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2177	Genomewide weighted hypothesis testing in family-based association studies, with an application to a 100K scan. <b>2007</b> , 81, 607-14	81
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2083	Disease associations and family-based tests. <b>2008</b> , Chapter 1, Unit 1.12	4
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2064	Comparison of mixed-model approaches for association mapping. <b>2008</b> , 178, 1745-54	199
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1798	IL28B is associated with response to chronic hepatitis C interferon-alpha and ribavirin therapy. <i>Nature Genetics</i> , <b>2009</b> , 41, 1100-4	36.3	1636
1797	Genome-wide association study identifies variants in TMPRSS6 associated with hemoglobin levels. <i>Nature Genetics</i> , <b>2009</b> , 41, 1170-2	36.3	179
1796	Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium. <i>Nature Genetics</i> , <b>2009</b> , 41, 1191-8	36.3	285
1795	A large-scale replication study identifies TNIP1, PRDM1, JAZF1, UHRF1BP1 and IL10 as risk loci for systemic lupus erythematosus. <i>Nature Genetics</i> , <b>2009</b> , 41, 1228-33	36.3	626
1794	Genome-wide association study in a Chinese Han population identifies nine new susceptibility loci for systemic lupus erythematosus. <i>Nature Genetics</i> , <b>2009</b> , 41, 1234-7	36.3	732
1793	Genetic variants in TPMT and COMT are associated with hearing loss in children receiving cisplatin chemotherapy. <i>Nature Genetics</i> , <b>2009</b> , 41, 1345-9	36.3	243
1792	Genetic variants at CD28, PRDM1 and CD2/CD58 are associated with rheumatoid arthritis risk. <i>Nature Genetics</i> , <b>2009</b> , 41, 1313-8	36.3	272
1791	HLA-C cell surface expression and control of HIV/AIDS correlate with a variant upstream of HLA-C. <i>Nature Genetics</i> , <b>2009</b> , 41, 1290-4	36.3	230
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1787	Reply to: "Experimental aspects of copy number variant assays at CCL3L1". <b>2009</b> , 15, 1117-20		22
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1783	Recent advances of genetic ancestry testing in biomedical research and direct to consumer testing. <b>2009</b> , 76, 225-35	29
1782	Tests of association for quantitative traits in nuclear families using principal components to correct for population stratification. <b>2009</b> , 73, 601-13	27
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1774	Genome-wide association and replication studies identified TRHR as an important gene for lean body mass. <b>2009</b> , 84, 418-23	89
1773	Genome-wide association analysis identifies PDE4D as an asthma-susceptibility gene. <b>2009</b> , 84, 581-93	264
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1591	Variation explained in mixed-model association mapping. <b>2010</b> , 105, 333-40	87
1590	Population substructure in continuous and fragmented stands of <i>Populus trichocarpa</i> . <b>2010</b> , 105, 348-57	23
1589	Population-based linkage analysis of schizophrenia and bipolar case-control cohorts identifies a potential susceptibility locus on 19q13. <b>2010</b> , 15, 319-25	34
1588	Genome-wide association scan for five major dimensions of personality. <b>2010</b> , 15, 647-56	214

1587	Genome-wide association study of recurrent major depressive disorder in two European case-control cohorts. <b>2010</b> , 15, 589-601		190
1586	Whole-genome association mapping of gene expression in the human prefrontal cortex. <b>2010</b> , 15, 779-84		60
1585	Genome-wide association study of 107 phenotypes in Arabidopsis thaliana inbred lines. <b>2010</b> , 465, 627-31		1257
1584	ITPA gene variants protect against anaemia in patients treated for chronic hepatitis C. <b>2010</b> , 464, 405-8		380
1583	Genome-wide SNP and haplotype analyses reveal a rich history underlying dog domestication. <b>2010</b> , 464, 898-902		526
1582	Assessing sources of inconsistencies in genotypes and their effects on genome-wide association studies with HapMap samples. <b>2010</b> , 10, 364-74		18
1581	Geographical genomics of human leukocyte gene expression variation in southern Morocco. <i>Nature Genetics</i> , <b>2010</b> , 42, 62-7	36.3	117
1580	Meta-analyses of genome-wide association studies identify multiple loci associated with pulmonary function. <i>Nature Genetics</i> , <b>2010</b> , 42, 45-52	36.3	467
1579	Genetic variation in SCN10A influences cardiac conduction. <i>Nature Genetics</i> , <b>2010</b> , 42, 149-52	36.3	209
1578	A genome-wide association study identifies pancreatic cancer susceptibility loci on chromosomes 13q22.1, 1q32.1 and 5p15.33. <i>Nature Genetics</i> , <b>2010</b> , 42, 224-8	36.3	463
1577	Plasmodium falciparum genome-wide scans for positive selection, recombination hot spots and resistance to antimalarial drugs. <i>Nature Genetics</i> , <b>2010</b> , 42, 268-71	36.3	164
1576	Genome-wide association study of hematological and biochemical traits in a Japanese population. <i>Nature Genetics</i> , <b>2010</b> , 42, 210-5	36.3	388
1575	Common variants in KCNN3 are associated with lone atrial fibrillation. <i>Nature Genetics</i> , <b>2010</b> , 42, 240-4	36.3	362
1574	Multiple common variants for celiac disease influencing immune gene expression. <i>Nature Genetics</i> , <b>2010</b> , 42, 295-302	36.3	727
1573	Variance component model to account for sample structure in genome-wide association studies. <i>Nature Genetics</i> , <b>2010</b> , 42, 348-54	36.3	1624
1572	Genome-wide association study of intracranial aneurysm identifies three new risk loci. <i>Nature Genetics</i> , <b>2010</b> , 42, 420-5	36.3	234
1571	Genetic loci influencing kidney function and chronic kidney disease. <i>Nature Genetics</i> , <b>2010</b> , 42, 373-5	36.3	205
1570	Genome-wide meta-analyses identify multiple loci associated with smoking behavior. <i>Nature Genetics</i> , <b>2010</b> , 42, 441-7	36.3	927

1569	Genome-wide association study meta-analysis identifies seven new rheumatoid arthritis risk loci. <i>Nature Genetics</i> , <b>2010</b> , 42, 508-14	36.3	969
1568	A regulatory variant in CCR6 is associated with rheumatoid arthritis susceptibility. <i>Nature Genetics</i> , <b>2010</b> , 42, 515-9	36.3	209
1567	Genome-wide association study identifies five new breast cancer susceptibility loci. <i>Nature Genetics</i> , <b>2010</b> , 42, 504-7	36.3	582
1566	Genome-wide meta-analyses identifies seven loci associated with platelet aggregation in response to agonists. <i>Nature Genetics</i> , <b>2010</b> , 42, 608-13	36.3	204
1565	Common SNPs explain a large proportion of the heritability for human height. <i>Nature Genetics</i> , <b>2010</b> , 42, 565-9	36.3	2935
1564	Genome-wide association studies identify IL23R-IL12RB2 and IL10 as Behçet's disease susceptibility loci. <i>Nature Genetics</i> , <b>2010</b> , 42, 703-6	36.3	392
1563	Excess of rare variants in genes identified by genome-wide association study of hypertriglyceridemia. <i>Nature Genetics</i> , <b>2010</b> , 42, 684-7	36.3	365
1562	Common genetic variation in the HLA region is associated with late-onset sporadic Parkinson's disease. <i>Nature Genetics</i> , <b>2010</b> , 42, 781-5	36.3	574
1561	Association of IFIH1 and other autoimmunity risk alleles with selective IgA deficiency. <i>Nature Genetics</i> , <b>2010</b> , 42, 777-80	36.3	122
1560	Genome-wide association study of esophageal squamous cell carcinoma in Chinese subjects identifies susceptibility loci at PLCE1 and C20orf54. <i>Nature Genetics</i> , <b>2010</b> , 42, 759-63	36.3	335
1559	A shared susceptibility locus in PLCE1 at 10q23 for gastric adenocarcinoma and esophageal squamous cell carcinoma. <i>Nature Genetics</i> , <b>2010</b> , 42, 764-7	36.3	403
1558	A genome-wide association study in the Japanese population identifies susceptibility loci for type 2 diabetes at UBE2E2 and C2CD4A-C2CD4B. <i>Nature Genetics</i> , <b>2010</b> , 42, 864-8	36.3	214
1557	A multi-stage genome-wide association study of bladder cancer identifies multiple susceptibility loci. <i>Nature Genetics</i> , <b>2010</b> , 42, 978-84	36.3	408
1556	Common variants at TRAF3IP2 are associated with susceptibility to psoriatic arthritis and psoriasis. <i>Nature Genetics</i> , <b>2010</b> , 42, 996-9	36.3	294
1555	Genome-wide association studies of 14 agronomic traits in rice landraces. <i>Nature Genetics</i> , <b>2010</b> , 42, 961-3	36.3	1414
1554	A genome-wide association study of Hodgkin's lymphoma identifies new susceptibility loci at 2p16.1 (REL), 8q24.21 and 10p14 (GATA3). <i>Nature Genetics</i> , <b>2010</b> , 42, 1126-1130	36.3	158
1553	Data quality control in genetic case-control association studies. <b>2010</b> , 5, 1564-73		741
1552	Empirical tests for compositional epistasis. <b>2010</b> , 11, 166		26

1551	Methodological challenges of genome-wide association analysis in Africa. <b>2010</b> , 11, 149-60	143
1550	New approaches to population stratification in genome-wide association studies. <b>2010</b> , 11, 459-63	774
1549	Statistical analysis strategies for association studies involving rare variants. <b>2010</b> , 11, 773-85	378
1548	Centralized Genomic Control: A Simple Approach Correcting for Population Structures. <b>2010</b> , 1	
1547	The coalescent and its descendants. 204-237	1
1546	CONVERGENCE AND PREDICTION OF PRINCIPAL COMPONENT SCORES IN HIGH-DIMENSIONAL SETTINGS. <b>2010</b> , 38, 3605-3629	47
1545	CoAIMs: a cost-effective panel of ancestry informative markers for determining continental origins. <b>2010</b> , 5, e13443	19
1544	Commercially available outbred mice for genome-wide association studies. <b>2010</b> , 6, e1001085	102
1543	Allelic selection of amplicons in glioblastoma revealed by combining somatic and germline analysis. <b>2010</b> , 6, e1001086	21
1542	The characterization of twenty sequenced human genomes. <b>2010</b> , 6, e1001111	133
1541	Analysis of population structure: a unifying framework and novel methods based on sparse factor analysis. <b>2010</b> , 6, e1001117	95
1540	Dementia revealed: novel chromosome 6 locus for late-onset Alzheimer disease provides genetic evidence for folate-pathway abnormalities. <b>2010</b> , 6, e1001130	111
1539	Risk of ovarian cancer and inherited variants in relapse-associated genes. <b>2010</b> , 5, e8884	22
1538	A new statistic to evaluate imputation reliability. <b>2010</b> , 5, e9697	47
1537	Theoretical formulation of principal components analysis to detect and correct for population stratification. <b>2010</b> , 5, e12510	13
1536	Genetic variants in nuclear-encoded mitochondrial genes influence AIDS progression. <b>2010</b> , 5, e12862	35
1535	A genome-wide association study of red blood cell traits using the electronic medical record. <b>2010</b> , 5, e13011	94
1534	Ancestral informative marker selection and population structure visualization using sparse Laplacian eigenfunctions. <b>2010</b> , 5, e13734	7

