Bernard D Keavney

List of Publications by Year in Descending Order

159 papers	9,486 citations	49 h-index	95 g-index
181 ext. papers	11,723 ext. citations	9.5 avg, IF	5.45 L-index

#	Paper	IF	Citations
159	Genetic resiliency associated with dominant lethal mutation causing atrial septal defect with high heritability.. *Cell Reports Medicine*, **2022**, 3, 100501	18	
158	Data-independent acquisition mass spectrometry in severe rheumatic heart disease (RHD) identifies a proteomic signature showing ongoing inflammation and effectively classifying RHD cases.. *Clinical Proteomics*, **2022**, 19, 7	5	1
157	Genetic analyses of circulating PUFA-derived mediators identifies heritable dihydroxyeicosatrienoic acid species.. *Prostaglandins and Other Lipid Mediators*, **2022**, 106638	3.7	
156	Common Genetic Variants Contribute to Risk of Transposition of the Great Arteries. *Circulation Research*, **2021**,	15.7	2
155	PROTEA, A Southern African Multicenter Congenital Heart Disease Registry and Biorepository: Rationale, Design, and Initial Results. *Frontiers in Pediatrics*, **2021**, 9, 763060	3.4	1
154	A novel RNA-mediated mechanism causing down-regulation of insulating promoter interactions in human embryonic stem cells. *Scientific Reports*, **2021**, 11, 23233	4.9	1
153	The physiological and pathological functions of VEGFR3 in cardiac and lymphatic development and related diseases. *Cardiovascular Research*, **2021**, 117, 1877-1890	9.9	3
152	Response to correspondence on "Reproducibility of CRISPR-Cas9 methods for generation of conditional mouse alleles: a multi-center evaluation". *Genome Biology*, **2021**, 22, 99	18.3	2
151	Uncovering genetic mechanisms of hypertension through multi-omic analysis of the kidney. *Nature Genetics*, **2021**, 53, 630-637	36.3	5
150	Circulating ceramides as biomarkers of cardiovascular disease: Evidence from phenotypic and genomic studies. *Atherosclerosis*, **2021**, 327, 18-30	3.1	10
149	Rationale and design of the African Cardiomyopathy and Myocarditis Registry Program: The IMHOTEP study. *International Journal of Cardiology*, **2021**, 333, 119-126	3.2	0
148	Rare variants in KDR, encoding VEGF Receptor 2, are associated with tetralogy of Fallot. *Genetics in Medicine*, **2021**, 23, 1952-1960	8.1	1
147	Identification of a Variant in a Family With Arrhythmogenic Cardiomyopathy and Left Ventricular Fibrosis. *Circulation Genomic and Precision Medicine*, **2021**, 14, e003138	5.2	1
146	Heritability and family-based GWAS analyses of the N-acyl ethanolamine and ceramide plasma lipidome. *Human Molecular Genetics*, **2021**, 30, 500-513	5.6	4
145	Defining the Normal Spectrum of Electrocardiographic and Left Ventricular Adaptations in Mixed-Race Male Adolescent Soccer Players. *Circulation*, **2021**, 143, 94-96	16.7	1
144	Congenital heart disease risk loci identified by genome-wide association study in European patients. *Journal of Clinical Investigation*, **2021**, 131,	15.9	9
143	Integrative analysis of genomic variants reveals new associations of candidate haploinsufficient genes with congenital heart disease. *PLoS Genetics*, **2021**, 17, e1009679	6	1

142	Clinical Genetic Risk Variants Inform a Functional Protein Interaction Network for Tetralogy of Fallot. *Circulation Genomic and Precision Medicine*, **2021**, 14, e003410	5.2	1
141	Association of Novel Locus With Rheumatic Heart Disease in Black African Individuals: Findings From the RHDGen Study. *JAMA Cardiology*, **2021**, 6, 1000-1011	16.2	7
140	Vector-based discrete element method for solid elastic materials. *Computer Physics Communications*, **2020**, 254, 107353	4.2	5
139	A Patient-Specific CFD Pipeline Using Doppler Echocardiography for Application in Coarctation of the Aorta in a Limited Resource Clinical Context. *Frontiers in Bioengineering and Biotechnology*, **2020**, 8, 409	5.8	9
138	CMV-independent increase in CD27-CD28+ CD8+ EMRA T cells is inversely related to mortality in octogenarians. *Npj Aging and Mechanisms of Disease*, **2020**, 6, 3	5.5	13
