MEDISYN
ΣΥΝΕΤΑΙΡΙΣΜΟΣ ΕΡΓΑΣΤΗΡΙΑΚΩΝ ΙΑΤΡΩΝ

ΓΟΝΙΔΙΑΚΟΣ ΕΛΕΓΧΟΣ ΥΓΕΙΑΣ & ΕΥΕΞΙΑΣ

NUTRIFIT PREMIUM DNA

ANALYSED GENES

A WAY TO YOUR IDEAL BODY WEIGHT

Gene	Analysis	Role of the gene
ADIPOQ	Weight loss-regain	*A gene expressed in fatty tissue. It regulates fat metabolism and sensitivity to insulin.*
INSIG2	Risk of being overweight	*A protein found in the endoplasmic reticulum of the cells and blocks the processing of the protein SREB in order to regulate the synthesis of cholesterol.*
MC4R	Risk of being overweight	*A receptor involved in many physiological processes, such as regulation of energy consumption/storage in the body, the formation of steroids and control of temperature.*
TNFA	Risk of being overweight	*A cytokine, which is secreted by macrophages. It has an important role in the immune response to infections.*
PCSK1	Risk of being overweight	*An enzyme which processes proinsulin type I, and, therefore, has an important role in regulating the biosynthesis of insulin.*
NRXN3	Risk of being overweight	*A protein from the family of neurexins, which function as adhesive molecules and receptors in the nervous system.*
FTO	Risk of being overweight	*A gene that determines the development of excess body weight.*
TMEM18	Risk of being overweight	*A highly conserved protein, which is predominantly expressed in brains.*
GNPDA2	Risk of being overweight	*A gene involved in the development of excess body weight.*
BDNF	Risk of being overweight	*A protein from the family of nerve growth factors. It is involved in the survival and differentiation of certain neurons.*
APOA2	Risk for being overweight	*A protein, which is the second most represented component of HDL particles. It has an important role in the HDL metabolism.*
APOA2	Response to saturated fats	*A protein, which is the second most represented component of HDL particles. It has an important role in the HDL metabolism.*
ADIPOQ	Response to monounsaturated fats	*A gene expressed in the fatty tissue. It regulates fat metabolism and sensitivity to insulin.*
PPAR alpha(1)	Response to polyunsaturated fats	*Regulator of the synthesis of fatty acids, the oxidation, gluconeogenesis and ketogenesis.*
FTO	Response to carbohydrates	*A gene involved in the development of excess body weight.*
KCTD10	Response to carbohydrates	*A gene that encodes the domain of the potassium channel, responsible for its selective transport through the cell membrane.*

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NUTRIFIT PREMIUM DNA

ANALYSED GENES

WHICH VITAMINS AND MINERALS DOES YOUR BODY NEED?

Gene	Analysis	Role of the gene
ALPL	Vitamin B6	*An enzyme which functions in an alkaline environment and is crucial for growth and development of bones and teeth, as it is involved in the process of mineralisation, which is the process of accumulation of calcium and phosphorus. It also influences the level of vitamin B6.*
MTHFR	Vitamin B9	*Reduces 5,10-methylene-tetra-hydro-folate into methyl-tetra-hydro-folate and is, therefore, important for absorption of vitamin B9.*
FUT2	Vitamin B12	*A protein which influences the level of vitamin B12.*
GC	Vitamin D	*Binding and transport of vitamin D and its metabolites through the body, and influencing the vitamin D level.*
DHCR7	Vitamin D	*7-dehydrocholesterol transforms vitamin D3, which is the precursor of 25-hydroxyvitamin D3, into cholesterol, and in this way eliminates the substrate from the synthetic pathway.*
CYP2R1	Vitamin D	*Transforms vitamin D into an active form, so that it can bind with the receptor for vitamin D.*
TMPRSS6	Iron	*An enzyme which is found on the cell surface and is involved in the uptake and recycling of iron.*
HFE	Iron	*An enzyme which is found on the cell surface. It detects the amount of iron in the body and regulates the production of protein hepcidin, which is the main iron-regulating hormone in the body.*
AGT	Sodium (salt)	*A gene expressed in the liver. It activates with low pressure through renin and angiotensin converting enzyme (ACE), where angiotensin II is formed. It is in charge of the maintenance of blood pressure and electrolyte homeostasis.*
CLCNKA	Sodium (salt)	*Chloride channel with 12 transmembrane domains, which is in charge of the maintenance of blood pressure.*
WNK1	Potassium	*A protein which is responsible for the transport of sodium and potassium. It is included in electrolyte homeostasis and regulation of blood pressure.*
COL1A1	Bone density	*Collagen type I built from two alpha 1 chains and one alpha 2 chain. Collagen is the main protein of the organic part of the bone matrix (98%).*
GPR177	Bone density	*A protein which is part of the evolutionary highly conserved Wnt signal pathway, which is important for the differentiation and development of bone cells, and the resorption of bone material.*
DCDC5	Bone density	*A highly conserved element, which serves as a template for protein links.*
ZBTB40(1)	Bone density	*A protein found in the bone tissue and which influences bone density.*
ZBTB40(2)	Bone density	*A protein found in the bone tissue and which influences bone density.*

