MW Jann, **JH Zhao**, T Sakai, H Zaher, K Wolff, AJ Makoff, DA Collier, RW Kerwin, FJ Gonzalez. Clozapine pharmacokinetics and Pharmacogenetics studied with CYP1A2-null mice. *J Psychopharmacol*, 2000, **14**, 353-359.
31. Li T, X Liu, Z Hong, **J Zhao**, X Hu, P Sham, D Collier. Association analysis of polymorphisms in the *mu* opiod gene and heroin abuse in Chinese subjects. *Addict Biol*, 2000, **5**:181-186.
32. Li T, X Liu, ZH Zhu, **J Zhao**, X Hu, DM Ball, PC Sham, DA Collier. No association between (AAT)<sub>n</sub> repeats in the cannabinoid receptor gene (CNR1) and heroin abuse in a Chinese population. *Mol Psychiatr*, 2000 **5**, 128-130.
33. Li T, D Ball, **J Zhao**, RM Murray, X Liu, PC Sham, DA Collier. Family-based linkage disequilibrium mapping using SNP marker haplotypes: application to a potential locus for schizophrenia at chromosome 22q11. *Mol Psychiatr*, 2000, **5**, 77-84.
34. Sham P, **JH Zhao**, SS Cherny, JK Hewitt. Variance components QTL linkage analysis of selected and non-normal samples: conditioning on trait values. *Genet Epidemiol*, 2000, **19**, (suppl 1), 22-28
35. Sham PC, **JH Zhao**. The power of genome-wide sib pair linkage scans for quantitative trait loci using the new Haseman-Elston regression method, *GeneScreen* 2000, **1**:103-106.
36. Koch HG, J McClay, EW Loh, S Higuchi, **JH Zhao**, P Sham, D Ball and IW Craig. Allele association studies with SSR and SNP markers at known physical distances within a 1MB region embracing from the ALDH2 locus in the Japanese. *Hum Mol Genet*, 2000, **9**:2993-2999
37. Sham PC, **JH Zhao**, I Waldman, D Curtis. Should ambiguous trios for {TDT} be discarded? *Ann Hum Genet* 2000, **64**:575-576.
38. Karwautz A, S Rabe-Hesketh, X Hu, **J Zhao**, P Sham, DA Collier, JL Treasure. Individual-specific risk factors for anorexia nervosa: a pilot study using a discordant sister-pair design. *Psych Med* 2001, **31**(2):317-329.
39. Meira-Lima IV, **JH Zhao**, P Sham, AC Pereira, JE Krieger and H Vallada. Association and linkage studies between bipolar affective disorder and the polymorphic CAG/CTG repeat loci ERDA1, SEF2-1B, MAB21L and KCNN3, *Mol Psych* 2001, **6**(5):565-569.
40. Mill J, S Curran, L Kent, S Richards, A Gould, V Virdee, L Hockett, J Sharp, C Batten, S Fernando, E Simanoff, M Thompson, **J Zhao**, P Sham, E Taylor, P Asherson. Attention deficit hyperactivity disorder (ADHD) and the dopamine D4 receptor gene: evidence of association but no linkage in a UK sample. *Mol Psych* 2001, **6**(4): 440-444.
41. Cai G, T Li, H Deng, **J Zhao**, X Hu, RM Murray, X Liu, PC Sham, DA Collier. Affected sibling pair linkage analysis of qualitative and quantitative traits for schizophrenia on chromosome 22 in a Chinese population. *Am J Med Genet* 2001, **105**(4):321-327.
42. Russ C, JF Powerll, **J Zhao**, M Baker, M Hutton, F Crawford, M Mullan, G Roks, M Cruts, S Lovestone. The microtubule associated protein Tau gene and Alzheimer's disease - an association study and meta-analysis. *Neurosci Lett* 2001, **314**(1-2):92-96.
