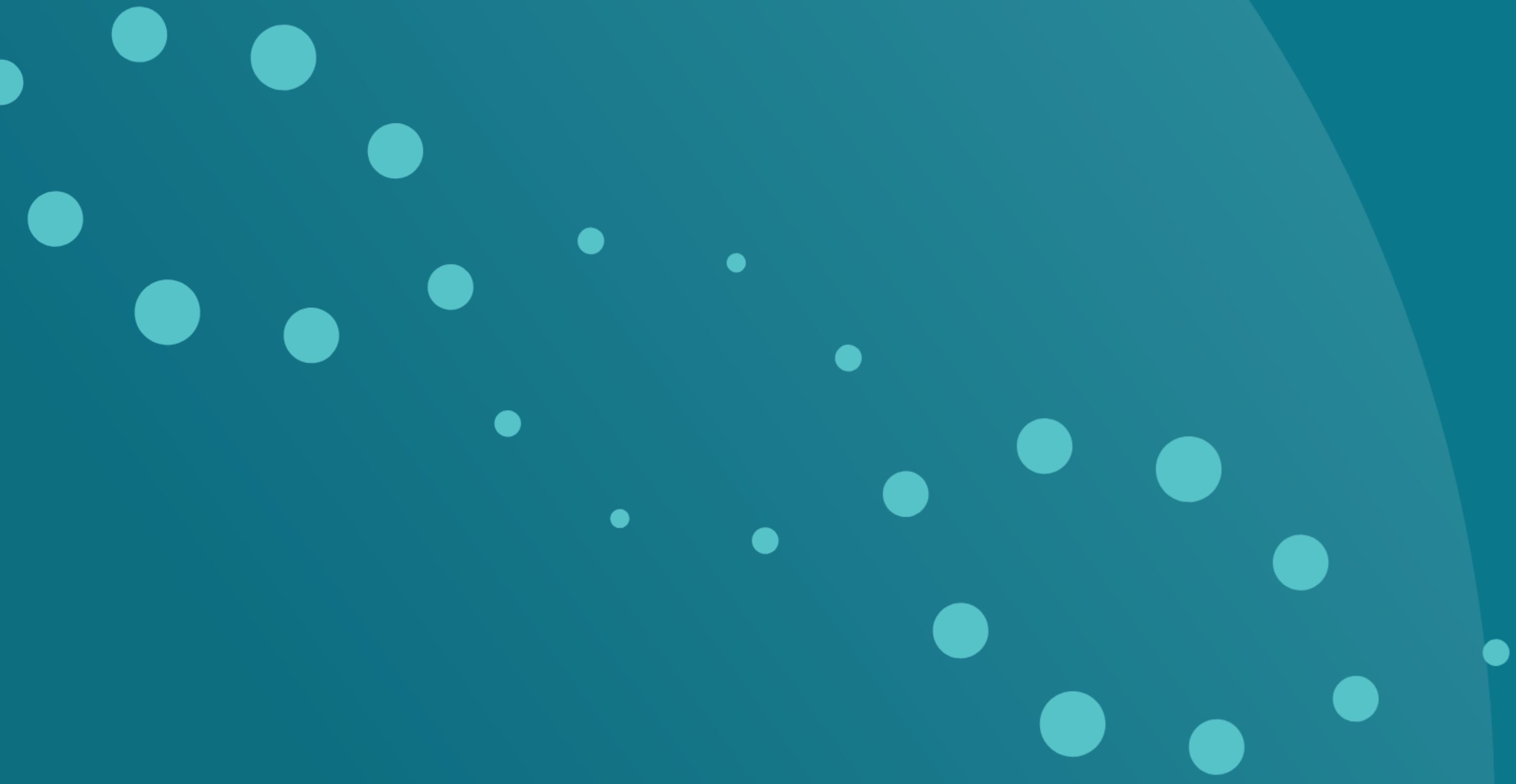
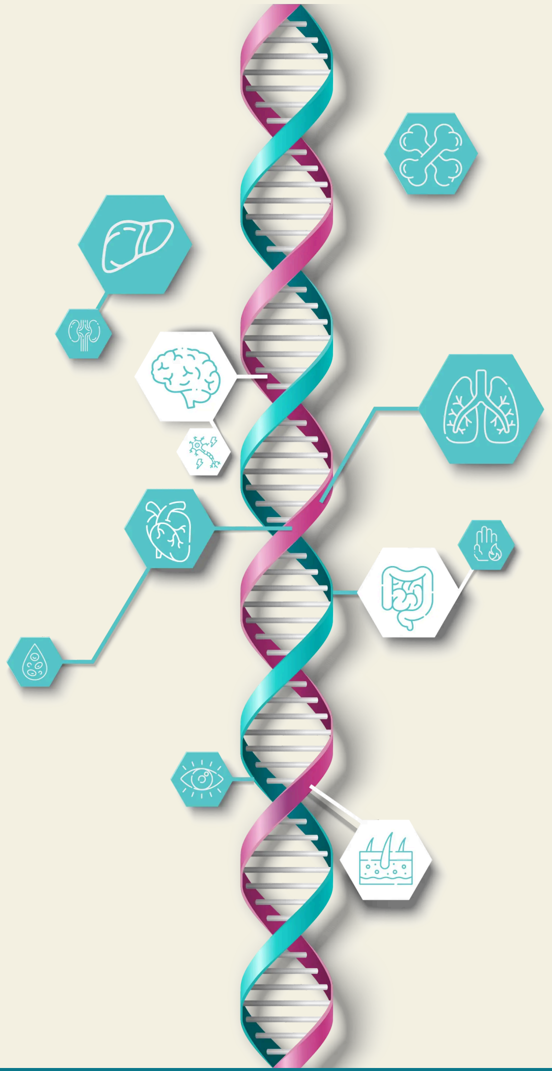
NEURO BIOLOGIX®

