# Jeanette Erdmann

## List of Publications by Citations



| | | | |
|---|---|---|---|
| 320 papers | 47,664 citations | 91 h-index | 217 g-index |
| 348 ext. papers | 58,165 ext. citations | 12 avg, IF | 6.03 L-index |

| # | Paper | IF | Citations |
|---|---|---|---|
| 320 | Biological, clinical and population relevance of 95 loci for blood lipids. *Nature*, **2010**, 466, 707-13 | 50.4 | 2742 |
| 319 | Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206 | 50.4 | 2687 |
| 318 | The mutational constraint spectrum quantified from variation in 141,456 humans. *Nature*, **2020**, 581, 434-443 | 50.4 | 2278 |
| 317 | Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. *Nature Genetics*, **2010**, 42, 937-48 | 36.3 | 2267 |
| 316 | Genomewide association analysis of coronary artery disease. *New England Journal of Medicine*, **2007**, 357, 443-53 | 59.2 | 1608 |
| 315 | Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. *Nature*, **2011**, 478, 103-9 | 50.4 | 1564 |
| 314 | Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. *Lancet, The*, **2012**, 380, 572-80 | 40 | 1523 |
| 313 | Hundreds of variants clustered in genomic loci and biological pathways affect human height. *Nature*, **2010**, 467, 832-8 | 50.4 | 1514 |
| 312 | Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. *Nature Genetics*, **2011**, 43, 333-8 | 36.3 | 1394 |
| 311 | Defining the role of common variation in the genomic and biological architecture of adult human height. *Nature Genetics*, **2014**, 46, 1173-86 | 36.3 | 1339 |
| 310 | A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. *Nature Genetics*, **2015**, 47, 1121-1130 | 36.3 | 1290 |
| 309 | Large-scale association analysis identifies new risk loci for coronary artery disease. *Nature Genetics*, **2013**, 45, 25-33 | 36.3 | 1172 |
| 308 | Genomewide Association Study of Severe Covid-19 with Respiratory Failure. *New England Journal of Medicine*, **2020**, 383, 1522-1534 | 59.2 | 913 |
| 307 | Genome-wide association of early-onset myocardial infarction with single nucleotide polymorphisms and copy number variants. *Nature Genetics*, **2009**, 41, 334-41 | 36.3 | 884 |
| 306 | Human metabolic individuality in biomedical and pharmaceutical research. *Nature*, **2011**, 477, 54-60 | 50.4 | 728 |
| 305 | Loss-of-function mutations in APOC3, triglycerides, and coronary disease. *New England Journal of Medicine*, **2014**, 371, 22-31 | 59.2 | 721 |
| 304 | Identification of seven loci affecting mean telomere length and their association with disease. *Nature Genetics*, **2013**, 45, 422-7, 427e1-2 | 36.3 | 624 |

| | | | |
|---|---|---|---|
| 303 | DNA methylation and body-mass index: a genome-wide analysis. *Lancet, The*, **2014**, 383, 1990-8 | 40 | 569 |
| 302 | Interleukin-6 receptor pathways in coronary heart disease: a collaborative meta-analysis of 82 studies. *Lancet, The*, **2012**, 379, 1205-13 | 40 | 522 |
| 301 | Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. *Nature*, **2015**, 518, 102-6 | 50.4 | 463 |
| 300 | Genetic Loci associated with C-reactive protein levels and risk of coronary heart disease. *JAMA - Journal of the American Medical Association*, **2009**, 302, 37-48 | 27.4 | 459 |
| 299 | Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. *Nature Genetics*, **2013**, 45, 501-12 | 36.3 | 437 |
| 298 | A genome-wide meta-analysis identifies 22 loci associated with eight hematological parameters in the HaemGen consortium. *Nature Genetics*, **2009**, 41, 1182-90 | 36.3 | 433 |
| 297 | Association between C reactive protein and coronary heart disease: mendelian randomisation analysis based on individual participant data. *BMJ, The*, **2011**, 342, d548 | 5.9 | 422 |
| 296 | Identification of ADAMTS7 as a novel locus for coronary atherosclerosis and association of ABO with myocardial infarction in the presence of coronary atherosclerosis: two genome-wide association studies. *Lancet, The*, **2011**, 377, 383-92 | 40 | 399 |
| 295 | The metabochip, a custom genotyping array for genetic studies of metabolic, cardiovascular, and anthropometric traits. *PLoS Genetics*, **2012**, 8, e1002793 | 6 | 395 |
| 294 | New susceptibility locus for coronary artery disease on chromosome 3q22.3. *Nature Genetics*, **2009**, 41, 280-2 | 36.3 | 389 |
| 293 | Genome-wide haplotype association study identifies the SLC22A3-LPAL2-LPA gene cluster as a risk locus for coronary artery disease. *Nature Genetics*, **2009**, 41, 283-5 | 36.3 | 374 |
| 292 | Association analyses based on false discovery rate implicate new loci for coronary artery disease. *Nature Genetics*, **2017**, 49, 1385-1391 | 36.3 | 361 |
| 291 | Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. *Nature Genetics*, **2011**, 43, 1005-11 | 36.3 | 338 |
| 290 | New gene functions in megakaryopoiesis and platelet formation. *Nature*, **2011**, 480, 201-8 | 50.4 | 330 |
| 289 | Novel loci for adiponectin levels and their influence on type 2 diabetes and metabolic traits: a multi-ethnic meta-analysis of 45,891 individuals. *PLoS Genetics*, **2012**, 8, e1002607 | 6 | 326 |
| 288 | Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. *Science*, **2016**, 351, 1166-71 | 33.3 | 325 |
| 287 | Coding Variation in ANGPTL4, LPL, and SVEP1 and the Risk of Coronary Disease. *New England Journal of Medicine*, **2016**, 374, 1134-44 | 59.2 | 325 |
| 286 | Common variants at 10 genomic loci influence hemoglobin A(C) levels via glycemic and nonglycemic pathways. *Diabetes*, **2010**, 59, 3229-39 | 0.9 | 314 |

| | | | |
|---|---|---|---|
| 285 | Repeated replication and a prospective meta-analysis of the association between chromosome 9p21.3 and coronary artery disease. *Circulation*, **2008**, 117, 1675-84 | 16.7 | 312 |
| 284 | Inactivating mutations in NPC1L1 and protection from coronary heart disease. *New England Journal of Medicine*, **2014**, 371, 2072-82 | 59.2 | 307 |
| 283 | FTO genotype is associated with phenotypic variability of body mass index. *Nature*, **2012**, 490, 267-72 | 50.4 | 304 |
| 282 | Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. *Nature Communications*, **2016**, 7, 10023 | 17.4 | 295 |
| 281 | Genome-wide association identifies nine common variants associated with fasting proinsulin levels and provides new insights into the pathophysiology of type 2 diabetes. *Diabetes*, **2011**, 60, 2624-34 | 0.9 | 285 |
| 280 | Sex-stratified genome-wide association studies including 270,000 individuals show sexual dimorphism in genetic loci for anthropometric traits. *PLoS Genetics*, **2013**, 9, e1003500 | 6 | 277 |
| 279 | The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. *Nature Genetics*, **2016**, 48, 1171-1184 | 36.3 | 251 |
| 278 | Shared genetic susceptibility to ischemic stroke and coronary artery disease: a genome-wide analysis of common variants. *Stroke*, **2014**, 45, 24-36 | 6.7 | 245 |
| 277 | Genome-wide association study in Han Chinese identifies four new susceptibility loci for coronary artery disease. *Nature Genetics*, **2012**, 44, 890-4 | 36.3 | 243 |
| 276 | The impact of low-frequency and rare variants on lipid levels. *Nature Genetics*, **2015**, 47, 589-97 | 36.3 | 229 |
| 275 | A genome-wide association study identifies two loci associated with heart failure due to dilated cardiomyopathy. *European Heart Journal*, **2011**, 32, 1065-76 | 9.5 | 228 |
| 274 | ANGPTL3 Deficiency and Protection Against Coronary Artery Disease. *Journal of the American College of Cardiology*, **2017**, 69, 2054-2063 | 15.1 | 226 |
| 273 | A trans-acting locus regulates an anti-viral expression network and type 1 diabetes risk. *Nature*, **2010**, 467, 460-4 | 50.4 | 224 |
| 272 | Cigarette smoking reduces DNA methylation levels at multiple genomic loci but the effect is partially reversible upon cessation. *Epigenetics*, **2014**, 9, 1382-96 | 5.7 | 222 |
| 271 | The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. *PLoS Genetics*, **2015**, 11, e1005378 | 6 | 220 |
| 270 | Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. *Nature Genetics*, **2013**, 45, 621-31 | 36.3 | 219 |
| 269 | Dysfunctional nitric oxide signalling increases risk of myocardial infarction. *Nature*, **2013**, 504, 432-6 | 50.4 | 185 |
| 268 | Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. *Nature Genetics*, **2017**, 49, 1113-1119 | 36.3 | 184 |

