Client Report

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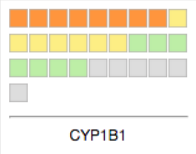
Welcome to Opus 23 Pro.

Opus 23 Pro interprets the 'raw data' provided by reporting services (such as 23andMe) into its medical significance. To do this Opus 23 Pro scans over 20 peer-reviewed, evidence-based scientific databases and cross-references their information with the results of your raw data. This report summarizes the findings from your genomic data that have been curated by your clinical team into a human-understandable format. However, before we begin, let's introduce a few genetic concepts to set the stage and advance your understanding a bit.

GENOMIC PROFILES

Although SNPs are the 'letters' of individuality, genes are in fact the words and vocabulary. After all, it is the genes that have to do the work, coding for the construction for a myriad of enzymes and proteins. Because gene function is central to any sort of biochemical prediction, Opus 23 Pro groups all the SNP outcomes under their parent gene, and presents its results as a reflection of their combined influence on the effectiveness of that gene. Although SNPs are pretty much unchangeable, our genes can be influenced (for better or worse) by lifestyle, diet, emotions and nutritional supplementation.

Each gene is depicted as a grid showing the result of its SNPs:



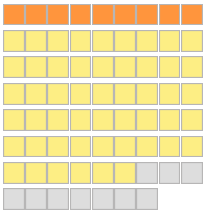
- The sum of the significant SNPs in the gene that indicate a higher (homozygous) risk are the orange squares
- The sum of the significant SNPs in the gene that indicate a lower (heterozygous) risk are the yellow squares
- The sum of the significant SNPs that are working just fine (no problem polymorphisms) risk are the gray squares
- You might even find that for some genes you may have a polymorphism that conveys some benefit. These are the green squares

NOTE: The genes that appear in this report have been selected for inclusion by your clinical team. Generally these are genes that the team feel are worthy of attention. Rest assured that this is but a small percentage of all the gene data the team has examined. In a way similar to conventional lab tests, all those normal results are great, but what we're really interested in is the problem areas!

Genetics can be complicated to the layperson. Sometimes a word is used to descibe a gene function that you might not recognize. If *Opus 23 Pro* thinks that you might need some help with a technical term, 'Mr. Smart Owl' will try to explain it to you. These terms are also included in a Glossary at the end of this report.

HPA AXIS GENOMICS

Our short-term responses to stress are produced by the 'Fight or Flight Response' which stimulates the sympathetic nervous system. Long term stress is regulated by the Hypothalamic Pituitary-Adrenal (HPA) system. Over-activation of the HPA system causes the adrenal cortex to release a stress hormone called cortisol. This can have a number of functions, including releasing stored glucose from the liver (for energy) and controlling swelling after injury. When disregulated or poorly controlled, the excess cortisol can suppress the immune system.



NR3C1

NR3C1

Full Name: 'nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)'

NR3C1 encodes the 'glucocorticoid receptor', which can activate glucocorticoid-responsive genes to activate their being 'read' (transcription) and having their instructions carried out. This receptor is typically found in the cell's cytoplasm, but upon binding, it is transported into the cell nucleus. It is involved in inflammatory responses and cellular proliferation Mutations in this gene are associated with generalized glucocorticoid resistance. Glucocorticoid s are part of the feedback mechanism in the immune system that turns immune activity (inflammation) down. They are therefore used in medicine to treat diseases caused by an overactive immune system, such as allergies, asthma and autoimmune diseases. There has been some association with variations in NR3C1 and bone mineral density, which is opposite for men and women.

Found in: Amygdala • Bone marrow • Brain • Colon • Eosinophil • Eye • Fetus • Heart • Hippocampus • Hypothalamus • Kidney • Leukocyte • Liver • Lung • Lymphocyte • Macrophage • Monocyte • Nasal mucosa • Neutrophil • Osteoblast • Pancreas • Peripheral blood cell • Pituitary gland • Placenta • Skeletal Muscle • Skin fibroblast • Spleen

Your clinical team considers this gene result **significant and actionable.**

New concepts:

- The **gene** is the fundamental physical and functional unit of heredity. A gene is an ordered sequence of nucleotides located in a particular position on a particular chromosome that encodes a specific product (i.e., a protein).
- The **nucleus** is the central part of most cells that contains genetic material and is enclosed in a membrane
- A **receptor** is a molecule in a cell membrane, that responds specifically to a particular neurotransmitter, hormone, antigen, or other substance.
- **Transcription** is the first step of gene expression, in which a particular segment of DNA is copied into RNA
- **Cytoplasm** is the material or protoplasm within a living cell, excluding the nucleus.

You have a few **especially noteworthy** SNP polymorphisms on **NR3C1:**

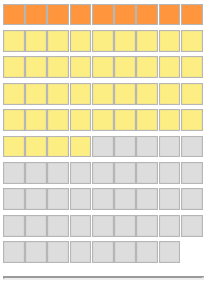
- **rs6191** *3298G>T (+-)
- **rs6196** (+-)
- **rs2918419** 1185-28620A>G (+-)
- **rs258813** 2023+335C>T (+-)
- **rs33388** 1185-3562T>A (+-)
- **rs6198** *3833A>G (++)

Your clinical team has identified these **high-value foods** that you should emphasize in your diet to improve *NR3C1* function:

- Chocolate • Pumpkin Seeds • Quinoa • Rice Bran

MISCELLANEOUS/ UNCATEGORIZED GENES

Genes listed here have been identified as significant by your clinical team, but do not have a convenient category to be classified under.



SLC22A5

SLC22A5

Full Name: 'solute carrier family 22 (organic cation/carnitine transporter), member 5'

Mutations in the SLC22A5 gene can result in an absent or dysfunctional OCTN2 protein, a mitochondrial fatty acid transporter. As a result, there is a shortage (deficiency) of carnitine within cells. Without carnitine, fatty acids cannot enter mitochondria and be used to make energy. Reduced energy production can lead to some features of primary carnitine deficiency, such as muscle weakness and hypoglycemia. Fatty acids may also build up in cells and damage the heart, liver, and muscles. This abnormal buildup causes the other signs and symptoms of the disorder.

Found in: Adrenal gland • Brain • Heart • Intestine • Kidney • Liver • Lung • Muscle • Nervous system • Pancreas • Placenta • Prostate • Thyroid gland • Trachea • Uterus

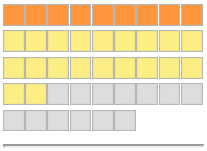
Your clinical team considers this gene result **significant and actionable.**

New concepts:

- **Mitochondria** are a cell constitutent (organelle) found in large numbers in most cells, in which the biochemical processes of respiration and energy production occur.
- **Proteins** are large molecules composed of one or more chains of amino acids. Proteins are required for the structure, function, and regulation of the bodys cells, tissues, and organs, and each protein has unique functions. Examples are hormones, enzymes, and antibodies.

You have a few **especially noteworthy** SNP polymorphisms on **SLC22A5:**

- **rs2631363** (+-)
- **rs2631361** (+-)
- **rs274558** (+-) **OPUS:** Associated with renal carnitine transport (risk)
- **rs13180186** LOC553103 (+-) **OPUS:** Associated with carnitine transport (risk)
- **rs274557** (+-) **OPUS:** Associated with renal carnitine transport (risk) **GWAS**: Plasma omega-6 polyunsaturated fatty acid levels (arachidonic acid)
- **rs4646301** (+-)
- **rs2631367** LOC553103 (++) **OPUS:** Associated with carnitine transport (risk)



USF1

USF1

Full Name: 'upstream transcription factor 1'

This gene encodes a member of the basic helix-loop-helix leucine zipper family, and can function as a cellular transcription factor. The encoded protein can activate transcription through pyrimidine-rich initiator (Inr) elements and E-box motifs. This gene has been linked to familial combined hyperlipidemia (FCHL). Alternative splicing of this gene results in multiple transcript variants. A related pseudogene has been defined on chromosome 21. [provided by RefSeq, Feb 2013] The upstream stimulatory factors (USF1 and USF2) are transcription factors that participate in the regulation of a large number of genes and especially USF2 appears to be crucial for the control of embryonic development, brain function, metabolism, iron homeostasis, fertility and growth whereas USF1 has roles in metabolism, as well as in the tanning and immune response (Sirito et al., 1998; Corre and Galibert, 2005). Furthermore, USFs seems to exhibit a tissue protective and tumor suppressive function in several cancer types (Ismail et al., 1999; Chen et al., 2006; Chang et al., 2005). Although the majority of mechanisms regulating USFs are largely unknown, phosphorylation appears to play an important role and the present review aims to summarize the current knowledge about the regulation of USFs by direct phosphorylation and the consequences for USF functions. [PMID: 25741280]

Found in: Ubiquitous

Your clinical team considers this gene result **significant and actionable.**

New concepts:

- **Homeostasis** is the tendency of a system, especially the physiological system of higher animals, to maintain internal stability, owing to the coordinated response of its parts to any situation or stimulus that would tend to disturb its normal condition or function.
- **Ribonucleic acid (RNA)** is a chemical found in the nucleus and cytoplasm of cells; it plays an important role in protein synthesis and other chemical activities of the cell.

You have a few **especially noteworthy** SNP polymorphisms on **USF1:**

- **rs2774276** (+-)
- **rs2073653** 306A>G (+-)
- **rs1556259** (+-)
- **rs2073658** -2083G>A (++) **OPUS:** Associated with hyperlipidemia• higher cholesterol • metabolic syndrome (risk)

RXRA

RXRA

Full Name: 'retinoid X receptor, alpha'

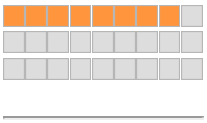
Retinoid X receptors (RXRs) and retinoic acid receptors (RARs) are receptors for the cell nucleus that activate the effects of retinoids (vitamin A). These receptors function as transcription factors, controlling the rate of activation of specific genes. RXRA provides instructions for making an enzyme called retinoid X receptor, alpha, which is a member of the family of transcriptional regulators of steroid and thyroid hormone receptors.

Found in: B Cell • Kidney • Liver • Lung fibroblast • Pituitary gland • Uterine stromal cell

Your clinical team considers this gene result **only for informational purposes**

ESTROGEN AND TESTOSTERONE GENOMICS

Estrogen and testosterone are key components to understanding the biology behind sexual differences between women and men. Although estrogen and testosterone are present in both sexes, the prevalence of estrogen in women and testosterone in males far outweigh the inverse, resulting in many distinct characteristics.



SHBG

SHBG

Full Name: 'sex hormone-binding globulin'

SHBG transports androgens (such as testosterone) and estrogens in the blood. Polymorphisms in this gene have been associated with polycystic ovary syndrome and type 2 diabetes mellitus. SHBG is produced mostly by the liver and is released into the bloodstream. SHBG levels are decreased by androgens, administration of anabolic steroids,[20] polycystic ovary syndrome, hypothyroidism, obesity, Cushing's syndrome, and acromegaly. Low SHBG levels increase the probability of Type 2 Diabetes. SHBG levels increase with estrogenic states (oral contraceptives), pregnancy, hyperthyroidism, cirrhosis, anorexia nervosa, and certain drugs. Long-term calorie restriction of more than 50 percent increases SHBG, while lowering free and total testosterone and estradiol.

Found in: Brain • Liver • Placenta • Plasma • Serum • Testis • Uterus

Your clinical team considers this gene result **significant and actionable.**

New concepts:

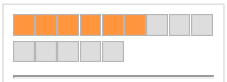
- An **androgen** is any natural or synthetic compound, usually a steroid hormone, that stimulates or controls the development and maintenance of male characteristics.