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ANALYSED GENES

WHICH VITAMINS AND MINERALS DOES YOUR BODY NEED?

Gene	Analysis	Role of the gene
ESR1	Bone density	*A transcription factor involved in the regulation of the expression of genes, which influences the proliferation of cells and differentiation of tissues. It is responsible for growth and maintenance of the strength of human bones.*
C6ORF97	Bone density	*A protein which influences bone density.*
SP7	Bone density	*Transcription factor and the activator of bone cell differentiation.*
AKAP11	Bone density	*Member of a structurally completely different group of proteins, which have a common function of binding the regulatory subunit of kinase A. It is highly expressed during spermatogenesis. It is found next to the RANKL gene, which has an important role in bone metabolism.*
TNFRSF11A	Bone density	*It is essential for RANKL-regulated osteoclastogenesis – the formation of osteoclasts (cells which break down bone cells).*
CA1	Zinc	*A gene that encodes a zinc-containing enzyme which catalyses the formation and dissociation of carbonic acid from carbon dioxide and water and plays an important role in carbon dioxide transport.*
PPCDC	Zinc	*A gene that encodes enzyme PPCDC and affects zinc status through effects on vitamin B5 (pantothenate) metabolism.*
NBDY	Zinc	*A gene that promotes dispersal of P-body components and is likely to play a role in the mRNA decapping process.*

IMPORTANT INFLUENCES ON YOUR EATING HABITS

Gene	Analysis	Role of the gene
ADRA2A	Sweet treats intake	*Regulates the transmission of the nervous impulse and influences our behavioural habits.*
NMB	Hunger	*Involved in the regulation of feeding processes.*
FTO	Satiety	*A protein involved in the development of excess body weight.*
SLC2A2	Perception of sweet taste	*Regulates glucose transport and is a glucose sensor.*
TAS2R38	Perception of bitter taste	*A transmembrane receptor, which determines the ability to detect bitter substances, found in the plant genus Brassica.*

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ANALYSED GENES

LIFESTYLE HABITS

Gene	Analysis	Role of the gene
CRP	Inflammation sensitivity	*C-Reactive Protein is involved in several host defense related functions. Consequently, the level of this protein in plasma increases greatly during acute phase response to infection or other inflammatory stimuli. It is often used as a marker for inflammation in blood tests.*
IL6R	Inflammation sensitivity	*IL6R gene encodes a subunit of the interleukin 6 (IL6) receptor complex. Interleukin 6 is a potent pleiotropic cytokine that regulates cell growth and differentiation and plays an important role in the immune response and inflammation.*
CLOCK	Sleep cycle	*A gene encoding a basic helix-loop-helix-PAS transcription factor (CLOCK) that affects both the persistence and period of circadian rhythms.*
NPAS	Sleep cycle	*A gene that functions as a part of a molecular clock operative in the mammalian forebrain.*