RESULTS FOR: Rachel Stanas
BIRTH GENDER: Female
BIRTH DATE: 06/26/1966
AGE: 59
REGISTRATION ID: NXRV6883





Your DNA Fingerprint: Unlike Any Other

You are completely unique. Among the 8 billion people on Earth, no one else carries your exact genetic blueprint—a one-of-a-kind combination of 3 billion DNA base pairs that will never be repeated. Even that tiny 0.1% of DNA that varies between humans represents millions of differences that shape everything from how you process nutrients and medications to your stress response, neurotransmitter balance, and metabolic patterns. This extraordinary uniqueness means your body has its own individual way of functioning, responding, and thriving. That's why this report doesn't offer generic advice—it provides insights tailored specifically to your genetic makeup, because your health journey should be as unique as your DNA.

Understanding Your Results

Use the color coding system for at-a-glance highlights of the results, to quickly determine top priorities and areas requiring support.

🟩 Normal Finding: Best outcome for this marker - No variant-related risk

🟨 Intermediate Finding: Partial effect expected - Heterozygous genotype

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I. Summary Plan

Selected by your provider

PEA SOOTHE SUPPORT

METHYLATION COMPLETE™

LONGEVITY MULTI

MAGNESIUM GLYCINATE COMPLEX

BERBERINE COMPLEX

Provider's Notes

I'm excited to help you progress along your wellness journey. We have some clear paths forward here that I'm confident will get you to your goals!

II. Results and Recommendations

Response & Recovery

Response and Recovery describes your body's natural defense and repair systems that protect and restore cellular health. When these processes remain activated for too long, they can create imbalances that may affect healthy tissue. This panel analyzes genetic variations that influence how your body responds to challenges and recovers afterward. It examines genes affecting immune function, cellular repair, and your body's ability to return to balance. Understanding your genetic profile helps identify your unique patterns of response and recovery from environmental stressors.

Products

Selected by your provider

OMEGACELL 1600 TG

A clean, sustainably-sourced Omega-3 formulawith 1600mg of EPA and DHA in an equal, 1:1 ratio to support cardiovascular, brain, and cellular health.

IMMUNE RESTORE DAILY

Our exclusive Immune Restore Daily formula combines six powerful ingredients to help modulate, balance, and regulate the immune response. Beta-glucans are known as "biological response modifiers" because of their ability to activate the immune system. Immune Restore Daily provides multifaceted support for the immune system.

BIOTIC SUPREME 50

Biotic Supreme 50 is a next-generation probiotic (NGP) formula that creates a powerful synergistic effect on GI ecology. It delivers over 50 billion CFU of Bifidobacterium, Lactobacillus, and Saccharomyces boulardii to support gut health, immune function, and normal bowel movements. It also includes 500 million AFU of the keystone probiotic Akkermansia muciniphila along with Clostridium butyricum and Bifidobacterium infantis to strengthen the structure and diversity of the entire gut ecosystem.* In addition to being formulated with an overage, Biotic Supreme 50

PEA SOOTHE SUPPORT

Palmitoylethanolamide (PEA) is a naturally occurring substance synthesized by healthy tissue in the human body and functions as a response to inflammation. Supplementing with PEA has been shown in over 300 medical studies to help reduce inflammation and pain naturally. This natural anti-inflammatory supports the nervous system and stabilizes immune responses.*

PEA SOOTHE SUPPORT TOPICAL

Palmitoylethanolamide (PEA) is a naturally occurring substance synthesized by healthy tissue in the human body and functions as a response to inflammation. Supplementing with PEA has been shown in over 300 medical studies to help reduce inflammation. This natural anti-inflammatory supports the nervous system and improves immune responses.

Provider Recommendations

The Soothe Support will be a great tool to get you started in addressing some of the underlying inflammation you may be feeling as a result of your autoimmune conditions. Consider the diet and sleep recommendations listed below that we emphasized.

Dietary Recommendations

- Adjust your calorie consumption to match your body's daily energy needs, with the goal of achieving and maintaining a healthy weight.
- Scrutinize labels to identify and reduce sources of added sugars, particularly in beverages and processed snacks (e.g., replace soda with sparkling water; choose plain yogurt and add fruit).
- Incorporate Omega-3 sources: Fatty fish twice weekly (e.g., salmon, herring, mackerel) and plant sources (e.g., walnuts, flaxseed, soybean oil).
- Increase flavanols: dark chocolate (70% or higher) or natural, non-alkalized cocoa powder added into smoothies or oatmeal.
- Anti-Inflammatory Focus: Emphasize polyphenol-rich foods (e.g., artichokes, berries, extra virgin olive oil).
- Adopt a diet rich in natural autophagy mimetics by incorporating polyphenol-containing foods (e.g, green tea and turmeric) alongside spermidine sources (e.g., fermented soybeans

and wheat germ).