137	Association of congenital cardiovascular malformation and neuropsychiatric phenotypes with 15q11.2 (BP1-BP2) deletion in the UK Biobank. *European Journal of Human Genetics*, **2020**, 28, 1265-1273	5.3	6
136	Cardiac Imaging of Aortic Valve Area From 34 287 UK Biobank Participants Reveals Novel Genetic Associations and Shared Genetic Comorbidity With Multiple Disease Phenotypes. *Circulation Genomic and Precision Medicine*, **2020**, 13, e003014	5.2	1
135	The use of missing values in proteomic data-independent acquisition mass spectrometry to enable disease activity discrimination. *Bioinformatics*, **2020**, 36, 2217-2223	7.2	12
134	Hypertension and renin-angiotensin system blockers are not associated with expression of angiotensin-converting enzyme 2 (ACE2) in the kidney. *European Heart Journal*, **2020**, 41, 4580-4588	9.5	22
133	Global prevalence of congenital heart disease in school-age children: a meta-analysis and systematic review. *BMC Cardiovascular Disorders*, **2020**, 20, 488	2.3	5
132	Identifying genetic factors that contribute to the increased risk of congenital heart defects in infants with Down syndrome. *Scientific Reports*, **2020**, 10, 18051	4.9	4
131	Heritability of haemodynamics in the ascending aorta. *Scientific Reports*, **2020**, 10, 14356	4.9	2
130	Reproducibility of CRISPR-Cas9 methods for generation of conditional mouse alleles: a multi-center evaluation. *Genome Biology*, **2019**, 20, 171	18.3	39
129	Human Y Chromosome Exerts Pleiotropic Effects on Susceptibility to Atherosclerosis. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2019**, 39, 2386-2401	9.4	15
128	Exploring Shared Susceptibility between Two Neural Crest Cells Originating Conditions: Neuroblastoma and Congenital Heart Disease. *Genes*, **2019**, 10,	4.2	8
127	Marked variation in heritability estimates of left ventricular mass depending on modality of measurement. *Scientific Reports*, **2019**, 9, 13556	4.9	1
126	Does rhythm matter in acute heart failure? An insight from the British Society for Heart Failure National Audit. *Clinical Research in Cardiology*, **2019**, 108, 1276-1286	6.1	6
125	Integration of Large-Scale Genomic Data Sources With Evolutionary History Reveals Novel Genetic Loci for Congenital Heart Disease. *Circulation Genomic and Precision Medicine*, **2019**, 12, 442-451	5.2	10

124	Global birth prevalence of congenital heart defects 1970-2017: updated systematic review and meta-analysis of 260 studies. *International Journal of Epidemiology*, **2019**, 48, 455-463	7.8	254
123	Whole Exome Sequencing Reveals the Major Genetic Contributors to Nonsyndromic Tetralogy of Fallot. *Circulation Research*, **2019**, 124, 553-563	15.7	62
122	Promoter interactome of human embryonic stem cell-derived cardiomyocytes connects GWAS regions to cardiac gene networks. *Nature Communications*, **2018**, 9, 2526	17.4	34
121	Structural modelling of the cardiovascular system. *Biomechanics and Modeling in Mechanobiology*, **2018**, 17, 1217-1242	3.8	12
120	Genomic Risk Prediction of Coronary Artery Disease in 480,000 Adults: Implications for Primary Prevention. *Journal of the American College of Cardiology*, **2018**, 72, 1883-1893	15.1	285
119	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. *Nature Genetics*, **2018**, 50, 1412-1425	36.3	386
118	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. *Nature Genetics*, **2017**, 49, 403-415	36.3	313
117	Induced pluripotent stem cell modelling of HLHS underlines the contribution of dysfunctional NOTCH signalling to impaired cardiogenesis. *Human Molecular Genetics*, **2017**, 26, 3031-3045	5.6	31
116	Protein-altering and regulatory genetic variants near GATA4 implicated in bicuspid aortic valve. *Nature Communications*, **2017**, 8, 15481	17.4	52
115	Non-muscle myosin IIB (Myh10) is required for epicardial function and coronary vessel formation during mammalian development. *PLoS Genetics*, **2017**, 13, e1007068	6	14