YOUR GENES, DETOXIFICATION AND ANTIOXIDANTS

Gene	Analysis	Role of the gene
CAT	Oxidative stress	*Catalase transforms reactive oxygen species into water and oxygen, and therefore reduces the toxic influence of hydrogen peroxide*
NQO1	Oxidative stress	*Enzyme which functions as quinone reductase in connection to the conjugation of hydroquinones. It is involved in numerous detoxification pathways and biosynthetic processes, such as vitamin K-dependent glutamate carboxylation.*
APOA5	Vitamin E	*Apolipoprotein A5 has an important role in the regulation of the level of chylomicrons and triglycerides in the plasma. Because vitamin E is fat-soluble, APOA5 through lipid concentration in the blood affects the vitamin E level.*
SEPP-1_1	Selenium	*Functions as an antioxidant. It is responsible for selenium transport, mostly to the brain and the testicles.*
SEPP-1_2	Selenium	*Functions as an antioxidant. It is responsible for selenium transport, mostly to the brain and the testicles.*
SLC23A1	Vitamin C	*One of the two transporters, responsible for the absorption/distribution of dietary vitamin C in our body, involving epithelial surfaces. A variant of this gene causes reduced absorption of vitamin C and is associated with lower plasma vitamin C concentrations.*

SPORTS AND RECREATION IN TUNE WITH YOUR GENES

Gene	Analysis	Role of the gene
ACTN3	Muscle structure	*A protein expressed in the muscles. It binds to actin and is, therefore, important for muscle contraction.*
PPAR alpha(2)	Muscle structure	*Regulates the expression of genes responsible for the oxidation fatty acids in the skeletal muscles and the heart muscle.*

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NUTRIFIT PREMIUM DNA

ANALYSED GENES

SPORTS AND RECREATION IN TUNE WITH YOUR GENES

Gene	Analysis	Role of the gene
INSIG2	Strength training	*A protein present in the endoplasmic reticulum, where it regulates the processing of binding protein for the steral regulatory element.*
ADRB2	VO2max	*β2 adrenergic receptor (ADRB2) is a member of the G-protein-coupled receptor superfamily and plays a pivotal role in the regulation of the cardiac, pulmonary, vascular, endocrine, and central nervous system.*
PPARGC1A	VO2max	*PPARGC1A is a transcriptional coactivator of the PPAR family and is involved in mitochondrial biogenesis, fatty acid oxidation, glucose utilisation, thermogenesis and angiogenesis.*
VEGFA	VO2max	*A variant in the VEGFA gene has been associated with VEGF protein expression. Several studies revealed associations of VEGFA gene polymorphisms with aerobic capacity in humans and endurance athlete status.*
ACE	VO2max	*ACE exerts a tonic regulatory function on circulatory homeostasis, through the synthesis of vasoconstrictor angiotensin II, which also drives aldosterone synthesis and the degradation of vasodilator kinins.*
PPAR alpha_2	VO2max	*Peroxisome proliferator-activated receptor alpha (PPAR-alpha) gene is implicated in the hypoxia-inducible factor (HIF) oxygen signalling pathway and regulation of erythropoiesis.*
CAT	Post-exercise recovery	*Catalase breaks down hydrogen peroxide (H2O2), which production is elevated during high-intensity training. At low levels, it is involved in several chemical signalling pathways, but at high levels it is toxic to cells.*
NQO1	Post-exercise recovery	*The enzyme functions as a quinone reductase in connection to the conjugation of hydroquinones. It is involved in numerous detoxification pathways and biosynthetic processes, such as vitamin K-dependent glutamate carboxylation.*
GPX1	Post-exercise recovery	*Glutathione peroxidase functions in the detoxification of hydrogen peroxide and is one of the most important antioxidant enzymes in humans.*
SOD2	Post-exercise recovery	*This gene is associated with the synthesis of superoxide dismutase, an enzyme found to be associated with the conversion of superoxide (O2-) into oxygen (O2) and hydrogen peroxide (H2O2). Superoxide dismutase is an important antioxidant which protects the cell from ionising radiation, oxidative stress and inflammatory cytokines.*
IL6	Inflammation	*Interleukine-6 pro-inflammatory molecule (IL6) stimulates the immune response to training and is involved in the inflammatory repair process. It plays a role in glucose and lipid metabolism.*
TNF	Inflammation	*Pro-inflammatory molecule. Elevated levels of TNF are associated with in an increase in the systemic immune response and inflammatory processes.*
CRP	Inflammation	*C-Reactive Protein is involved in several host defense related functions. Consequently, the level of this protein in plasma increases greatly during acute phase response to infection or other inflammatory stimuli. It is often used as a marker for inflammation in blood tests.*
IL6R	Inflammation	*IL6R gene encodes a subunit of the interleukin 6 (IL6) receptor complex. Interleukin 6 is a potent pleiotropic cytokine that regulates cell growth and differentiation and plays an important role in the immune response and inflammation.*
MMP3	Soft tissue injury risk	*It codes for the enzyme Matrix Metallopeptidase 3, which is responsible for the breakdown of fibronectin, collagen and proteoglycans of the cartilage. As such, it is involved in wound repair and progression of atherosclerosis.*