| | | | |
|---|---|---|---|
| 267 | Systematic screening for mutations in the human serotonin-2A (5-HT2A) receptor gene: identification of two naturally occurring receptor variants and association analysis in schizophrenia. *Human Genetics*, **1996**, 97, 614-9 | 6.3 | 181 |
| 266 | Large-scale gene-centric analysis identifies novel variants for coronary artery disease. *PLoS Genetics* , **2011**, 7, e1002260 | 6 | 175 |
| 265 | Novel missense mutations (p.T596M and p.P1797H) in NOTCH1 in patients with bicuspid aortic valve. *Biochemical and Biophysical Research Communications*, **2006**, 345, 1460-5 | 3.4 | 168 |
| 264 | Genetic variants associated with cardiac structure and function: a meta-analysis and replication of genome-wide association data. *JAMA - Journal of the American Medical Association*, **2009**, 302, 168-78 | 27.4 | 164 |
| 263 | Mutation spectrum in a large cohort of unrelated consecutive patients with hypertrophic cardiomyopathy. *Clinical Genetics*, **2003**, 64, 339-49 | 4 | 162 |
| 262 | Genetically determined height and coronary artery disease. *New England Journal of Medicine*, **2015**, 372, 1608-18 | 59.2 | 152 |
| 261 | Genetic determinants of circulating sphingolipid concentrations in European populations. *PLoS Genetics*, **2009**, 5, e1000672 | 6 | 150 |
| 260 | Integrative genomics reveals novel molecular pathways and gene networks for coronary artery disease. *PLoS Genetics*, **2014**, 10, e1004502 | 6 | 147 |
| 259 | Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. *Journal of the American College of Cardiology*, **2017**, 69, 823-836 | 15.1 | 146 |
| 258 | Inheritance of coronary artery disease in men: an analysis of the role of the Y chromosome. *Lancet, The*, **2012**, 379, 915-922 | 40 | 145 |
| 257 | Abdominal aortic aneurysm is associated with a variant in low-density lipoprotein receptor-related protein 1. *American Journal of Human Genetics*, **2011**, 89, 619-27 | 11 | 145 |
| 256 | Nexilin mutations destabilize cardiac Z-disks and lead to dilated cardiomyopathy. *Nature Medicine*, **2009**, 15, 1281-8 | 50.5 | 142 |
| 255 | Distinct heritable patterns of angiographic coronary artery disease in families with myocardial infarction. *Circulation*, **2005**, 111, 855-62 | 16.7 | 138 |
| 254 | Design of the Coronary ARtery DIsease Genome-Wide Replication And Meta-Analysis (CARDIoGRAM) Study: A Genome-wide association meta-analysis involving more than 22 000 cases and 60 000 controls. *Circulation: Cardiovascular Genetics*, **2010**, 3, 475-83 | | 135 |
| 253 | Peroxisome proliferator--activated receptor alpha gene regulates left ventricular growth in response to exercise and hypertension. *Circulation*, **2002**, 105, 950-5 | 16.7 | 135 |
| 252 | A common polymorphism in KCNH2 (HERG) hastens cardiac repolarization. *Cardiovascular Research*, **2003**, 59, 27-36 | 9.9 | 133 |
| 251 | A genome-wide association study reveals variants in ARL15 that influence adiponectin levels. *PLoS Genetics*, **2009**, 5, e1000768 | 6 | 129 |
| 250 | CD163+ macrophages promote angiogenesis and vascular permeability accompanied by inflammation in atherosclerosis. *Journal of Clinical Investigation*, **2018**, 128, 1106-1124 | 15.9 | 126 |

| | | | |
|---|---|---|---|
| 249 | Genetic variation at chromosome 1p13.3 affects sortilin mRNA expression, cellular LDL-uptake and serum LDL levels which translates to the risk of coronary artery disease. *Atherosclerosis*, **2010**, 208, 183-9 | 3.1 | 123 |
| 248 | Common genetic loci influencing plasma homocysteine concentrations and their effect on risk of coronary artery disease. *American Journal of Clinical Nutrition*, **2013**, 98, 668-76 | 7 | 122 |
| 247 | A decade of genome-wide association studies for coronary artery disease: the challenges ahead. *Cardiovascular Research*, **2018**, 114, 1241-1257 | 9.9 | 121 |
| 246 | Novel mutations in sarcomeric protein genes in dilated cardiomyopathy. *Biochemical and Biophysical Research Communications*, **2002**, 298, 116-20 | 3.4 | 120 |
| 245 | Clinical and genetic association of serum paraoxonase and arylesterase activities with cardiovascular risk. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2012**, 32, 2803-12 | 9.4 | 119 |
| 244 | Lifelong reduction of LDL-cholesterol related to a common variant in the LDL-receptor gene decreases the risk of coronary artery disease--a Mendelian Randomisation study. *PLoS ONE*, **2008**, 3, e2986 | 3.7 | 117 |
| 243 | Genetic regulation of serum phytosterol levels and risk of coronary artery disease. *Circulation: Cardiovascular Genetics*, **2010**, 3, 331-9 | | 116 |
| 242 | Genetics and heritability of coronary artery disease and myocardial infarction. *Clinical Research in Cardiology*, **2007**, 96, 1-7 | 6.1 | 112 |
| 241 | A novel variant on chromosome 7q22.3 associated with mean platelet volume, counts, and function. *Blood*, **2009**, 113, 3831-7 | 2.2 | 109 |
| 240 | Multiethnic meta-analysis of genome-wide association studies in >100 000 subjects identifies 23 fibrinogen-associated Loci but no strong evidence of a causal association between circulating fibrinogen and cardiovascular disease. *Circulation*, **2013**, 128, 1310-24 | 16.7 | 107 |
| 239 | Integrating genome-wide genetic variations and monocyte expression data reveals trans-regulated gene modules in humans. *PLoS Genetics*, **2011**, 7, e1002367 | 6 | 99 |
| 238 | A genome-wide association study identifies LIPA as a susceptibility gene for coronary artery disease. *Circulation: Cardiovascular Genetics*, **2011**, 4, 403-12 | | 98 |
| 237 | Genetic variation of the 5-HT2A receptor and response to clozapine. *Lancet, The*, **1995**, 346, 908-9 | 40 | 97 |
| 236 | Spectrum of clinical phenotypes and gene variants in cardiac myosin-binding protein C mutation carriers with hypertrophic cardiomyopathy. *Journal of the American College of Cardiology*, **2001**, 38, 322-30 | 15.1 | 96 |
| 235 | Bradykinin B2BKR receptor polymorphism and left-ventricular growth response. *Lancet, The*, **2001**, 358, 1155-6 | 40 | 96 |
| 234 | Genetic association study identifies HSPB7 as a risk gene for idiopathic dilated cardiomyopathy. *PLoS Genetics*, **2010**, 6, e1001167 | 6 | 93 |
| 233 | A genome-wide association study for coronary artery disease identifies a novel susceptibility locus in the major histocompatibility complex. *Circulation: Cardiovascular Genetics*, **2012**, 5, 217-25 | | 92 |
| 232 | Genome-wide association study identifies a new locus for coronary artery disease on chromosome 10p11.23. *European Heart Journal*, **2011**, 32, 158-68 | 9.5 | 92 |