43. RYL Chen, P Sham, EYH Chen, T Li, EFC Cheung, TCK Hui, CL Kwok, F Lieh-Mak, **JH Zhao**, D Collier, R Murray. No association between T102C polymorphism of serotonin-2A receptor gene and clinical phenotypes of Chinese schizophrenic patients. *Psychitr Res* 2001, **105**: 175-185
44. **Zhao JH**, PC Sham. Faster allelic association using unrelated individuals. *Hum Hered* 2002, **53**: 36-41.
45. Li T, X Liu, **J Zhao**, X Hu, DM Ball, E-W Loh PC Sham and DA Collier. Allelic association analysis of the dopamine D2, D3, 5-HT(2A) and GABA(A)gamma2 receptors and the serotonin transporter genes with heroin abuse in Chinese subjects. *Am J Med Genet* 2002, **114**: 329-334.
46. Mallett R, J Leff, D Bhugra, D Pang, **JH Zhao**. Social environment, ethnicity and schizophrenia: a case-control study. *Social Psychiatr and Psychiatric Epidemiol* 2002, **37**: 329-335.
47. **Zhao JH**, S Lissarrague, L Essioux, PC Sham. GENECOUNTING: haplotype analysis with missing genotypes. *Bioinformatics* 2002, **18**: 1694-1695.
48. **Zhao JH**, PC Sham. Generic number system and haplotype analysis. *Comp Meth Prog Biomed* 2003, **70**: 1-9.

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49. Gabrovsek M, M Breclj-Anderluh, L Bellodi, E Cellini, D Di Bella, X Estivill, F Fernandez-Aranda, B Freeman, F Geller, M Gratacos, R Haigh, J Hebebrand, A Hinney, J Holliday, X Hu, A Karwautz, B Nacmias, M Ribases, H Remschmidt, R Komel, S Sorbi, M Tomori, J Treasure, G Wagner, **J Zhao**, DA Collier. Combined family trio and case-control analysis of the COMT val158met polymorphism in European patients with anorexia nervosa *Am J Med Genet B (Neuropsychiatric Genet)* 2004, **124B**:68–72
50. Huang Y, T Li, Y Wang, J Ansar, G Lanting, X Liu, **JH Zhao**, X Hu, PC Sham, D Collier. Linkage disequilibrium analysis of polymorphisms in the gene for myelin oligodendrocyte glycoprotein in Tourette's syndrome patients from a Chinese sample. *Am J Med Genet. (Neuropsychiatric Genet)* 2004, **124B**:76-80.
51. Shi J, S Zhang, C Ma, X Liu, T Li, M Tang, H Han, Y Guo, **JH Zhao**, K Zheng, X Kong, K Zhang, Z Su, Z Zhao. Association between apolipoprotein C1 HpaI polymorphism and sporadic Alzheimer's disease in Chinese. *Acta Neurol Scan* 2004, **109**:140-145.
52. Shi J, S Zhang, M Tang, X Liu, T Li, H Han, Y Wang, Y Guo, **J Zhao**, H Li, C Ma. Possible association between Cys311Ser polymorphism of paraoxonase 2 gene and late-onset Alzheimer's disease in Chinese. *Mol Brain Res* 2004, **120**:201–204.
53. Tan Q, **JH Zhao**, I Iachine, J Hjelmberg, W Vach, JW Vaupel, Christensen K, TA Kruse. Power of non-parametric linkage analysis in mapping genes contributing to human longevity *Genet Epidemiol* 2004, **26**:245-253.
54. **Zhao JH**. 2LD, GENECOUNTING and HAP: Computer programs for linkage disequilibrium analysis. *Bioinformatics* 2004, **20**:1325-1326.
55. **Zhao JH**, Book review: Lachin JM (2000): Biostatistical methods: the assessment of relative risks. New York: John Wiley. *Stat Methods Med Res* 2004; **13**: 414-415.
56. Parsian A, R Sinha, B Racette, **JH Zhao**, JS Perlmutter. Association of a variation in the promotor of the brain-derived neurotrophic factor gene with familial parkinson's disease. *Parkinsonism and Related Disorders* 2004, **10**:213-219.