114	Biochemical Screening for Nonadherence Is Associated With Blood Pressure Reduction and Improvement in Adherence. *Hypertension*, **2017**, 70, 1042-1048	8.5	81
113	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. *Hypertension*, **2017**,	8.5	85
112	Association analyses based on false discovery rate implicate new loci for coronary artery disease. *Nature Genetics*, **2017**, 49, 1385-1391	36.3	361
111	4D flow MRI assessment of right atrial flow patterns in the normal heart - influence of caval vein arrangement and implications for the patent foramen ovale. *PLoS ONE*, **2017**, 12, e0173046	3.7	8
110	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. *Nature Genetics*, **2016**, 48, 1462-1472	36.3	198
109	A genome-wide association study of congenital cardiovascular left-sided lesions shows association with a locus on chromosome 20. *Human Molecular Genetics*, **2016**, 25, 2331-2341	5.6	18
108	Forward and back aspiration during ST-elevation myocardial infarction: a feasibility study. *EuroIntervention*, **2016**, 11, e1639-48	3.1	8
107	Definition and delivery of an aortopathy bundle of care (ABC): a tool for improving diagnosis and management of Marfan syndrome and related conditions. *Clinical Medicine*, **2016**, 16 Suppl 3, s30	1.9	1

106	Distinct genetic architectures for syndromic and nonsyndromic congenital heart defects identified by exome sequencing. *Nature Genetics*, **2016**, 48, 1060-5	36.3	200
105	Impact of age on access site-related outcomes in 469,983 percutaneous coronary intervention procedures: Insights from the British Cardiovascular Intervention Society. *Catheterization and Cardiovascular Interventions*, **2015**, 86, 965-72	2.7	22
104	Genetic variants associated with risk of atrial fibrillation regulate expression of PITX2, CAV1, MYOZ1, C9orf3 and FANCC. *Journal of Molecular and Cellular Cardiology*, **2015**, 85, 207-14	5.8	31
103	Stroke following percutaneous coronary intervention: type-specific incidence, outcomes and determinants seen by the British Cardiovascular Intervention Society 2007-12. *European Heart Journal*, **2015**, 36, 1618-28	9.5	50
102	Positional mapping of PRKD1, NRP1 and PRDM1 as novel candidate disease genes in truncus arteriosus. *Journal of Medical Genetics*, **2015**, 52, 322-9	5.8	23
101	Using population data for assessing next-generation sequencing performance. *Bioinformatics*, **2015** , 31, 56-61	7.2	
100	Concise Review: Cardiac Disease Modeling Using Induced Pluripotent Stem Cells. *Stem Cells*, **2015**, 33, 2643-51	5.8	35
99	Association analysis identifies new risk loci for congenital heart disease in Chinese populations. *Nature Communications*, **2015**, 6, 8082	17.4	19
98	Myocardial ischemia and reperfusion leads to transient CD8 immune deficiency and accelerated immunosenescence in CMV-seropositive patients. *Circulation Research*, **2015**, 116, 87-98	15.7	23
97	Increased Power for Detection of Parent-of-Origin Effects via the Use of Haplotype Estimation. *American Journal of Human Genetics*, **2015**, 97, 419-34	11	11
96	Impact of age on the prognostic value of left ventricular function in relation to procedural outcomes following percutaneous coronary intervention: insights from the British Cardiovascular Intervention Society. *Catheterization and Cardiovascular Interventions*, **2015**, 85, 944-51	2.7	7
95	Targeted Next-Generation Sequencing Analysis of 1,000 Individuals with Intellectual Disability. *Human Mutation*, **2015**, 36, 1197-204	4.7	122
94	Chromosomal Imbalances in Patients with Congenital Cardiac Defects: A Meta-analysis Reveals Novel Potential Critical Regions Involved in Heart Development. *Congenital Heart Disease*, **2015**, 10, 193-208	3.1	18
93	T lymphocytes and fractalkine contribute to myocardial ischemia/reperfusion injury in patients. *Journal of Clinical Investigation*, **2015**, 125, 3063-76	15.9	85
92	Research capacity. Enabling the genomic revolution in Africa. *Science*, **2014**, 344, 1346-8	33.3	256