| | | | |
|---|---|---|---|
| 231 | Coronary heart disease-associated variation in TCF21 disrupts a miR-224 binding site and miRNA-mediated regulation. *PLoS Genetics*, **2014**, 10, e1004263 | 6 | 91 |
| 230 | Long-range DNA looping and gene expression analyses identify DEXI as an autoimmune disease candidate gene. *Human Molecular Genetics*, **2012**, 21, 322-33 | 5.6 | 91 |
| 229 | Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. *Journal of the American College of Cardiology*, **2019**, 73, 58-66 | 15.1 | 86 |
| 228 | ADAMTS-7 inhibits re-endothelialization of injured arteries and promotes vascular remodeling through cleavage of thrombospondin-1. *Circulation*, **2015**, 131, 1191-201 | 16.7 | 84 |
| 227 | Cardiometabolic effects of genetic upregulation of the interleukin 1 receptor antagonist: a Mendelian randomisation analysis. *Lancet Diabetes and Endocrinology,the*, **2015**, 3, 243-53 | 18.1 | 81 |
| 226 | Common polymorphisms influencing serum uric acid levels contribute to susceptibility to gout, but not to coronary artery disease. *PLoS ONE*, **2009**, 4, e7729 | 3.7 | 81 |
| 225 | Genome-wide association study and targeted metabolomics identifies sex-specific association of CPS1 with coronary artery disease. *Nature Communications*, **2016**, 7, 10558 | 17.4 | 79 |
| 224 | Association of angiotensin-converting enzyme 2 (ACE2) gene polymorphisms with parameters of left ventricular hypertrophy in men. Results of the MONICA Augsburg echocardiographic substudy. *Journal of Molecular Medicine*, **2006**, 84, 88-96 | 5.5 | 78 |
| 223 | Genetic linkage and association of the growth hormone secretagogue receptor (ghrelin receptor) gene in human obesity. *Diabetes*, **2005**, 54, 259-67 | 0.9 | 78 |
| 222 | Sex in basic research: concepts in the cardiovascular field. *Cardiovascular Research*, **2017**, 113, 711-724 | 9.9 | 77 |
| 221 | A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. *Science Translational Medicine*, **2016**, 8, 341ra76 | 17.5 | 77 |
| 220 | Coronary artery disease-associated locus on chromosome 9p21 and early markers of atherosclerosis. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2008**, 28, 1679-83 | 9.4 | 77 |
| 219 | Exome sequencing and directed clinical phenotyping diagnose cholesterol ester storage disease presenting as autosomal recessive hypercholesterolemia. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2013**, 33, 2909-14 | 9.4 | 76 |
| 218 | Genetics of myocardial infarction: a progress report. *European Heart Journal*, **2010**, 31, 918-25 | 9.5 | 76 |
| 217 | Common genetic variation in the 3MBCL11B gene desert is associated with carotid-femoral pulse wave velocity and excess cardiovascular disease risk: the AortaGen Consortium. *Circulation: Cardiovascular Genetics*, **2012**, 5, 81-90 | | 76 |
| 216 | Effect of the angiotensin II type 2-receptor gene (+1675 G/A) on left ventricular structure in humans. *Journal of the American College of Cardiology*, **2001**, 37, 175-82 | 15.1 | 76 |
| 215 | Lack of association between the Trp719Arg polymorphism in kinesin-like protein-6 and coronary artery disease in 19 case-control studies. *Journal of the American College of Cardiology*, **2010**, 56, 1552-63 | 15.1 | 75 |
| 214 | Association of the T8590C polymorphism of CYP4A11 with hypertension in the MONICA Augsburg echocardiographic substudy. *Hypertension*, **2005**, 46, 766-71 | 8.5 | 75 |

| | | | |
|---|---|---|---|
| 213 | The impact of newly identified loci on coronary heart disease, stroke and total mortality in the MORGAM prospective cohorts. *Genetic Epidemiology*, **2009**, 33, 237-46 | 2.6 | 73 |
| 212 | Circulating brain-derived neurotrophic factor concentrations and the risk of cardiovascular disease in the community. *Journal of the American Heart Association*, **2015**, 4, e001544 | 6 | 70 |
| 211 | The novel genetic variant predisposing to coronary artery disease in the region of the PSRC1 and CELSR2 genes on chromosome 1 associates with serum cholesterol. *Journal of Molecular Medicine*, **2008**, 86, 1233-41 | 5.5 | 69 |
| 210 | Novel mutation in the alpha-tropomyosin gene and transition from hypertrophic to hypocontractile dilated cardiomyopathy. *Circulation*, **2000**, 102, E112-6 | 16.7 | 66 |
| 209 | Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. *Journal of the American Heart Association*, **2017**, 6, | 6 | 65 |
| 208 | Genetic markers enhance coronary risk prediction in men: the MORGAM prospective cohorts. *PLoS ONE*, **2012**, 7, e40922 | 3.7 | 65 |
| 207 | Cystatin C and Cardiovascular Disease: A Mendelian Randomization Study. *Journal of the American College of Cardiology*, **2016**, 68, 934-45 | 15.1 | 65 |
| 206 | Prediction of Causal Candidate Genes in Coronary Artery Disease Loci. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2015**, 35, 2207-17 | 9.4 | 64 |
| 205 | Association of common polymorphisms in GLUT9 gene with gout but not with coronary artery disease in a large case-control study. *PLoS ONE*, **2008**, 3, e1948 | 3.7 | 64 |
| 204 | Identification of genetic variation in the human serotonin 1D beta receptor gene. *Biochemical and Biophysical Research Communications*, **1994**, 205, 1194-200 | 3.4 | 62 |
| 203 | Functional Characterization of the Coronary Artery Disease Risk Locus. *Circulation*, **2017**, 136, 476-489 | 16.7 | 61 |
| 202 | Genetic evidence for PLASMINOGEN as a shared genetic risk factor of coronary artery disease and periodontitis. *Circulation: Cardiovascular Genetics*, **2015**, 8, 159-67 | | 61 |
| 201 | Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. *American Journal of Human Genetics*, **2016**, 99, 40-55 | 11 | 61 |
| 200 | No association of interleukin-6 gene polymorphism (-174 G/C) with myocardial infarction or traditional cardiovascular risk factors. *International Journal of Cardiology*, **2004**, 97, 205-12 | 3.2 | 61 |
| 199 | Ahnak is critical for cardiac Ca(V)1.2 calcium channel function and its beta-adrenergic regulation. *FASEB Journal*, **2005**, 19, 1969-77 | 0.9 | 60 |
| 198 | Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. *PLoS Genetics*, **2015**, 11, e1005230 | 6 | 59 |
| 197 | White Blood Cells and Blood Pressure: A Mendelian Randomization Study. *Circulation*, **2020**, 141, 1307-1317 | 16.7 | 58 |
| 196 | Association of low-grade urinary albumin excretion with left ventricular hypertrophy in the general population: the MONICA/KORA Augsburg Echocardiographic Substudy. *Nephrology Dialysis Transplantation*, **2006**, 21, 2780-7 | 4.3 | 58 |