You have an especially noteworthy SNP polymorphism on **SHBG:**

- **rs12150660** (++) **OPUS:** Associated with lower blood testosterone levels (risk)

ADIPOCYTOKINE GENOMICS

Adipocytokines are chemical messengers inside the cell that respond to changes in the environment such as a drop or increase in nutrients. Adipocytokines are very active in adipose (fat) tissue, and play important roles in the development of insulin resistance and associated metabolic complications such as elevated blood lipids, hypertension, diabetes, obesity and premature heart disease. Adipocytokines are though to be the molecular connection between poor metabolism and inflammation. Many of the genes involved in adipocytokine signalling play an important role in metabolic syndrome.



MTOR

MTOR

Full Name: 'mechanistic target of rapamycin (serine/threonine kinase)'

The mechanistic target of rapamycin, also known as MTOR, is a protein that in humans is encoded by the MTOR gene. MTOR regulates cell growth, cell proliferation, cell motility, cell survival, protein synthesis, autophagy, and transcription. The MTOR signaling pathway senses and integrates a variety of environmental cues to regulate organismal growth and homeostasis. The pathway regulates many major cellular processes and is implicated in an increasing number of pathological conditions, including cancer, obesity, type 2 diabetes, and neurodegeneration. It is hypothesized that some dietary regimes, like caloric restriction and methionine restriction, cause lifespan extension by decreasing MTOR activity. Decreased MTOR activity has been found to increase life span in animal studies. MTOR has important effects on 'autophagy' the process by which cells remove debris, and the failure of autophagy is thought to be one of the main reasons for the accumulation of cell damage and aging.

Found in: Brain • Heart • Kidney • Liver • Lung • Pancreas • Placenta • Skeletal Muscle • T Cell

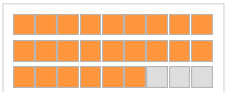
Your clinical team considers this gene result **significant and actionable.**

New concepts:

- **Autophagy** (from the Greek "to eat self") is the natural, regulated process by which the cell removes unnecessary or dysfunctional cellular components, such as worn-out or mis-folded proteins and other cellular debris.
- **Motility** is exhibiting or being capable of movement.

You have an especially noteworthy SNP polymorphism on **MTOR:**

- **rs1057079** (++)



IL13

IL13

Full Name: 'interleukin 13'

IL13 is one of a class of immune hormones known as 'cytokines'. IL13 down-regulates the activity of white blood cells known as 'macrophages', and thereby inhibits the production of pro-inflammatory cytokines and chemokines. This cytokine is found to be critical to the pathogenesis of allergen-induced asthma but operates through mechanisms independent of IgE and eosinophils. Dietary lectins have been shown to produce immunologic reactions due to their ability to stimulate IL13.

Found in: Lymphocyte • Serum • Skin • T Cell

Your clinical team considers this gene result **significant and actionable.**

New concepts:

- **Pathogenesis** is the development of a disease and the chain of events leading to that disease.
- **Cytokines** are chemicals important in cell signaling. They are released by cells and affect the behavior of other cells. Cytokines include chemokines, interferons and interleukins. Cytokines are produced by a broad range of cells, including immune cells like macrophages, B lymphocytes and T lymphocytes.
- A **pathogen** is a bacterium, virus, or other microorganism that can cause disease.

You have a few **especially noteworthy** SNP polymorphisms on **IL13:**

- **rs1295685** +2525G/A (++) **OPUS:** Associated with psoriasis • autoimmune syndromes (risk)
- **rs1800925** (++) **OPUS:** Associated with IgE (allergic antibodies) • psoriasis • autoimmune syndromes (risk)
- **rs20541** (++) **OPUS:** Associated with elevated IgE (allergic antibodies) levels immunoglobulin E • asthma (risk) **GWAS**: Self-reported allergy • IgE levels • Psoriasis

BONE DENSITY GENOMICS

Bone density refers to the amount of mineral matter in bone. Bone density is used in clinical medicine as an indirect indicator of osteoporosis and fracture risk.There is association between poor bone density and higher probability of fracture. Fractures of the legs and pelvis due to falls are a significant public health problem, especially in elderly women, leading to much medical cost, inability to live independently, and evsuffering.

CYP24A1

CYP24A1

Full Name: 'cytochrome P450, family 24, subfamily A, polypeptide 1'

CYP24A1 is a phase I detoxifying/ metabolizing enzyme. CYP24A1 initiates the breakdown of 1,25-dihydroxyvitamin D3, the physiologically active form of vitamin D3. In regulating the level of vitamin D3, this enzyme plays a role in calcium homeostasis and the vitamin D endocrine system.

Found in: Fetus • Monocyte • Proximal convoluted tubule • Skin

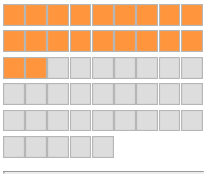
Your clinical team considers this gene result **significant and actionable.**

New concepts:

- **Endocrine** relates to, or denotes glands that secrete hormones or other products directly into the blood.

You have an especially noteworthy SNP polymorphism on **CYP24A1:**

- **rs2296241** (++) **OPUS:** Associated with cholesterol/ steroid/ lipid synthesis • vitamin D3 regulation • calcium homeostasis • drug metabolism (risk)



VDR

VDR

Full Name: 'vitamin D (1,25- dihydroxyvitamin D3) receptor'

Vitamin D receptor. VDR Fok is involved with Blood sugar regulation. VDR mutations oppose COMT mutations in the regulation of dopamine levels. A VDR mutation means that a person is less sensitive to methyl group supplement levels. (Mood swings.) A VDR mutation can result in behaviors opposite to a COMT mutation. The vitamin D receptor plays an important role in regulating the hair cycle. Loss of VDR is associated with hair loss in experimental animals. Glucocorticoids are known to decrease expression of VDR, which is expressed in most tissues of the body and regulate intestinal transport of calcium, iron and other minerals. The VDR SNP rs1544410 has been associated with low bone mineral density and osteoporosis. Mutations in the VDR gene cause vitamin D-dependent rickets type 2 (VDDR2), also known as hereditary vitamin D-resistant rickets (HVDRR). This disorder of bone development is characterized by low levels of calcium (hypocalcemia) and phosphate (hypophosphatemia) in the blood, which lead to soft, weak bones (rickets) that are prone to fracture. A common feature of this condition is bowed legs. The VDR gene mutations that cause this condition prevent the VDR protein from functioning properly. Some changes in the VDR gene lead to an abnormally short version of the VDR protein; others result in the production of an abnormal receptor that cannot bind to calcitriol, to RXR, or to DNA. Despite plenty of calcitriol in the body, the altered VDR cannot stimulate gene activity important for mineral absorption. The lack of calcium and phosphate absorption in the intestines slows deposition of these minerals into developing bone (bone mineralization), which leads to soft, weak bones and other features of VDDR2. Hypocalcemia also causes muscle weakness and seizures in some affected individuals. Most VDR gene mutations impair hair growth, leading to alopecia; however, mutations that block VDR's ability to interact with calcitriol do not cause alopecia, indicating that calcitriol is not necessary for the receptor's role in hair development.

Found in: Lymphocyte • Ubiquitous

Your clinical team considers this gene result **significant and actionable.**

Clinician Notes:

- Could be a factor in immune function.

New concepts:

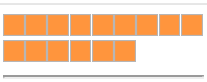
- A **mutation** is an alteration of genetic material such that a new variation is produced.
- A **methyl group** is one of the commonest structural units of organic compounds, consisting of three hydrogen atoms bonded to a carbon atom, which is linked to the remainder of the molecule.

You have a few **especially noteworthy** SNP polymorphisms on **VDR:**

- **rs7975232** ApaI (++)
- **rs731236** (++) **OPUS:** Associated with taq1 dopamine synthesis • breast cancer susceptibility (risk)
- **rs1544410** BsmI (++) **OPUS:** Associated with bone density • Hashimoto's thyroiditis • infertility (risk)
- **rs4516035** A-1012G (++) **OPUS:** Associated with melanoma (risk)

Your clinical team has identified the following **nutraceuticals** to be of potential value:

- **Vitamin D (calciferols)** (9 additional gene hits)



WNT16

WNT16

Full Name: 'wingless-type MMTV integration site family, member 16'

The WNT gene family consists of structurally related genes which encode secreted signaling proteins. These proteins have been implicated in oncogenesis and in several developmental processes, including regulation of cell fate and patterning during embryogenesis. This gene is a member of the WNT gene family. It contains two transcript variants diverging at the 5' termini. These two variants are proposed to be the products of separate promoters and not to be splice variants from a single promoter. They are differentially expressed in normal tissues, one of which (variant 2) is expressed at significant levels only in the pancreas, whereas another one (variant 1) is expressed more ubiquitously with highest levels in adult kidney, placenta, brain, heart, and spleen. [provided by RefSeq, Jul 2008]

Found in: Brain • Heart • Kidney • Leukocyte • Lung • Pancreas • Placenta • Skeletal Muscle • Small Intestine • Spleen

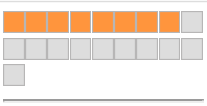
Your clinical team considers this gene result **significant and actionable.**

New concepts:

- **Embryogenesis** is the formation and development of an embryo.
- **Oncogenesis** is the production or causation of tumors; called also tumorigenesis.
- An **oncogene** is a gene found in the chromosomes of tumor cells whose activation is associated with the initial and continuing conversion of normal cells into cancer cells.
- In genetics, a **promoter** is a region of DNA that initiates transcription of a particular gene.

You have an especially noteworthy SNP polymorphism on **WNT16:**

- **rs3801387** (++) **OPUS:** Associated with bone mineral density (risk) **GWAS**: Bone mineral density (LSBMD)



HSD11B1

HSD11B1

Full Name: 'hydroxysteroid (11-beta) dehydrogenase 1'

HSD11B1 catalyzes the conversion of the stress hormone cortisol to the inactive metabolite cortisone. In addition, the encoded protein can catalyze the reverse reaction, the conversion of cortisone to cortisol. Too much cortisol can lead to central obesity, and a particular variation in this gene has been associated with obesity and insulin resistance in children.

Found in: Adipocyte • Adipose tissue stromal cell • Cerebellum • Decidua • Granulosa lutein cell • Liver • Lung • Oocyte • Osteoblast • Osteoclast • Pituitary gland • Placenta • Renal medulla • Spleen • Zona fasciculata • Zona glomerulosa • Zona reticularis

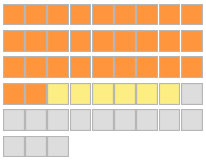
Your clinical team considers this gene result **noteworthy but not actionable**

New concepts:

- To **Catalyze** is to cause or accelerate (a reaction) by acting as a catalyst.
- A **metabolite** is a product of metabolism; a substance essential to the metabolism of a particular organism or to a particular metabolic process.

CATECHOLAMINE GENOMICS

Included among catecholamines are epinephrine (adrenaline), norepinephrine (noradrenaline), and dopamine, all of which are produced from phenylalanine and tyrosine. Release of the hormones epinephrine and norepinephrine from the adrenal medulla of the adrenal glands is part of the fight-or-flight response. Excessive catecholamine activity can cause increases in heart rate, blood pressure, blood glucose levels, and a general reaction of the sympathetic nervous system.