1533	Estimating the total number of susceptibility variants underlying complex diseases from genome-wide association studies. <b>2010</b> , 5, e13898	13
1532	Genomic selection in admixed and crossbred populations. <b>2010</b> , 88, 32-46	141
1531	A Genome-Wide Association Study of Educational Attainment. <b>2010</b> ,	0
1530	Characterizing allelic association in the genome era. <b>2010</b> , 92, 461-70	2
1529	Optimizing copy number variation analysis using genome-wide short sequence oligonucleotide arrays. <b>2010</b> , 38, 3275-86	15
1528	Host determinants of HIV-1 control in African Americans. <b>2010</b> , 201, 1141-9	125
1527	European lactase persistence genotype shows evidence of association with increase in body mass index. <b>2010</b> , 19, 1129-36	50
1526	GWAS analyzer: integrating genotype, phenotype and public annotation data for genome-wide association study analysis. <b>2010</b> , 26, 560-4	22
1525	A genome-wide association study in 19 633 Japanese subjects identified LHX3-QSOX2 and IGF1 as adult height loci. <b>2010</b> , 19, 2303-12	91
1524	Genetic variants in ABO blood group region, plasma soluble E-selectin levels and risk of type 2 diabetes. <b>2010</b> , 19, 1856-62	131
1523	COMT val108/158 met genotype affects neural but not cognitive processing in healthy individuals. <b>2010</b> , 20, 672-83	47
1522	Novel associations of multiple genetic loci with plasma levels of factor VII, factor VIII, and von Willebrand factor: The CHARGE (Cohorts for Heart and Aging Research in Genome Epidemiology) Consortium. <b>2010</b> , 121, 1382-92	260
1521	Clinical Approach to Sudden Cardiac Death Syndromes. <b>2010</b> ,	2
1520	Genome-wide association study of major recurrent depression in the U.K. population. <b>2010</b> , 167, 949-57	194
1519	Association of genome-wide variation with the risk of incident heart failure in adults of European and African ancestry: a prospective meta-analysis from the cohorts for heart and aging research in genomic epidemiology (CHARGE) consortium. <b>2010</b> , 3, 256-66	147
1518	Common variants in the calcium-sensing receptor gene are associated with total serum calcium levels. <b>2010</b> , 19, 4296-303	77
1517	EGLN1 involvement in high-altitude adaptation revealed through genetic analysis of extreme constitution types defined in Ayurveda. <b>2010</b> , 107, 18961-6	122
1516	A comprehensive genetic study on left atrium size in Caribbean Hispanics identifies potential candidate genes in 17p10. <b>2010</b> , 3, 386-92	13



1515	Predicting sensation seeking from dopamine genes. A candidate-system approach. <b>2010</b> , 21, 1282-90	84
1514	A genome-wide association study reveals susceptibility variants for non-small cell lung cancer in the Korean population. <b>2010</b> , 19, 4948-54	65
1513	Genome-wide association study of prostate cancer mortality. <b>2010</b> , 19, 2869-76	42
1512	Association of single nucleotide polymorphisms on chromosome 9p21.3 with platelet reactivity: a potential mechanism for increased vascular disease. <b>2010</b> , 3, 445-53	48
1511	Robust relationship inference in genome-wide association studies. <b>2010</b> , 26, 2867-73	1238
1510	Signatures of founder effects, admixture, and selection in the Ashkenazi Jewish population. <b>2010</b> , 107, 16222-7	81
1509	Genome-wide association of anthropometric traits in African- and African-derived populations. <b>2010</b> , 19, 2725-38	81
1508	Positionally cloned genes and age-specific effects in asthma and atopy: an international population-based cohort study (ECRHS). <b>2010</b> , 65, 124-31	20
1507	Saliva-derived DNA performs well in large-scale, high-density single-nucleotide polymorphism microarray studies. <b>2010</b> , 19, 794-8	47
1506	Genetic variation of genes involved in dihydrotestosterone metabolism and the risk of prostate cancer. <b>2010</b> , 19, 229-39	42
1505	Variant ABO blood group alleles, secretor status, and risk of pancreatic cancer: results from the pancreatic cancer cohort consortium. <b>2010</b> , 19, 3140-9	67
1504	Genome-wide association study identifies variants at the IL18-BCO2 locus associated with interleukin-18 levels. <b>2010</b> , 30, 885-90	62
1503	European ancestry as a risk factor for atrial fibrillation in African Americans. <b>2010</b> , 122, 2009-15	171
1502	Correction for hidden confounders in the genetic analysis of gene expression. <b>2010</b> , 107, 16465-70	107
1501	Multistage genomewide association study identifies a locus at 1q41 associated with rate of HIV-1 disease progression to clinical AIDS. <b>2010</b> , 201, 618-26	60
1500	Efficient genome-wide association testing of gene-environment interaction in case-parent trios. <b>2010</b> , 172, 116-22	30
1499	Identification of epistatic effects using a protein-protein interaction database. <b>2010</b> , 19, 4345-52	21
1498	Pesticide use modifies the association between genetic variants on chromosome 8q24 and prostate cancer. <b>2010</b> , 70, 9224-33	34

1497	Genetic structure of a unique admixed population: implications for medical research. <b>2010</b> , 19, 411-9	86
1496	BDNF Val66Met is associated with introversion and interacts with 5-HTTLPR to influence neuroticism. <b>2010</b> , 35, 1083-9	85
1495	Evidence for CRHR1 in multiple sclerosis using supervised machine learning and meta-analysis in 12,566 individuals. <b>2010</b> , 19, 4286-95	17
1494	Identity-by-descent matrix decomposition using latent ancestral allele models. <b>2010</b> , 185, 1045-57	16
1493	Genome-wide association study identifies polymorphisms in LEPR as determinants of plasma soluble leptin receptor levels. <b>2010</b> , 19, 1846-55	63
1492	Genome-wide association study of height and body mass index in Australian twin families. <b>2010</b> , 13, 179-93	51
1491	In silico replication of the genome-wide association results of the Type 1 Diabetes Genetics Consortium. <b>2010</b> , 19, 2534-8	14
1490	Variation at 8q24 and 9p24 and risk of epithelial ovarian cancer. <b>2010</b> , 13, 43-56	14
1489	Genome-wide association studies in cancer--current and future directions. <b>2010</b> , 31, 111-20	82
1488	Correcting population stratification in genetic association studies using a phylogenetic approach. <b>2010</b> , 26, 798-806	29
1487	Dealing with heterogeneity between cohorts in genomewide SNP association studies. <b>2010</b> , 9, Article 8	18
1486	Mapping of numerous disease-associated expression polymorphisms in primary peripheral blood CD4+ lymphocytes. <b>2010</b> , 19, 4745-57	94
1485	Assessment of LD matrix measures for the analysis of biological pathway association. <b>2010</b> , 9, Article35	2
1484	Advances in genomic analysis of stroke: what have we learned and where are we headed?. <b>2010</b> , 41, 825-32	64
1483	Dense mapping of MYH9 localizes the strongest kidney disease associations to the region of introns 13 to 15. <b>2010</b> , 19, 1805-15	56
1482	A novel adaptive method for the analysis of next-generation sequencing data to detect complex trait associations with rare variants due to gene main effects and interactions. <b>2010</b> , 6, e1001156	180
1481	. <b>2010</b> ,	
1480	A risk allele for focal segmental glomerulosclerosis in African Americans is located within a region containing APOL1 and MYH9. <b>2010</b> , 78, 698-704	125

1479	BioSMACK: A linux Live CD for analysis of genome-wide association. <b>2010</b> ,	
1478	Genome-wide association studies for the identification of biomarkers in metabolic diseases. <b>2010</b> , 4, 39-51	6
1477	Prostate cancer susceptibility variants confer increased risk of disease progression. <b>2010</b> , 19, 2124-32	37
1476	Identification and frequency estimation of inversion polymorphisms from haplotype data. <b>2010</b> , 17, 517-31	21
1475	Pancreatic cancer risk and ABO blood group alleles: results from the pancreatic cancer cohort consortium. <b>2010</b> , 70, 1015-23	168
1474	Variant of TYR and autoimmunity susceptibility loci in generalized vitiligo. <b>2010</b> , 362, 1686-97	281
1473	Genome-wide associations and functional genomic studies of musculoskeletal adverse events in women receiving aromatase inhibitors. <b>2010</b> , 28, 4674-82	175
1472	Clinical Summaries. <b>2010</b> , 121, 1375-1376	
1471	Genomic variation associated with mortality among adults of European and African ancestry with heart failure: the cohorts for heart and aging research in genomic epidemiology consortium. <b>2010</b> , 3, 248-55	66
1470	Common genetic variation and susceptibility to partial epilepsies: a genome-wide association study. <b>2010</b> , 133, 2136-47	115
1469	Using association mapping to dissect the genetic basis of complex traits in plants. <b>2010</b> , 9, 157-65	117
1468	Genome-wide association study of homocysteine levels in Filipinos provides evidence for CPS1 in women and a stronger MTHFR effect in young adults. <b>2010</b> , 19, 2050-8	57
1467	Improved prediction of cardiovascular disease based on a panel of single nucleotide polymorphisms identified through genome-wide association studies. <b>2010</b> , 3, 468-74	76
1466	Genome-wide association identifies OBFC1 as a locus involved in human leukocyte telomere biology. <b>2010</b> , 107, 9293-8	209
1465	A genome-wide association study of alcohol dependence. <b>2010</b> , 107, 5082-7	367
1464	Examination of association with candidate genes for diabetic nephropathy in a Mexican American population. <b>2010</b> , 5, 1072-8	23
1463	Characterization of the oral fungal microbiome (mycobiome) in healthy individuals. <b>2010</b> , 6, e1000713	659
1462	Common genetic variants near the Brittle Cornea Syndrome locus ZNF469 influence the blinding disease risk factor central corneal thickness. <b>2010</b> , 6, e1000947	106