| | | | |
|---|---|---|---|
| 195 | Functional gene testing of the Glu298Asp polymorphism of the endothelial NO synthase. *Journal of Hypertension*, **2000**, 18, 1767-73 | 1.9 | 58 |
| 194 | Systematic screening for mutations in the promoter and the coding region of the 5-HT1A gene. *American Journal of Medical Genetics Part A*, **1995**, 60, 393-9 | | 57 |
| 193 | Investigation of the human serotonin 6 (5-HT6) receptor gene in bipolar affective disorder and schizophrenia **2000**, 96, 217-221 | | 56 |
| 192 | A genome-wide association study identifies nucleotide variants at SIGLEC5 and DEFA1A3 as risk loci for periodontitis. *Human Molecular Genetics*, **2017**, 26, 2577-2588 | 5.6 | 55 |
| 191 | New insights into the genetics of X-linked dystonia-parkinsonism (XDP, DYT3). *European Journal of Human Genetics*, **2015**, 23, 1334-40 | 5.3 | 55 |
| 190 | Transcript expression-aware annotation improves rare variant interpretation. *Nature*, **2020**, 581, 452-458 | 50.4 | 55 |
| 189 | Analysis of predicted loss-of-function variants in UK Biobank identifies variants protective for disease. *Nature Communications*, **2018**, 9, 1613 | 17.4 | 55 |
| 188 | How to include chromosome X in your genome-wide association study. *Genetic Epidemiology*, **2014**, 38, 97-103 | 2.6 | 55 |
| 187 | Epigenetics in health and disease: heralding the EWAS era. *Lancet, The*, **2014**, 383, 1952-4 | 40 | 55 |
| 186 | Systems Genetics Analysis of Genome-Wide Association Study Reveals Novel Associations Between Key Biological Processes and Coronary Artery Disease. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2015**, 35, 1712-22 | 9.4 | 55 |
| 185 | Genetic predisposition to higher blood pressure increases coronary artery disease risk. *Hypertension*, **2013**, 61, 995-1001 | 8.5 | 55 |
| 184 | Evaluating drug targets through human loss-of-function genetic variation. *Nature*, **2020**, 581, 459-464 | 50.4 | 53 |
| 183 | Phenotypic Consequences of a Genetic Predisposition to Enhanced Nitric Oxide Signaling. *Circulation*, **2018**, 137, 222-232 | 16.7 | 53 |
| 182 | 5-HT2A receptor and bipolar affective disorder: association studies in affected patients. *Neuroscience Letters*, **1997**, 224, 95-8 | 3.3 | 52 |
| 181 | Detection of four polymorphic sites in the human dopamine D1 receptor gene (DRD1). *Human Molecular Genetics*, **1994**, 3, 209 | 5.6 | 52 |
| 180 | A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease. *PLoS Genetics*, **2020**, 16, e1008629 | 6 | 49 |
| 179 | Meta-analysis of gene-level associations for rare variants based on single-variant statistics. *American Journal of Human Genetics*, **2013**, 93, 236-48 | 11 | 49 |
| 178 | An alternative splice variant in Abcc6, the gene causing dystrophic calcification, leads to protein deficiency in C3H/He mice. *Journal of Biological Chemistry*, **2008**, 283, 7608-15 | 5.4 | 49 |

| | | | |
|---|---|---|---|
| 177 | Systematic analysis of variants related to familial hypercholesterolemia in families with premature myocardial infarction. *European Journal of Human Genetics*, **2016**, 24, 191-7 | 5.3 | 48 |
| 176 | Genome-wide haplotype analysis of cis expression quantitative trait loci in monocytes. *PLoS Genetics*, **2013**, 9, e1003240 | 6 | 47 |
| 175 | Genetic analysis for a shared biological basis between migraine and coronary artery disease. *Neurology: Genetics*, **2015**, 1, e10 | 3.8 | 46 |
| 174 | Dissecting the roles of microRNAs in coronary heart disease via integrative genomic analyses. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2015**, 35, 1011-21 | 9.4 | 46 |
| 173 | Novel correlations between the genotype and the phenotype of hypertrophic and dilated cardiomyopathy: results from the German Competence Network Heart Failure. *European Journal of Heart Failure*, **2011**, 13, 1185-92 | 12.3 | 46 |
| 172 | Novel approach identifies SNPs in SLC2A10 and KCNK9 with evidence for parent-of-origin effect on body mass index. *PLoS Genetics*, **2014**, 10, e1004508 | 6 | 45 |
| 171 | Genetics of coronary artery disease and myocardial infarction--2013. *Current Cardiology Reports*, **2013**, 15, 368 | 4.2 | 43 |
| 170 | Aldosterone synthase (CYP11B2) -344 C/T polymorphism is associated with left ventricular structure in human arterial hypertension. *Journal of the American College of Cardiology*, **2001**, 37, 878-84 | 15.1 | 43 |
| 169 | Familial aggregation of left main coronary artery disease and future risk of coronary events in asymptomatic siblings of affected patients. *European Heart Journal*, **2007**, 28, 2432-7 | 9.5 | 41 |
| 168 | Association of a functional polymorphism in the CYP4A11 gene with systolic blood pressure in survivors of myocardial infarction. *Journal of Hypertension*, **2006**, 24, 1965-70 | 1.9 | 41 |
| 167 | Pyrophosphate Supplementation Prevents Chronic and Acute Calcification in ABCC6-Deficient Mice. *American Journal of Pathology*, **2017**, 187, 1258-1272 | 5.8 | 40 |
| 166 | Associations of autozygosity with a broad range of human phenotypes. *Nature Communications*, **2019**, 10, 4957 | 17.4 | 40 |
| 165 | Assessing the causal association of glycine with risk of cardio-metabolic diseases. *Nature Communications*, **2019**, 10, 1060 | 17.4 | 38 |
| 164 | Genome-wide association study of L-arginine and dimethylarginines reveals novel metabolic pathway for symmetric dimethylarginine. *Circulation: Cardiovascular Genetics*, **2014**, 7, 864-72 | | 38 |
| 163 | Psoriasis and cardiometabolic traits: modest association but distinct genetic architectures. *Journal of Investigative Dermatology*, **2015**, 135, 1283-1293 | 4.3 | 38 |
| 162 | Lack of association between the MEF2A gene and myocardial infarction. *Circulation*, **2008**, 117, 185-91 | 16.7 | 38 |
| 161 | Loss of Cardioprotective Effects at the Locus as a Result of Gene-Smoking Interactions. *Circulation*, **2017**, 135, 2336-2353 | 16.7 | 36 |
| 160 | Meta-analysis of genome-wide association studies of aggressive and chronic periodontitis identifies two novel risk loci. *European Journal of Human Genetics*, **2019**, 27, 102-113 | 5.3 | 36 |