COMT

COMT

Full Name: 'catechol-O-methyltransferase'

Catechol-O-methyltransferase (COMT) gene helps break down dopamine and norepinephrine. A defect will cause higher dopamine due to slower breakdown which can contribute to anxiety and insomnia. More susceptible to dopamine fluctuations, therefore mood swings. People without COMT mutations are generally more even tempered. Studies of Val158Met polymorphism have shown to affect cognitive tasks rated as executive function(1), aggression(2) and working memory and ratings of subjective well-being (3). Implicated in ADD/ADHD and bipolar disorders. A functioning VDR FOKI and/or supplementing with vitamin D enhances dopamine formation. COMT is important in the metabolism of catechol drugs used in the treatment of hypertension, asthma, and Parkinson disease. Catechol-estrogens like 4-OH Estrone, and catechol-containing flavinoids are metabolised by this enzyme and plays a role in the risk of cancer.

Found in: Adrenal gland • Intestine • Lacrimal gland • Mammary gland • Monocyte • Tear

Your clinical team considers this gene result **significant and actionable.**

New concepts:

- A **polymorphism** is a difference in DNA sequence among individuals.

You have a few **especially noteworthy** SNP polymorphisms on **COMT:**

- **rs4680** V158M 472AA (++) **OPUS:** Associated with COMT enzyme • dopamine • stress • blood metabolites • breast cancer • pain • memory • attention • (risk) **GWAS**: Blood metabolite levels (X-01911) • Blood metabolite levels (X-11593--O-methylascorbate)
- **rs4633** H62H (++) **OPUS:** Associated with pain sensitivity • paranoid schizophrenia • homocysteine • hyperactivity • chronic fatigue syndrome (risk)
- **rs4646312** -91-385T>C (++) **OPUS:** Associated with estrogen and androgen metabolizing (risk)

Your clinical team has identified the following **nutraceuticals** to be of potential value:

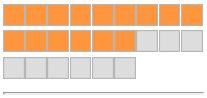
- **Pyridoxal 5' phosphate** (3 additional gene hits)
- **Magnesium** (2 additional gene hits)

Your clinical team has identified these **high-value foods** that you should emphasize in your diet to improve *COMT* function:

- Chocolate • Pumpkin Seeds • Quinoa • Rice Bran

Your clinical team has identified several **environmental risk factors** that can influence the function of COMT:

- Noise • Aluminum Compounds • Minerals • Vasopressins • Organoplatinum Compounds • Disulfides • Neurotoxins • Oxidopamine • Testosterone • Ergonovine • Sulfonylurea Compounds • Pyrimidines • Fatty Acids, Unsaturated • Somatomedins • Amino Acids, Diamino • Fruit • Fatty Acids, Omega-3 • Calcium Compounds • Polychlorinated Biphenyls • Hydroxybenzoic Acids • Dideoxynucleosides • Phosphorus Compounds • Testosterone Congeners • Carotenoids • Dipeptides • Captopril • Fatty Acids, Essential • Pyrethrins • Ergolines • Tetanus Toxoid • Antacids



DDC

DDC

Full Name: 'dopa decarboxylase (aromatic L-amino acid decarboxylase)'

The DDC gene provides instructions for making the aromatic l-amino acid decarboxylase (AADC) enzyme, which is important in the brain and nervous system. This enzyme takes part in the pathway that produces dopamine and serotonin, which are chemical messengers that transmit signals between nerve cells (neurotransmitters). DDC is responsible for the synthesis of dopamine and serotonin from L-DOPA and L-5-hydroxytryptophan, respectively.

Found in: Ubiquitous

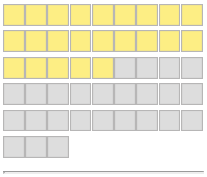
Your clinical team considers this gene result **noteworthy but not actionable**

New concepts:

- **Amino acid** are small molecules that are the components of proteins. There are 20 different kinds of amino acids in living things. Proteins are composed of different combinations of amino acids assembled in chain-like molecules.

METHYLATION GENOMICS

Methylation is the addition of a single carbon and three hydrogen atoms (called a methyl group) to another molecule. The removal of a methyl group is called demethylation. The addition or removal of methyl groups act as on/off switches inside the body, controlling everything from our stress response, the production of energy from food, brain chemistry and detoxification. Researchers are only now beginning to appreciate the diverse role of methylation and its importance to our health.



MTHFR

MTHFR

Full Name: 'methylenetetrahydrofolate reductase (NAD(P)H)'

Perhaps the most studied SNP-containing gene of all, Methylene tetrahydrofolate reductase (MTHFR) allows conversion of 5,10-methylenetetrahydrofolate to 5-methyltetrahydrofolate, needed for conversion of homocysteine (HCy) to the protein-building amino acid methionine via methylation, in the rate-limiting step of the methyl cycle. MTHFR is a highly polymorphic gene, and genetic variation influences susceptibility to occlusive vascular disease, neural tube defects, colon cancer and acute leukemia, and mutations in this gene are associated with methylenetetrahydrofolate reductase deficiency. Lower MTHFR enzyme activity results in lower levels of methylated folate, leading to elevated homocysteine (HCy). Natural variation in this gene is common in healthy people. Although some variants have been reported to influence susceptibility to occlusive vascular disease, neural tube defects, Alzheimer's disease and other forms of dementia, colon cancer, and acute leukemia, findings from small early studies have not been consistently reproduced. Two of the most investigated are C677T (rs1801133) and A1298C (rs1801131) single nucleotide polymorphisms (SNPs).

- Individuals with two copies of 677C (677CC) have the most common genotype. 677TT individuals (homozygous) have lower MTHFR activity than CC or CT (heterozygous) individuals.
- 1298AA is the "normal" homozygous, 1298AC the heterozygous, and 1298CC the homozygous for the "variant". The C mutation does not appear to affect the MTHFR protein. It does not result in thermolabile MTHFR and does not appear to affect homocysteine levels. It does, however, affect the conversion of MTHF to BH4 (tetrahydrobiopterin), an important cofactor in the production of neurotransmitters, production of nitric oxide, and detoxification of ammonia.

Found in: Brain • Colon • Heart • Intestine • Kidney • Liver • Lung • Muscle • Placenta • Spleen • Stomach • Testis

Your clinical team considers this gene result **significant and actionable.**

New concepts:

- The **genotype** is the genetic makeup of an individual. Genotype can refer to a person's entire genetic makeup or the alleles at a particular locus
- A **nucleotide** is subunit of DNA or RNA consisting of a nitrogenous base (adenine, guanine, thymine, or cytosine), a phosphate molecule, and a sugar molecule. Thousands of nucleotides are linked to form a DNA or RNA molecule.
- A **homozygous** genotype has the same allele at the same locus (location) on both chromosomes. Homozygous also refers to a genotype consisting of two identical alleles of a gene for a particular trait.
- A **heterozygous** genotype consists of two different alleles of a gene for a particular trait. Individuals who are heterozygous for a trait are referred to as heterozygotes.
- The **rate limiting step** is the slowest step in a metabolic pathway or series of chemical reactions, which determines the overall rate of the other reactions in the pathway.
- **Methylation** is the addition of a single carbon and three hydrogen atoms (called a methyl group) to another molecule. The removal of a methyl group is called demethylation. Methylation is a key mechanism behind the regulation of gene expression.

You have a few **especially noteworthy** SNP polymorphisms on **MTHFR:**

- **rs1801133** (+-) **OPUS:** Associated with cancer • migraine headache • homocysteine (risk) **GWAS**: Homocysteine levels (WGHS) • Homocysteine levels
- **rs1801131** A1298C (+-) **OPUS:** Associated with neurotransmitter synthesis (risk)

Your clinical team has identified the following **nutraceuticals** to be of potential value:

- **5-methyltetrahydrofolate** (3 additional gene hits)

Your clinical team has identified these **high-value foods** that you should emphasize in your diet to improve *MTHFR* function:

- Chocolate • Pumpkin Seeds • Quinoa • Rice Bran

Your clinical team has identified several **environmental risk factors** that can influence the function of MTHFR:

- Helium • Angiotensin II Type 1 Receptor Blockers • Palmitic Acids • Venoms • Tetrazoles • Water Pollutants • Pyrazoles • Adrenergic Agents • Sleep Apnea Syndromes • Cacao • Air Pollutants • Citrus • Sialic Acids • Dioxoles • Cardiac Glycosides • Tyramine • Valine • Pyrethrins • Belladonna Alkaloids • Plant Components, Aerial • Polymethacrylic Acids • Viper Venoms • Floxuridine • Daunorubicin • Quercetin • Sodium, Dietary • Cinnamates • Cocos • Tropanes • Hydroxycholecalciferols • Smoke • Cyclopropanes • Hydroxybenzoic Acids • Pesticides • Immunization, Passive • Alkaloids • Fatty Acids, Essential • Sodium • Hypoglycemic Agents

FOLH1

FOLH1

Full Name: 'folate hydrolase (prostate-specific membrane antigen) 1'

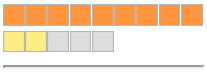
The FOLH1 gene provides instructions for making folate hydrolase 1, a type II transmembrane glycoprotein belonging to the M28 peptidase family. The protein acts as a glutamate carboxypeptidase on various substrates, including the nutrient folate and the neuropeptide N-acetyl-l-aspartyl-l-glutamate. It is found in a number of tissues such as the prostate (it is also known as prostate-specific membrane antigen), the central and peripheral nervous system and the kidney. Variation in this gene may be associated with impaired intestinal absorption of dietary folates, resulting in low blood folate levels and consequent high levels of the toxic protein homocysteine. In the brain, activity of this protein may be involved in a number of pathological conditions associated with toxicity from excess glutamate. In the prostate the protein is found at higher levels in cancerous cells, and as such, is used as an effective diagnostic and prognostic indicator of prostate cancer (PSA).

Found in: Brain • Colon • Heart • Kidney • Liver • Lung • Ovary • Pancreas • Placenta • Prostate • Salivary gland • Semen • Skeletal Muscle • Small Intestine • Spleen • Testis

Your clinical team considers this gene result **noteworthy but not actionable**

PHASE I DETOXIFICATION

The body's detoxification usually proceeds in three 'phases', with each phase passing the toxin to the next phase after its completes its work. The first stage ('phase I') involves enzymes known as 'cytochromes' (usually identified by the prefix 'CYP" in their name.) There are many different cytochromes and each one does a particular, specific job. Phase I reactions transform the toxin into a chemical form that can be metabolized by the phase II enzymes. The phase I cytochromes are an important starting point for the metabolism of many drugs, and individuals who have compromised cytochrome function may have problems eliminating pharmaceutical effectively.



DRD2

DRD2

Full Name: 'dopamine receptor D2'

This gene encodes a dopamine receptor. A missense mutation in this gene causes the rare myoclonus dystonia; other mutations have been associated with schizophrenia.

Found in: Brain • CNS • Kidney • Nervous system • Pituitary gland • Retina • Vascular system

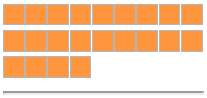
Your clinical team considers this gene result **significant and actionable.**

You have an especially noteworthy SNP polymorphism on **DRD2:**

- **rs6277** Pro290Pro (++) **OPUS:** Associated with schizophrenia • substance abuse • dopamine (risk)

PHASE II DETOXIFICATION

The second stage of detoxification ('phase II') involves the further processing of toxins, chemicals and drugs after their initial transformation in phase I. Phase II usually involves the conversion of the toxin into a relatively benign end product by attaching (conjugating) the toxin to other water-soluble substances to increase its solubility. Each of the different types of phase II enzymes catalyzes a different type of conjugation reaction.