1461	Haplotype-based pharmacogenetic analysis for longitudinal quantitative traits in the presence of dropout. <b>2010</b> , 20, 334-50	3
1460	Genome-wide association studies of hypertension: light at the end of the tunnel. <b>2010</b> , 2010, 509581	8
1459	Exploratory data analysis in large-scale genetic studies. <b>2010</b> , 11, 70-81	7
1458	Analysis of genetic variants in never-smokers with lung cancer facilitated by an Internet-based blood collection protocol: a preliminary report. <b>2010</b> , 16, 755-63	69
1457	Genome-wide association identifies ATOH7 as a major gene determining human optic disc size. <b>2010</b> , 19, 2716-24	118
1456	Recurrent microdeletions at 15q11.2 and 16p13.11 predispose to idiopathic generalized epilepsies. <b>2010</b> , 133, 23-32	347
1455	European population substructure correlates with systemic lupus erythematosus endophenotypes in North Americans of European descent. <b>2010</b> , 11, 515-21	15
1454	An integration of genome-wide association study and gene expression profiling to prioritize the discovery of novel susceptibility Loci for osteoporosis-related traits. <b>2010</b> , 6, e1000977	163
1453	Genome-wide association study in Asian populations identifies variants in ETS1 and WDFY4 associated with systemic lupus erythematosus. <b>2010</b> , 6, e1000841	316
1452	Genome-wide association study identifies ALDH7A1 as a novel susceptibility gene for osteoporosis. <b>2010</b> , 6, e1000806	88
1451	Web-based, participant-driven studies yield novel genetic associations for common traits. <b>2010</b> , 6, e1000993	332
1450	Association between common variation in genes encoding sweet taste signaling components and human sucrose perception. <b>2010</b> , 35, 579-92	70
1449	Whole-genome linkage and association scan in primary, nonsyndromic vesicoureteric reflux. <b>2010</b> , 21, 113-23	51
1448	Rapid assessment of genetic ancestry in populations of unknown origin by genome-wide genotyping of pooled samples. <b>2010</b> , 6, e1000866	33
1447	Quantification of population structure using correlated SNPs by shrinkage principal components. <b>2010</b> , 70, 9-22	40
1446	Identification of a functional genetic variant at 16q12.1 for breast cancer risk: results from the Asia Breast Cancer Consortium. <b>2010</b> , 6, e1001002	93
1445	Genome-wide association study of blood pressure extremes identifies variant near UMOD associated with hypertension. <b>2010</b> , 6, e1001177	255
1444	The 5p15.33 locus is associated with risk of lung adenocarcinoma in never-smoking females in Asia. <b>2010</b> , 6, e1001051	141

1443	Experimental approaches for identifying schizophrenia risk genes. <b>2010</b> , 4, 587-610	4
1442	Locus category based analysis of a large genome-wide association study of rheumatoid arthritis. <b>2010</b> , 19, 3863-72	11
1441	Multiple genetic loci influence serum urate levels and their relationship with gout and cardiovascular disease risk factors. <b>2010</b> , 3, 523-30	243
1440	Common variations in PSMD3-CSF3 and PLCB4 are associated with neutrophil count. <b>2010</b> , 19, 2079-85	44
1439	Comprehensive analysis of genomic variation in the LPA locus and its relationship to plasma lipoprotein(a) in South Asians, Chinese, and European Caucasians. <b>2010</b> , 3, 39-46	95
1438	CNVineta: a data mining tool for large case-control copy number variation datasets. <b>2010</b> , 26, 2208-9	4
1437	Multi-population GWA mapping via multi-task regularized regression. <b>2010</b> , 26, i208-16	51
1436	Association Analysis under Population Stratification: A Two-Stage Procedure Utilizing Population- and Family-Based Analyses. <b>2010</b> , 69, 160-70	6
1435	Delta-centralization fails to control for population stratification in genetic association studies. <b>2010</b> , 69, 285-94	4
1434	Genetic differences between five European populations. <b>2010</b> , 70, 141-9	24
1433	Associations between genetic variants in the ACE, AGT, AGTR1 and AGTR2 genes and renal function in the Multi-ethnic Study of Atherosclerosis. <b>2010</b> , 32, 156-62	18
1432	Systematic removal of outliers to reduce heterogeneity in case-control association studies. <b>2010</b> , 70, 227-31	4
1431	Conditions under which genome-wide association studies will be positively misleading. <b>2010</b> , 186, 1045-52	131
1430	Genomewide linkage and peakwide association analyses of carotid plaque in Caribbean Hispanics. <b>2010</b> , 41, 2750-6	30
1429	Support for TGFB1 as a susceptibility gene for high myopia in individuals of Chinese descent. <b>2010</b> , 128, 1081-4	19
1428	Radiation pharmacogenomics: a genome-wide association approach to identify radiation response biomarkers using human lymphoblastoid cell lines. <b>2010</b> , 20, 1482-92	114
1427	Gene expression levels as endophenotypes in genome-wide association studies of Alzheimer disease. <b>2010</b> , 74, 480-6	29
1426	Correcting for cryptic relatedness in population-based association studies of continuous traits. <b>2010</b> , 69, 28-33	7

1425	Association of mu-opioid receptor variants and response to citalopram treatment in major depressive disorder. <b>2010</b> , 167, 565-73	52
1424	Interrogating local population structure for fine mapping in genome-wide association studies. <b>2010</b> , 26, 2961-8	58
1423	Association of genetic variation in the MET proto-oncogene with schizophrenia and general cognitive ability. <b>2010</b> , 167, 436-43	30
1422	Meta-analysis confirms CR1, CLU, and PICALM as alzheimer disease risk loci and reveals interactions with APOE genotypes. <b>2010</b> , 67, 1473-84	330
1421	Establishment of a standardized system to perform population structure analyses with limited sample size or with different sets of SNP genotypes. <b>2010</b> , 55, 525-33	6
1420	The regulation-of-autophagy pathway may influence Chinese stature variation: evidence from elder adults. <b>2010</b> , 55, 441-7	19
1419	Examination of disease-based selection, demographic history and population structure in European Y-chromosome haplogroup I. <b>2010</b> , 55, 613-20	3
1418	Polymorphisms in the Hsp70 gene locus are genetically associated with systemic lupus erythematosus. <b>2010</b> , 69, 1983-9	25
1417	Variants in linkage disequilibrium with the late cornified envelope gene cluster deletion are associated with susceptibility to psoriatic arthritis. <b>2010</b> , 69, 2199-203	35
1416	Candidate gene studies in the GWAS era: the MET proto-oncogene, neurocognition, and schizophrenia. <b>2010</b> , 167, 369-72	8
1415	Mexican-American admixture mapping analyses for diabetic nephropathy in type 2 diabetes mellitus. <b>2010</b> , 30, 141-9	7
1414	Methods: genetic epidemiology. <b>2010</b> , 30, 795-814	
1413	Analysis of the impact of genetic variation on human gene expression. <b>2010</b> , 628, 321-39	5
1412	Radial basis function regression methods for predicting quantitative traits using SNP markers. <b>2010</b> , 92, 209-25	35
1411	Trends and Statistical Challenges in Genomewide Association Studies. <b>2010</b> , 283-308	
1410	Two-stage testing strategies for genome-wide association studies in family-based designs. <b>2010</b> , 620, 485-96	5
1409	Dimension reduction for high-dimensional data. <b>2010</b> , 620, 417-34	25
1408	Improved reporting of statistical design and analysis: guidelines, education, and editorial policies. <b>2010</b> , 620, 563-98	10

1407	Genomic similarity and kernel methods I: advancements by building on mathematical and statistical foundations. <b>2010</b> , 70, 109-31	71
1406	Gene dosage of the common variant 9p21 predicts severity of coronary artery disease. <b>2010</b> , 56, 479-86	121
1405	Genome-wide association study of asthma identifies RAD50-IL13 and HLA-DR/DQ regions. <b>2010</b> , 125, 328-335.e11	250
1404	Application of genetic/genomic approaches to allergic disorders. <b>2010</b> , 126, 425-36; quiz 437-8	15
1403	PDE11A associations with asthma: results of a genome-wide association scan. <b>2010</b> , 126, 871-873.e9	39
1402	Ineffectiveness of telephone-based environmental control intervention to improve asthma outcomes. <b>2010</b> , 126, 873-5	8
1401	A genomewide association study of citalopram response in major depressive disorder. <b>2010</b> , 67, 133-8	251
1400	Genome-wide association scan of trait depression. <b>2010</b> , 68, 811-7	114
1399	[Systemic lupus erythematosus. ¿What do we know and where are we heading?¿]. <b>2010</b> , 6, 1-2	1
1398	A genome-wide meta-analysis identifies novel loci associated with schizophrenia and bipolar disorder. <b>2010</b> , 124, 192-9	163
1397	A genome-wide association scan on estrogen receptor-negative breast cancer. <b>2010</b> , 12, R93	32
1396	Systemic lupus erythematosus. ¿What do we know and where are we heading?¿ <b>2010</b> , 6, 1-2	
1395	Genetic variation in IL28B is associated with chronic hepatitis C and treatment failure: a genome-wide association study. <b>2010</b> , 138, 1338-45, 1345.e1-7	956
1394	Genetic approaches to functional gastrointestinal disorders. <b>2010</b> , 138, 1276-85	77
1393	Genetic regulation of serum phytosterol levels and risk of coronary artery disease. <b>2010</b> , 3, 331-9	116
1392	Genome-wide association study for adiponectin levels in Filipino women identifies CDH13 and a novel uncommon haplotype at KNG1-ADIPOQ. <b>2010</b> , 19, 4955-64	86
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1390	Common genetic variation in multiple metabolic pathways influences susceptibility to low HDL-cholesterol and coronary heart disease. <b>2010</b> , 51, 3524-32	50