| | | | |
|---|---|---|---|
| 159 | Identification of the BCAR1-CFDP1-TMEM170A locus as a determinant of carotid intima-media thickness and coronary artery disease risk. *Circulation: Cardiovascular Genetics*, **2012**, 5, 656-65 | | 35 |
| 158 | Evaluation of three polymorphisms in the promoter region of the angiotensin II type I receptor gene. *Journal of Hypertension*, **2000**, 18, 267-72 | 1.9 | 35 |
| 157 | Angiotensin II type 2 receptor gene polymorphism and cardiovascular phenotypes: the GLAECO and GLAOLD studies. *European Journal of Heart Failure*, **2002**, 4, 707-12 | 12.3 | 34 |
| 156 | Expression quantitative trait Loci acting across multiple tissues are enriched in inherited risk for coronary artery disease. *Circulation: Cardiovascular Genetics*, **2015**, 8, 305-15 | | 33 |
| 155 | Epistatic interaction between haplotypes of the ghrelin ligand and receptor genes influence susceptibility to myocardial infarction and coronary artery disease. *Human Molecular Genetics*, **2007** , 16, 887-99 | 5.6 | 33 |
| 154 | Myeloid CD34+CD13+ precursor cells transdifferentiate into chondrocyte-like cells in atherosclerotic intimal calcification. *American Journal of Pathology*, **2010**, 177, 473-80 | 5.8 | 32 |
| 153 | Network analysis of coronary artery disease risk genes elucidates disease mechanisms and druggable targets. *Scientific Reports*, **2018**, 8, 3434 | 4.9 | 31 |
| 152 | Macrophage cholesterol efflux correlates with lipoprotein subclass distribution and risk of obstructive coronary artery disease in patients undergoing coronary angiography. *Lipids in Health and Disease*, **2009**, 8, 14 | 4.4 | 31 |
| 151 | RANTES/CCL5 and risk for coronary events: results from the MONICA/KORA Augsburg case-cohort, Athero-Express and CARDIoGRAM studies. *PLoS ONE*, **2011**, 6, e25734 | 3.7 | 31 |
| 150 | Rare Protein-Truncating Variants in APOB, Lower Low-Density Lipoprotein Cholesterol, and Protection Against Coronary Heart Disease. *Circulation Genomic and Precision Medicine*, **2019**, 12, e002376 | 5.2 | 30 |
| 149 | Intronic ANG II type 2 receptor gene polymorphism 1675 G/A modulates receptor protein expression but not mRNA splicing. *American Journal of Physiology - Regulatory Integrative and Comparative Physiology*, **2005**, 289, R1729-35 | 3.2 | 30 |
| 148 | Powerful identification of cis-regulatory SNPs in human primary monocytes using allele-specific gene expression. *PLoS ONE*, **2012**, 7, e52260 | 3.7 | 30 |
| 147 | SPG7 variant escapes phosphorylation-regulated processing by AFG3L2, elevates mitochondrial ROS, and is associated with multiple clinical phenotypes. *Cell Reports*, **2014**, 7, 834-47 | 10.6 | 29 |
| 146 | Characterization of the GNAQ promoter and association of increased Gq expression with cardiac hypertrophy in humans. *European Heart Journal*, **2008**, 29, 888-97 | 9.5 | 28 |
| 145 | Genetic variation in the arachidonate 5-lipoxygenase-activating protein (ALOX5AP) is associated with myocardial infarction in the German population. *Clinical Science*, **2008**, 115, 309-15 | 6.5 | 27 |
| 144 | Retrospective study of the parental origin of the extra chromosome in trisomy 18 (Edwards syndrome). *Human Genetics*, **1993**, 92, 347-9 | 6.3 | 26 |
| 143 | Runs of Homozygosity: Association with Coronary Artery Disease and Gene Expression in Monocytes and Macrophages. *American Journal of Human Genetics*, **2015**, 97, 228-37 | 11 | 25 |
| 142 | Polymorphisms in the promoter region of the dimethylarginine dimethylaminohydrolase 2 gene are associated with prevalence of hypertension. *Pharmacological Research*, **2009**, 60, 488-93 | 10.2 | 25 |

| | | | |
|---|---|---|---|
| 141 | KCNJ11 polymorphisms and sudden cardiac death in patients with acute myocardial infarction. *Journal of Molecular and Cellular Cardiology*, **2004**, 36, 287-93 | 5.8 | 25 |
| 140 | Serum microRNA-1233 is a specific biomarker for diagnosing acute pulmonary embolism. *Journal of Translational Medicine*, **2016**, 14, 120 | 8.5 | 24 |
| 139 | Genome-wide meta-analysis of common variant differences between men and women. *Human Molecular Genetics*, **2012**, 21, 4805-15 | 5.6 | 24 |
| 138 | Genetic causes of myocardial infarction: new insights from genome-wide association studies. *Deutsches Ärzteblatt International*, **2010**, 107, 694-9 | 2.5 | 24 |
| 137 | SNPtoGO: characterizing SNPs by enriched GO terms. *Bioinformatics*, **2008**, 24, 146-8 | 7.2 | 24 |
| 136 | Association of the Ghrelin receptor gene region with left ventricular hypertrophy in the general population: results of the MONICA/KORA Augsburg Echocardiographic Substudy. *Hypertension*, **2006**, 47, 920-7 | 8.5 | 24 |
| 135 | Ultrafine mapping of Dyscalc1 to an 80-kb chromosomal segment on chromosome 7 in mice susceptible for dystrophic calcification. *Physiological Genomics*, **2007**, 28, 203-12 | 3.6 | 24 |
| 134 | The power of genetic diversity in genome-wide association studies of lipids. *Nature*, **2021**, | 50.4 | 24 |
| 133 | Genetic variants primarily associated with type 2 diabetes are related to coronary artery disease risk. *Atherosclerosis*, **2015**, 241, 419-26 | 3.1 | 23 |
| 132 | Lymphotoxin-alpha and galectin-2 SNPs are not associated with myocardial infarction in two different German populations. *Journal of Molecular Medicine*, **2007**, 85, 997-1004 | 5.5 | 23 |
| 131 | The ABO blood group locus and a chromosome 3 gene cluster associate with SARS-CoV-2 respiratory failure in an Italian-Spanish genome-wide association analysis | | 23 |
| 130 | Genome-wide association study in takotsubo syndrome - Preliminary results and future directions. *International Journal of Cardiology*, **2017**, 236, 335-339 | 3.2 | 22 |
| 129 | Role of sGC-dependent NO signalling and myocardial infarction risk. *Journal of Molecular Medicine*, **2015**, 93, 383-94 | 5.5 | 22 |
| 128 | Human 5-HT5A receptor gene: systematic screening for DNA sequence variation and linkage mapping on chromosome 7q34-q36 using a polymorphism in the 5Ṁntranslated region. *Biochemical and Biophysical Research Communications*, **1997**, 233, 6-9 | 3.4 | 22 |
| 127 | The common Y402H variant in complement factor H gene is not associated with susceptibility to myocardial infarction and its related risk factors. *Clinical Science*, **2007**, 113, 213-8 | 6.5 | 22 |
| 126 | Novel genetic approach to investigate the role of plasma secretory phospholipase A2 (sPLA2)-V isoenzyme in coronary heart disease: modified Mendelian randomization analysis using PLA2G5 expression levels. *Circulation: Cardiovascular Genetics*, **2014**, 7, 144-50 | | 21 |
| 125 | Functional interaction of osteogenic transcription factors Runx2 and Vdr in transcriptional regulation of Opn during soft tissue calcification. *American Journal of Pathology*, **2013**, 183, 60-8 | 5.8 | 21 |
| 124 | Heterozygous Gene Deficiency and Risk of Coronary Artery Disease. *Circulation Genomic and Precision Medicine*, **2020**, 13, 417-423 | 5.2 | 21 |