Lifestyle Recommendations

- Sleep Hygiene: Enhance sleep quality by establishing a consistent pre-sleep "wind-down" routine (e.g., reading, gentle stretching) and limiting blue light exposure from screens for at least 60-90 minutes before bedtime.
- Environmental Awareness: Be mindful of your immediate living and working environments to support well-being (e.g., ensure adequate ventilation, seek natural light exposure).
- Physical Activity: Engage in regular physical activity (e.g., at least 150 minutes of moderate-intensity aerobic activity per week, plus muscle-strengthening activities on 2 or more days), advised by a professional.
- Health Monitoring: Engage in routine preventive health check-ups with a healthcare provider.
- Mindfulness Practice: Dedicate at least 10 minutes daily to a specific stress-reduction practice (e.g., guided mindfulness meditation, journaling).
- Substance Use: Actively avoid tobacco products and secondhand smoke, and limit alcohol consumption (e.g., striving for no more than 1 drink per day for women, 2 for men).
- Environmental Control: Focus on a comprehensive reduction of environmental toxins. Conduct a formal assessment for mold and other potential allergens in the home.
- Symptom Tracking: Keep a detailed log to track symptom patterns in relation to diet, environment, and lifestyle.

Response & Recovery Genes

The table below presents each gene and rsID, the genotype for each variant, and a description, all organized by topic.

IL2 **rs2069762**	**AA**	IL2 produces a cytokine essential for T cell proliferation, B cell maturation, regulatory T cell production, and activation of immune cells. The promoter rs2069762 variant affects IL2 production - the C allele increases transcription leading to elevated IL2 and excessive immune activation. C allele carriers show dose-dependent increased risk for inflammatory diseases, with CC homozygotes having highest susceptibility to ulcerative colitis, late-onset psoriasis, and endometriosis due to chronic inflammation, while the A allele reduces inflammatory disease risk.

IL4 rs2243250	CC	IL4 is a Th2 cytokine that promotes Th2 differentiation, enhances B-cell proliferation and IgE production, suppresses Th1 responses, and reduces pro-inflammatory cytokines. The promoter rs2243250 variant's T allele increases IL4 expression, shifting immunity toward Th2 dominance. This protects against Th1-mediated conditions like multiple sclerosis in Caucasians but increases susceptibility to antibody-mediated autoimmune disorders - TT homozygotes show increased Hashimoto thyroiditis risk and T carriers have higher rheumatoid arthritis risk.
IL5 rs2069812	AG	IL5 is a Th2 cytokine that stimulates B cell growth and eosinophil activation, mediating allergic responses and autoimmune conditions. The promoter rs2069812 G allele upregulates IL5 production, enhancing Th2 responses that facilitate autoantibody damage to thyroid and orbital tissues. G allele carriers show increased Graves' disease and Graves' ophthalmopathy susceptibility compared to AA genotype, with risk amplified when combined with other Th2 cytokine variants, particularly in East Asian populations.
IL6 rs1800795	GG	IL6 encodes a proinflammatory cytokine central to immune response, inflammation, acute phase responses, and metabolic regulation via JAK/STAT3 pathways. The promoter rs1800795 variant's G allele increases IL6 expression and inflammation, while C allele reduces production. The G allele increases hepatitis B/C, hepatocellular carcinoma, and NASH susceptibility through chronic inflammation but protects against PCOS. The C allele increases PCOS risk by reducing IL6 activity needed for normal ovarian function.
IL6 rs1800797	GG	IL6 encodes interleukin-6, crucial for immune regulation, inflammation, and metabolism. It activates JAK/STAT3, MAPK, and PI3K/Akt pathways affecting acute-phase responses and lymphocyte activation. The promoter rs1800797 variant modulates IL6 transcription by altering transcription factor binding. The G allele correlates with higher IL6 expression during inflammation, potentially increasing lumbar disc disease and distal interphalangeal osteoarthritis risk.
IL13 rs1800925	CT	IL13 is a Th2 cytokine that regulates pro-inflammatory cytokines, induces IgE production, and enhances airway mucus secretion, key in asthma and COPD. The promoter rs1800925 T allele creates a YY1 binding site that increases IL13 transcription in Th2 cells. T allele carriers show increased type 2 inflammatory conditions - enhanced COPD airway inflammation, dose-dependent allergic inflammation risk (TT>CT>CC), and higher appendicitis risk in TT homozygotes.