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1388	Genetic susceptibility to type 2 diabetes is associated with reduced prostate cancer risk. <b>2010</b> , 69, 193-201	30
1387	Population Genetic Principles and Human Populations. <b>2010</b> , 487-506	
1386	Consanguinity, Genetic Drift, and Genetic Diseases in Populations with Reduced Numbers of Founders. <b>2010</b> , 507-528	15
1385	Genetic Epidemiology. <b>2010</b> , 617-634	
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1382	Exploring genetic susceptibility to cancer in diverse populations. <b>2010</b> , 20, 330-5	25
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1378	Patterns of population structure and environmental associations to aridity across the range of loblolly pine ( <i>Pinus taeda</i> L., Pinaceae). <b>2010</b> , 185, 969-82	283
1377	Genetics of Susceptibility and Resistance to Infection. <b>2010</b> , 37, 67-99	1
1376	A framework for feature selection in clustering. <b>2010</b> , 105, 713-726	346
1375	A genome-wide association study of nasopharyngeal carcinoma identifies three new susceptibility loci. <i>Nature Genetics</i> , <b>2010</b> , 42, 599-603	36.3 306
1374	Effect of pravastatin therapy on coronary events in carriers of the KIF6 719Arg allele from the cholesterol and recurrent events trial. <b>2010</b> , 105, 1300-5	28
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1370	Genetic variants and risk of lung cancer in never smokers: a genome-wide association study. <b>2010</b> , 11, 321-30	190
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1366	Mapping genes that predict treatment outcome in admixed populations. <b>2010</b> , 10, 465-77	27
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1364	IL-1 gene cluster is not linked to aggressive periodontitis. <b>2010</b> , 89, 457-61	19
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1360	Methods: genetic epidemiology. <b>2010</b> , 33, 15-34	
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1358	Genome Wide Association Studies. <b>2010</b> , 159-175	
1357	A whole genome association study of mother-to-child transmission of HIV in Malawi. <b>2010</b> , 2, 17	40
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1354	Quality control for genome-wide association studies. <b>2010</b> , 628, 341-72	83

1353	Update on the genetic risk factors for rheumatoid arthritis. <b>2010</b> , 6, 61-75		26
1352	Simultaneously accounting for population structure, genotype by environment interaction, and spatial variation in marker-trait associations in sugarcane. <b>2010</b> , 53, 973-81		46
1351	The FOXE1 locus is a major genetic determinant for radiation-related thyroid carcinoma in Chernobyl. <b>2010</b> , 19, 2516-23		122
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1347	Reviews of Science for Science Librarians: Genome-Wide Association Studies (GWAS). <b>2011</b> , 30, 229-243		1
1346	Candidate genes versus genome-wide associations: which are better for detecting genetic susceptibility to infectious disease?. <b>2011</b> , 278, 1183-8		54
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1344	A germline variant in the interferon regulatory factor 4 gene as a novel skin cancer risk locus. <b>2011</b> , 71, 1533-9		38
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1340	Genome-wide association mapping reveals a rich genetic architecture of complex traits in <i>Oryza sativa</i> . <b>2011</b> , 2, 467		875
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1338	Genome-wide association study identifies FCGR2A as a susceptibility locus for Kawasaki disease. <i>Nature Genetics</i> , <b>2011</b> , 43, 1241-6	36.3	236
1337	A genome-wide association study identifies two new risk loci for Graves' disease. <i>Nature Genetics</i> , <b>2011</b> , 43, 897-901	36.3	209
1336	Screening ethnically diverse human embryonic stem cells identifies a chromosome 20 minimal amplicon conferring growth advantage. <b>2011</b> , 29, 1132-44		406

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1334	Control for confounding in case-control studies using the stratification score, a retrospective balancing score. <b>2011</b> , 173, 752-60		19
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1331	A quantitative-trait genome-wide association study of alcoholism risk in the community: findings and implications. <b>2011</b> , 70, 513-8		157
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1327	Genome-wide association study identifies a susceptibility locus for schizophrenia in Han Chinese at 11p11.2. <i>Nature Genetics</i> , <b>2011</b> , 43, 1228-31	36.3	231
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1325	A geographic cline of skull and brain morphology among individuals of European Ancestry. <b>2011</b> , 72, 35-44		17
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1320	Genome-wide association study identifies three new melanoma susceptibility loci. <i>Nature Genetics</i> , <b>2011</b> , 43, 1108-13	36.3	203
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1317	A genome-wide association study identifies new susceptibility loci for non-cardia gastric cancer at 3q13.31 and 5p13.1. <i>Nature Genetics</i> , <b>2011</b> , 43, 1215-8	36.3	215
1316	Quality control procedures for genome-wide association studies. <b>2011</b> , Chapter 1, Unit1.19		199
1315	Identification of common variants influencing risk of the tauopathy progressive supranuclear palsy. <i>Nature Genetics</i> , <b>2011</b> , 43, 699-705	36.3	386
1314	A genome-wide perspective on the evolutionary history of enigmatic wolf-like canids. <b>2011</b> , 21, 1294-305		222
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1308	Different differences: the use of 'genetic ancestry' versus race in biomedical human genetic research. <b>2011</b> , 41, 5-30		185
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1306	The Fundamentals of Modern Statistical Genetics. <b>2011</b> ,		42
1305	Genome-wide association study identifies three new susceptibility loci for adult asthma in the Japanese population. <i>Nature Genetics</i> , <b>2011</b> , 43, 893-6	36.3	252
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1300	Planning a genome-wide association study: points to consider. <b>2011</b> , 43, 451-60		14

1299	hzAnalyzer: detection, quantification, and visualization of contiguous homozygosity in high-density genotyping datasets. <b>2011</b> , 12, R21	3
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1296	Genetic Epidemiology. <b>2011</b> ,	2
1295	From sequence to function: Insights from natural variation in budding yeasts. <b>2011</b> , 1810, 959-66	19
1294	Ancestry of African Americans with sickle cell disease. <b>2011</b> , 47, 41-5	23
1293	SNPs on chromosome 5p15.3 associated with myocardial infarction in Japanese population. <b>2011</b> , 56, 47-51	26
1292	Perspectives on human population structure at the cusp of the sequencing era. <b>2011</b> , 12, 245-74	58
1291	A triple combination strategy corrects population stratification bias and saves genotyping cost. <b>2011</b> , 64, 517-24	1
1290	Genetic association study suggests a role for SP110 variants in lymph node tuberculosis but not pulmonary tuberculosis in north Indians. <b>2011</b> , 72, 576-80	16
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1288	Genome-wide association study of blood pressure response to methylphenidate treatment of attention-deficit/hyperactivity disorder. <b>2011</b> , 35, 466-72	21
1287	A genome-wide association study of aging. <b>2011</b> , 32, 2109.e15-28	110
1286	The neuronal transporter gene SLC6A15 confers risk to major depression. <b>2011</b> , 70, 252-65	161
1285	Genome-wide association studies reveal genetic variants in CTNND2 for high myopia in Singapore Chinese. <b>2011</b> , 118, 368-75	103
1284	Association mapping. <b>2011</b> , 760, 35-52	2
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1282	Genome-wide association study identifies two new susceptibility loci for atopic dermatitis in the Chinese Han population. <i>Nature Genetics</i> , <b>2011</b> , 43, 690-4	363 153

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1280	A genome-wide set of SNPs detects population substructure and long range linkage disequilibrium in wild sheep. <b>2011</b> , 11, 314-22		68
1279	Comparison of F(ST) outlier tests for SNP loci under selection. <b>2011</b> , 11 Suppl 1, 184-94		343
1278	A genome-wide linkage study of mammographic density, a risk factor for breast cancer. <b>2011</b> , 13, R132		7
1277	Variants in the pregnancy-associated plasma protein-A2 gene on Bos taurus autosome 16 are associated with daughter calving ease and productive life in Holstein cattle. <b>2011</b> , 94, 1552-8		18
1276	Population Substructure in Association Studies. <b>2011</b> , 125-137		
1275	Accuracy of Pseudo-Inverse Covariance Learning--A Random Matrix Theory Analysis. <b>2011</b> , 33, 1470-81		23
1274	Association of a polymorphism of BTN2A1 with myocardial infarction in East Asian populations. <b>2011</b> , 215, 145-52		42
1273	Statistical Optimization of Pharmacogenomics Association Studies: Key Considerations from Study Design to Analysis. <b>2011</b> , 9, 41-66		10
1272	Association Mapping of Malting Quality Quantitative Trait Loci in Winter Barley: Positive Signals from Small Germplasm Arrays. <b>2011</b> , 4, 256-272		35
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1269	Current gene discovery strategies for ocular conditions. <b>2011</b> , 52, 7761-70		3
1268	Data Quality Control. <b>2011</b> , 95-108		3
1267	Genetic Association Study Design. <b>2011</b> , 25-48		1
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1264	Gene by sex interaction for measures of obesity in the framingham heart study. <b>2011</b> , 2011, 329038		16

1263	Capitalizing on admixture in genome-wide association studies: a two-stage testing procedure and application to height in African-Americans. <b>2011</b> , 2,	5
1262	A genome-wide association study of upper aerodigestive tract cancers conducted within the INHANCE consortium. <b>2011</b> , 7, e1001333	136
1261	Copy number variation of KIR genes influences HIV-1 control. <b>2011</b> , 9, e1001208	111
1260	Testing for an unusual distribution of rare variants. <b>2011</b> , 7, e1001322	465
1259	Differential genetic associations for systemic lupus erythematosus based on anti-dsDNA autoantibody production. <b>2011</b> , 7, e1001323	167
1258	Genome-wide association analysis identifies variants associated with nonalcoholic fatty liver disease that have distinct effects on metabolic traits. <b>2011</b> , 7, e1001324	629
1257	Differences in candidate gene association between European ancestry and African American asthmatic children. <b>2011</b> , 6, e16522	52
1256	Tracing cattle breeds with principal components analysis ancestry informative SNPs. <b>2011</b> , 6, e18007	27
1255	A preliminary study of genetic factors that influence susceptibility to bovine tuberculosis in the British cattle herd. <b>2011</b> , 6, e18806	22
1254	Behavior of QQ-plots and genomic control in studies of gene-environment interaction. <b>2011</b> , 6, e19416	73
1253	A genetic risk score combining ten psoriasis risk loci improves disease prediction. <b>2011</b> , 6, e19454	74
1252	Knowledge-driven multi-locus analysis reveals gene-gene interactions influencing HDL cholesterol level in two independent EMR-linked biobanks. <b>2011</b> , 6, e19586	55
1251	Genes involved in vasoconstriction and vasodilation system affect salt-sensitive hypertension. <b>2011</b> , 6, e19620	48
1250	Common variants in a novel gene, FONG on chromosome 2q33.1 confer risk of osteoporosis in Japanese. <b>2011</b> , 6, e19641	27
1249	Validation of a cost-efficient multi-purpose SNP panel for disease based research. <b>2011</b> , 6, e19699	5
1248	From SNPs to genes: disease association at the gene level. <b>2011</b> , 6, e20133	50
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1246	Genetic association study of common mitochondrial variants on body fat mass. <b>2011</b> , 6, e21595	24