| | | | |
|---|---|---|---|
| 123 | LDL triglycerides, hepatic lipase activity, and coronary artery disease: An epidemiologic and Mendelian randomization study. *Atherosclerosis*, **2019**, 282, 37-44 | 3.1 | 20 |
| 122 | Genetically modulated educational attainment and coronary disease risk. *European Heart Journal*, **2019**, 40, 2413-2420 | 9.5 | 20 |
| 121 | Association between arterial pressure and coronary artery calcification. *Journal of Hypertension*, **2007**, 25, 1731-8 | 1.9 | 19 |
| 120 | Angiotensin converting enzyme gene polymorphism and myocardial infarction a large association and linkage study. *International Journal of Biochemistry and Cell Biology*, **2003**, 35, 955-62 | 5.6 | 19 |
| 119 | Association of NOS3 gene polymorphisms with essential hypertension in Sudanese patients: a case control study. *BMC Medical Genetics*, **2017**, 18, 128 | 2.1 | 18 |
| 118 | No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. *Scientific Reports*, **2016**, 6, 35278 | 4.9 | 18 |
| 117 | Ultrahigh-resolution, high-speed spectral domain optical coherence phase microscopy. *Optics Letters*, **2014**, 39, 45-7 | 3 | 18 |
| 116 | Whole-exome sequencing in an extended family with myocardial infarction unmasks familial hypercholesterolemia. *BMC Cardiovascular Disorders*, **2014**, 14, 108 | 2.3 | 18 |
| 115 | Coronary artery disease associated gene Phactr1 modulates severity of vascular calcification in vitro. *Biochemical and Biophysical Research Communications*, **2017**, 491, 396-402 | 3.4 | 18 |
| 114 | Genome-wide and gene-centric analyses of circulating myeloperoxidase levels in the charge and care consortia. *Human Molecular Genetics*, **2013**, 22, 3381-93 | 5.6 | 18 |
| 113 | Screening the human bradykinin B2 receptor gene in patients with cardiovascular diseases: Identification of a functional mutation in the promoter and a new coding variant (T21M). *American Journal of Medical Genetics Part A*, **1998**, 80, 521-525 | | 18 |
| 112 | Knock-out of nexilin in mice leads to dilated cardiomyopathy and endomyocardial fibroelastosis. *Basic Research in Cardiology*, **2016**, 111, 6 | 11.8 | 17 |
| 111 | Relation of the G protein beta3-subunit polymorphism with left ventricle structure and function. *Hypertension*, **2002**, 40, 162-7 | 8.5 | 17 |
| 110 | Novel intronic polymorphism (+1675G/A) in the human angiotensin II subtype 2 receptor gene. *Human Mutation*, **2000**, 15, 487 | 4.7 | 17 |
| 109 | Lack of genetically determined structural variants of the human serotonin-1E (5-HT1E) receptor protein points to its evolutionary conservation. *Molecular Brain Research*, **1995**, 29, 387-90 | | 17 |
| 108 | Genome-wide association meta-analysis of coronary artery disease and periodontitis reveals a novel shared risk locus. *Scientific Reports*, **2018**, 8, 13678 | 4.9 | 17 |
| 107 | Genome-Wide Association and Functional Studies Identify and as Novel Susceptibility Genes for Coronary Artery Disease. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2018**, 38, 964-975 | 9.4 | 15 |
| 106 | Stimulators of the soluble guanylyl cyclase: promising functional insights from rare coding atherosclerosis-related GUCY1A3 variants. *Basic Research in Cardiology*, **2016**, 111, 51 | 11.8 | 15 |

| | | | |
|---|---|---|---|
| 105 | APOE alleles are not associated with calcific aortic stenosis. *Heart*, **2006**, 92, 1463-6 | 5.1 | 15 |
| 104 | Genetic variants in the promoter (g983G>T) and coding region (A92T) of the human cardiotrophin-1 gene (CTF1) in patients with dilated cardiomyopathy. *Human Mutation*, **2000**, 16, 448 | 4.7 | 15 |
| 103 | Systematic screening for mutations in the human serotonin 1F receptor gene in patients with bipolar affective disorder and schizophrenia. *American Journal of Medical Genetics Part A*, **1996**, 67, 225-8 | | 15 |
| 102 | Additional Candidate Genes for Human Atherosclerotic Disease Identified Through Annotation Based on Chromatin Organization. *Circulation: Cardiovascular Genetics*, **2017**, 10, | | 14 |
| 101 | Proatherosclerotic Effect of the 1-Subunit of Soluble Guanylyl Cyclase by Promoting Smooth Muscle Phenotypic Switching. *American Journal of Pathology*, **2016**, 186, 2220-2231 | 5.8 | 14 |
| 100 | Reversal of Aging-Induced Increases in Aortic Stiffness by Targeting Cytoskeletal Protein-Protein Interfaces. *Journal of the American Heart Association*, **2018**, 7, | 6 | 14 |
| 99 | Genome-wide association analysis in dilated cardiomyopathy reveals two new players in systolic heart failure on chromosomes 3p25.1 and 22q11.23. *European Heart Journal*, **2021**, 42, 2000-2011 | 9.5 | 14 |
| 98 | Common and Rare Genetic Variation in CCR2, CCR5, or CX3CR1 and Risk of Atherosclerotic Coronary Heart Disease and Glucometabolic Traits. *Circulation: Cardiovascular Genetics*, **2016**, 9, 250-8 | | 14 |
| 97 | Association between PPARalpha gene polymorphisms and myocardial infarction. *Clinical Science*, **2008**, 115, 301-8 | 6.5 | 13 |
| 96 | Arterial calcification in mice after freeze-thaw injury. *Annals of Anatomy*, **2006**, 188, 235-42 | 2.9 | 12 |
| 95 | Binding properties of the naturally occurring human 5-HT1A receptor variant with the Ile28Val substitution in the extracellular domain. *Naunyn-Schmiedeberg's Archives of Pharmacology*, **1995**, 352, 455-8 | 3.4 | 12 |
| 94 | DNA Sequence Variation in Encoding the Activin Receptor-Like Kinase 7 Influences Body Fat Distribution and Protects Against Type 2 Diabetes. *Diabetes*, **2019**, 68, 226-234 | 0.9 | 12 |
| 93 | Druggability of Coronary Artery Disease Risk Loci. *Circulation Genomic and Precision Medicine*, **2018**, 11, e001977 | 5.2 | 12 |
| 92 | Lack of association between a common polymorphism near the INSIG2 gene and BMI, myocardial infarction, and cardiovascular risk factors. *Obesity*, **2009**, 17, 1390-5 | 8 | 11 |
| 91 | Robust association of the APOE epsilon4 allele with premature myocardial infarction especially in patients without hypercholesterolaemia: the Aachen study. *European Journal of Clinical Investigation*, **2007**, 37, 106-8 | 4.6 | 11 |
| 90 | No association of the CYP3A5*1 allele with blood pressure and left ventricular mass and geometry: the KORA/MONICA Augsburg echocardiographic substudy. *Clinical Science*, **2006**, 111, 365-72 | 6.5 | 11 |
| 89 | Association of Genetic Variation at Locus with Vascular Depression. *Biomolecules*, **2018**, 8, | 5.9 | 11 |
| 88 | Genetic Susceptibility Loci for Cardiovascular Disease and Their Impact on Atherosclerotic Plaques. *Circulation Genomic and Precision Medicine*, **2018**, 11, e002115 | 5.2 | 11 |