57. Walshe M, C McDonald, M Taylor, **J Zhao**, P Sham, A Grech, K Schulze, E Bramon, R Murray. Obstetric complications in patients with Schizophrenia and their unaffected siblings *European Psychiatr* 2005, **20**:28-34.
58. Shi J, S Zhang, M Tang, C Ma, **J Zhao**, T Li, X Liu, Y Sun, Y Guo, H Han, Y Ma, Z Zhao. Mutation screening and association study of the neprilysin gene in sporadic Alzheimer's disease in Chinese persons. *J Gerontology Bio Sci* 2005, **60A**: 301-306.
59. Tan Q, L Christiansen, L Bathum, **JH Zhao**, AI Yashin, JW Vaupel, K Christensen, TA Kruse. Estimating haplotype relative risks on human survival in population-based association studies. *Hum Hered* 2005, **59**:88-97.
60. Tan Q, L Christiansen, L Bathum, **JH Zhao**, W Vach, JW Vaupel, K Christensen, TA Kruse. Haplotype effects on human survival: logistic regression models applied to unphased genotype data. *Ann Hum Genet* 2005, **69**: 168-175.
61. **Zhao JH**, EJ Brunner, M Kumari, A Singh-Manoux, E Hawe, PJ Talmud, MG Marmot, SE Humphries. APOE polymorphism, socioeconomic status and cognitive function in later mid-life: The Whitehall II longitudinal study. *Soc Psychiatr and Psychiatr Epidemiol* 2005, **40**:557-563.
62. **Zhao JH**. Mixed-effects Cox models of alcohol dependence in extended families. *BMC Genetics* 2005, (Suppl) **6**:127.
63. Tan Q, K Christensen, L Christiansen, L Bathum, S Li, **JH Zhao**, TK Kruse. Haplotype association analysis of human disease traits using multi-locus genotype data of unrelated subjects. *Genetical Res* 2005, **86**: 223-231.
64. **Zhao JH**, Q Tan. Integrated analysis of genetic data with R. *Hum Genomics* 2006, **2**(4):258-265.
65. **Zhao JH**, Drawing pedigree diagrams with R and graphviz, *R News* 6:38-41, 2006
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68. **Zhao JH**, Luan JA, Tan Q, Loos R, Wareham NJ. Analysis of large genomic data *in silico*: the EPIC-Norfolk study of obesity. In DS Huang, L Heutte, and M Loog (Eds). *Advanced Intelligent Computing Theories and Applications with Aspects of Contemporary Intelligent Computing Techniques*, Third International Conference on Intelligent Computing (ICIC) 2007: 781-790.
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70. Tan Q, Christiansen L, Brasch-Andersen C, **Zhao JH**, Kruse TA, Christensen K. Retrospective analysis of main and interaction effects in genetic association studies of human complex traits. *BMC Genet* 2007, **8**:70.
71. **Zhao JH**, J Luan, F Baksh, Q Tan. Mining gene networks with application to GAW15 problem 1. *BMC Proc* 2007, **1** (Suppl 1):S52
72. **Zhao JH**. gap: genetic analysis package. *J Stat Soft* 2007, **23** (8):1-18.
73. Sandhu MS, et al. LDL-cholesterol concentrations: a genome-wide association study. *Lancet* 2008, **371**:483-491.
74. Tan Q, M Thomassen, KM Jochumsen, **JH Zhao**, K Christensen, TA Kruse. Evolutionary Algorithm for Feature Subset Selection in Predicting Tumor Outcomes Using Microarray Data. I. Măndoiu, R. Sunderraman, and A. Zelikovsky (Eds.): ISBRA 2008, LNBI 4983, pp. 426–433, 2008. © Springer-Verlag Berlin Heidelberg 2008
75. Weedon MN, et al. Genome-wide association analysis identifies 20 loci that influence adult height. *Nat Genet* 2008, **40**:575-583.