GSR

GSR

Full Name: 'glutathione reductase'

GSR is a central enzyme of cellular antioxidant defense. Glutathione plays a key role in maintaining proper function and preventing oxidative stress in human cells. It can act as a scavenger for hydroxyl radicals, singlet oxygen, and various electrophiles. Reduced glutathione reduces the oxidized form of the enzyme glutathione peroxidase, which in turn reduces hydrogen peroxide (H_2O_2), a dangerously reactive species within the cell. In addition, it plays a key role in the metabolism and clearance of xenobiotics, acts as a cofactor in certain detoxifying enzymes, participates in transport, and regenerates antioxidants such and Vitamins E and C to their reactive forms. Some patients exhibit deficient levels of glutathione activity as a result of not consuming enough riboflavin in their diets.

Found in: Brain • Epidermis • Fetus • Lacrimal gland • Lens • Leukocyte • Neutrophil • Oesophagus • Placenta • Red blood cell • Semen • Tear • Urine

Your clinical team considers this gene result **significant and actionable.**

New concepts:

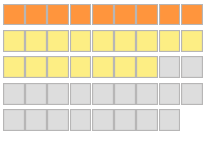
- A **xenobiotic** is a chemical compound foreign to the body. Xenobiotics include drugs, and environmental compounds such as pollutants that are not produced by the body. In the environment, xenobiotics include synthetic pesticides, herbicides, and industrial pollutants that would not be found in nature.
- **Singlet oxygen** is a high energy form of oxygen. Singlet oxygen is one of the reactive oxygen species, which is linked to oxidation of LDL cholesterol and resultant cardiovascular effects.
- **Oxidative stress** reflects an imbalance between the levels of reactive oxygen species and the body's ability to readily detoxify the reactive intermediates or to repair the resulting damage.
- In chemistry, an **electrophile** (literally electron lover) is a molecule attracted to electrons. It participates in a chemical reaction by accepting an electron pair in order to bond to a other molecules that want to give them up.

You have a few **especially noteworthy** SNP polymorphisms on **GSR:**

- **rs3594** (++) **OPUS:** Associated with anemia • autism • bipolar (risk)
- **rs2551715** (++) **OPUS:** Associated with lupus (risk)

OXIDATIVE/ ANTIOXIDANT GENOMICS

Oxidative stress reflects an imbalance between the systemic manifestation of reactive oxygen species (free radicals) and the body's ability to readily detoxify the reactive intermediates or to repair the resulting damage. Polyunsaturated fatty acids, particularly arachidonic acid and linoleic acid, are primary targets for free radical and singlet oxygen oxidations. The best studied cellular antioxidants are the enzymes superoxide dismutase (SOD), catalase, and glutathione peroxidase. Oxidative stress is also thought to contribute to the aging process.



GCLC

GCLC

Full Name: 'glutamate-cysteine ligase, catalytic subunit'

Glutamate-cysteine ligase, also known as gamma-glutamylcysteine synthetase is the first rate-limiting enzyme of glutathione synthesis. Glutathione (GSH) is an important antioxidant in plants, animals, fungi, and some bacteria and archaea, preventing damage to important cellular components caused by reactive oxygen species such as free radicals, peroxides, lipid peroxides and heavy metals. Cigarette smoke has been shown to epigenetically induce hypermethylation of the GCLC, depressing its activity. S-adenosylmethionine (SAMe) has been shown to increase cellular glutathione content in persons suffering from a disease-related glutathione deficiency.

Found in: Kidney • Liver

Your clinical team considers this gene result **significant and actionable.**

New concepts:

- **Hypermethylation** is an increase in the epigenetic methylation of cytosine and adenosine residues in DNA.

You have a few **especially noteworthy** SNP polymorphisms on **GCLC:**

- **rs2277108** 1281+176C>T (+-)
- **rs13437395** 1281+1881A>G (+-)
- **rs617066** 446+1658C>T (++)

Your clinical team has identified the following **nutraceuticals** to be of potential value:

- **Vitamin D (calciferols)** (9 additional gene hits)

CARDIOVASCULAR GENOMICS

Cardiovascular disease (CVD) is a class of diseases that involve the heart or blood vessels. Cardiovascular diseases are the leading cause of death globally. There are several risk factors for heart diseases: age, gender, tobacco use, physical inactivity, excessive alcohol consumption, unhealthy diet, obesity, family history of cardiovascular disease, raised blood pressure (hypertension), raised blood sugar (diabetes mellitus), raised blood cholesterol, psychosocial factors, poverty and low educational status, and air pollution. It is estimated that 90% of CVD is preventable.

PSRC1

PSRC1

Full Name: 'proline/serine-rich coiled-coil 1'

This gene encodes a target for regulation by the tumor suppressor protein p53. Thus its main role appears to be the supression of unwarranted growth. Variations appear to be associated with increased risk of coronary artery disease.

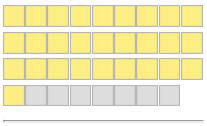
Your clinical team considers this gene result **significant and actionable.**

New concepts:

- A **tumor suppressor** is a gene whose function is to limit cell proliferation and loss of whose function leads to cell transformation and tumor growth.

You have an especially noteworthy SNP polymorphism on **PSRC1:**

- **rs599839** (++)



CETP

CETP

Full Name: 'cholesteryl ester transfer protein, plasma'

Cholesteryl ester transfer protein (CETP), also called plasma lipid transfer protein, assists the transport of cholesterol components and triglycerides between the lipoproteins. It collects triglycerides from very-low-density (VLDL) or low-density lipoproteins (LDL) and exchanges them for cholesterol components from high-density lipoproteins (HDL), and vice versa. Most of the time CETP trades a triglyceride for a cholesterol component or a cholesterol component for a triglyceride.

Found in: Adipose tissue • Adrenal gland • Blood • Heart • Liver • Plasma • Skeletal Muscle • Small Intestine • Spleen • Urine

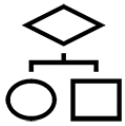
Your clinical team considers this gene result **significant and actionable.**

You have a few **especially noteworthy** SNP polymorphisms on **CETP:**

- **rs1800775** -656C>A (+-) **OPUS:** Associated with HDL cholesterol • lipid levels • venous thromboembolism (risk) **GWAS**: Triglycerides (HDL) • Lipid traits (HDL-C) • Blood metabolite levels (X-12038) • Triglycerides (apoA-1) • HDL cholesterol
- **rs3764261** (+-) **OPUS:** Associated with HDL LDL cholesterol triglycerides (risk) **GWAS**: Lipoprotein-associated phospholipase A2 activity and mass (mass) • Cholesterol, total • Lipid traits (HDL) • Hematological and biochemical traits (HDL) • Age-related macular degeneration • Triglycerides • Metabolic syndrome (HDL) • HDL cholesterol • Metabolic syndrome (bivariate traits) (BP-HDLC) • LDL cholesterol

Your clinical team has identified several **environmental risk factors** that can influence the function of CETP:

- Helium • Polymethacrylic Acids • Thiazepines • Palmitic Acids • Pituitary Hormones • Floxuridine • Quercetin • Cinnamates • Quinolones • Cocos • Flavoring Agents • Hydroxycholecalciferols • Glutamates • Adrenergic Agents • Cyclopropanes • Cacao • Sialic Acids • Sleep Disorders • Fats • Dioxoles • Cardiac Glycosides • Tyramine • Sodium



MULTI-SNP ALGORITHMS

Algorithms are perhaps the most significant and flexible aspect of your Opus 23 data. They are usually the easiest result for the non-medical person to understand, because their conclusions are usually simplified statements in everyday language.

Many correlations between SNPs and various traits exist as 'haplotypes,' clusters of SNPs, often on different genes, that must be evaluated as 'true' or 'false' based on their total outcome values. Some algorithms may identify risks for certain problems, while others identify special strengths or benefits you might possess. It's helpful to think of an Opus 23 algorithm as a tiny flowchart, that depending on which way the result branches, generates a 'true or false' result.

For example, a simple algorithm to determine if you should get out of bed might be:

- If you hear the alarm clock, open your eyes.
- If it's dark outside, go back to bed.
- If it's light outside, check the time.
- If it's earlier than 7AM, go back to bed.
- If it's later than 7AM, get up, check calendar
- If it's Saturday, go back to bed.

As can be seen, there are a lot of ways you can go back to bed with this algorithm! And this is also true as well for the Opus 23 Pro algorithms: In order for an algorithm to be true, it must fufill all of several conditions. *If even one condition fails, the whole algorithm will be false.*

Each algorithm is displayed in its own box, and contain information about the genes and SNPs used in its creation. The title of the algorithm is generally its conclusion. Typically, your report contains only true algoriths, although your clinical team may choose to include false algorithms as well, especially if it would be helpful to make you aware of something you're likely to not be prone to. Thus:

- An algorithm that returns a **true** will have a 'check' icon in the bottom left-hand box. The conclusions of these algorithms **pertain** to you based on your genomic data results.
- An algorithm that returns a **false** will have a 'cross' icon in the bottom left-hand box. The conclusions of these algorithms **do not pertain** to you based on your genomic data, other than perhaps the added knowledge that this is one less thing in life to worry about.

CLASSIC GENETICS

Probably A blood group (genotype AO) | TRUE

Genes: ABO
Repute: NEUTRAL
Magnitude: 2
Frequency: 38%

INTERPRETATION: You are likely blood type A carrying one 'A' allele and one 'O' on the ABO gene (genotype AO). You will be an ABO type AO if you are carrying a type O allele (i.e., the rs8176719(DI) genotype), and if you are rs8176746(GG) and rs8176747(CC). A small number of individuals have had this genotype and reported that they were blood group O. If you are unsure of your ABO blood type you may want to opt for a serologic (blood test) to confirm this result.

This Classic Genetics algorithm is **true** for you

Your results: rs8176746 (**GG**) | rs8176719 (**DI**) | rs8176747 (**CC**)

Blood group A subtype A1 | TRUE

Genes: ABO
Repute: NEUTRAL
Magnitude: 2
Frequency: 80%

INTERPRETATION: You have the blood group A subtype A2. The A blood type contains about 20 subgroups, of which A1 and A2 are the most common (over 99%). A1 makes up about 80% of all A-type blood, with A2 making up almost all of the rest. These two subgroups are not always interchangeable as far as transfusion is concerned, as some A2 individuals produce antibodies against the A1 antigen. Complications can sometimes arise in rare cases when typing the blood. A2 type A has less enzyme reactivity than A1 and some researchers speculate that there must have been evolutionary pressure on this gene to develop such variants, possibly as a result of viral outbreaks among different human populations living in various ecosystems.

This Classic Genetics algorithm is **true** for you

Your results: rs8176704 (**GG**) | rs8176750 (**N/A**)

Secretor | TRUE

Genes: FUT2
Repute: NEUTRAL
Magnitude: 2
Frequency: 77%

INTERPRETATION: You are a ABH 'secretor'. rs601338 is found on chromosome 19 in the alpha(1,2)-fucosyltransferase FUT2 gene. The wild-type rs601338(G) encodes the "secretor" (Se) allele, while rs601338(A) encodes the "non-secretor" (se) allele. A study of 115 Swedish adults concluded that secretor rs601338(GG) homozygotes and heterozygotes have a genetic susceptibility to infection by the Norwalk norovirus, a major (and contagious) cause of acute gastroenteritis worldwide among adults.