| | | | |
|---|---|---|---|
| 87 | Etidronate prevents dystrophic cardiac calcification by inhibiting macrophage aggregation. *Scientific Reports*, **2018**, 8, 5812 | 4.9 | 10 |
| 86 | A genomic exploration identifies mechanisms that may explain adverse cardiovascular effects of COX-2 inhibitors. *Scientific Reports*, **2017**, 7, 10252 | 4.9 | 10 |
| 85 | Molecular variants of soluble guanylyl cyclase affecting cardiovascular risk. *Circulation Journal*, **2015**, 79, 463-9 | 2.9 | 10 |
| 84 | Cloning and characterization of the 5′flanking region of the human cardiotrophin-1 gene. *Biochemical and Biophysical Research Communications*, **1998**, 244, 494-7 | 3.4 | 10 |
| 83 | Association of the coronary artery disease risk gene GUCY1A3 with ischaemic events after coronary intervention. *Cardiovascular Research*, **2019**, 115, 1512-1518 | 9.9 | 9 |
| 82 | The assertion that a G21V mutation in AGTR2 causes mental retardation is not supported by other studies. *Human Genetics*, **2004**, 114, 396; author reply 397 | 6.3 | 9 |
| 81 | Lack of association of a 9 bp insertion/deletion polymorphism within the bradykinin 2 receptor gene with myocardial infarction. *Clinical Science*, **2004**, 107, 505-11 | 6.5 | 9 |
| 80 | Population Bias in Polygenic Risk Prediction Models for Coronary Artery Disease. *Circulation Genomic and Precision Medicine*, **2020**, 13, e002932 | 5.2 | 9 |
| 79 | Rheumatoid Arthritis and Coronary Artery Disease: Genetic Analyses Do Not Support a Causal Relation. *Journal of Rheumatology*, **2017**, 44, 4-10 | 4.1 | 8 |
| 78 | A locus on chromosome 10 influences C-reactive protein levels in two independent populations. *Human Genetics*, **2007**, 122, 95-102 | 6.3 | 8 |
| 77 | Comprehensive exploration of the effects of miRNA SNPs on monocyte gene expression. *PLoS ONE*, **2012**, 7, e45863 | 3.7 | 8 |
| 76 | A familial congenital heart disease with a possible multigenic origin involving a mutation in BMPR1A. *Scientific Reports*, **2019**, 9, 2959 | 4.9 | 7 |
| 75 | Shared genetic aetiology of coronary artery disease and atherosclerotic stroke - 2015. *Current Atherosclerosis Reports*, **2015**, 17, 498 | 6 | 7 |
| 74 | Two polymorphisms in the Cx40 promoter are associated with hypertension and left ventricular hypertrophy preferentially in men. *Clinical and Experimental Hypertension*, **2015**, 37, 580-6 | 2.2 | 7 |
| 73 | Genetic variants associated with celiac disease and the risk for coronary artery disease. *Molecular Genetics and Genomics*, **2015**, 290, 1911-7 | 3.1 | 7 |
| 72 | Lack of association between polymorphisms of angiotensin II receptor genes and response to short-term angiotensin II infusion. *Journal of Hypertension*, **2000**, 18, 1573-8 | 1.9 | 7 |
| 71 | Systematic screening for mutations in the human serotonin-2A (5-HT2A) receptor gene: Identification of two naturally occurring receptor variants and association analysis in schizophrenia **1996**, 97, 614 | | 7 |
| 70 | Qtlizer: comprehensive QTL annotation of GWAS results. *Scientific Reports*, **2020**, 10, 20417 | 4.9 | 7 |

| | | | |
|---|---|---|---|
| 69 | Increased Serum Levels of Asymmetric Dimethylarginine and Symmetric Dimethylarginine and Decreased Levels of Arginine in Sudanese Patients with Essential Hypertension. *Kidney and Blood Pressure Research*, **2020**, 45, 727-736 | 3.1 | 6 |
| 68 | Dare to Compare. Development of Atherosclerotic Lesions in Human, Mouse, and Zebrafish. *Frontiers in Cardiovascular Medicine*, **2020**, 7, 109 | 5.4 | 6 |
| 67 | Five novel genetic variants in the promoter and coding region of the alpha B-crystallin gene (CRYAB): -652G>A, -650C>G, -249G>C, S41Y, P51L. *Human Mutation*, **2000**, 16, 374 | 4.7 | 6 |
| 66 | Cis-epistasis at the LPA locus and risk of cardiovascular diseases. *Cardiovascular Research*, **2021**, | 9.9 | 6 |
| 65 | Coronary Artery Ectasia Are Frequently Observed in Patients With Bicuspid Aortic Valves With and Without Dilatation of the Ascending Aorta. *Circulation: Cardiovascular Interventions*, **2016**, 9, | 6 | 6 |
| 64 | miR-128a Acts as a Regulator in Cardiac Development by Modulating Differentiation of Cardiac Progenitor Cell Populations. *International Journal of Molecular Sciences*, **2020**, 21, | 6.3 | 5 |
| 63 | Classification of ADAMTS binding sites: The first step toward selective ADAMTS7 inhibitors. *Biochemical and Biophysical Research Communications*, **2016**, 471, 380-5 | 3.4 | 5 |
| 62 | Forty-five years to diagnosis. *Neuromuscular Disorders*, **2013**, 23, 503-5 | 2.9 | 5 |
| 61 | Identification of a single SNP that affects the promoter activity in the Moroccan prolific DMman breed. *Journal of Animal Science*, **2015**, 93, 2064-73 | 0.7 | 5 |
| 60 | Single nucleotide polymorphisms with cis-regulatory effects on long non-coding transcripts in human primary monocytes. *PLoS ONE*, **2014**, 9, e102612 | 3.7 | 5 |
| 59 | A proteomic atlas of the neointima identifies novel druggable targets for preventive therapy. *European Heart Journal*, **2021**, 42, 1773-1785 | 9.5 | 5 |
| 58 | Discovery and systematic characterization of risk variants and genes for coronary artery disease in over a million participants | | 5 |
| 57 | Genetics of coronary artery disease: Short people at risk?. *Expert Review of Cardiovascular Therapy*, **2015**, 13, 1169-72 | 2.5 | 4 |
| 56 | CYP17A1 deficient XY mice display susceptibility to atherosclerosis, altered lipidomic profile and atypical sex development. *Scientific Reports*, **2020**, 10, 8792 | 4.9 | 4 |
| 55 | Utilization of Mental Health Care, Treatment Patterns, and Course of Psychosocial Functioning in Northern German Coronary Artery Disease Patients with Depressive and/or Anxiety Disorders. *Frontiers in Psychiatry*, **2018**, 9, 75 | 5 | 4 |
| 54 | Differentiation of human iPSCs into VSMCs and generation of VSMC-derived calcifying vascular cells. *Stem Cell Research*, **2018**, 31, 62-70 | 1.6 | 4 |
| 53 | Assignment of the human serotonin 1F receptor gene (HTR1F) to the short arm of chromosome 3 (3p13-p14.1). *Molecular Membrane Biology*, **1997**, 14, 133-5 | 3.4 | 4 |
| 52 | Molecular signatures of cardiovascular disease risk: potential for test development and clinical application. *Molecular Diagnosis and Therapy*, **2008**, 12, 281-7 | 4.5 | 4 |