91	Atorvastatin induces T cell proliferation by a telomerase reverse transcriptase (TERT) mediated mechanism. *Atherosclerosis*, **2014**, 236, 312-20	3.1	28
90	Major bleeding after percutaneous coronary intervention and risk of subsequent mortality: a systematic review and meta-analysis. *Open Heart*, **2014**, 1, e000021	3	75
89	Bariatric surgery and its impact on cardiovascular disease and mortality: a systematic review and meta-analysis. *International Journal of Cardiology*, **2014**, 173, 20-8	3.2	186

88	Functionally significant, rare transcription factor variants in tetralogy of Fallot. *PLoS ONE*, **2014**, 9, e95453	37	42
87	Atrial fibrillation associated with ivabradine treatment: meta-analysis of randomised controlled trials. *Heart*, **2014**, 100, 1506-10	5.1	107
86	Utility of NT-proBNP as a rule-out test for left ventricular dysfunction in very old people with limiting dyspnoea: the Newcastle 85+ Study. *BMC Cardiovascular Disorders*, **2014**, 14, 128	2.3	7
85	Chromosome 16q22 variants in a region associated with cardiovascular phenotypes correlate with ZFHX3 expression in a transcript-specific manner. *BMC Genetics*, **2014**, 15, 136	2.6	6
84	Impact of left ventricular function in relation to procedural outcomes following percutaneous coronary intervention: insights from the British Cardiovascular Intervention Society. *European Heart Journal*, **2014**, 35, 3004-12a	9.5	52
83	Human Tra2 proteins jointly control a CHEK1 splicing switch among alternative and constitutive target exons. *Nature Communications*, **2014**, 5, 4760	17.4	35
82	Renal denervation and blood pressure reduction in resistant hypertension: a systematic review and meta-analysis. *Open Heart*, **2014**, 1, e000092	3	4
81	An induced pluripotent stem cell model of hypoplastic left heart syndrome (HLHS) reveals multiple expression and functional differences in HLHS-derived cardiac myocytes. *Stem Cells Translational Medicine*, **2014**, 3, 416-23	6.9	57
80	Genome-wide association study of multiple congenital heart disease phenotypes identifies a susceptibility locus for atrial septal defect at chromosome 4p16. *Nature Genetics*, **2013**, 45, 822-4	36.3	91
79	Genetic information and the prediction of incident type 2 diabetes in a high-risk multiethnic population: the EpiDREAM genetic study. *Diabetes Care*, **2013**, 36, 2836-42	14.6	20
78	Low-frequency intermediate penetrance variants in the ROCK1 gene predispose to Tetralogy of Fallot. *BMC Genetics*, **2013**, 14, 57	2.6	9
77	Mutations in FAM111B cause hereditary fibrosing poikiloderma with tendon contracture, myopathy, and pulmonary fibrosis. *American Journal of Human Genetics*, **2013**, 93, 1100-7	11	45
76	Ebstein anomaly associated with left ventricular noncompaction: an autosomal dominant condition that can be caused by mutations in MYH7. *American Journal of Medical Genetics, Part C: Seminars in Medical Genetics*, **2013**, 163C, 178-84	3.1	35
75	Quantitative variation in plasma angiotensin-I converting enzyme activity shows allelic heterogeneity in the ABO blood group locus. *Annals of Human Genetics*, **2013**, 77, 465-71	2.2	14
74	Defining cardiac adaptations and safety of endurance training in patients with m.3243A>G-related mitochondrial disease. *International Journal of Cardiology*, **2013**, 168, 3599-608	3.2	29
73	Concentric hypertrophic remodelling and subendocardial dysfunction in mitochondrial DNA point mutation carriers. *European Heart Journal Cardiovascular Imaging*, **2013**, 14, 650-8	4.1	20
72	Association between C677T polymorphism of methylene tetrahydrofolate reductase and congenital heart disease: meta-analysis of 7697 cases and 13,125 controls. *Circulation: Cardiovascular Genetics*, **2013**, 6, 347-53		26
71	Loss of function of parathyroid hormone receptor 1 induces Notch-dependent aortic defects during zebrafish vascular development. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2013**, 33, 1257-63	9.4	13