1245	Copy number variation in CNP267 region may be associated with hip bone size. <b>2011</b> , 6, e22035	5
1244	A genome-wide association study confirms previously reported loci for type 2 diabetes in Han Chinese. <b>2011</b> , 6, e22353	49
1243	The genetic structure of the Swedish population. <b>2011</b> , 6, e22547	53
1242	Identification of KIF3A as a novel candidate gene for childhood asthma using RNA expression and population allelic frequencies differences. <b>2011</b> , 6, e23714	41
1241	Genetic variants of TSLP and asthma in an admixed urban population. <b>2011</b> , 6, e25099	35
1240	Copy number variants in extended autism spectrum disorder families reveal candidates potentially involved in autism risk. <b>2011</b> , 6, e26049	61
1239	The fat mass and obesity associated gene, FTO, is also associated with osteoporosis phenotypes. <b>2011</b> , 6, e27312	28
1238	Sensitivity of genome-wide-association signals to phenotyping strategy: the PROP-TAS2R38 taste association as a benchmark. <b>2011</b> , 6, e27745	32
1237	Genome-wide association study in bipolar patients stratified by co-morbidity. <b>2011</b> , 6, e28477	40
1236	Genome-wide association study of hepatocellular carcinoma in Southern Chinese patients with chronic hepatitis B virus infection. <b>2011</b> , 6, e28798	53
1235	Accounting for population stratification in practice: a comparison of the main strategies dedicated to genome-wide association studies. <b>2011</b> , 6, e28845	39
1234	Statistical epistasis and functional brain imaging support a role of voltage-gated potassium channels in human memory. <b>2011</b> , 6, e29337	5
1233	Molecular Genetics and Economics. <b>2011</b> , 25, 57-82	75
1232	Genome-wide association study of personality traits in bipolar patients. <b>2011</b> , 21, 190-4	36
1231	Genes linked to energy metabolism and immunoregulatory mechanisms are associated with subcutaneous adipose tissue distribution in HIV-infected men. <b>2011</b> , 21, 798-807	17
1230	Common polymorphisms in FMO1 are associated with nicotine dependence. <b>2011</b> , 21, 397-402	16
1229	Xenobiotic-metabolizing gene variants, pesticide use, and the risk of prostate cancer. <b>2011</b> , 21, 615-23	36
1228	The contribution of common CYP2A6 alleles to variation in nicotine metabolism among European-Americans. <b>2011</b> , 21, 403-16	68



1227	Genetic association of bipolar disorder with the $\beta$ nicotinic receptor subunit gene. <b>2011</b> , 21, 77-84	8
1226	Mixed model association mapping for fusarium head blight resistance in tunisian-derived durum wheat populations. <b>2011</b> , 1, 209-18	46
1225	Generalizability and epidemiologic characterization of eleven colorectal cancer GWAS hits in multiple populations. <b>2011</b> , 20, 70-81	66
1224	GCH1, BH4 and pain. <b>2011</b> , 12, 1728-41	41
1223	Screening low-frequency SNPS from genome-wide association study reveals a new risk allele for progression to AIDS. <b>2011</b> , 56, 279-84	25
1222	Cytogenetics. <b>2011</b> , 156-168	
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1220	When the negative is positive. <b>2011</b> , 117, 1441-2	2
1219	Identification of a specific intronic PEAR1 gene variant associated with greater platelet aggregability and protein expression. <b>2011</b> , 118, 3367-75	82
1218	Platelet CD36 surface expression levels affect functional responses to oxidized LDL and are associated with inheritance of specific genetic polymorphisms. <b>2011</b> , 117, 6355-66	74
1217	Prothrombin 20210G>A genotype and C-reactive protein level. <b>2011</b> , 118, 4495-6	1
1216	Response: genetic admixture in sickle cell disease. <b>2011</b> , 118, 4495-4495	1
1215	Germline mutations in MSR1, ASCC1, and CTHRC1 in patients with Barrett esophagus and esophageal adenocarcinoma. <b>2011</b> , 306, 410-9	77
1214	Bayesian variable selection regression for genome-wide association studies and other large-scale problems. <b>2011</b> , 5,	220
1213	Accuracy and Training Population Design for Genomic Selection on Quantitative Traits in Elite North American Oats. <b>2011</b> , 4,	171
1212	Association Mapping for Enhancing Maize (Zea mays L.) Genetic Improvement. <b>2011</b> , 51, 433-449	233
1211	Rationale for an international consortium to study inherited genetic susceptibility to childhood acute lymphoblastic leukemia. <b>2011</b> , 96, 1049-54	32
1210	Introduction to Population Diversity and Genetic Testing. 3-11	

1209	Genetic variation in UGT1A1 typical of Gilbert syndrome is associated with unconjugated hyperbilirubinemia in patients receiving tocilizumab. <b>2011</b> , 21, 365-74	15
1208	A genome-wide association study of DSM-IV cannabis dependence. <b>2011</b> , 16, 514-8	58
1207	Understanding the population structure of North American patients with cystic fibrosis. <b>2011</b> , 79, 136-46	20
1206	Bayesian non-parametric multivariate statistical models for testing association between quantitative traits and candidate genes in structured populations. <b>2011</b> , 60, 207-219	
1205	Mixture modelling as an exploratory framework for genotype-trait associations. <b>2011</b> , 60, 355-375	1
1204	Whole-genome association study for fatty acid composition of oleic acid in Japanese Black cattle. <b>2011</b> , 42, 141-8	45
1203	Assessment of the functionality of genome-wide canine SNP arrays and implications for canine disease association studies. <b>2011</b> , 42, 181-90	11
1202	A comparison of association methods correcting for population stratification in case-control studies. <b>2011</b> , 75, 418-27	64
1201	Mitochondria-wide association study of common variants in osteoporosis. <b>2011</b> , 75, 569-74	22
1200	Efficient genomewide selection of PCA-correlated tSNPs for genotype imputation. <b>2011</b> , 75, 707-22	3
1199	A novel method to detect gene-gene interactions in structured populations: MDR-SP. <b>2011</b> , 75, 742-54	13
1198	Asymptotic conditional singular value decomposition for high-dimensional genomic data. <b>2011</b> , 67, 344-52	31
1197	Control of population stratification by correlation-selected principal components. <b>2011</b> , 67, 967-74	24
1196	Analysis of dyslexia candidate genes in the Raine cohort representing the general Australian population. <b>2011</b> , 10, 158-65	43
1195	CNTNAP2 variants affect early language development in the general population. <b>2011</b> , 10, 451-6	128
1194	A genome-wide association study for quantitative traits in schizophrenia in China. <b>2011</b> , 10, 734-9	26
1193	Genome-wide association study of renal cell carcinoma identifies two susceptibility loci on 2p21 and 11q13.3. <i>Nature Genetics</i> , <b>2011</b> , 43, 60-5	36.3 199
1192	Genome-wide association analysis in primary sclerosing cholangitis identifies two non-HLA susceptibility loci. <i>Nature Genetics</i> , <b>2011</b> , 43, 17-9	36.3 181

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1189	Association of a functional variant downstream of TNFAIP3 with systemic lupus erythematosus. <i>Nature Genetics</i> , <b>2011</b> , 43, 253-8	36.3	208
1188	A genome-wide association study in Europeans and South Asians identifies five new loci for coronary artery disease. <i>Nature Genetics</i> , <b>2011</b> , 43, 339-44	36.3	528
1187	Genome-wide association study identifies 12 new susceptibility loci for primary biliary cirrhosis. <i>Nature Genetics</i> , <b>2011</b> , 43, 329-32	36.3	396
1186	Common variants at MS4A4/MS4A6E, CD2AP, CD33 and EPHA1 are associated with late-onset Alzheimer's disease. <i>Nature Genetics</i> , <b>2011</b> , 43, 436-41	36.3	1367
1185	Genome-wide association study identifies a common variant associated with risk of endometrial cancer. <i>Nature Genetics</i> , <b>2011</b> , 43, 451-4	36.3	121
1184	Genome partitioning of genetic variation for complex traits using common SNPs. <i>Nature Genetics</i> , <b>2011</b> , 43, 519-25	36.3	659
1183	Genome-wide association study identifies susceptibility loci for open angle glaucoma at TMCO1 and CDKN2B-AS1. <i>Nature Genetics</i> , <b>2011</b> , 43, 574-8	36.3	329
1182	Genome-wide association study of prostate cancer in men of African ancestry identifies a susceptibility locus at 17q21. <i>Nature Genetics</i> , <b>2011</b> , 43, 570-3	36.3	171
1181	A twist on admixture mapping. <i>Nature Genetics</i> , <b>2011</b> , 43, 178-9	36.3	4
1180	Family-based designs for genome-wide association studies. <b>2011</b> , 12, 465-74		211
1179	Genome-wide association study of bronchial asthma in the Volga-Urals region of Russia. <b>2011</b> , 45, 911-920		20
1178	Genome-wide association study of anthropometric traits and evidence of interactions with age and study year in Filipino women. <b>2011</b> , 19, 1019-27		65
1177	ADIPOQ, ADIPOR1, and ADIPOR2 polymorphisms in relation to serum adiponectin levels and BMI in black and white women. <b>2011</b> , 19, 2053-62		36
1176	A genome-wide analysis of population structure in the Finnish Saami with implications for genetic association studies. <b>2011</b> , 19, 347-52		16
1175	Caution in generalizing known genetic risk markers for breast cancer across all ethnic/racial populations. <b>2011</b> , 19, 243-5		17
1174	A candidate gene study of the type I interferon pathway implicates IKBKE and IL8 as risk loci for SLE. <b>2011</b> , 19, 479-84		51