TNF **rs1800629**	**GA**	TNF-α is a pro-inflammatory cytokine that regulates cytokine production, adhesion molecules, neutrophil activation, and immune cell recruitment. The promoter rs1800629 A allele increases TNF-α production compared to G allele. The A allele shows complex associations - increases asthma and SLE risk, has ethnicity-dependent rheumatoid arthritis effects (risk in Latin Americans, protective in Asians), and protects against psoriatic arthritis where G allele increases susceptibility.
TNF **rs361525**	**GG**	TNF regulates inflammatory cascades, cytokine production, adhesion molecules, leukocyte recruitment, and tissue remodeling, playing key roles in immune regulation and host defense. The promoter rs361525 variant shows the A allele reduces ankylosing spondylitis and rheumatoid arthritis susceptibility, while the G allele is associated with standard or increased risk for these inflammatory autoimmune conditions, emphasizing disease-specific interpretation of TNF genotypes.
STAT4 **rs10181656**	**CG**	STAT4 is a transcription factor activated by IL-12, IL-23, IL-27, and interferons that regulates Th1 differentiation, IFN-γ production, and Th17 development, mediating pro-inflammatory responses. The intronic rs10181656 G allele increases STAT4 expression, enhancing Th1/Th17 activation and autoantibody production. G allele carriers show elevated susceptibility to rheumatoid arthritis, systemic lupus erythematosus, Graves' disease, and Hashimoto's thyroiditis due to excessive inflammatory responses and loss of immune tolerance.
IL23R **rs11209026**	**GG**	IL23R encodes the interleukin-23 receptor on T cells (especially Th17), NK cells, and immune cells, which activates JAK2/STAT3 signaling to produce pro-inflammatory cytokines (IL-17A, IL-17F, IL-22, IL-21) central to Th17 function and mucosal immunity. The rs11209026 variant causes R381Q substitution - the A allele creates a hypofunctional receptor that reduces STAT3 activation and IL-17 production, shifting away from Th17 responses. The A allele strongly protects against Crohn's Disease and Ulcerative Colitis by reducing gut inflammation, while the G risk allele maintains pro-inflammatory IL-23/Th17 signaling associated with elevated IBD and autoimmune disease risk.
IL2RA **rs12722489**	**CC**	L2RA encodes part of the IL-2 receptor complex essential for T cell proliferation and regulatory T cell maintenance, crucial for immune tolerance. The intronic rs12722489 variant influences IL2RA expression through regulatory elements and epigenetic modifications. The C allele significantly increases Multiple Sclerosis and Crohn's disease risk in Caucasians by modifying IL2RA expression, potentially impairing regulatory T cell function and fostering excessive effector T cell activity, disrupting self-tolerance.

CTLA4 **rs231775**	**AG**	CTLA4 is an inhibitory checkpoint molecule on regulatory T cells that suppresses T-cell activation by competing for ligands on antigen-presenting cells, maintaining immune homeostasis and peripheral tolerance. The rs231775 variant's G allele causes diminished CTLA4 functionality, particularly in regulatory T cells. The G allele increases autoimmune disease susceptibility including rheumatoid arthritis and type 1 diabetes due to reduced capacity to regulate autoreactive T cells and compromised immune tolerance.
PTPN22 **rs2476601**	**CC**	PTPN22 encodes LYP, a negative regulator of T cell receptor signaling that reduces T cell activation by dephosphorylating key signaling proteins. The rs2476601 variant (R620W) disrupts LYP-Csk interaction, altering TCR signaling regulation and promoting autoreactive lymphocyte survival. The T allele is a major non-HLA risk factor for rheumatoid arthritis, type 1 diabetes, SLE, and Graves' disease. Notably, the C allele (not T) increases Crohn's disease risk, showing disease-specific effects.
CD14 **rs2569191**	**CC**	CD14 rs2569191 is a promoter variant that alters CD14 gene expression and immune responses depending on environmental exposures. The C allele increases risk for elevated IgE, allergen sensitization, and atopic asthma in low microbial environments like urban, pet-free households where reduced microbial exposure promotes allergic Th2 immune responses. Early-life microbial exposure may help reduce this risk.
TRAF1 **rs3761847**	**AG**	TRAF1 is an intracellular signaling protein that regulates TNF receptor signaling, functioning as a negative regulator that inhibits TNF-driven inflammation by modulating NF-κB activity. The rs3761847 G risk allele disrupts TRAF1's ability to inhibit TNF responses, augmenting joint tissue inflammation characteristic of rheumatoid arthritis. G allele carriers show modestly increased susceptibility to anti-CCP-positive rheumatoid arthritis, establishing TRAF1-C5 as a significant non-HLA genetic risk locus through impaired regulation of TNF-induced inflammation.
TLR3 **rs3775291**	**CT**	TLR3 provides antiviral defense through TRIF-dependent signaling, producing type I interferons and pro-inflammatory cytokines vital for antiviral and adaptive immune responses. The rs3775291 variant affects antiviral signaling through modified RNA binding and TRIF activation. The T allele generally increases viral infection susceptibility, though effects vary by genetic background, highlighting the importance of personalized immune response management.