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SPORTS AND RECREATION IN TUNE WITH YOUR GENES

Gene	Analysis	Role of the gene
COL5A1	Soft tissue injury risk	*It has been shown the variant within COL5A1 gene affects our (in)flexibility (passive straight leg and a sit-and-reach measurement), which consequently affects our soft tissue injury risk.*
COL1A1	Soft tissue injury risk	*COL1A1 encodes for collagen type I, a protein that strengthens and support many tissues in the body, including cartilage, bone and tendon.*
GDF5	Soft tissue injury risk	*GDF5 (growth differentiation factor 5) is a member of the bone morphogenetic protein (BMP) family and the TGF-beta superfamily and can affect our soft tissue injury risk.*
CREB1	Heart capacity	*CREB1 has been found to be involved in the generation of long-term cardiac memory, a process leading to adaptation of ventricular repolarisation (indexed by electrocardiographic T wave) to ventricular pacing.*
ACE	Heart capacity	*ACE exerts a tonic regulatory function in circulatory homeostasis, through the synthesis of vasoconstrictor angiotensin II, which also drives aldosterone synthesis, and the degradation of vasodilator kinins.*
IL15RA	Muscle volume gene	*Growth factor that is expressed in muscle and has been demonstrated to have anabolic effects, with increased levels being linked to muscle growth in various studies.*
COMT	Warrior gene	*COMT is one of several enzymes that degrade dopamine, epinephrine, and norepinephrine. COMT breaks down dopamine mostly in the part of the brain responsible for higher cognitive or executive function (prefrontal cortex).*
TRHR_1	Lean body mass	*TRHR encodes the thyrotropin-releasing hormone (TRH) receptor. The TRH response to TRHR is the first step in the hormonal cascade that eventually leads to the release of thyroxin, which is important in the development of skeletal muscle.*
TRHR_2	Lean body mass	*TRHR encodes the thyrotropin-releasing hormone (TRH) receptor. The TRH response to TRHR is the first step in the hormonal cascade that eventually leads to the release of thyroxin, which is important in the development of skeletal muscle.*
MCT-1	Gene for muscle fatigue	*A gene associated with the synthesis of MCT1, a molecule that transports lactic acid across the muscle cell membrane.*

CARDIOVASCULAR HEALTH

Gene	Analysis	Role of the gene
FADS1-2-3_1	HDL, LDL cholesterol, Triglycerides	*The family of desaturases which incorporate double bonds into fatty acids.*
CETP_1	HDL, LDL cholesterol	*A protein which collects triglycerides from VLDL and LDL, and replaces them with cholesterol esters from HDL and vice versa.*
APOA1	HDL, LDL cholesterol, Triglycerides	*The main lipoprotein of HDL particles.*
ANGPTL3	LDL cholesterol, Triglycerides	*A protein which, through liver receptor X, influences the level of plasma lipids.*
GALNT2	HDL cholesterol, Triglycerides	*A protein responsible for the biosynthesis of oligosaccharides.*