1173	Evaluation of the TREX1 gene in a large multi-ancestral lupus cohort. <b>2011</b> , 12, 270-9	194
1172	The role of HLA-DR-DQ haplotypes in variable antibody responses to anthrax vaccine adsorbed. <b>2011</b> , 12, 457-65	30
1171	Fine mapping the TAGAP risk locus in rheumatoid arthritis. <b>2011</b> , 12, 314-8	32
1170	Overview of techniques to account for confounding due to population stratification and cryptic relatedness in genomic data association analyses. <b>2011</b> , 106, 511-9	60
1169	Investigating population stratification and admixture using eigenanalysis of dense genotypes. <b>2011</b> , 107, 413-20	25
1168	Genome-wide association study of recurrent early-onset major depressive disorder. <b>2011</b> , 16, 193-201	206
1167	Novel loci for major depression identified by genome-wide association study of Sequenced Treatment Alternatives to Relieve Depression and meta-analysis of three studies. <b>2011</b> , 16, 202-15	209
1166	Genome-wide pharmacogenomic analysis of response to treatment with antipsychotics. <b>2011</b> , 16, 76-85	124
1165	Genome-wide association with MRI atrophy measures as a quantitative trait locus for Alzheimer's disease. <b>2011</b> , 16, 1130-8	111
1164	TMEM132D, a new candidate for anxiety phenotypes: evidence from human and mouse studies. <b>2011</b> , 16, 647-63	120
1163	Genome-wide association study of conduct disorder symptomatology. <b>2011</b> , 16, 800-8	88
1162	LUPA: a European initiative taking advantage of the canine genome architecture for unravelling complex disorders in both human and dogs. <b>2011</b> , 189, 155-9	79
1161	A meta-analysis of two genome-wide association studies identifies 3 new loci for alcohol dependence. <b>2011</b> , 45, 1419-25	67
1160	Choice of population structure informative principal components for adjustment in a case-control study. <b>2011</b> , 12, 64	10
1159	Genome-wide association analysis of gender differences in major depressive disorder in the Netherlands NESDA and NTR population-based samples. <b>2011</b> , 133, 516-21	37
1158	Imputation of sequence variants for identification of genetic risks for Parkinson's disease: a meta-analysis of genome-wide association studies. <b>2011</b> , 377, 641-9	733
1157	Genome-wide association study for coronary artery calcification with follow-up in myocardial infarction. <b>2011</b> , 124, 2855-64	213
1156	Genome-wide association study identifies two loci strongly affecting transferrin glycosylation. <b>2011</b> , 20, 3710-7	27

1155	Association of the sirtuin and mitochondrial uncoupling protein genes with carotid plaque. <b>2011</b> , 6, e27157	46
1154	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. <b>2011</b> , 88, 6-18	103
1153	GCTA: a tool for genome-wide complex trait analysis. <b>2011</b> , 88, 76-82	3838
1152	Identification of a systemic lupus erythematosus susceptibility locus at 11p13 between PDHX and CD44 in a multiethnic study. <b>2011</b> , 88, 83-91	69
1151	Genetic basis of autoantibody positive and negative rheumatoid arthritis risk in a multi-ethnic cohort derived from electronic health records. <b>2011</b> , 88, 57-69	98
1150	Whole-exome sequencing links a variant in DHDDS to retinitis pigmentosa. <b>2011</b> , 88, 201-6	130
1149	Estimating missing heritability for disease from genome-wide association studies. <b>2011</b> , 88, 294-305	737
1148	Genetic variants at 13q12.12 are associated with high myopia in the Han Chinese population. <b>2011</b> , 88, 805-813	95
1147	Rare-variant association testing for sequencing data with the sequence kernel association test. <b>2011</b> , 89, 82-93	1573
1146	Recent admixture in an Indian population of African ancestry. <b>2011</b> , 89, 111-20	23
1145	GWAS findings for human iris patterns: associations with variants in genes that influence normal neuronal pattern development. <b>2011</b> , 89, 334-43	47
1144	Variants near FOXE1 are associated with hypothyroidism and other thyroid conditions: using electronic medical records for genome- and phenome-wide studies. <b>2011</b> , 89, 529-42	199
1143	Comparison of SSRs and SNPs in assessment of genetic relatedness in maize. <b>2011</b> , 139, 1045-54	74
1142	A combined analysis of genome-wide association studies in breast cancer. <b>2011</b> , 126, 717-27	85
1141	Risk of contralateral breast cancer associated with common variants in BRCA1 and BRCA2: potential modifying effect of BRCA1/BRCA2 mutation carrier status. <b>2011</b> , 127, 819-29	7
1140	ASIP genetic variants and the number of non-melanoma skin cancers. <b>2011</b> , 22, 495-501	8
1139	Association study of type 2 diabetes genetic susceptibility variants and risk of pancreatic cancer: an analysis of PanScan-I data. <b>2011</b> , 22, 877-83	48
1138	Association mapping of quantitative resistance for <i>Leptosphaeria maculans</i> in oilseed rape ( <i>Brassica napus</i> L.). <b>2011</b> , 27, 271-287	61

1137	Characterization of a global germplasm collection and its potential utilization for analysis of complex quantitative traits in maize. <b>2011</b> , 28, 511-526	217
1136	Mapping QTLs for improving grain yield using the USDA rice mini-core collection. <b>2011</b> , 234, 347-61	60
1135	Uncovering hidden variance: pair-wise SNP analysis accounts for additional variance in nicotine dependence. <b>2011</b> , 129, 177-88	8
1134	Genome-wide linkage and peak-wide association study of obesity-related quantitative traits in Caribbean Hispanics. <b>2011</b> , 129, 209-19	23
1133	A genome-wide screen of gene-gene interactions for rheumatoid arthritis susceptibility. <b>2011</b> , 129, 473-85	26
1132	Genomic and genealogical investigation of the French Canadian founder population structure. <b>2011</b> , 129, 521-31	52
1131	Potential novel candidate polymorphisms identified in genome-wide association study for breast cancer susceptibility. <b>2011</b> , 130, 529-37	39
1130	Haplotype structure in Ashkenazi Jewish BRCA1 and BRCA2 mutation carriers. <b>2011</b> , 130, 685-99	15
1129	Current status of genome-wide association studies in cancer. <b>2011</b> , 130, 59-78	142
1128	Robust association tests under different genetic models, allowing for binary or quantitative traits and covariates. <b>2011</b> , 41, 768-75	51
1127	Population structure and linkage disequilibrium in oat ( <i>Avena sativa</i> L.): implications for genome-wide association studies. <b>2011</b> , 122, 623-32	54
1126	Association mapping for quality traits in soft winter wheat. <b>2011</b> , 122, 961-70	98
1125	Association mapping of grain color, phenolic content, flavonoid content and antioxidant capacity in dehulled rice. <b>2011</b> , 122, 1005-16	79
1124	Effect of population structure corrections on the results of association mapping tests in complex maize diversity panels. <b>2011</b> , 122, 1149-60	44
1123	Genome-wide association mapping reveals epistasis and genetic interaction networks in sugar beet. <b>2011</b> , 123, 109-18	43
1122	Determination of genetic structure of germplasm collections: are traditional hierarchical clustering methods appropriate for molecular marker data?. <b>2011</b> , 123, 195-205	82
1121	Identification of novel genomic regions associated with resistance to <i>Pyrenophora tritici-repentis</i> races 1 and 5 in spring wheat landraces using association analysis. <b>2011</b> , 123, 1029-41	50
1120	Genome-wide association mapping of agronomic traits in sugar beet. <b>2011</b> , 123, 1121-31	51

1119	Population structure and marker-trait association analysis of the US peanut ( <i>Arachis hypogaea</i> L.) mini-core collection. <b>2011</b> , 123, 1307-17	82
1118	Genome-wide association and meta-analysis in populations from Starr County, Texas, and Mexico City identify type 2 diabetes susceptibility loci and enrichment for expression quantitative trait loci in top signals. <b>2011</b> , 54, 2047-55	90
1117	Homozygous carriers of the G allele of rs4664447 of the glucagon gene (GCG) are characterised by decreased fasting and stimulated levels of insulin, glucagon and glucagon-like peptide (GLP)-1. <b>2011</b> , 54, 2820-31	14
1116	Genetic analysis of vertebral trabecular bone density and cross-sectional area in older men. <b>2011</b> , 22, 1079-90	23
1115	Bayes factors in the presence of population stratification. <b>2011</b> , 81, 836-841	1
1114	Multiple phenotypes in genome-wide genetic mapping studies. <b>2011</b> , 2, 519-22	7
1113	Identifying QTLs and Epistasis in Structured Plant Populations Using Adaptive Mixed LASSO. <b>2011</b> , 16, 170-184	32
1112	Genetics of hypertension and cardiovascular disease and their interconnected pathways: lessons from large studies. <b>2011</b> , 13, 46-54	25
1111	GWAS for discovery and replication of genetic loci associated with sudden cardiac arrest in patients with coronary artery disease. <b>2011</b> , 11, 29	53
1110	Using emergency department-based inception cohorts to determine genetic characteristics associated with long term patient outcomes after motor vehicle collision: methodology of the CRASH study. <b>2011</b> , 11, 14	32
1109	A follow-up study for left ventricular mass on chromosome 12p11 identifies potential candidate genes. <b>2011</b> , 12, 100	14
1108	Combined analysis of three genome-wide association studies on vWF and FVIII plasma levels. <b>2011</b> , 12, 102	49
1107	Comprehensive genetic assessment of a functional TLR9 promoter polymorphism: no replicable association with asthma or asthma-related phenotypes. <b>2011</b> , 12, 26	23
1106	Genome-wide association study of Stevens-Johnson Syndrome and Toxic Epidermal Necrolysis in Europe. <b>2011</b> , 6, 52	86
1105	SNP-PRAGE: SNP-based parametric robust analysis of gene set enrichment. <b>2011</b> , 5 Suppl 2, S11	2
1104	Association analyses of the MAS-QTL data set using grammar, principal components and Bayesian network methodologies. <b>2011</b> , 5 Suppl 3, S8	5
1103	Stratify or adjust? Dealing with multiple populations when evaluating rare variants. <b>2011</b> , 5 Suppl 9, S101	5
1102	Identification of multiple rare variants associated with a disease. <b>2011</b> , 5 Suppl 9, S103	3

1101	Association screening for genes with multiple potentially rare variants: an inverse-probability weighted clustering approach. <b>2011</b> , 5 Suppl 9, S106	4
1100	Application of Bayesian network structure learning to identify causal variant SNPs from resequencing data. <b>2011</b> , 5 Suppl 9, S109	9
1099	Improved power by collapsing rare and common variants based on a data-adaptive forward selection strategy. <b>2011</b> , 5 Suppl 9, S114	3
1098	Effect of population stratification analysis on false-positive rates for common and rare variants. <b>2011</b> , 5 Suppl 9, S116	15
1097	Comparative study of statistical methods for detecting association with rare variants in exome-resequencing data. <b>2011</b> , 5 Suppl 9, S33	5
1096	Methods for adjusting population structure and familial relatedness in association test for collective effect of multiple rare variants on quantitative traits. <b>2011</b> , 5 Suppl 9, S35	5
1095	Resampling procedures to identify important SNPs using a consensus approach. <b>2011</b> , 5 Suppl 9, S59	1
1094	Detecting rare functional variants using a wavelet-based test on quantitative and qualitative traits. <b>2011</b> , 5 Suppl 9, S70	4
1093	Gene-based multiple trait analysis for exome sequencing data. <b>2011</b> , 5 Suppl 9, S75	5
1092	Linkage analysis merging replicate phenotypes: an application to three quantitative phenotypes in two African samples. <b>2011</b> , 5 Suppl 9, S81	4
1091	Genome-wide joint SNP and CNV analysis of aortic root diameter in African Americans: the HyperGEN study. <b>2011</b> , 4, 4	14
1090	Combinations of newly confirmed Glioma-Associated loci link regions on chromosomes 1 and 9 to increased disease risk. <b>2011</b> , 4, 63	17
1089	Novel human genetic variants associated with extrapulmonary tuberculosis: a pilot genome wide association study. <b>2011</b> , 4, 28	23
1088	Population-genetic comparison of the Sorbian isolate population in Germany with the German KORA population using genome-wide SNP arrays. <b>2011</b> , 12, 67	22
1087	Genome-wide distribution of genetic diversity and linkage disequilibrium in elite sugar beet germplasm. <b>2011</b> , 12, 484	15
1086	Replication of MAPT and SNCA, but not PARK16-18, as susceptibility genes for Parkinson's disease. <b>2011</b> , 26, 819-23	55
1085	Genomewide linkage study of modifiers of LRRK2-related Parkinson's disease. <b>2011</b> , 26, 2039-44	7
1084	Genome-wide association study of theta band event-related oscillations identifies serotonin receptor gene HTR7 influencing risk of alcohol dependence. <b>2011</b> , 156B, 44-58	61