TLR4 **rs4986791**	**CT**	TLR4 detects bacterial lipopolysaccharide and other pathogen patterns, triggering cytokine release and adaptive immunity activation, crucial for infection control. The rs4986791 variant may alter receptor conformation and signaling. The T allele increases type 2 diabetes and asthma risk, possibly through chronic low-grade inflammation from altered TLR4 recognition that impairs insulin signaling and promotes airway inflammation.
AOC1 **rs10156191**	**CC**	AOC1 encodes diamine oxidase (DAO), the main enzyme for degrading histamine in the gut and other tissues. The rs10156191 T allele is associated with reduced DAO activity in an additive manner - each T allele copy further decreases enzyme levels. T allele carriers have diminished histamine degradation capacity, predisposing to histamine intolerance, especially with high dietary histamine, DAO-inhibiting substances (alcohol, certain medications), or intestinal damage that limits DAO production.
HNMT **rs11558538**	**CC**	HNMT encodes histamine N-methyltransferase, the main enzyme inactivating histamine through methylation, particularly in bronchial epithelium and central nervous system. The rs11558538 variant (C314T in exon 4) T allele reduces protein stability, increasing degradation and lowering enzyme concentrations. This decreases histamine clearance capacity in a dose-dependent manner, with TT homozygotes most affected. Diminished histamine inactivation is associated with higher asthma and allergic disorder susceptibility.
HNMT **rs1050891**	**GG**	HNMT is the principal enzyme inactivating intracellular histamine in the central nervous system and immune cells through methylation. The 3'UTR rs1050891 variant's A allele diminishes mRNA stability, resulting in decreased HNMT enzyme levels and reduced histamine clearance, increasing histamine availability. The A allele is associated with increased ADHD hyperactivity and heightened myasthenia gravis susceptibility.
FUT2 **rs492602**	**AG**	FUT2 encodes α(1,2) fucosyltransferase, determining secretor status and ABO antigen expression on epithelial cells and body fluids. The rs492602 G allele is linked to elevated Crohn's disease vulnerability, possibly due to enzyme function loss, absence of ABO(H) antigens in secretions, and dysbiosis that disrupts mucosal immune homeostasis.
NOS2 **rs2248814**	**GG**	The intronic rs2248814 variant in nitric oxide synthase 2 (NOS2) affects inflammatory pathways. The A allele is associated with dysregulated iNOS activity and altered nitric oxide levels, worsening oxidative stress and impairing inflammatory response regulation. A allele carriers show adverse cigarette smoking effects on age-related macular degeneration risk, especially AA homozygotes, and increased pulmonary tuberculosis susceptibility through impaired macrophage antimicrobial responses.

HLA-DQA1 **rs2187668**	**CC**	HLA-DQA1 encodes the alpha-chain of HLA-DQ, crucial for presenting gluten peptides to T cells in intestinal mucosa, central to celiac disease pathogenesis. The intronic rs2187668 variant serves as a precise marker for the HLA-DQ2.5cis haplotype, the predominant celiac disease genetic risk factor. The T allele indicates significantly elevated celiac disease risk, making this SNP valuable for clinical diagnostics and population screening.

Autophagy

Autophagy describes your body's cellular recycling system that breaks down and removes damaged cell parts while recovering useful materials. Like a cellular cleaning crew, this process helps maintain healthy cells by clearing out old or dysfunctional components and making room for new ones. This panel analyzes genetic variations that affect how efficiently your cells perform this essential housekeeping, including genes that control the formation of cellular "recycling containers" and the breakdown process itself. Understanding your autophagy genetics helps identify how well your body maintains cellular health, removes cellular waste, and renews itself at the microscopic level.

Products

Selected by your provider

INTRACELLULAR DETOX COMPLEX

Our exclusive Intracellular Detox Complex is a potent combination of well-studied ingredients known to optimize multiple biologic pathways within the cell. This anti-inflammatory powerhouse protects cells from oxidative stressors and damage while combating aging and promoting autophagy.

Provider Recommendations

As you mentioned, let's focus on the lifestyle recommendation below including a consistent exercise plan.

Dietary Recommendations

- Scrutinize labels to identify and reduce sources of added sugars, particularly in beverages and processed snacks (e.g., replace soda with sparkling water; choose plain yogurt and add fruit).
- Replace sources of saturated fat with unsaturated fats (e.g., replace butter with olive oil; choose lean poultry over fatty red meat; use low-fat cheese instead of full-fat).
- Incorporate Omega-3 sources: Fatty fish twice weekly (e.g., salmon, herring, mackerel) and plant sources (e.g., walnuts, flaxseed, soybean oil).

- Increase flavanols: dark chocolate (70% or higher) or natural, non-alkalized cocoa powder added into smoothies or oatmeal.
- Strictly minimize or avoid ultra-processed items (e.g., sugary drinks, packaged snacks, fast food, processed meats).
- Therapeutic foods, such as garlic, ginger, green tea, onions and turmeric, generously into your cooking as part of a healthy, plant-rich dietary pattern.

Lifestyle Recommendations

- Mindfulness Practice: Dedicate at least 10 minutes daily to a stress-reduction practice like meditation.
- Physical Activity: Ensure your exercise routine is regular and of moderate intensity, and advised by a professional.
- Stress Management: Make stress management an essential focus due to its impact on cellular health.
- Therapeutic Practices: Consider incorporating heat therapy (e.g., sauna) if available and tolerated, as it has been studied for its effects on cellular stress responses.
- Mindfulness: Commit to a daily meditation or mindfulness practice to manage the gut-brain axis.
- Circadian Rhythm: Strictly optimize your circadian rhythm by managing light exposure (morning sun, avoiding night-time blue light).

Autophagy Genes

The table below presents each gene and rsID, the genotype for each variant, and a description, all organized by topic.