70	Genome-wide association study identifies loci on 12q24 and 13q32 associated with tetralogy of Fallot. *Human Molecular Genetics*, **2013**, 22, 1473-81	5.6	68
69	Common variation neighbouring micro-RNA 22 is associated with increased left ventricular mass. *PLoS ONE*, **2013**, 8, e55061	3.7	5
68	Nonsynonymous variants in the SMAD6 gene predispose to congenital cardiovascular malformation. *Human Mutation*, **2012**, 33, 720-7	4.7	90
67	Apolipoprotein(a) genetic sequence variants associated with systemic atherosclerosis and coronary atherosclerotic burden but not with venous thromboembolism. *Journal of the American College of Cardiology*, **2012**, 60, 722-9	15.1	118
66	Prevalence of left ventricular dysfunction in a UK community sample of very old people: the Newcastle 85+ study. *Heart*, **2012**, 98, 1418-23	5.1	24
65	Contribution of global rare copy-number variants to the risk of sporadic congenital heart disease. *American Journal of Human Genetics*, **2012**, 91, 489-501	11	213
64	Mutations in multidomain protein MEGF8 identify a Carpenter syndrome subtype associated with defective lateralization. *American Journal of Human Genetics*, **2012**, 91, 897-905	11	55
63	Functional significance of SRJ domain mutations in CITED2. *PLoS ONE*, **2012**, 7, e46256	3.7	17
62	High-throughput 13-parameter immunophenotyping identifies shifts in the circulating T-cell compartment following reperfusion in patients with acute myocardial infarction. *PLoS ONE*, **2012**, 7, e47155	3.7	24
61	A new phenotype of brain iron accumulation with dystonia, optic atrophy, and peripheral neuropathy. *Movement Disorders*, **2012**, 27, 789-93	7	39
60	Left ventricular torsion, energetics, and diastolic function in normal human aging. *American Journal of Physiology - Heart and Circulatory Physiology*, **2012**, 302, H885-92	5.2	55
59	A common variant in the PTPN11 gene contributes to the risk of tetralogy of Fallot. *Circulation: Cardiovascular Genetics*, **2012**, 5, 287-92		25
58	Phenotype-specific effect of chromosome 1q21.1 rearrangements and GJA5 duplications in 2436 congenital heart disease patients and 6760 controls. *Human Molecular Genetics*, **2012**, 21, 1513-20	5.6	83
57	Common variation in the CD36 (fatty acid translocase) gene is associated with left-ventricular mass. *Journal of Hypertension*, **2011**, 29, 690-5	1.9	12
56	Exome sequencing identifies GATA-2 mutation as the cause of dendritic cell, monocyte, B and NK lymphoid deficiency. *Blood*, **2011**, 118, 2656-8	2.2	316
55	Assessment of a large panel of candidate biomarkers of ageing in the Newcastle 85+ study. *Mechanisms of Ageing and Development*, **2011**, 132, 496-502	5.6	90
54	Genetic mechanisms mediating atherosclerosis susceptibility at the chromosome 9p21 locus. *Current Atherosclerosis Reports*, **2011**, 13, 193-201	6	36
53	Mutations in the sarcomere gene MYH7 in Ebstein anomaly. *Circulation: Cardiovascular Genetics*, **2011**, 4, 43-50		114

52	Common variation at the 11-hydroxysteroid dehydrogenase type 1 gene is associated with left ventricular mass. *Circulation: Cardiovascular Genetics*, **2011**, 4, 156-62		9
51	C reactive protein and the risk of cardiovascular disease. *BMJ, The*, **2011**, 342, d144	5.9	7
50	Genotype at the P554L variant of the hexose-6 phosphate dehydrogenase gene is associated with carotid intima-medial thickness. *PLoS ONE*, **2011**, 6, e23248	3.7	6
49	22q11.2 Deletion Syndrome is under-recognised in adult patients with tetralogy of Fallot and pulmonary atresia. *Heart*, **2010**, 96, 621-4	5.1	38
48	Coronary artery disease-related genetic variant on chromosome 10q11 is associated with carotid intima-media thickness and atherosclerosis. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2010**, 30, 2678-83	9.4	28
47	Variation at the NFATC2 locus increases the risk of thiazolidinedione-induced edema in the Diabetes REduction Assessment with ramipril and rosiglitazone Medication (DREAM) study. *Diabetes Care*, **2010**, 33, 2250-3	14.6	32