1083	The ATXN1 and TRIM31 genes are related to intelligence in an ADHD background: evidence from a large collaborative study totaling 4,963 subjects. <b>2011</b> , 156, 145-57	16
1082	Genome-wide association analysis of age at onset and psychotic symptoms in bipolar disorder. <b>2011</b> , 156B, 370-8	39
1081	Genome-wide association analysis of age at onset in schizophrenia in a European-American sample. <b>2011</b> , 156B, 671-80	22
1080	A test of the influence of continental axes of orientation on patterns of human gene flow. <b>2011</b> , 146, 515-29	17
1079	CR1 is associated with amyloid plaque burden and age-related cognitive decline. <b>2011</b> , 69, 560-9	128
1078	Genome-wide meta-analysis identifies novel multiple sclerosis susceptibility loci. <b>2011</b> , 70, 897-912	263
1077	New sequential treatment with chemotherapy and reduced-intensity conditioning for allogeneic stem-cell transplantation in very high-risk acute myeloid leukemia. <b>2011</b> , 86, 619-21	3
1076	The impact of osteoporosis (as measured by lumbar spine quantitative computed tomography) on disease activity and survival in myeloma patients: a 13-year prospective study. <b>2011</b> , 86, 617-9	5
1075	Fetal hemoglobin in sickle cell anemia: Saudi patients from the Southwestern province have similar HBB haplotypes but higher HbF levels than African Americans. <b>2011</b> , 86, 612-4	26
1074	Hematological characteristics and effective screening for compound heterozygosity for Hb constant spring and deletional $\beta$ -thalassemia. <b>2011</b> , 86, 615-7	4
1073	Proportions of bone marrow lymphocyte subsets at diagnosis may predict survival in patients with newly diagnosed diffuse large B-cell lymphoma independently of the international prognostic index. <b>2011</b> , 86, 622-4	
1072	Predictors of complete responses with denileukin diftitox in cutaneous T-cell lymphoma. <b>2011</b> , 86, 627-30	9
1071	Comparison of autologous stem cell transplantation versus consolidation chemotherapy for patients with cytogenetically normal acute myeloid leukemia (CN-AML) and FLT3ITD. <b>2011</b> , 86, 625-7	7
1070	Nilotinib treatment-associated peripheral artery disease and sudden death: yet another reason to stick to imatinib as front-line therapy for chronic myelogenous leukemia. <b>2011</b> , 86, 610-1	61
1069	Investigation of maternal effects, maternal-fetal interactions and parent-of-origin effects (imprinting), using mothers and their offspring. <b>2011</b> , 35, 19-45	59
1068	Propensity score-based nonparametric test revealing genetic variants underlying bipolar disorder. <b>2011</b> , 35, 125-32	36
1067	The impact of self-identified race on epidemiologic studies of gene expression. <b>2011</b> , 35, 93-101	11
1066	Sample size requirements to detect gene-environment interactions in genome-wide association studies. <b>2011</b> , 35, 201-10	73

1065	On the follow-up of genome-wide association studies: an overall test for the most promising SNPs. <b>2011</b> , 35, 303-9	4
1064	An improved score test for genetic association studies. <b>2011</b> , 35, 350-9	13
1063	Evaluation of methods accounting for population structure with pedigree data and continuous outcomes. <b>2011</b> , 35, 427-36	3
1062	Bias due to two-stage residual-outcome regression analysis in genetic association studies. <b>2011</b> , 35, 592-6	17
1061	A test of Hardy-Weinberg equilibrium in structured populations. <b>2011</b> , 35, 671-8	15
1060	Sifting the wheat from the chaff: prioritizing GWAS results by identifying consistency across analytical methods. <b>2011</b> , 35, 745-54	7
1059	Pitfalls of merging GWAS data: lessons learned in the eMERGE network and quality control procedures to maintain high data quality. <b>2011</b> , 35, 887-98	55
1058	Rare variants, common markers: synthetic association and beyond. <b>2011</b> , 35 Suppl 1, S80-4	9
1057	Regression and data mining methods for analyses of multiple rare variants in the Genetic Analysis Workshop 17 mini-exome data. <b>2011</b> , 35 Suppl 1, S92-100	3
1056	Identification of homogeneous genetic architecture of multiple genetically correlated traits by block clustering of genome-wide associations. <b>2011</b> , 26, 1261-71	45
1055	Genome-wide association study of rheumatoid arthritis in Koreans: population-specific loci as well as overlap with European susceptibility loci. <b>2011</b> , 63, 884-93	111
1054	Fine mapping of a major histocompatibility complex in ankylosing spondylitis: association of the HLA-DPA1 and HLA-DPB1 regions. <b>2011</b> , 63, 3305-12	15
1053	Effective sample size: Quick estimation of the effect of related samples in genetic case-control association analyses. <b>2011</b> , 35, 40-9	14
1052	Differential serum cytokine levels are associated with cytokine gene polymorphisms in north Indians with active pulmonary tuberculosis. <b>2011</b> , 11, 1015-22	28
1051	Inherited variants in mitochondrial biogenesis genes may influence epithelial ovarian cancer risk. <b>2011</b> , 20, 1131-45	50
1050	Carotid plaque and candidate genes related to inflammation and endothelial function in Hispanics from northern Manhattan. <b>2011</b> , 42, 889-96	30
1049	Type 2 deiodinase and host responses of sepsis and acute lung injury. <b>2011</b> , 45, 1203-11	50
1048	CUBN is a gene locus for albuminuria. <b>2011</b> , 22, 555-70	170

1047	Polygenic dissection of the bipolar phenotype. <b>2011</b> , 198, 284-8	57
1046	Heritability of the weight loss response to gastric bypass surgery. <b>2011</b> , 96, E1630-3	63
1045	Genome-wide association study identifies genetic variants influencing F-cell levels in sickle-cell patients. <b>2011</b> , 56, 316-23	57
1044	Attempted replication of 50 reported asthma risk genes identifies a SNP in RAD50 as associated with childhood atopic asthma. <b>2011</b> , 71, 97-105	38
1043	Common SNPs/haplotypes in IL18R1 and IL18 genes are associated with variations in humoral immunity to smallpox vaccination in Caucasians and African Americans. <b>2011</b> , 204, 433-41	31
1042	Genome-wide association study identifies BICD1 as a susceptibility gene for emphysema. <b>2011</b> , 183, 43-9	88
1041	Temporal evolution of financial-market correlations. <b>2011</b> , 84, 026109	58
1040	Human polymorphisms at long non-coding RNAs (lncRNAs) and association with prostate cancer risk. <b>2011</b> , 32, 1655-9	107
1039	Correcting for Population Stratification in Genomewide Association Studies. <b>2011</b> , 106, 997-1008	11
1038	Duffy-null-associated low neutrophil counts influence HIV-1 susceptibility in high-risk South African black women. <b>2011</b> , 52, 1248-56	62
1037	Replication of breast cancer GWAS susceptibility loci in the Women's Health Initiative African American SHARe Study. <b>2011</b> , 20, 1950-9	48
1036	The meta-analysis of genome-wide association studies. <b>2011</b> , 12, 259-69	49
1035	Assessment of hepatocyte growth factor in ovarian cancer mortality. <b>2011</b> , 20, 1638-48	30
1034	Associations between genetic polymorphisms of insulin-like growth factor axis genes and risk for age-related macular degeneration. <b>2011</b> , 52, 9099-107	17
1033	Host genetic determinants of T cell responses to the MRKAd5 HIV-1 gag/pol/nef vaccine in the step trial. <b>2011</b> , 203, 773-9	31
1032	Genetic variation in NCAM1 contributes to left ventricular wall thickness in hypertensive families. <b>2011</b> , 108, 279-83	37
1031	Progress and promise of genome-wide association studies for human complex trait genetics. <b>2011</b> , 187, 367-83	406
1030	Genetic variation predicting cisplatin cytotoxicity associated with overall survival in lung cancer patients receiving platinum-based chemotherapy. <b>2011</b> , 17, 5801-11	79

1029	Acetaminophen-NAPQI hepatotoxicity: a cell line model system genome-wide association study. <b>2011</b> , 120, 33-41	50
1028	Chromosome 9p21 haplotypes and prognosis in white and black patients with coronary artery disease. <b>2011</b> , 4, 169-78	21
1027	Genome-wide association study of HPV seropositivity. <b>2011</b> , 20, 4714-23	20
1026	Impact of phenotype definition on genome-wide association signals: empirical evaluation in human immunodeficiency virus type 1 infection. <b>2011</b> , 173, 1336-42	18
1025	Genome-wide association study for serum urate concentrations and gout among African Americans identifies genomic risk loci and a novel URAT1 loss-of-function allele. <b>2011</b> , 20, 4056-68	86
1024	Genome-wide association study of smoking behaviours in patients with COPD. <b>2011</b> , 66, 894-902	78
1023	Genome-wide association study identifies nidogen 1 (NID1) as a susceptibility locus to cutaneous nevi and melanoma risk. <b>2011</b> , 20, 2673-9	43
1022	Ecologically and evolutionarily important SNPs identified in natural populations. <b>2011</b> , 28, 1817-26	37
1021	A genetic variant near the PMAIP1/Noxa gene is associated with increased bleomycin sensitivity. <b>2011</b> , 20, 820-6	10
1020	A genome-wide association study reveals evidence of association with sarcoidosis at 6p12.1. <b>2011</b> , 38, 1127-35	40
1019	An increased burden of common and rare lipid-associated risk alleles contributes to the phenotypic spectrum of hypertriglyceridemia. <b>2011</b> , 31, 1916-26	73
1018	ADRB2 Gly16Arg polymorphism, asthma control and lung function decline. <b>2011</b> , 38, 1029-35	18
1017	Genetic variability of smoking persistence in African Americans. <b>2011</b> , 4, 729-34	9
1016	Identification of cis- and trans-acting genetic variants explaining up to half the variation in circulating vascular endothelial growth factor levels. <b>2011</b> , 109, 554-63	57
1015	Large-scale fine mapping of the HNF1B locus and prostate cancer risk. <b>2011</b> , 20, 3322-9	22
1014	Genome-wide association study implicates PARD3B-based AIDS restriction. <b>2011</b> , 203, 1491-502	45
1013	Genome-wide association study of survival in non-small cell lung cancer patients receiving platinum-based chemotherapy. <b>2011</b> , 103, 817-25	73
1012	Validation of a small set of ancestral informative markers for control of population admixture in African Americans. <b>2011</b> , 173, 587-92	36