This Classic Genetics algorithm is **true** for you

Your results: rs601338 (**AG**)

Iris color and morphology | TRUE

Genes: SEMA3A,TRAF3IP1,CHR14-92773663,HERC1,TYR,HERC2
Repute: NEUTRAL
Magnitude: 0.1
Frequency: N/A

INTERPRETATION: The iris is the colored part of the eye, and patterns in the iris are highly variable. Research has investigated a possible relationship between iris patterns and the development of the nervous system. Large studies on four characteristics of the iris (the numbers of crypts, or recesses, iris furrows, presence of pigmented rings around the pupils, and number of nevi, or marks in the iris) were carried out with Australian people of European descent. An association was found between the frequency of crypts and the following variants: rs1533995 of the SEMA3A gene affecting nerve cells; furrows and variants within the rs3739070 SNP of the cytoskeleton gene TRAF3IP1; and the pigmented ring and variants at rs12896399 SNP, an intergenic location near the well-known pigmentation SLC24A4 gene. These findings individually accounted for around 1.5%-3% of the variance for these iris characteristics. These findings suggest that genes involved in normal nerve development may also affect the appearance of the iris. With regard to overall eye color, rs1393350 in the TYR gene, rs12896399 as mentioned above and rs1667394 in HERC2 were found to influence the likelihood of blue or green eyes in people with non-brown eyes.

Morphology	Appearance	Gene	Genotype
Crypts	Typical appearance	SEMA3A	rs1533995 (AG)
Furrow contractions	Typical appearance	TRAF3IP1	rs3739070 (AA)
Furrow contractions	Shorter, less distinct or absent	TRAF3IP1	rs3739070 (GG)
Pigmentation rings around pupil	Typical pigmentation	CHR14-92773663	rs12896399 (GT)
Eye color if non-brown	Typical likelihood of blue instead of green	CHR14-92773663	rs12896399 (GT)
Iris nevi	Slightly more pronounced	HERC1	rs11630290 (GG)
Eye color if non-brown	More likely to have blue eyes instead of green	HERC2	rs1667394 (TT)

This Classic Genetics algorithm is **true** for you

Your results: rs1533995 (**AG**) | rs3739070 (**AA**) | rs12896399 (**GT**) | rs11630290 (**CC**) | rs1393350 (**GG**) | rs1667394 (**TT**)

NEURODEGENERATIVE DISEASE

APOE E2/E3 Genotype | TRUE

Genes: APOE
Repute: BENEFIT
Magnitude: 2
Frequency: 10.8~13.3~7.9~APOE%

INTERPRETATION: You have one APOE-ε2 allele and one APOE-ε3 allele. This is associated with a slightly lower risk of Alzheimer's disease. A study found that children with an apo E2E3 genotype had lower concentrations of low-density lipoprotein cholesterol (LDL-C) and apolipoprotein B (apo B) than those with an apo E4E3.

This Neurodegenerative Disease algorithm is **true** for you

Your results: rs429358 (**TT**) | rs7412 (**CT**)

Increased risk of Parkinson's Disease | TRUE

Genes: MTHFR,COMT
Repute: RISK
Magnitude: 2
Frequency: N/A

INTERPRETATION: The risk of Parkinson's disease was found to be higher in people with two copies of the catechol-O methyltransferase (COMT) gene variant alleles, rs4680 (AA) and rs4633 (TT). The risk is even higher when the variant form of the methylene tetrahydrofolate reductase (MTHFR) gene rs1801133 C677T (A) allele is present, which may indicate high homocysteine concentrations in the blood.

This Neurodegenerative Disease algorithm is **true** for you

Your results: rs1801133 (**AG**) | rs4680 (**AA**) | rs4633 (**TT**)

Elevated brain and cerebrospinal fluid concentrations of kynurenic acid | TRUE

Genes: KMO
Repute: RISK
Magnitude: 2.1
Frequency: N/A

INTERPRETATION: Kynurenic acid (KYNA or KYN) is a product of the normal metabolism of amino acid L-tryptophan. It has been shown that kynurenic acid possesses neuroactive activity. It acts as an antiexcitotoxic and anticonvulsant, most likely through acting as an antagonist at excitatory amino acid receptors. Because of this activity, it may influence important neurophysiological and neuropathological processes. Patients with schizophrenia show increased brain and cerebrospinal fluid (CSF) concentrations of kynurenic acid. The KMO polymorphism rs1053230 is situated in the part of the gene sequence coding for positions outside of the mitochondria membrane. You have the minor allele (T) of the KMO SNP rs1053230 which was strongly associated with increased CSF concentrations of KYNA. Numerous studies suggest that brain KYNA is a biologic marker of neuroinflammation. As KYNA production is increased in animals on a ketogenic diet, this type of diet may not be optimum for you.

This Neurodegenerative Disease algorithm is **true** for you

Your results: rs1053230 (**TT**)

MIND/ BODY

Significantly heightened placebo effect | TRUE

Genes: COMT,TPH2
Repute: NEUTRAL
Magnitude: 3
Frequency: 7%

INTERPRETATION: This client is heterozygous for the COMT rs4680(AA) variant (often referred to as 'val158met'). This variation produces a valine to methionine substitution, resulting in a less thermostable COMT enzyme that exhibits a 3-fold reduction in activity. Lower COMT enzymatic activity results higher dopamine levels; lower pain threshold, enhanced vulnerability to stress. Yet this genotype also appears to be also more efficient at processing information under most conditions. val158met has been associated with a more 'exploratory' personality'. A recent study showed that as the number of COMT val158met met alleles increased progressively from rs4680(GG) to rs4680(AG) to rs4680(AA), and COMT activity decreased (theoretically making more dopamine available in the prefrontal cortex), placebo responses increased in a linear fashion.

This placebo effect is greatly enhanced by this client also carrying the COMT rs4633 (TT) allele as rs4633 was found to be in strong linkage disequilibrium with rs4680.

This Mind/ Body algorithm is **true** for you

Your results: rs4680 (**AA**) | rs4633 (**TT**) | rs4570625 (**TT**)

Oxytocin 'social/ empathy' polymorphism | TRUE

Genes: OXTR
Repute: BENEFIT
Magnitude: 3
Frequency: N/A

INTERPRETATION: rs53576 is a silent G to A change in the oxytocin receptor (OXTR) gene. You have the GG genotype, which appears to predispose to gaining benefits in the managment of stress form seeking social support. Understress, individuals with with one or more copies of the G version of rs53576 were more likely to seek emotional support from their friends, compared to those with two copies of the A version. Studies have demonstrated that individuals with the G allele are more empathetic, feel less lonely, employ more sensitive parenting techniques, and have lower rates of autism. GG genotype rs53576 also tend to be on average more optimistic and empathetic and handle stress well.

This Mind/ Body algorithm is **true** for you

Your results: rs53576 (**GG**)

METHYLATION

Significantly reduced MTHFR enzyme activity | TRUE

Genes: MTHFR,CBS
Repute: RISK
Magnitude: 3.3
Frequency: N/A

INTERPRETATION: MTHFR is a key enzyme in the methylation pathway and is responsible for converting folate into its active state. The two main variants that are well understood and tested for are C677T and A1298C. The end results of having one of these SNPs are reduced enzyme activity and a reduced amount of usable folate. MTHFR is most commonly associated with homocysteinemia, especially in conjunction with low B vitamin status. Homocysteinemia is associated with many cardiovascular disorders such as increased risk of atherosclerosis, stroke, abdominal aortic aneurysm, essential hypertension, and venous thrombosis. Other conditions correlated with MTHFR polymorphisms are increased risk of diabetic depression, schizophrenia, autism, osteoporosis, certain cancers, and pregnancy-related disorders.The A1298C is associated with a decreased enzyme activity but not to the same degree as the C677T mutation. In the C677T SNP, the enzyme activity is reduced by each mutant allele present.

CBS variant noted: Having the variant form of the CBS (cystathionine beta synthase) gene at rs234706(A), known as the C699T polymorphism may help to keep your homocysteine levels normal, despite the effect of reduced MTHFR enzyme activity. Having the CBS 699T minor allele will not affect other potential issues relating to folate metabolism however: the formation of DNA and neurotransmitters can also be influenced by other genes.

C677T (rs1801133)	A1298C (rs1801131)	Result
-/-	-/-	Normal enzyme activity
-/-	+/-	8-10% reduced enzyme activity
-/-	+/+	30-40% reduced enzyme activity
+/-	-/-	30-40% reduced enzyme activity
+/-	+/-	50-60% reduced enzyme activity
+/+	-/-	60-70% reduced enzyme activity
+/+	+/-	60-70% reduced enzyme activity

This Methylation algorithm is **true** for you

ADDITIONAL THERAPEUTICS:
The CBS C699T variant will work to reduce the neuroexcitatory effects of homocysteine levels but should also be supported with pyridoxal-5-phosphate because of a probable bottleneck at CBS due to potential lack of SAMe from the methionine cycle.

Your results: rs1801133 (**AG**) | rs1801131 (**GT**) | rs234706 (**AG**)

AUTO-IMMUNE/ INFLAMMATORY

Slight 'outside-in' causality to atopic dermatitis | TRUE

Genes: FLG
Repute: RISK
Magnitude: 1.5
Frequency: N/A

INTERPRETATION: Atopic dermatitis (AD, 'eczema') is a multifactorial disease associated with a barrier disruption of the skin and intense systemic inflammation. The immunologic features of AD are well established, controversy remains as to whether AD is caused by systemic inflammation triggering barrier dysfunction (the 'inside-out' hypothesis) or from the epidermal skin barrier disruption triggering immunologic imbalance (the 'outside-in' hypothesis). The genetic basis is incompletely understood; however, loss of function mutations in the filaggrin gene (FLG) are the most significant and widely replicated genetic risk factor reported to date. Filaggrin gene mutations are associated with persistent AD, and it has been posited that environmental factors such as temperature and humidity also can affect filaggrin production as it relates to barrier function. Skin barrier disruption results in increased cutaneous and systemic lymphocyte Th2 cell responses. Inflammatory Th2 cells triggered by an impaired skin barrier also may predispose patients to the development of allergic diseases such as asthma, in line with 'Atopic March', or the progression of AD to other forms of atopy (eg, food allergy, asthma). Filaggrin polymorphisms have been associated with significantly high levels of serum FFA compared with controls. Epidermal de novo fatty acid synthesis plays an important role in permeability barrier homeostasis. Disruption of the permeability barrier results in a rapid and marked increase in fatty acid synthesis. Barrier disruption increases the activity and mRNA levels of both of the key enzymes required for de novo fatty acid synthesis, acetyl CoA carboxylase and fatty acid synthase.

This Auto-Immune/ Inflammatory algorithm is **true** for you

ADDITIONAL THERAPEUTICS:
A topical probiotic may be indicated in filaggrin-relatec atopic dermatitis. One study reported that levels of filaggrin protein — a critical component of the skin barrier — were twice as high in skin treated with a probiotic extract than in untreated skin. This may have to do with disruption of S. aureus biofilms. Two strains, L. reuteri and B. bifidus appear to be the best indicated, as well as ammonia oxidizing bacteria such as Nitrosomonas eutropha.

Your results: rs11584340 (**--**) | rs61816761 (**N/A**) | rs11582620 (**AA**) | rs6700998 (**GG**)

Risk of autoimmune disorder/ gluten sensitivity | TRUE

Genes: KIAA1109
Repute: RISK
Magnitude: 4
Frequency: 6%

INTERPRETATION: Of SNPs outside the HLA region, rs13119723(G) and rs6822844(G) in the region of the IL21 gene showed the strongest association with celiac disease in a study of ~800 Caucasian patients and a meta-analysis of two further populations.[PMID 17558408] This constellation also showed a signficant association with rheumatoid arthritis and psoriasis.