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ANALYSED GENES

CARDIOVASCULAR HEALTH

Gene	Analysis	Role of the gene	Ge
PLTP	HDL cholesterol, Triglycerides	*A transport protein for phospholipids, which is present in the blood plasma. It transports phospholipids from lipoproteins, rich in triglycerides on HDL.*	
MLXIPL	HDL cholesterol, Triglycerides	*In relation to glucose, it binds and activates motifs of carbohydrate response elements (ChoRE) and motifs, responsible for the synthesis of triglycerides.*	
TRIB1_3	HDL, LDL cholesterol, Triglycerides	*A protein involved in the regulation of inflammation in the fatty tissue, and in obesity, induced by a high-fat content diet.*	
PPARalfa_1	HDL cholesterol	*Regulator of the synthesis of fatty acids, the oxidation, gluconeogenesis and ketogenesis.*	
APOE_1	HDL cholesterol, LDL cholesterol	*A rotein essential for the breaking down of lipoproteins, rich in triglycerides.*	
APOB_1	HDL, LDL cholesterol, Triglycerides	*The main lipoprotein of chylomicrons and LDL particles.*	
ABCG5/8	LDL cholesterol	*Proteins which regulate the cell export of cholesterol. Incorrect functioning is expressed in the accumulation of sterols.*	
LDLR	LDL cholesterol	*A protein which binds LDL particles on the surface of cells, and enables their transport into cells.*	
PPP1R3B	HDL, LDL cholesterol	*Inhibits the inactivation of glycogen phosphorylase, and limits the breakdown of glycogen.*	
ABCA1	HDL, LDL cholesterol, Triglycerides	*A membrane transporter, which regulates the transport of cholesterol and phospholipids, and the formation of HDL.*	
LIPC	HDL cholesterol	*A receptor for cholesterol, phospholipids, glycerides and acyl-CoA thioesters.*	
LCAT	HDL cholesterol	*It esters the cholesterol, which is crucial for the transport of cholesterol.*	
LIPG	HDL cholesterol	*A protein,which enables the hydrolysis of HDL particles.*	
HLA	LDL cholesterol, Triglycerides	*It helps to differentiate between the body's own and the foreign substances.*	
GCKR_1	LDL cholesterol, Triglycerides	*Inhibits the activity of glucokinase, which is an important enzyme in glucose metabolism.*	
TIMD4	LDL cholesterol, Triglycerides	*Phosphatidylserine receptor that enhances the engulfment of apoptotic cells.*	
IL6R	LDL cholesterol	*The IL6R gene encodes a subunit of the interleukin 6 (IL6) receptor complex. Interleukin 6 is a potent pleiotropic cytokine that regulates cell growth and differentiation and plays an important role in the immune response.*	
APOA5	Triglycerides	*Apolipoprotein A5 has an important role in the regulation of the level of chylomicrons and triglycerides in the plasma.*	
LPL	HDL cholesterol, Triglycerides	*Lipoprotein, which eliminates fats from chylomicrons and VLDL.*	

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CARDIOVASCULAR HEALTH

Gene	Analysis	Role of the gene
LRP1	HDL cholesterol, Triglycerides	*A protein involved in cellular lipid homeostasis.*
IRS1	HDL cholesterol, Triglycerides	*A protein which is phosphorylated by insulin receptor tyrosine kinase.*
TCF7L2	Blood sugar	*A transcription factor which is involved in the Wingless-type (Wnt) signal path through which it influences diabetes type II.*
SLC30A8	Blood sugar	*The main component of zinc supply for the production of insulin, and it is involved in processes of storage in insulin-secreting beta-cells of the pancreas.*
G6PC2	Blood sugar	*Catalytic subunit of an enzyme glucose-6-phosphatase, and it, therefore, important influences the blood glucose level.*
MTNR1B	Blood sugar	*Receptor for melatonin, influencing circadian rhythms.*
DGKB	Blood sugar	*Diacylglycerol kinase regulates the level of diacylglycerol and the secretion of insulin.*
GCKR	Blood sugar	*Inhibitor of glucokinase (GCK), which regulates the first step of metabolic pathways of sugars.*
ADCY5	Blood sugar	*Enzyme cyclase, responsible for the synthesis of cAMP which regulates the activity of glucagon and adrenaline.*
FADS1	Omega-3 metabolism	*An enzyme encoded by this gene is involved in conversion of ALA (α-linolenic acid) omega-3 fatty acid to EPA (eicosapentaenoic acid) and DHA (docosahexaenoic acid).*
FADS1	Omega-3 and triglycerides	*An enzyme encoded by this gene is involved in conversion of ALA (α-linolenic acid) omega-3 fatty acid to EPA (eicosapentaenoic acid) and DHA (docosahexaenoic acid).*
PCSK1	Insulin sensitivity	*An enzyme which processes proinsulin type I, and, therefore, has an important role in regulating the biosynthesis of insulin.*
ADIPOQ	Insulin sensitivity	*A gene expressed in fatty tissue. It regulates fat metabolism and sensitivity to insulin.*
TCF7L2	Insulin sensitivity	*A transcription factor which is involved in the Wingless-type (Wnt) signal path through which it influences diabetes type II.*
ADIPOQ	Adiponectin	*A gene expressed in fatty tissue. It regulates fat metabolism and sensitivity to insulin.*
CRP	C-reactive protein (CRP)	*The protein encoded by this gene is involved in several host defence related functions based on its ability to recognize foreign pathogens and damaged cells.*
IL6R_1	C-reactive protein (CRP)	*IL6R gene encodes a subunit of the interleukin 6 (IL6) receptor complex. Interleukin 6 is a potent pleiotropic cytokine that regulates cell growth and differentiation and plays an important role in the immune response.*
HNF1A	C-reactive protein (CRP)	*The protein encoded by this gene is a transcription factor required for the expression of several liver-specific genes.*
APOE_1	C-reactive protein (CRP)	*Protein, essential for the breaking down of lipoproteins, rich in triglycerides.*