ATG16L1 **rs10210302**	**CT**	ATG16L1 encodes a key autophagy protein that forms a complex with ATG5 and ATG12 to facilitate autophagosome membrane expansion, essential for degrading intracellular debris, pathogens, and damaged organelles, thereby maintaining intestinal epithelial homeostasis. The rs10210302 polymorphism (C>T) affects autophagy pathway function, with the T allele disrupting autophagic processes and impairing bacterial clearance. Clinically, T allele carriers show increased Crohn's disease susceptibility with an additive effect - TT homozygotes exhibit highest risk, heterozygotes intermediate risk - as impaired bacterial clearance leads to chronic intestinal inflammation, making this variant vital for disease risk assessment and a potential therapeutic target.
ATG5 **rs510432**	**TT**	ATG5 (autophagy-related 5) is a key protein involved in autophagy, facilitating the degradation and recycling of proteins, damaged organelles, and pathogens. In the context of the immune response and sepsis, ATG5 plays a critical role in autophagosome formation. It interacts with ATG12 and ATG16L1 to facilitate the expansion and maturation of autophagosome membranes, which is a crucial component of autophagy. In immune regulation, proper ATG5 function is essential for modulating inflammation. A deficiency in ATG5 leads to an augmented production of pro-inflammatory cytokines (such as TNF-α, IL-1β, and IL-6) subsequent to LPS exposure. The promoter region rs510432 T allele is linked to increased sepsis progression and severity by diminishing ATG5 expression, thereby exacerbating inflammatory cytokine production under stress conditions.
FOXO3 **rs2802292**	**GG**	FOXO3, a transcription factor in the insulin/IGF-1 pathway, regulates genes vital for stress resistance, metabolism, autophagy, and longevity, helping prevent age-related neurodegenerative and cardiovascular diseases. The rs2802292 SNP (intron 2, T>G substitution) shows the G allele associated with enhanced cognitive function, decreased cardiovascular/metabolic risks, and extended longevity, while the T allele lacks these protective effects. Benefits vary by sex and environment - males show stronger cardiovascular/cognitive advantages, females reduced blood glucose, though pollution exposure may mitigate benefits.

Methylation

Methylation describes a vital process where your body adds small chemical tags to DNA and other molecules, controlling how genes work and supporting countless cellular functions. This process depends on B vitamins, especially folate and B12, working together in a complex cycle. This panel analyzes genetic variations affecting how your body absorbs, processes, and uses these crucial nutrients for methylation. Understanding your methylation genetics helps identify how efficiently your body performs this essential process that influences energy production, detoxification, mood balance, and overall cellular health.

Products

Selected by your provider

OPTIMAL B COMPLEX

Optimal B Complex provides a potent and comprehensive blend of essential B-complex vitamins. Our formula delivers superior B complex vitamin support for those who may have trouble metabolizing traditional B vitamin supplements. This supplement enhances practical use in the body by creating select B vitamin pairings for our key ingredients.

BIOACTIVE B12 FOLATE

Bioactive B12-Folate® provides methylation support necessary to carry out essential life processes. Vitamin B12 works closely with vitamin B9, also called folate or folic acid, to help make red blood cells and to help iron work better in the body.

METHYL FOLATE PLUS™

Our exclusive Methyl Folate Plus™ formula provides the metabolically bioactive form folate (Vit B9), L-5- methylfolate. In conjunction with folinic acid and niacinamide this formula offers a complete folate support to the nervous and immune systems. Use this product in conjunction with either Methylation Complete Pro or Methylation Pro Topical for complete methylation support.

TOPICAL METHYLATION COMPLETE

Our exclusive Topical Methylation Complete combines methylfolate with essential cofactors, especially important for those with methylation deficiencies, including MTHFR and VDR Taq mutations. The unique topical delivery system assures that our professional-grade cream promotes and enhances the entire complex methylation process to support the nervous and immune systems.

METHYLATION COMPLETE™

Methylation Complete™ allows maximum delivery of B12, B6 and 5-MTHF to the nervous and immune systems. Fast-dissolving tablets allow for quick release into the bloodstream and may be especially beneficial for persons who are vegetarian or have gastrointestinal issues due to aging, illness, surgery, or a methylation deficiency. Improved methylation has many benefits for the immune and nervous systems.

Provider Recommendations

After two weeks, let's start this product. In the immediate, be sure to implement the sleep protocols and alcohol reduction we discussed.

Dietary Recommendations

- Support the stomach acid needed to properly absorb Vitamin B12 from your food by taking a small amount of apple cider vinegar in water before meals, while avoiding antacids when possible.
- To potentially optimize Vitamin B12 absorption, consider separating your B12-rich meals (e.g., meat or fish) from high-dose calcium supplements by a few hours.
- Increase B12-rich foods into your diet (e.g., clams, beef liver, salmon, or fortified nutritional yeast).
- Regularly include cruciferous vegetables (e.g., broccoli, cauliflower, cabbage) and alliums (e.g., garlic, onions) in your diet.
- Provide the essential fuel for methylation by regularly eating key "methyl donor" foods (e.g., egg yolks, beets, salmon, sunflower seeds).
- Ensure a steady daily intake of B12 foods at least one or two of your main meals (e.g., eggs for breakfast or tuna for lunch).

- Support your key methylation enzymes by eating foods rich in riboflavin (B2) (e.g., almonds, mushrooms, spinach).
- Consider adding fortified nutritional yeast to your meals as a reliable, non-animal source of essential B vitamins, especially B12.
- Registered dietitian supervision.
- Advanced metabolic diet protocols.