| | | | |
|---|---|---|---|
| 51 | Lack of association of genetic variants in the LRP8 gene with familial and sporadic myocardial infarction. *Journal of Molecular Medicine*, **2008**, 86, 1163-70 | 5.5 | 4 |
| 50 | Genetic factors for overweight and CAD. *Herz*, **2006**, 31, 189-99 | 2.6 | 4 |
| 49 | A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease | | 4 |
| 48 | Long-term prevention after myocardial infarction in young patients ≤45 years: the Intensive Prevention Program in the Young (IPP-Y) study. *European Journal of Preventive Cardiology*, **2020**, 27, 2264-2266 | 3.9 | 4 |
| 47 | Studies in Zebrafish Demonstrate That and Are Most Likely the Causal Genes at the Blood Pressure-Associated Locus on Human Chromosome 10q24.32. *Frontiers in Cardiovascular Medicine*, **2020**, 7, 135 | 5.4 | 4 |
| 46 | The C5a/C5a receptor 1 axis controls tissue neovascularization through CXCL4 release from platelets. *Nature Communications*, **2021**, 12, 3352 | 17.4 | 4 |
| 45 | New technologies for intensive prevention programs after myocardial infarction: rationale and design of the NET-IPP trial. *Clinical Research in Cardiology*, **2021**, 110, 153-161 | 6.1 | 4 |
| 44 | CARDIoGRAM celebrates its 10th Anniversary. *European Heart Journal*, **2019**, 40, 1664-1666 | 9.5 | 3 |
| 43 | Genetics of educational attainment and coronary risk in Mendelian randomization studies. *European Heart Journal*, **2020**, 41, 894-895 | 9.5 | 3 |
| 42 | Quantitative analysis of cardiomyocyte dynamics with optical coherence phase microscopy **2012**, | | 3 |
| 41 | Genomic correlates of glatiramer acetate adverse cardiovascular effects lead to a novel locus mediating coronary risk. *PLoS ONE*, **2017**, 12, e0182999 | 3.7 | 3 |
| 40 | Qtlizer: comprehensive QTL annotation of GWAS results | | 3 |
| 39 | Identification of two novel bullous pemphigoid- associated alleles, HLA-DQA1*05:05 and -DRB1*07:01, in Germans. *Orphanet Journal of Rare Diseases*, **2021**, 16, 228 | 4.2 | 3 |
| 38 | Mental Health and Psychosocial Functioning Over the Lifespan of German Patients Undergoing Cardiac Catheterization for Coronary Artery Disease. *Frontiers in Psychiatry*, **2018**, 9, 338 | 5 | 3 |
| 37 | Transcriptome-wide association study of coronary artery disease identifies novel susceptibility genes.. *Basic Research in Cardiology*, **2022**, 117, 6 | 11.8 | 3 |
| 36 | Mendelian randomization analysis does not support causal associations of birth weight with hypertension risk and blood pressure in adulthood. *European Journal of Epidemiology*, **2020**, 35, 685-697 | 12.1 | 2 |
| 35 | Genetic basis of myocardial infarction: Novel insights from genome-wide association studies. *Current Cardiovascular Risk Reports*, **2009**, 3, 426-433 | 0.9 | 2 |
| 34 | Impact of diabetes on QT dynamicity in patients with and without myocardial infarction: The KORA Family Heart Study. *PACE - Pacing and Clinical Electrophysiology*, **2007**, 30 Suppl 1, S183-7 | 1.6 | 2 |

| | | | |
|---|---|---|---|
| 33 | Mutation in the beta amyloid precursor protein gene and schizophrenia. *Biological Psychiatry*, **1993**, 34, 502 | 7.9 | 2 |
| 32 | Osteoclast imbalance in primary familial brain calcification: evidence for its role in brain calcification. *Brain*, **2020**, 143, e1 | 11.2 | 2 |
| 31 | Induced Pluripotent Stem Cells (iPSCs) in Vascular Research: from Two- to Three-Dimensional Organoids. *Stem Cell Reviews and Reports*, **2021**, 17, 1741-1753 | 7.3 | 2 |
| 30 | Polymorphisms in the Mitochondrial Genome Are Associated With Bullous Pemphigoid in Germans. *Frontiers in Immunology*, **2019**, 10, 2200 | 8.4 | 2 |
| 29 | Lp-PLA2, scavenger receptor class B type I gene (SCARB1) rs10846744 variant, and cardiovascular disease. *PLoS ONE*, **2018**, 13, e0204352 | 3.7 | 2 |
| 28 | Sharing lessons learnt across European cardiovascular research consortia. *Drug Discovery Today*, **2020**, 25, 787-792 | 8.8 | 1 |
| 27 | Functional evaluation of GUCY1A3 mutations associated with myocardial infarction risk. *BMC Pharmacology & Toxicology*, **2015**, 16, | 2.6 | 1 |
| 26 | Well kept secrets of the genome. *European Heart Journal*, **2003**, 24, 501-3 | 9.5 | 1 |
| 25 | Outcome of clinical versus genetic family screening in hypertrophic cardiomyopathy with focus on cardiac beta-myosin gene mutations: prediction of clinical status--is molecular genetics a new tool for the management of hypertrophic cardiomyopathy in clinical practice?. *Cardiovascular Research*, **2003**, 57, 298-301 | 9.9 | 1 |
| 24 | Heterozygous ATP-binding Cassette Transporter G5 Gene Deficiency and Risk of Coronary Artery Disease | | 1 |
| 23 | Cis-epistasis at the LPA locus and risk of coronary artery disease | | 1 |
| 22 | Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. *Circulation Genomic and Precision Medicine*, **2020**, 13, e002769 | 5.2 | 1 |
| 21 | sGC Activity and Regulation of Blood Flow in a Zebrafish Model System. *Frontiers in Physiology*, **2021**, 12, 633171 | 4.6 | 1 |
| 20 | Identification of a Functional Variant at the Chromosome 4q27 Coronary Artery Disease Locus in an Extended Myocardial Infarction Family. *Circulation*, **2021**, 144, 662-665 | 16.7 | 1 |
| 19 | Erbliche Grundlagen der KHK. *CardioVasc*, **2012**, 12, 56-60 | 0 | 0 |
| 18 | Current Developments of Clinical Sequencing and the Clinical Utility of Polygenic Risk Scores in Inflammatory Diseases. *Frontiers in Immunology*, **2020**, 11, 577677 | 8.4 | 0 |
| 17 | What can we learn from common variants associated with unexpected phenotypes in rare genetic diseases?. *Orphanet Journal of Rare Diseases*, **2021**, 16, 41 | 4.2 | 0 |
| 16 | Identification of a novel ovine LH-beta promoter region, which dramatically enhances its promoter activity. *SpringerPlus*, **2015**, 4, 466 | | |

| | | |
|---|---|---|
| 15 | Retraction notice to "Differentiation of human iPSCs into VSMCs and generation of VSMC-derived calcifying vascular cells" [Stem Cell Res. 31 (2018) 62-70]. *Stem Cell Research*, **2020**, 45, 101830 | 1.6 |
| 14 | Tippfehler im Genom: erbliche Ursachen von Herzerkrankungen. *BioSpektrum*, **2013**, 19, 642-644 | 0.1 |
| 13 | Genetik des Herzinfarktes. Der lange Weg von der positiven Familienanamnese zum Gen. *Chemie in Unserer Zeit*, **2009**, 43, 288-295 | 0.2 |
| 12 | Genetik der koronaren Herzkrankheit und des Herzinfarkts. *Medizinische Genetik*, **2007**, 19, 316-320 | 0.5 |
| 11 | Identification of genetic variants (g789C>T and G111S) in the human HSPB2 gene. *Human Mutation*, **2001**, 17, 81 | 4.7 |
| 10 | Common polymorphisms in the cannabinoid CB2 receptor gene (CNR2) are not associated with myocardial infarction and cardiovascular risk factors. *International Journal of Molecular Medicine*, **1998**, 22, 165 | 4.4 |
| 9 | Dinucleotide repeat polymorphism at the D18S99 locus. *Human Molecular Genetics*, **1993**, 2, 91 | 5.6 |
| 8 | Dinucleotide repeat polymorphism at the D18S365 locus. *Human Molecular Genetics*, **1993**, 2, 1747 | 5.6 |
| 7 | The Genetics of Coronary Heart Disease. *Cardiac and Vascular Biology*, **2019**, 141-168 | 0.2 |
| 6 | Genetics of (Premature) Coronary Artery Disease **2020**, 413-430 | |
| 5 | Genetics of (Premature) Coronary Artery Disease **2016**, 355-371 | |
| 4 | Genetics of (Premature) Coronary Artery Disease **2011**, 369-383 | |
| 3 | SNPboost: Interaction Analysis and Risk Prediction on GWA Data. *Lecture Notes in Computer Science*, **2011**, 111-118 | 0.9 |
| 2 | The CAD risk locus 9p21 increases the risk of vascular calcification in an iPSC-derived VSMC model. *Stem Cell Research and Therapy*, **2021**, 12, 166 | 8.3 |
| 1 | A1268 Association of Serum Levels of Asymmetric Dimethylarginine with Essential Hypertension in Sudanese Patients. *Journal of Hypertension*, **2018**, 36, e9-e10 | 1.9 |