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ANALYSED GENES

REJUVENATION

Gene	Analysis	Role of the gene
CAT	Skin antioxidant capacity	*Catalase transforms reactive oxygen species into water and oxygen, and, therefore, reduces the toxic influence of hydrogen peroxide.*
NQO1	Skin antioxidant capacity	*Glutathione peroxidase functions in the detoxification of hydrogen peroxide and is one of the most important antioxidant enzymes in humans.*
SOD2	Skin antioxidant capacity	*This gene is associated with the synthesis of superoxide dismutase, which is an important antioxidant which protects the cell from ionising radiation, oxidative stress and inflammatory cytokines.*
GPX1	Skin antioxidant capacity	*The enzyme which functions as a quinone reductase in connection to the conjugation of hydroquinones. It is involved in numerous detoxification pathways and biosynthetic processes.*
GLO1	Glycation protection	*GLO1 gene encodes an enzyme which is responsible for the protection of our cells against AGEs (advanced glycation end products).*
GLO1	Glycation protection	*GLO1 gene encodes an enzyme which is responsible for the protection of our cells against AGEs (advanced glycation end products).*
ACE2	Cellulite	*This gene encodes for an enzyme responsible for the conversion of angiotensin I to angiotensin II and catabolism of bradykinin. Studies have shown that circulating angiotensin II is a major regulator of fasting adipose blood flow and can therefore influence our susceptibility to cellulite development.*
HIF1A	Cellulite	*This gene encodes the alpha subunit of HIF-1, which is a transcription factor. Activation of HIF1A impairs healthy adipose endocrine function and may in this way affect the formation of cellulite.*
AQP3	Skin hydration	*A protein which acts as a glycerol transporter in the skin and plays an important role in regulating stratum corneum and epidermal glycerol content. It is involved in skin hydration, wound healing, and tumorigenesis.*
MMP1	Skin elasticity	*The protein encoded by this gene belong to the enzyme family called matrix metalloproteinase. Upregulation of the MMP1 gene leads to faster dermal collagen degradation.*
MMP3	Skin elasticity	*This gene encodes an enzyme which degrades fibronectin, laminin, collagens III, IV, IX, and X, and cartilage proteoglycans.*
IL6	Skin elasticity	*Gene that plays a major role in cell proliferation, and collagen synthesis.*
ELN	Skin elasticity	*This gene encodes for elastin, a major component of elastic fibres, which provides reversible extensibility to connective tissue. Studies have shown that mutations in the ELN gene affects its expression which results in lower amounts of elastin in our body.*
HMCN	Stretch marks	*This gene encodes for elastin, a major component of elastic fibres, which provides reversible extensibility to connective tissue. Studies have shown that mutations in the ELN gene affects its expression which results in lower amounts of elastin in our body.*
ELN	Stretch marks	*HMCN1 plays an important role in the organisation of hemidesmosomes in the epidermis.*