76. Loos R, et al. Common variants near *MC4R* are associated with fat mass, weight and risk of obesity. *Nat Genet* 2008, **40**:768-775.
77. Tan Q, **J Zhao**, S Li, L Christiansen, TA Kruse, K Christensen. Differential and correlation analyses of microarray gene expression data in the CEPH Utah families. *Genomics* 2008, **92**:94-100.
78. Tan Q, **JH Zhao**, TA Kruse, K Christensen. Power for genetic association study of human longevity using the case-control design. *Am J Epidemiol* 2008, **168**:890-896.
79. E Vassos, PC Sham, G Cai, H Deng, X Liu, X Sun, **J Zhao**, RM Murray, DA Collier, T Li. Correlation and familial aggregation of dimensions of psychosis in affected sibling pairs from China. *Brit J Psychiat* 2008, **193**:305-310.
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83. Patra B, Parsian AJ, Racette BA, **Zhao JH**, Perlmutter JS, Parsian A. LRRK2 gene G2019S mutation and SNPs [haplotypes] in subtypes of Parkinson's disease. *Parkinsonism Relat Disord*, 2009, **15**:175-180.
84. Ong KK, Elks CE, Li S, **Zhao JH**, Luan J, Andersen LB, Bingham SA, Brage S, Smith GD, Ekelund U, Gillson CJ, Glaser B, Golding J, Hardy R, Khaw KT, Kuh D, Luben R, Marcus M, McGeehin MA, Ness AR, Northstone K, Ring SM, Rubin C, Sims MA, Song K, Strachan DP, Vollenweider P, Waeber G, Waterworth DM, Wong A, Deloukas P, Barroso I, Mooser V, Loos RJ,



- Wareham NJ. Genetic variation in *LIN28B* is associated with the timing of puberty. *Nat Genet* 2009, **41**:729-733.
85. Newton-Cheh C, et al. Genome-wide association study identifies eight loci associated with blood pressure. *Nat Genet* 2009, **41**:666-676.
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90. Li S, **Zhao JH**, Luan J, Luben RN, Rodwell SA, Khaw K-T, Ong KK, Wareham NJ, Loos RJF. Cumulative effects and predictive value of common obesity-susceptibility variants identified by genome-wide association studies. *Am J Clin Nutr*. 2010, **91**:184-190.
91. Repapi E, et al. Genome-wide association study identifies five loci associated with lung function. *Nat Genet*. 2010, **42**(1):36-44.
92. Dupuis J, et al. Novel genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. *Nat Genet*. 2010, **42**:105-116
93. Saxena R, et al. Genetic variation in *GIPR* influences the glucose and insulin responses to an oral glucose challenge. *Nat Genet* 2010, **42**:142-148
94. Peng Q, **Zhao JH**, Xue F. PCA-based bootstrap confidence interval tests for gene-disease association involving multiple SNPs. *BMC Genet* 2010, **11**:6
95. Peng Q, **Zhao JH**, Xue F. A gene-based method for detecting gene-gene co-association in a case-control association study. *Eur J Hum Genet* 2010, **18**:582-587
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98. Lango Allen, H., K. Estrada, et al. Hundreds of variants clustered in genomic loci and biological pathways affect human height. *Nature* 2010, **467**(7317): 832-838.
99. Tan Q, **Zhao JH**, Li S, Kruse TA, Christensen K. Power assessment for genetic association study of human longevity using offspring of long-lived families. *Eur J Epidemiol* **21**:501-506, 2010.
100. Yang Q, et al. Racial/Ethnic Differences in Association of Fasting Glucose–Associated Genomic Loci With Fasting Glucose, HOMA-B, and Impaired Fasting Glucose in the U.S. Adult population *Diabetes Care* 2010, **33**:2370-2377.
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102. Speliotes EK, et al. Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. *Nat Genet* 2010, **42**(11):937-948.
103. Heid IM, et al. Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution *Nat Genet* 2010, **42**(11):949-960.
104. Elks CE, et al. Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies *Nat Genet* 2010; **42**:1077-1085
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