46	Chromosome 9p21 SNPs Associated with Multiple Disease Phenotypes Correlate with ANRIL Expression. *PLoS Genetics*, **2010**, 6, e1000899	6	291
45	Systematic survey of variants in TBX1 in non-syndromic tetralogy of Fallot identifies a novel 57 base pair deletion that reduces transcriptional activity but finds no evidence for association with common variants. *Heart*, **2010**, 96, 1651-5	5.1	47
44	Elevated heart rate and cardiovascular outcomes in patients with coronary artery disease: clinical evidence and pathophysiological mechanisms. *Atherosclerosis*, **2010**, 212, 1-8	3.1	42
43	The interleukin-1 cluster, dyslipidaemia and risk of myocardial infarction. *BMC Medicine*, **2010**, 8, 6	11.4	3
42	Genetic variation in VEGF does not contribute significantly to the risk of congenital cardiovascular malformation. *PLoS ONE*, **2009**, 4, e4978	3.7	13
41	Familial and phenotypic associations of the aldosterone Renin ratio. *Journal of Clinical Endocrinology and Metabolism*, **2009**, 94, 4324-33	5.6	38
40	Genetic variants associated with myocardial infarction risk factors in over 8000 individuals from five ethnic groups: The INTERHEART Genetics Study. *Circulation: Cardiovascular Genetics*, **2009**, 2, 16-25		54
39	STK39 polymorphisms and blood pressure: an association study in British Caucasians and assessment of cis-acting influences on gene expression. *BMC Medical Genetics*, **2009**, 10, 135	2.1	26
38	Ambulatory blood pressure is associated with polymorphic variation in P2X receptor genes. *Hypertension*, **2008**, 52, 980-5	8.5	49
37	Circulating endothelial progenitor cells exhibit diurnal variation. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2008**, 28, e21-2	9.4	34
36	More evidence against a causal association between C-reactive protein and diabetes. *PLoS Medicine* , **2008**, 5, e174	11.6	3
35	Genome-wide linkage analysis of electrocardiographic and echocardiographic left ventricular hypertrophy in families with hypertension. *European Heart Journal*, **2008**, 29, 525-30	9.5	29

34	Association of cholesteryl ester transfer protein genotypes with CETP mass and activity, lipid levels, and coronary risk. *JAMA - Journal of the American Medical Association*, **2008**, 299, 2777-88	27.4	385
33	Plasma potassium level is associated with common genetic variation in the beta-subunit of the epithelial sodium channel. *American Journal of Physiology - Regulatory Integrative and Comparative Physiology*, **2008**, 294, R1068-72	3.2	6
32	Correction of population stratification in large multi-ethnic association studies. *PLoS ONE*, **2008**, 3, e1382	3.7	53
31	Telomere length is associated with left ventricular function in the oldest old: the Newcastle 85+ study. *European Heart Journal*, **2007**, 28, 172-6	9.5	69
30	The C-532T polymorphism of the angiotensinogen gene is associated with pulse pressure: a possible explanation for heterogeneity in genetic association studies of AGT and hypertension. *International Journal of Epidemiology*, **2007**, 36, 1356-62	7.8	17
29	Association of apolipoprotein E genotypes with lipid levels and coronary risk. *JAMA - Journal of the American Medical Association*, **2007**, 298, 1300-11	27.4	546
28	Association between aldosterone production and variation in the 11beta-hydroxylase (CYP11B1) gene. *Journal of Clinical Endocrinology and Metabolism*, **2006**, 91, 5051-6	5.6	22
27	Fibrinogen and coronary heart disease: test of causality by ‘Mendelian randomization’. *International Journal of Epidemiology*, **2006**, 35, 935-43	7.8	112
26	Seven haemostatic gene polymorphisms in coronary disease: meta-analysis of 66,155 cases and 91,307 controls. *Lancet, The*, **2006**, 367, 651-8	40	334
25	INSIG-2 promoter polymorphism and obesity related phenotypes: association study in 1428 members of 248 families. *BMC Medical Genetics*, **2006**, 7, 83	2.1	48