This Auto-Immune/ Inflammatory algorithm is **true** for you

Your results: rs6822844 (**GT**) | rs13119723 (**AG**)

C-Reactive Protein Genotypes, Nutritional Status and Inflammation | TRUE

Genes: CRP
Repute: SEE TABLE
Magnitude: 4
Frequency: N/A

INTERPRETATION: C-reactive protein is a protein produced by the CRP gene in response to inflammatory signals from interleukin 6. It activates complement, which enhances the ability of the immune system to remove pathogens. Inflammation, as indicated by CRP levels in the blood, is a risk factor for chronic diseases. Several SNPs (rs3093058, rs3093062, rs2808630) on the CRP gene are related to foods influencing genetic susceptibility to heightened systemic inflammation. This algorithm uses a combination of major and minor alleles for these three SNPS to determine your potential risk for several diet-related factors. The results of your algorithm calculations are summarized inthe following table.

Effects of cholesterol/ triglycerides	You are unlikely to experience increased inflammation as a result of high CRP if you have cholesterol and triglycerides in your diet.
Effects of weight loss	You will most likely not experience reduced inflammation as a result of lower CRP levels when you lose weight.

This Auto-Immune/ Inflammatory algorithm is **true** for you

Your results: rs3093058 (**TT**) | rs3093062 (**CC**) | rs2808630 (**TT**)

HLA genotypes and haplotypes | TRUE

Genes: HLA-A,HLA-C,HLA-D,HLA-DRB1,HLA-DQA1,IFHI1
Repute: SEE CHART
Magnitude: 3.5
Frequency: N/A

INTERPRETATION:

Disease Trait	Risk/benefit	Type	Genes	SNP Details	Risk Genotype	PMID
BAD	**Psoriasis**	Increased risk (2.8x)	SNP	HLA-C*06	rs10484554 (T)	18369459
BAD	**Psoriasis**	Increased risk	SNP	HLA-C*0602	rs1265181(G)	19169255
GOOD	**Crohns Disease**	Decreased risk	SNP	HLA-DRB1	rs9271366 (A)	21699788
GOOD	**Ulcerative colitis**	Significantly decreased risk (.58x)	SNP	HLA-DQ A*0101	rs2395185(TT)	19122664
BAD	**Type I diabetes**	Significantly increased risk (9.47x)	SNP	HLA-DQ A*0101	rs2395185(TT)	19837788
BAD	**Hay fever (allergic rhinitis)**	Increased risk	SNP	HLA-DRB1	rs2155219(T)	22036096
BAD	**Rheumatoid arthritis**	Increased risk (2.3x)	SNP	HLA-DRB1	rs6457617(T)	17554300
BAD	**Graves Disease (TSHR autoantibodies)**	Increased risk	SNP	HLA-DRB1	rs6457617(T)	21841780
BAD	**Rheumatoid arthritis**	Significant increased risk (5.2x)	SNP	HLA-DRB1	rs6457617(TT)	17554300
BAD	**Graves Disease (TSHR autoantibodies)**	Significant increased risk	SNP	HLA-DRB1	rs6457617(TT)	21841780

This Auto-Immune/ Inflammatory algorithm is **true** for you

Your results:	rs2187668 (**CC**)	rs1265181 (**CG**)	rs2395185 (**TT**)	rs9271366 (**AA**)	rs3135388 (**GG**)	rs1061235 (**AA**)
rs10484554 (**CT**)	rs7775228 (**TT**)	rs2155219 (**GT**)	rs6457617 (**TT**)			

DIET AND LIFESTYLE

Any type of exercise results in weight loss | TRUE

Genes: ADRB2,ADRB3
Repute: BENEFIT
Magnitude: 2.5
Frequency: 12%

INTERPRETATION: 88% of peoples' bodies resist burning fat during low intensity exercise. You are part of the 12% of the population who can lose weight with any type of exercise.

This Diet and Lifestyle algorithm is **true** for you

Your results: rs1042713 (**AA**) | rs4994 (**AA**)

Benefits from low-fat diet | TRUE

Genes: PPARG,ADRB2,ADRB3
Repute: BENEFIT
Magnitude: 2
Frequency: 39%

INTERPRETATION: You will lose 2.5 times as much weight on a low fat diet.

This Diet and Lifestyle algorithm is **true** for you

Your results: rs1042713 (**AA**) | rs4994 (**AA**) | rs1801282 (**CC**) | rs1042714 (**CC**)

AGING RELATED

Evidence of markers of longevity | TRUE

Genes: CAMK4,MINPP1,TOMM40,CDKN2B,APOC1
Repute: BENEFIT
Magnitude: 3
Frequency: N/A

INTERPRETATION: You have a considerable number of poymorphisms that are associated with longevity. Many of the genetic mechanisms for extreme longevity involves the avoidance of certain risk alleles that predispose to common diseases, including coronary artery disease, Alzheimer's disease, high cholesterol and chronic kidney disease. Besides some disease SNPs that are depleted in centenarians, it is also plausible that centenarians carry a different genetic background than the normal population consisting of protective SNPs that predispose for extreme longevity.

This Aging Related algorithm is **true** for you

Your results: rs10491334 (**CC**) | rs9664222 (**CC**) | rs4977756 (**AG**) | rs2075650 (**AA**) | rs4420638 (**N/A**)

Bone mineral density | TRUE

Genes: WNT16
Repute: RISK
Magnitude: 3.5
Frequency: 37.4%

INTERPRETATION: You may have weaker bones and potential for decreased mineral density. The WNT16 gene is part of the regulatory process for bone density. The risk genotype for lower bone density in the rs2707466 SNP of WNT16 is the homozygous (CC), whereas the (TT) genotype is associated with greater bone density and stronger bones.

This Aging Related algorithm is **true** for you

Your results: rs2707466 (**CC**)

Reduced memory abilities | TRUE

Genes: WWC1
Repute: RISK
Magnitude: 3
Frequency: 15%

INTERPRETATION: Your genotype suggests you may have reduced memory abilities. A study found that carriers of the T allele of rs17070145 in the KIBRA gene had 24% better free recall performance 5 minutes after word presentation and 19% better free recall performance 24 hours after word presentation than did non-carriers. T allele carriers had significantly better memory scores than non-carriers in the Buschke's Selective Reminding Test. Performance on another episodic memory task, the Rey Auditory Verbal Learning Test, was also significantly different between people with different alleles.

This Aging Related algorithm is **true** for you

Your results: rs17070145 (**CC**)

HEREDITARY METABOLIC

Probably lactose tolerant | TRUE

Genes: LAC,MCM6
Repute: BENEFIT
Magnitude: 2
Frequency: N/A

INTERPRETATION: The milk sugar lactose is digested by the lactase enzyme. Most people stop producing lactase after weaning, becoming lactose intolerant. Some people have developed lactase tolerance, or persistence, in which lactase production continues into adulthood. Intolerance is more common than lactase persistence. You are probably lactose tolerant. Two SNPs in the MCM6 gene rs182549 and rs4988235, linked to the lactase LCT gene, are the most common genetic causes in European Caucasian populations of hypolactasia, or lactose intolerance. The 'T' allele in rs182549 and the 'A' alele in rs4988235 are associated with lactose tolerance.

This Hereditary Metabolic algorithm is **true** for you

Your results: rs4988235 (**AA**) | rs182549 (**TT**)

Increased hypersensitivity response to non-steroidal anti-inflammatory drugs | TRUE

Genes: AOC1
Repute: RISK
Magnitude: 4
Frequency: 58%

INTERPRETATION: Non-steroidal anti-inflammatory drugs (NSAIDs) are the drugs most frequently involved in drug reactions. In the allergic response to NSAIDs histamine is released, and this is responsible for some of the clinical symptoms. The AOC1 (diamine oxidase) 16 Met allele rs10156191(T), which causes decreased metabolic capacity, is common among patients with hypersensitivity to NSAIDs.

This Hereditary Metabolic algorithm is **true** for you

Your results: rs10156191 (**CT**)

Increased risk of metabolic syndrome/ consequences | TRUE

Genes: GNB3
Repute: RISK
Magnitude: 4
Frequency: 55.1%

INTERPRETATION: rs5443, a SNP in the G-protein beta3 subunit (GNB3) gene that is more commonly known as the C825T variant, has been linked to a number of metabolic conditions including obesity, coronary artery disease, insulin resistance and therefore diabetes, left ventricular hypertrophy, and hypertension.

This Hereditary Metabolic algorithm is **true** for you

Your results: rs5443 (**CT**)

Moderately increased risk of T2DM from decreased capacity to scavenge ROS | TRUE

Genes: SOD2
Repute: RISK
Magnitude: 3.3
Frequency: 16%

INTERPRETATION: Superoxide is produced as a byproduct of using oxygen in the body, and if not regulated, causes cell damage. Superoxide dismutase (SOD) is an antioxidant enzyme that helps break down the damaging superoxide free radical into either ordinary molecular oxygen (O2) or hydrogen peroxide (H2O2). SOD is an important antioxidant defense in cells exposed to oxygen. Mitochondria, the energy-producing parts of the cell, use a type of SOD called SOD2 that uses manganese in its structure. The rs4880(A) allele of SOD2 is the more common SNP. A study showed a significant link between rs4880 (A) or (AA) and type 2 diabetes in the Chinese Han population. Insufficient scavenging of reactive oxygen species might be associated with a susceptibility to type 2 diabetes.

This Hereditary Metabolic algorithm is **true** for you

Your results: rs4880 (**AG**)

Lower serum levels of vitamin B12 | TRUE

Genes: FUT2
Repute: RISK
Magnitude: 3.1
Frequency: 77%

INTERPRETATION: You are a secretor of your blood type as a result of having the FUT2 (fucosyltransferase 2) secretor phenotype. There is a link with FUT2 secretor status and infection with the H. pylori bacteria, a risk factor for inflammation of the stomach. Being a secretor of your blood type is associated with lower vitamin B12 levels in the blood, potentially due to inactivation of the intrinsic factor (GIF) needed for B12 absorption. [PMID: 23402911]

This Hereditary Metabolic algorithm is **true** for you

Your results: rs601338 (**AG**)

Blood levels of vitamins | TRUE

Genes:
MTHFR,NBPF3,ALPL,TCN1,FUT2,BCO1,G6PD,SLC23A1,GC,CHR11-LOC116733008
Repute: SEE CHART
Magnitude: 3.5
Frequency: N/A

INTERPRETATION: The correlation of genetic variations with blood levels of vitamins is an indication of tendencies from the general population, and may not be relevant to your actual current situation. There are many other influences on vitamin levels, such as vitamin intake, absorption and usage in the body. Discuss with your practitioner the need to match your genetic patterns with further examination or testing.

Trait	Risk	Type	Genes	SNP Details	Risk Genotype	PMID
BAD	**Vitamin B6**	Lower levels	SNP	TCN1	rs526934(G)	19744961
BAD	**B12**	Lower absorption (non-secretor)	SNP	FUT2	rs602662(A)	19303062
BAD	**Vitamin E (tocopherols)**	Lower levels	SNP	CHR11-LOC116733008	rs12272004(C)	20190752

This Hereditary Metabolic algorithm is **true** for you

Your results:	rs12272004 (**CC**)	rs2282679 (**TT**)	rs33972313 (**CC**)	rs5030868 (**G**)	rs7501331 (**CC**)	rs12934922 (**TT**)
rs526934 (**AG**)	rs602662 (**AG**)	rs4654748 (**TT**)	rs1780324 (**AG**)	rs1801133 (**AG**)		

Possible risk of hypomagnesemia | TRUE

Genes: MUC1,SHROOM3,DCDC5,MECOM
Repute: RISK
Magnitude: 1.5
Frequency: N/A

INTERPRETATION: A large genome-wide study of serum magnesium levels in 15,366 subjects found that common genetic variants in the genomic regions in or near the MUC1, SHROOM3, DCDC5 and MECOM genes were significantly and reproducibly associated with serum magnesium levels and clinically defined lower levels of magnesium in the blood. Magnesium is a critical mineral, and is often missing in sufficient amounts in our diet.