1011	A pilot genome-wide association study shows genomic variants enriched in the non-tumor cells of patients with well-differentiated neuroendocrine tumors of the ileum. <b>2011</b> , 18, 171-80	19
1010	Invited commentary: dietary pattern analysis. <b>2011</b> , 173, 1105-8; discussion 1109-10	24
1009	Risk alleles for systemic lupus erythematosus in a large case-control collection and associations with clinical subphenotypes. <b>2011</b> , 7, e1001311	130
1008	Power comparison between population-based case-control studies and family-based transmission-disequilibrium tests: An empirical study. <b>2011</b> , 17 Suppl 1, S27-31	8
1007	LIN28B polymorphisms influence susceptibility to epithelial ovarian cancer. <b>2011</b> , 71, 3896-903	70
1006	Genome-wide association study identifies two major loci affecting calving ease and growth-related traits in cattle. <b>2011</b> , 187, 289-97	84
1005	Dissection of the genetics of Parkinson's disease identifies an additional association 5' of SNCA and multiple associated haplotypes at 17q21. <b>2011</b> , 20, 345-53	178
1004	Genome-wide association study confirms BST1 and suggests a locus on 12q24 as the risk loci for Parkinson's disease in the European population. <b>2011</b> , 20, 615-27	139
1003	Collagen-related genes influence the glaucoma risk factor, central corneal thickness. <b>2011</b> , 20, 649-58	127
1002	Genome-wide association studies in Asians confirm the involvement of ATOH7 and TGFBR3, and further identify CARD10 as a novel locus influencing optic disc area. <b>2011</b> , 20, 1864-72	79
1001	The MYH9/APOL1 region and chronic kidney disease in European-Americans. <b>2011</b> , 20, 2450-6	74
1000	Using genetic and clinical data to understand response to disease-modifying anti-rheumatic drug therapy: data from the Brigham and Women's Hospital Rheumatoid Arthritis Sequential Study. <b>2011</b> , 50, 40-6	71
999	A functional variant in ZNF512B is associated with susceptibility to amyotrophic lateral sclerosis in Japanese. <b>2011</b> , 20, 3684-92	42
998	Genetic diversity and population structure of Indonesian native chickens based on single nucleotide polymorphism markers. <b>2011</b> , 90, 2471-8	10
997	Genome-wide association study identifies HLA-DP as a susceptibility gene for pediatric asthma in Asian populations. <b>2011</b> , 7, e1002170	100
996	The influence of three genes on whether adolescents use contraception, USA 1994-2002. <b>2011</b> , 65, 253-71	16
995	Genome-wide association study identifies novel alleles associated with risk of cutaneous basal cell carcinoma and squamous cell carcinoma. <b>2011</b> , 20, 3718-24	80
994	High-dimensional pharmacogenetic prediction of a continuous trait using machine learning techniques with application to warfarin dose prediction in African Americans. <b>2011</b> , 27, 1384-9	48

993	MicroRNA processing and binding site polymorphisms are not replicated in the Ovarian Cancer Association Consortium. <b>2011</b> , 20, 1793-7	18
992	Interactions between genetic variants of folate metabolism genes and lifestyle affect plasma homocysteine concentrations in the Boston Puerto Rican population. <b>2011</b> , 14, 1805-12	14
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966	Robust linear regression methods in association studies. <b>2011</b> , 27, 815-21		27
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938	Genome-wide association of familial late-onset Alzheimer's disease replicates BIN1 and CLU and nominates CUGBP2 in interaction with APOE. <b>2011</b> , 7, e1001308	179
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936	Identification, replication, and functional fine-mapping of expression quantitative trait loci in primary human liver tissue. <b>2011</b> , 7, e1002078	171
935	Genetic architecture of aluminum tolerance in rice ( <i>Oryza sativa</i> ) determined through genome-wide association analysis and QTL mapping. <b>2011</b> , 7, e1002221	278
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930	Genome-wide association of pericardial fat identifies a unique locus for ectopic fat. <b>2012</b> , 8, e1002705	42
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927	A quantitative comparison of the similarity between genes and geography in worldwide human populations. <b>2012</b> , 8, e1002886	83
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917	Chapter 11: Genome-wide association studies. <b>2012</b> , 8, e1002822	708
916	Chapter 13: Mining electronic health records in the genomics era. <b>2012</b> , 8, e1002823	122
915	Genome-wide association study identifies chromosome 10q24.32 variants associated with arsenic metabolism and toxicity phenotypes in Bangladesh. <b>2012</b> , 8, e1002522	124
914	Genome-wide association study in east Asians identifies novel susceptibility loci for breast cancer. <b>2012</b> , 8, e1002532	118
913	Genome-wide association for abdominal subcutaneous and visceral adipose reveals a novel locus for visceral fat in women. <b>2012</b> , 8, e1002695	199
912	Brain expression genome-wide association study (eGWAS) identifies human disease-associated variants. <b>2012</b> , 8, e1002707	174
911	Genetic variants on chromosome 1q41 influence ocular axial length and high myopia. <b>2012</b> , 8, e1002753	77
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890	Surrogate variable analysis using partial least squares (SVA-PLS) in gene expression studies. <b>2012</b> , 28, 799-806	40
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883	Gene set analysis of survival following ovarian cancer implicates macrolide binding and intracellular signaling genes. <b>2012</b> , 21, 529-36	7
882	A genome-wide association study of overall survival in pancreatic cancer patients treated with gemcitabine in CALGB 80303. <b>2012</b> , 18, 577-84	81
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873	Lessons from genome-wide association studies for epidemiology. <b>2012</b> , 23, 363-7	13
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848	Genome-wide copy number variation association analyses for age at menarche. <b>2012</b> , 97, E2133-9	2
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845	Investigating the contribution of common genetic variants to the risk and pathogenesis of ADHD. <b>2012</b> , 169, 186-94	147
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836	A high-performance computing toolset for relatedness and principal component analysis of SNP data. <b>2012</b> , 28, 3326-8	1094
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831	Comprehensive evaluation of imputation performance in African Americans. <b>2012</b> , 57, 411-21	11
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829	A functional haplotype of UBE2L3 confers risk for systemic lupus erythematosus. <b>2012</b> , 13, 380-7	45
828	Genome-wide association study of serious blistering skin rash caused by drugs. <b>2012</b> , 12, 96-104	28
827	Genome-wide association study identifies common variants at TNFRSF13B associated with IgG level in a healthy Chinese male population. <b>2012</b> , 13, 509-13	14
826	Genome-wide association study of antipsychotic-induced QTc interval prolongation. <b>2012</b> , 12, 165-72	61
825	Background gene expression networks significantly enhance drug response prediction by transcriptional profiling. <b>2012</b> , 12, 446-52	5
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823	UGT1A1 is a major locus influencing bilirubin levels in African Americans. <b>2012</b> , 20, 463-8	54
822	Association of common genetic variants in GPCPD1 with scaling of visual cortical surface area in humans. <b>2012</b> , 109, 3985-90	43
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820	Lupus-associated causal mutation in neutrophil cytosolic factor 2 (NCF2) brings unique insights to the structure and function of NADPH oxidase. <b>2012</b> , 109, E59-67	124
819	Association of SCARB1 variants with subclinical atherosclerosis and incident cardiovascular disease: the multi-ethnic study of atherosclerosis. <b>2012</b> , 32, 1991-9	34
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811	A genome-wide association study in Han Chinese identifies multiple susceptibility loci for IgA nephropathy. <i>Nature Genetics</i> , <b>2011</b> , 44, 178-82	36.3 195
810	A genome-wide search for loci interacting with known prostate cancer risk-associated genetic variants. <b>2012</b> , 33, 598-603	27
809	Opportunities and challenges for genome sequencing in the clinic. <b>2012</b> , 89, 65-83	9
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807	The implications of genotype-environment correlation for establishing causal processes in psychopathology. <b>2012</b> , 24, 1253-64	39
806	Pediatric Biomedical Informatics. <b>2012</b> ,	3
805	Pharmacogenetic determinants of statin-induced reductions in C-reactive protein. <b>2012</b> , 5, 58-65	27
804	Novel loci associated with PR interval in a genome-wide association study of 10 African American cohorts. <b>2012</b> , 5, 639-46	41
803	Genetic variants in Arhgef11 are associated with kidney injury in the Dahl salt-sensitive rat. <b>2012</b> , 60, 1157-68	25
802	Excess variants in AFF2 detected by massively parallel sequencing of males with autism spectrum disorder. <b>2012</b> , 21, 4356-64	26
801	Genome-wide association study of antidepressant treatment-emergent suicidal ideation. <b>2012</b> , 37, 797-807	62
800	Evaluation of genome-wide association study-identified type 2 diabetes loci in African Americans. <b>2012</b> , 176, 995-1001	32
799	Robust estimation of local genetic ancestry in admixed populations using a nonparametric Bayesian approach. <b>2012</b> , 191, 1295-308	17
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796	Nonlinear dimension reduction with Wright-Fisher kernel for genotype aggregation and association mapping. <b>2012</b> , 28, i375-i381	3



795	The Minnesota Center for Twin and Family Research genome-wide association study. <b>2012</b> , 15, 767-74	59
794	HTR1B, ADIPOR1, PPARGC1A, and CYP19A1 and obesity in a cohort of Caucasians and African Americans: an evaluation of gene-environment interactions and candidate genes. <b>2012</b> , 175, 11-21	35
793	Investigation of the genetic association between quantitative measures of psychosis and schizophrenia: a polygenic risk score analysis. <b>2012</b> , 7, e37852	53
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