24	Genotype at the -174G/C polymorphism of the interleukin-6 gene is associated with common carotid artery intimal-medial thickness: family study and meta-analysis. *Stroke*, **2005**, 36, 2215-9	6.7	36
23	Genetic variation at the locus encompassing 11-beta hydroxylase and aldosterone synthase accounts for heritability in cortisol precursor (11-deoxycortisol) urinary metabolite excretion. *Journal of Clinical Endocrinology and Metabolism*, **2005**, 90, 1072-7	5.6	46
22	Association between common polymorphisms of the proopiomelanocortin gene and body fat distribution: a family study. *Diabetes*, **2005**, 54, 2492-6	0.9	57
21	Commentary: Katan’s remarkable foresight: genes and causality 18 years on. *International Journal of Epidemiology*, **2004**, 33, 11-4	7.8	16
20	Lipid-related genes and myocardial infarction in 4685 cases and 3460 controls: discrepancies between genotype, blood lipid concentrations, and coronary disease risk. *International Journal of Epidemiology*, **2004**, 33, 1002-13	7.8	47
19	Four paraoxonase gene polymorphisms in 11212 cases of coronary heart disease and 12786 controls: meta-analysis of 43 studies. *Lancet, The*, **2004**, 363, 689-95	40	260
18	Measured haplotype analysis of the aldosterone synthase gene and heart size. *European Journal of Human Genetics*, **2003**, 11, 395-401	5.3	17
17	Large-scale evidence that the cardiotoxicity of smoking is not significantly modified by the apolipoprotein E epsilon2/epsilon3/epsilon4 genotype. *Lancet, The*, **2003**, 361, 396-8	40	41

16	In search of genetic precision. *Lancet, The*, **2003**, 361, 1909-1910	40	2
15	Genetic epidemiological studies of coronary heart disease. *International Journal of Epidemiology*, **2002**, 31, 730-6	7.8	36
14	Genotype at a promoter polymorphism of the interleukin-6 gene is associated with baseline levels of plasma C-reactive protein. *Cardiovascular Research*, **2002**, 53, 1029-34	9.9	206
13	Common genetic polymorphisms and coronary heart disease. *Seminars in Vascular Medicine*, **2002**, 2, 233-41		
12	Angiotensin converting enzyme insertion or deletion polymorphism and coronary restenosis: meta-analysis of 16 studies. *BMJ, The*, **2002**, 325, 517-20	5.9	33
11	Genetics of coronary heart disease: current knowledge and research principles. *American Heart Journal*, **2000**, 140, S11-26	4.9	55
10	Recommendations for national and local regulatory authorities concerning research in genetic markers of disease. *American Heart Journal*, **2000**, 140, S3-5	4.9	
9	Large-scale test of hypothesised associations between the angiotensin-converting-enzyme insertion/deletion polymorphism and myocardial infarction in about 5000 cases and 6000 controls. International Studies of Infarct Survival (ISIS) Collaborators. *Lancet, The*, **2000**, 355, 434-42	40	228
8	Fine-mapping of an ancestral recombination breakpoint in DCP1. *Nature Genetics*, **1999**, 23, 270-1	36.3	40
7	Measured haplotype analysis of the angiotensin-I converting enzyme gene. *Human Molecular Genetics*, **1998**, 7, 1745-51	5.6	177
6	Evaluation of the angiotensinogen locus in human essential hypertension: a European study. *Hypertension*, **1998**, 31, 725-9	8.5	85
5	Prediction of patient responses to antihypertensive drugs using genetic polymorphisms: investigation of renin-angiotensin system genes. *Journal of Hypertension*, **1996**, 14, 259-62	1.9	80
4	U.K. Prospective Diabetes Study. XV: Relationship of renin-angiotensin system gene polymorphisms with microalbuminuria in NIDDM. *Kidney International*, **1995**, 48, 1907-11	9.9	57
3	Heritability and family-based GWAS analyses of the N-acyl ethanolamine and ceramide plasma lipidome		1
2	Genome-wide association study in European patients with congenital heart disease identifies risk loci for transposition of the great arteries and anomalies of the thoracic arteries and veins and expression of discovered candidate genes in the developing heart		1
1	Genetic analysis of over one million people identifies 535 novel loci for blood pressure		4