Interpretation: **Possible risk of low serum magnesium levels**

Gene	SNP	Risk Allele	You
MUC1	rs4072037	C	CT
SHROOM3	rs13146355	G	
DCDC5	rs3925584	C	CC
MECOM	rs448378	G	AG

This Hereditary Metabolic algorithm is **true** for you

Your results:	rs4072037 (**CT**)	rs13146355 (**N/A**)	rs3925584 (**CC**)	rs448378 (**AG**)

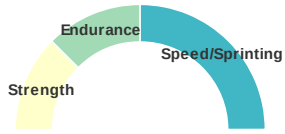
MUSCULO-SKELETAL

Training spectrum and traits indicative of elite athlete status | TRUE

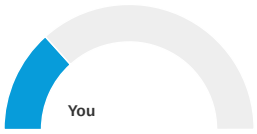
Genes: HIF1A,ACTN3,IL6,PPARGC1A,KDR,ADRB3
Repute: NEUTRAL
Magnitude: 3.2
Frequency: N/A

INTERPRETATION: Several genetic variations have been associated with improved athletic performance. The following SNPs have been identified in your genotyoe and may contribute to improvement or specific variations in athletic prowess:

- α-Actinin-3 (ACTN3) has been proposed to regulate skeletal muscle growth through its interaction with the signalling protein calcineurin. Expression of α-actininin-3 (ACTN3) is limited to fast muscle fibers responsible for generating force at high velocity. A common genetic variation in the ACTN3 gene (rs1815739/T) completely prevents the production of functional α-actinin-3 protein. This polymorphism is overepresented in strength and endurance athletes, while the CT/CC genotype is more common in sprinters.
  You have the ACTN3 genotype (CT) which is associated with a mix of muscle types/ probably best at sprinting or intermediate endurance athletics.
- Interleukin-6 (IL6), has been called by some authors 'an exercise factor' due to its pleiotropic effects (pleiotropy occurs when one gene influences two or more seemingly unrelated phenotypic traits.) Studies revealed that the frequency of the IL6 rs1800795 GG genotype were significantly higher in the power-orientated athletes compared to controls.
  You have the rs1800795 genotype (CG) which may indicate an improved ability in power-oriented sports.
- rs8192678 encodes a SNP in PPARGC1A. This gene is a 'coactivator' that regulates the genes involved in energy metabolism. The T allele appears to be more common in sprinters while the CT/CC genotypes are associated with increased endurance performance ability.
  You have the rs8192678 genotype (CT) which may indicate an improved ability in sprinter-oriented sports.



Your ability distribution



Your elite athlete potential

This Musculo-skeletal algorithm is **true** for you

Your results: rs11549465 (**CC**) | rs1815739 (**CT**) | rs1800795 (**CG**) | rs8192678 (**CT**) | rs1870377 (**N/A**) | rs4994 (**AA**)

Higher risk of lumbar disc disease | TRUE

Genes: CILP
Repute: RISK
Magnitude: 2.4
Frequency: 49%

INTERPRETATION: The Cartilage Intermediate Layer Protein, made by the CILP gene, is found in intervertebral discs, and is found at higher levels when disc degeneration happens. The lumbar discs between the spinal vertebrae in the low back are more prone to degeneration. The rs2073711 SNP is related to CILP levels, and your (GG) genotype indicates a higher of lumbar disc disease.

This Musculo-skeletal algorithm is **true** for you

Your results: rs2073711 (**GG**)

CARDIOLOGY

Increased risk of venous thromboembolism | TRUE

Genes: PON1,CCR2,CETP
Repute: RISK
Magnitude: 2
Frequency: 75%

INTERPRETATION: A small study of patients with genetic risk factors in recurring thromboembolisms (blood clots) in the veins suggested that the G variants of rs1799864 on the CCR5 gene (a receptor on white blood cells) and rs662 on PON1 (an enzyme that breaks down the toxic metabolites of some organophosphate insecticides) are associated with increased risk, while the A variant of rs1800775 on CETP (an enzyme for the transfer of cholesterol from high density lipoprotein to other lipoproteins) was associated with a reduced risk. This client's genotype suggests an increased risk of venous thromboembolism.

This Cardiology algorithm is **true** for you

Your results: rs662 (**CT**) | rs1799864 (**GG**) | rs1800775 (**AC**)

Lower heart attack risk (59%) than average | TRUE

Genes: DBH
Repute: BENEFIT
Magnitude: 2.6
Frequency: N/A

INTERPRETATION: You are in the ~30 % of people who carry two variant alleles at two SNPs, rs1108580 and rs1611115. People with these variants have 59% of risk of a heart attack or cardiovascular incident compared with people who carry none of the variant alleles for these two SNPs, based on a study of 3,000 African-Americans enrolled in the Jackson Heart Study.

This Cardiology algorithm is **true** for you

Your results: rs1108580 (**AG**) | rs1611115 (**CT**)

Higher HDL levels | TRUE

Genes: PLTP
Repute: BENEFIT
Magnitude: 3
Frequency: N/A

INTERPRETATION: The (T) allele of rs3843763 was associated with risk for lower high-density lipoprotein (HDL; the so-called 'good cholesterol') cholesterol plasma levels in studies of three independent populations, including both Caucasians and African-Americans.

This Cardiology algorithm is **true** for you

Your results: rs3843763 (**CC**)

Significant risk of salt-sensitive hypertension | TRUE

Genes: SLC4A5,GRK4,DRD2
Repute: RISK
Magnitude: 3.5
Frequency: N/A

INTERPRETATION: Studies of high blood pressure resulting from salt consumption found relevant SNPs in three genes: SLC4A5 (a sodium bicarbonate transporter), DRD2 (a dopamine receptor) and GRK4 (an enzyme that deactivates cellular sensing mechanisms). Of these, the AA mutation of rs7571842 in SLC4A5 was highly significant. , with the G allele conferring protection. Lesser effects were observed for the risk alleles of rs2960306 in GRK4 and rs6276 in DRD2. The effects of these mutations were relevant regardless of body mass index (BMI) and age.

This Cardiology algorithm is **true** for you

Your results: rs7571842 (**AA**) | rs2960306 (**GG**) | rs6276 (**N/A**)

ONCOLOGY

Significantly increased risk of prostate cancer | TRUE

Genes: FUNDC2P2,CCAT2
Repute: RISK
Magnitude: 3.6
Frequency: N/A

INTERPRETATION: Although it is a 'normal' haplotype (a common combination of SNP genotypes), having a haplotype in gene location 8q24 still increases the risk of prostate cancer. The rs1447295 (A) allele could be responsible for about seven percent of prostate cancer cases in white men of north European descent. Thus, taken together with rs6983267 (G), having these two alleles could account for as much as one quarter of prostate cancer cases in white men. In studies, the increased risk was observed for all age groups. rs1447295 (A) has about an 1.4x increased risk of prostate cancer; rs1447295 (AA) has about an 1.7x increased risk of prostate cancer. rs6983267 (G) has about an 1.3x increased risk of prostate cancer; rs6983267 (GG) has about an 1.6x increased risk of prostate cancer. Variation in the rs6983267 SNP has also been reported to affect the way aspirin decreases the risk of cancer.

This Oncology algorithm is **true** for you

Your results: rs6983267 (**GT**) | rs1447295 (**CC**)

DETOXIFICATION

NAT2 Slow Metabolizer | TRUE

Genes: NAT2
Repute: RISK
Magnitude: 3
Frequency: N/A

INTERPRETATION: You are a 'NAT2 Slow Metabolizer.' NAT2 is a phase II detoxifying enzyme that performs its work by 'acetylating' toxic compounds, allowing them to be excreted through the organs of elimination. Most non-Scandinavian Caucasians and approximately half of African-Americans are slow metabolizers. This variation is important because of its primary role in the deactivation of many chemicals in the body's environment, including those produced by caffeine, smoked or broiled meats, and cigarettes as well as aromatic amine and hydrazine drugs used medicinally. In general, slow metabolizers have higher rates of certain types of cancer and are more susceptible to side effects from chemicals metabolized by NAT2. Both slow and rapid acetylators are at increased risk for toxic overload if they are exposed to environmental toxins. Do not eat fried foods and avoid well-done meats as these may substantially increase your risk of certain cancers.

This Detoxification algorithm is **true** for you

Your results: rs1041983 (**CT**) | rs1801280 (**CT**) | rs1799929 (**CT**) | rs1799930 (**AG**) | rs1208 (**AG**) | rs1799931 (**GG**) | rs1495741 (**AA**)

CYP1A2 'slow metabolizer' Caffeine sensitivity | TRUE

Genes: CYP1A2
Repute: RISK
Magnitude: 2.5
Frequency: N/A

INTERPRETATION: You appear to have a common genotype in the gene CYP1A2 (cytochrome P450 1A2) which metabolizes coffee more slowly ('slow metabolizer') than people with some other forms. The same amount of caffeine will tend to have more stimulating effect on you than on fast metabolizers, and this genotype may also affect your metabolism of the antibiotic Ciprofloxacin.

This Detoxification algorithm is **true** for you

Your results: rs762551 (**AC**) | rs12720461 (**CC**) | rs2069526 (**TT**) | rs28399424 (**CC**)

PHARMACOGENOMICS

Preferred form(s) of B12 supplementation | TRUE

Genes: COMT,VDR
Repute: NEUTRAL
Magnitude: 1.3
Frequency: N/A

INTERPRETATION: Evidence suggests that polymorphisms in the COMT rs4680 (V158M) and VDR (Taq) rs731236 SNPs may help determine the optimum forms of vitamin B12 supplementation.

Your optimum B12 combination: **A combination of hydroxy B12 and adenosyl B12**

COMT	VDR	Result
AA	GG	• **Adenosylcobalamin B12:** The energy formation that occurs during the Citric Acid (energy production) cycle requires this form of B12. Although naturally occurring, it is the least stable of the four types of B12 outside the human body • **Hydroxycobalamin B12:** Bacteria naturally creates this form of vitamin B12, making it the main type found in most foods. It easily converts into methylcobalamin in the body. • **You should avoid Cyanocobalamin B12:** This synthetic version of vitamin B12 is created in a lab, which makes it the cheapest supplement option. It offers the most stable form of B12, although it does so through the presence of a cyanide molecule. While the amount of cyanide is not dangerous, it does require the body to expend energy to convert and remove it. This form of vitamin B12 should be avoided if possible.

This Pharmacogenomics algorithm is **true** for you

Your results: rs4680 (**AA**) | rs731236 (**GG**)

Normal statin metabolizer | TRUE

Genes: SLCO1B1
Repute: BENEFIT
Magnitude: 3
Frequency: 69%

INTERPRETATION: The SLCO1B1 gene codes for a protein produced in the liver that mediates the uptake and metabolism of statins. Three SLCO1B1 rs4149056 genotypes have been identified and classified in terms of their effect on statin metabolism in the liver. Normal activity is linked to the rs4149056(TT) genotype, decreased activity is linked to the rs4149056 (TC) genotype, and markedly decreased activity is linked to the rs4149056(CC) genotype.Your rs4149056(TT) genotype (valine/valine) is classified as normal statin metabolizers. You have a normal ability to metabolize statins (about 70% of the population). Standard doses of statins, if indicated, are recommended for LDL-C lowering.

