Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 30, 2024

National Genome Research Network

RRID:SCR_006626
Type: Tool

Proper Citation

National Genome Research Network (RRID:SCR_006626)

Resource Information

URL: http://www.ngfn.de/en/start.html

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Description: The program of medical genome research is a large-scale biomedical research project which extends the national genome research net (NGFN) and will be funded by the federal ministry of education and research (BMBF) from 2008-2013. Currently the program includes two fields: * Research ** NGFN-Plus: With the aim on combating diseases that are central to health policy, several hundred researchers are systematically investigating the complex molecular interactions of the human body. They are organized in 26 Integrated Genome Research Networks. * Application ** NGFN-Transfer: The rapid transfer of results from medical genome research into medical and industrial application is the aim of the scientists from research institutes and biomedical enterprises that cooperate in eight Innovation Alliances. AREAS OF DISEASE * Cardiovascular disease * Cancer * Neuronal diseases * Infections and Inflammations * Environmental factors

Abbreviations: NGFN

Synonyms: NGFN - National Genome Research Network, German National Genome Research Network

Resource Type: organization portal, portal, data or information resource

Keywords: genome, research, gene, disease

Related Condition: Cardiovascular disease, Cancer, Neuronal disease, Infectious disease, Inflammation, Disease linked to environment

Funding Agency: BMBF

Resource Name: National Genome Research Network

Resource ID: SCR_006626

Alternate IDs: nlx_151595

Ratings and Alerts

No rating or validation information has been found for National Genome Research Network.

No alerts have been found for National Genome Research Network.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 26 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Ellinghaus E, et al. (2017) Genome-wide association analysis for chronic venous disease identifies EFEMP1 and KCNH8 as susceptibility loci. Scientific reports, 7, 45652.

Cleynen I, et al. (2016) Inherited determinants of Crohn's disease and ulcerative colitis phenotypes: a genetic association study. Lancet (London, England), 387(10014), 156.

Yuan H, et al. (2016) A Novel Genetic Variant in Long Non-coding RNA Gene NEXN-AS1 is Associated with Risk of Lung Cancer. Scientific reports, 6, 34234.

Schedel M, et al. (2016) 1,25D3 prevents CD8(+)Tc2 skewing and asthma development through VDR binding changes to the Cyp11a1 promoter. Nature communications, 7, 10213.

Betz RC, et al. (2015) Genome-wide meta-analysis in alopecia areata resolves HLA associations and reveals two new susceptibility loci. Nature communications, 6, 5966.

Witt SH, et al. (2014) Investigation of manic and euthymic episodes identifies state- and trait-specific gene expression and STAB1 as a new candidate gene for bipolar disorder. Translational psychiatry, 4(8), e426.

, et al. (2014) Genetic determinants of common epilepsies: a meta-analysis of genome-wide association studies. The Lancet. Neurology, 13(9), 893.

Gewies A, et al. (2013) Prdm6 is essential for cardiovascular development in vivo. PloS one, 8(11), e81833.

Liu JZ, et al. (2013) Dense genotyping of immune-related disease regions identifies nine new risk loci for primary sclerosing cholangitis. Nature genetics, 45(6), 670.

Schurmann C, et al. (2012) Analyzing illumina gene expression microarray data from different tissues: methodological aspects of data analysis in the metaxpress consortium. PloS one, 7(12), e50938.

Klinkenberg M, et al. (2012) Restriction of trophic factors and nutrients induces PARKIN expression. Neurogenetics, 13(1), 9.

Elsharawy A, et al. (2012) Improving mapping and SNP-calling performance in multiplexed targeted next-generation sequencing. BMC genomics, 13, 417.

Pattaro C, et al. (2012) Genome-wide association and functional follow-up reveals new loci for kidney function. PLoS genetics, 8(3), e1002584.

Becker N, et al. (2011) Elastic SCAD as a novel penalization method for SVM classification tasks in high-dimensional data. BMC bioinformatics, 12, 138.

Kam-Thong T, et al. (2011) Epistasis detection on quantitative phenotypes by exhaustive enumeration using GPUs. Bioinformatics (Oxford, England), 27(13), i214.

Rivas MA, et al. (2011) Deep resequencing of GWAS loci identifies independent rare variants associated with inflammatory bowel disease. Nature genetics, 43(11), 1066.

Menssen A, et al. (2011) Differential gene expression profiling of human bone marrow-derived mesenchymal stem cells during adipogenic development. BMC genomics, 12, 461.

Liebl C, et al. (2009) Gene expression profiling following maternal deprivation: involvement of the brain Renin-Angiotensin system. Frontiers in molecular neuroscience, 2, 1.

Dräger A, et al. (2009) Modeling metabolic networks in C. glutamicum: a comparison of rate laws in combination with various parameter optimization strategies. BMC systems biology, 3, 5.

Vera J, et al. (2008) A systems biology approach to analyse amplification in the JAK2-STAT5 signalling pathway. BMC systems biology, 2, 38.