Lifestyle Recommendations

- Environmental Awareness: Be mindful of your immediate living and working environments to support well-being (e.g., ensure adequate ventilation, seek natural light exposure).
- Health Monitoring: Engage in routine preventive health check-ups with a healthcare provider.
- Stress Management: Incorporate basic stress management techniques into your daily routine (e.g., diaphragmatic breathing exercises, short walks in nature).
- Physical Activity: Engage in regular physical activity (e.g., at least 150 minutes of moderate-intensity aerobic activity per week, plus muscle-strengthening activities on 2 or more days), advised by a professional.
- Stress Management: Implement daily stress reduction practices, as chronic stress can impact metabolic processes.
- Sleep Quality: Enhance and prioritize sleep quality.
- Supportive Practices: Consider gentle practices that support the body's natural detoxification systems (e.g., staying well-hydrated, ensuring adequate dietary fiber).
- Self-Monitoring: Monitor your energy levels closely, as fatigue can be an early sign of B12 issues.
- Stress Protocol: Implement a comprehensive stress management strategy, as stress hormones can significantly influence metabolic pathways.
- Gut Health: Optimize gut health, as digestive function directly impacts B12 absorption.
- Sleep Optimization: Make sleep optimization a crucial and non-negotiable aspect of your daily routine.
- Healthcare professional may consider routine B12 testing and medication review to identify and address drug-nutrient interactions affecting B12 status.

- Alcohol: Emphasize the importance of limiting alcohol due to its direct negative effect on folate pathways.
- Symptom Tracking: Meticulously document any neurological symptoms (e.g., memory issues, balance problems, mood changes) for a healthcare provider.
- Supportive Practices: Focus on consistently supporting the body's natural detoxification systems through lifestyle (e.g., hydration, diet, sweating). If tolerated and not medically contraindicated.
- Professional guidance: Work with a healthcare provider to develop a comprehensive B12 strategy, which may include discussing functional B12 testing (e.g., MMA, homocysteine).

Methylation Genes

The table below presents each gene and rsID, the genotype for each variant, and a description, all organized by topic.

FOLR1 **rs2071010**	**GG**	FOLR1 encodes Folate Receptor 1, a membrane protein that transports folate into cells, especially through the placenta during pregnancy. Folate is essential for DNA synthesis and cell division - defects in folate transport can affect heart development, causing congenital anomalies.The GG genotype of FOLR1 SNP rs2071010 increases the risk of ventricular septal defect (VSD), particularly in the absence of folic acid supplementation, whereas the A allele offers protection. Patients with epilepsy who have the AA genotype are at greater risk of elevated homocysteine levels, necessitating monitoring to avert complications.
MTHFS **rs6495446**	**CC**	MTHFS encodes methenyltetrahydrofolate synthetase, crucial for folate turnover and accumulation, converting folate intermediates essential for DNA synthesis, repair, and methylation. The intronic rs6495446 variant's C allele is associated with diminished renal function and elevated chronic kidney disease risk in whites through altered gene expression and folate cycle modulation. The C allele shows additive effect for kidney disease progression, making it a biomarker for identifying individuals at heightened genetic susceptibility to CKD.
MTHFD1 **rs1076991**	**CC**	The T allele of the MTHFD1 SNP rs1076991 decreases gene expression by reducing promoter activity, which heightens the risk of acute myocardial infarction (AMI), especially when B vitamin supplements are taken. Individuals with the CC genotype face a higher risk of AMI when their glycine levels are low. Tailored therapy that considers a person's genotype and metabolic profile could enhance treatment outcomes.

SLC19A1 **rs1051266**	**TC**	The C allele (Arg) in SLC19A1 rs1051266 SNP reduces folate transport, decreasing intracellular folate, which affects DNA synthesis and methylation, increasing the risk of neural tube defects and heart disorders, especially in homozygous CC individuals or those with low folic acid. It also affects brain folate-dependent processes, reducing delayed memory performance. Individuals with the CC genotype might require additional folic acid to reduce these risks.
MTHFR **rs1801131**	**TG**	MTHFR encodes methylenetetrahydrofolate reductase, crucial for DNA synthesis, methylation, and preventing homocysteine accumulation. The rs1801131 variant causes glutamate-to-alanine substitution in the regulatory domain, decreasing enzyme activity. GG homozygotes show greatest reduction in MTHFR activity, which can be mitigated with folic acid supplementation. The GG genotype is associated with increased male infertility risk, particularly azoospermia.
MTHFR **rs1801133**	**GA**	MTHFR encodes methylenetetrahydrofolate reductase, essential for folate metabolism, DNA synthesis/repair, methylation, and homocysteine control. The rs1801133 variant (also called C677T) causes Ala222Val substitution, making the enzyme thermolabile with reduced activity. The A allele causes dose-dependent elevation of homocysteine and decreased folate, strongest in AA homozygotes. Associated with increased risk of spina bifida (especially with low folate), male infertility, and migraine with aura. Optimizing folate intake may reduce these risks.
MTRR **rs1801394**	**GG**	The G allele of the rs1801394 SNP in the MTRR gene hinders enzyme activity, leading to hyperhomocysteinemia and decreased effectiveness of folic acid treatment. This allele is linked to elevated homocysteine levels, a poor response to folate therapy, and greater risks of maternal Down syndrome and neural tube defects in cases of low B12. Individuals carrying the G allele might need alternative treatments, and those with the GG genotype could benefit from tailored preconception guidance and nutritional plans.
MTR **rs1805087**	**AA**	MTR uses folate and B12 to convert homocysteine to methionine, producing S-adenosylmethionine for DNA methylation and other processes. The rs1805087 variant (A2756G) G allele reduces homocysteine-to-methionine conversion efficiency, affecting methylation patterns. G carriers (AG, GG) show increased folate deficiency risk, particularly with inadequate folate/B12 intake. Higher intake of methyl donors (folate, B12, choline) helps support proper methylation and homocysteine metabolism in G allele carriers. Personalized nutrition especially important for metabolic balance.