This Pharmacogenomics algorithm is **true** for you

Your results: rs4149056 (**TT**)

Impaired NSAID drug metabolism | TRUE

Genes: CYP2C9,CYP2C8
Repute: RISK
Magnitude: 3.1
Frequency: N/A

INTERPRETATION: You have impaired metabolism of non-steroidal anti-inflammatory (NSAID) drugs, which increases the risk for gastrointestinal bleeding when taking any of these medications: aceclofenac, celecoxib, diclofenac, ibuprofen, indomethazine, lornoxicam, meloxicam, naproxen, piroxicam, tenoxicam and valdecoxib. This is due to mutations in CYP2C8*3 (rs11572080 and rs10509681) or CYP2C9*2 (rs1799853) or CYP2C9*3 (rs1057910)

This Pharmacogenomics algorithm is **true** for you

Your results: rs1799853 (**CC**) | rs1057910 (**AC**) | rs11572080 (**CC**) | rs10509681 (**TT**)

ENVIRONMENTAL/ CAUSATIVE FACTORS

This table displays the results when your SNP and gene data is cross-referenced against two major databases, the 'etiome' (the network of all causative factors, or 'etiologies') and the 'diseaseome' (the network of all diseases linked to these causative factors). This is important information, because, although not in themselves diseases, these environmental and lifestyle factors may in themselves complicate efforts to resolve health problems. Therefore they should be addressed as part of a total approach to health.

Factor	Magnitude	Factor	Magnitude
Polychlorinated Biphenyls		Fatty Acids, Unsaturated	
Immunosuppressive Agents		Sleep Disorders	
Contraceptives, Oral		Testosterone	
Anti-Inflammatory Agents, Non-Steroidal		Hormone Replacement Therapy	
Alkaloids		Anti-HIV Agents	
Antacids		Testosterone Congeners	
Minerals		Venoms	
Pyrazoles		Dipeptides	
Estrogens		Daunorubicin	
Vitamin B Deficiency		Calcium Compounds	
Neurotoxins		Antiviral Agents	
Hormone Antagonists		Flavoring Agents	
Glutamates		Thiazepines	
Disulfides		Sulfonamides	
Anticoagulants		Salicylic Acids	
Pyrimidines		Fatty Acids, Omega-3	
Tamoxifen		Organoplatinum Compounds	
Lactones		Vitamin B 12 Deficiency	
Tetrazoles		Immunization, Passive	
Citrus		Captopril	
Somatomedins		Tetanus Toxoid	
Helium		Hydroxybenzoic Acids	
Sialic Acids		Pyrethrins	
Sulfonylurea Compounds		Heparin	
Angiotensin II Type 1 Receptor Blockers		Quinolines	
Belladonna Alkaloids		Viper Venoms	
Tropanes		Hypoglycemic Agents	
Smoking		4-Hydroxycoumarins	
Carotenoids		Progesterone Congeners	
Quinolones		Ergolines	

BENEFICIAL FOODS

Based on an analysis of their micronutrient levels and special needs defined by your SNP and gene outcomes, this table lists specific foods that you may want to consider increasing your consumption of.

Food	Magnitude	Food	Magnitude
Kale *(Vitamin C total ascorbic acid, Antioxidant, Glucosinolates)*		**Chocolate** *(Magnesium, Antioxidant)*	
Broccoli *(Vitamin C total ascorbic acid, Glucosinolates)*		**Goji, Wolfberry** *(Vitamin C total ascorbic acid, Antioxidant)*	
Quinoa *(Magnesium)*		**Rice Bran** *(Vitamin B6, Magnesium)*	
Pumpkin Seeds *(Magnesium)*		**Parsley** *(Vitamin C total ascorbic acid, Antioxidant)*	
Grapefruit *(Vitamin C total ascorbic acid, Antioxidant)*		**Watercress** *(Antioxidant, Glucosinolates)*	
Lemon *(Vitamin C total ascorbic acid, Antioxidant)*		**Elderberries** *(Vitamin C total ascorbic acid, Antioxidant)*	
Escarole *(Vitamin C total ascorbic acid)*		**Onion, all types** *(Antioxidant)*	
Cilantro *(Antioxidant)*		**Bok Choy, Pak Choi** *(Glucosinolates)*	
Pineapple *(Vitamin C total ascorbic acid)*			

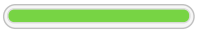
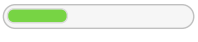
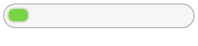
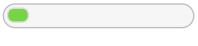
PROBLEMATIC FOODS

Based on an analysis of their micronutrient levels and special needs defined by your SNP and gene outcomes, this table lists specific foods that you may want to consider limiting your consumption of.

Food	Magnitude	Food	Magnitude
Crab *(Sodium, Purine High)*		**American Cheese** *(Sodium)*	
Gruyere Cheese *(Cholesterol)*		**Milk, Buttermilk** *(Cholesterol)*	
Cream Cheese *(Cholesterol)*		**High Fructose Corn Syrup** *(Fructose)*	

NATURAL PRODUCTS/ AGENTS

These are high-value natural products and agents which Opus 23 has determined to be worthy of consideration for inclusion into a rational dietary supplement program.

Agent	Magnitude	Agent	Magnitude
Vitamin D (calciferols) *(VDR, GCLC, CYP3A4, HLA-DRB1, CYP2J2, CYP27A1, NOS3, TPH2, MAOA)*		**5-methyltetrahydrofolate** *(MTHFR, MTRR, MTR)*	
Pyridoxal 5' phosphate *(COMT, SHMT1, CBS)*		**Magnesium** *(COMT, CBS)*	
N-acetylcysteine (NAC) *(NOS3)*		**Incremental Carbohydrate:Protein meals** *(TPH2)*	
Ashwagandha (Withania somnifera) *(MAOA)*		**Progesterone** *(MAOA)*	

UNIQUE DRUG REACTIONS

This table lists prescription medicines which your SNP data indicates you may be at risk of developing a unique drug reaction. Potential adverse reactions are indicated by an orange power bar; potential unique benefits by a green power bar. You should discuss these results with the prescribing physician before beginning any drug therapy involving these pharmaceuticals.

Drug	Reaction	Magnitude
Thiazide	*Thiazide-induced adverse metabolic effects in hypertensive patients*	
Cisplatin	*Adverse response to chemotherapy (neutropenia/leucopenia) * Ototoxicity (hearing loss) * Tinnitus, hearing impairment, Raynaud syndrome*	
Cyclophosphamide/ Doxorubicin/ Fluorouracil	*Adverse response to chemotherapy in breast cancer (alopecia)*	
Carbamazepine	*Carbamazepine resistant therapy, higher maintenance dose * Macropapular eruption*	
Docetaxel	*Adverse response to chemotherapy (neutropenia/leucopenia) * Adverse response to chemotherapy in breast cancer (alopecia)*	
Citalopram	*Elevated suicide risk * Homozygosity for the rs6295 G is associated with lower response rate in patients treated for major depression * Improved response to antidepressant medication*	
Venlafaxine	*Nausea, vomiting diarrhea * Poor drug metabolizer, lower dose requirements, nausea, vomiting and diarrhea*	
Fluorouracil	*Adverse response to chemotherapy (neutropenia/leucopenia) * Hematological toxicity, gastrointestinal toxicity * Neutropenia, diarrhea*	
Anti-microtubule drugs	*Adverse response to chemotherapy in breast cancer (alopecia)*	
Paclitaxel	*Adverse response to chemotherapy (neutropenia/leucopenia) * Adverse response to chemotherapy in breast cancer (alopecia)*	
Morphine	*Better response to pain relief drugs*	
All antimetabolite drugs	*Adverse response to chemotherapy (neutropenia/leucopenia)*	
Phenytoin	*Increased phenytoin effects due to higher plasma phenytoin levels * Poor drug metabolizer, lower dose requirements*	
All anthracycline-based drugs	*Adverse response to chemotherapy (neutropenia/leucopenia)*	
Trastuzumab	*Cardiotoxicity * Reduced response to herceptin*	
Carvedilol	*Better response to drug therapy * Improved response to blood pressure medication*	
Carboplatin	*Adverse response to chemotherapy (neutropenia/leucopenia)*	
All antimicrotubule drugs	*Adverse response to chemotherapy (neutropenia/leucopenia)*	
Daunorubicin	*Myelosuppression, cardiac toxicity, cytotoxicty*	
Paclitaxel/ Carboplatin	*Adverse response to chemotherapy (neutropenia/leucopenia)*	
Codeine	*Poor drug metabolizer, lower dose requirements*	
Clobazam	*Adverse drug reaction*	
Irinotecan	*Leukopenia, thrombpocytopenia*	
Budesonide	*Improved response for long-term asthma treatment*	
Cyclophosphamide/ Epirubicin/ Fluorouracil	*Adverse response to chemotherapy in breast cancer (alopecia)*	
Infliximab	*Better ACR20 response*	
Cyclosporine	*Gingival overgrowth, periodontal disease*	
Naltrexone	*Those with the AG genotype respond better to therapy (increase number of abstinent days)*	
Eletriptan	*Better response to drug treatment*	
Modafinil	*Poor response to modafinil*	
All platinum-based drugs	*Adverse response to chemotherapy (neutropenia/leucopenia)*	
Rizatriptan	*Better response to drug treatment*	
Ramipril	*More rapid response to drug treatment*	
Rosuvastatin	*Improved response to statin drugs*	
Gemcitabine	*Neutropenia*	
Simvastatin	*Improved response to statin drugs*	
Celecoxib	*Poor drug metabolizer, lower dose requirements*	

Zolmitriptan	*Better response to drug treatment*
Leflunomide	*Diarrhea, vomiting, liver toxicity, headache, insomnia, rash, alopecia, hypertension, leucopenia, asthma*
Sumatriptan	*Better response to drug treatment*
Metoprolol	*Improved response to blood pressure medication*
Acitretin	*Psoriasis*
Abacavir	*Presence of this SNP is predicative of hypersenitivity reaction when abacavir is given to HIV+ patients.*
Isoniazid	*Hepatotoxicity*
Sildenafil	*Better response to drug treatment*
Naratriptan	*Better response to drug treatment*
Dextromethorphan	*Poor drug metabolizer, lower dose requirements*
Amitriptyline	*Postural hypotension*
Cyclophosphamide	*Adverse response to chemotherapy (neutropenia/leucopenia)*
Etoposide	*Adverse response to chemotherapy (neutropenia/leucopenia)*
Acetylsalicylic acid	*Poor drug metabolizer, lower dose requirements*
Camptothecin	*Adverse response to chemotherapy (neutropenia/leucopenia)*
Caffeine	*Myocardial infarction*
Almotriptan	*Better response to drug treatment*
Pravastatin	*Improved response to statin drugs*
Amlodipine	*Adverse drug reaction*
Methamphetamine	*Methamphetamine psychosis and addiction*
Atenolol	*Better response to drug therapy*
Glipizide	*Poor drug metabolizer, lower dose requirements*
Verapamil	*Better response to drug therapy*
Clopidogrel	*Poor drug metabolizer, lower dose requirements, higher risk for drug-drug interactions*
Nortriptyline	*Postural hypotension*
Tolbutamide	*Poor drug metabolizer, lower dose requirements*
Frovatriptan	*Better response to drug treatment*
Methotrexate	*Mucositis, hepatic toxicity, thrombocytopenia, alopecia*