TCN1 **rs526934**	**GG**	TCN1 encodes transcobalamin I, a protein that binds and protects vitamin B12 in blood and facilitates intestinal absorption. The intronic rs526934 variant affects B12 transport. The G allele is associated with reduced vitamin B12 levels in a dose-dependent manner - each G allele copy decreases circulating B12 compared to the A allele. This reduction likely results from diminished cobalamin transport. GG homozygotes show lowest B12 levels, AG intermediate, and AA highest, indicating functional significance for B12 status.
TCN2 **rs1801198**	**CG**	TCN2 encodes transcobalamin II, which transports vitamin B12 from gut to cells. After intestinal absorption, B12 binds to TCII forming holotranscobalamin (active B12) for cellular delivery. The rs1801198 variant (Arg259Pro) affects this transport system. The GG genotype is associated with lower holotranscobalamin levels, reducing vitamin B12 availability for cellular uptake. Individuals with GG genotype have increased risk of subclinical but functionally relevant B12 deficiency, potentially requiring monitoring or supplementation.

Cellular Energy

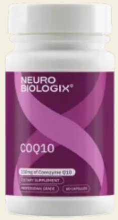
Cellular Energy describes how your cells produce and manage the energy needed to power all body functions. Your mitochondria, often called cellular powerhouses, convert nutrients into usable energy while managing the stress this process creates. This panel analyzes genetic variations that affect how efficiently your cells generate energy, how well your mitochondria function and multiply, and how your body protects these energy systems from damage. Understanding your cellular energy genetics helps identify your natural energy production patterns, exercise recovery ability, and how your body responds to different energy demands throughout the day.

Products

Selected by your provider

LONGEVITY MULTI

Longevity Multi is a high-potency, professional-grade, iron-free multivitamin and mineral formula for optimalwellness.*



COQ10

CoQ10 (Coenzyme Q10) is a naturally occurring nutrient essential for cell growth and maintenance. Aging decreases the body's ability to process and produce ubiquinol, the biologically functioning form of CoQ10. Illness, poor nutrient intake, and certain medications can result in inadequate internal production of CoQ10 to sustain optimal organ function.

Provider Recommendations

This will be a great all-around product that can help you here and in many other areas we'll review in the future.

Dietary Recommendations

- Regularly include magnesium-rich foods in your diet (e.g, dark leafy greens, almonds, pumpkin seeds, avocados).
- Regularly include high-polyphenol foods in your diet (e.g., berries, green tea, high-cacao dark chocolate).
- Prioritize a consistent intake of Vitamin E (e.g., almonds, sunflower seeds, spinach).
- Include selenium-rich foods in your diet (e.g., seafood or a single Brazil nut per day).

Lifestyle Recommendations

- Advanced Sleep Hygiene: Fully optimize the sleep environment to be completely dark, quiet, and cool.
- Mindfulness: Establish a regular meditation practice.
- Sleep Optimization: Make sleep optimization a critical, non-negotiable priority, aiming for 8+ hours if necessary for full recovery.
- Stress Management: Make daily, structured stress management a mandatory part of your routine.

Cellular Energy Genes

The table below presents each gene and rsID, the genotype for each variant, and a description, all organized by topic.

PPARGC1A **rs8192678**	**CC**	PPARGC1A encodes PGC-1α, a key regulator for mitochondrial biogenesis, oxidative metabolism, and glucose uptake in high-energy tissues. PGC-1α works with transcription factors to enhance GLUT4 expression and activate mitochondrial genes. The rs8192678 variant changes glycine to serine at position 482. The C allele maintains normal PGC-1α function supporting mitochondrial formation, while the T allele decreases its activity. T allele carriers show diminished aerobic adaptability with reduced VO2max improvements, impaired muscle fiber remodeling, and lower mitochondrial activity following training, indicating impaired cellular energy adaptation and increased metabolic stress susceptibility.

SIRT1 **rs7895833**	**GA**	SIRT1 encodes a NAD+-dependent enzyme that regulates mitochondrial biogenesis by activating PGC-1α, promoting ATP production and cellular energy balance while protecting against oxidative stress. The rs7895833 variant affects SIRT1-mediated mitochondrial regulation. G allele carriers demonstrate enhanced mitochondrial function with improved energy metabolism, lower BMI, and decreased obesity risk, while A allele carriers show elevated obesity risk and higher BMI due to reduced mitochondrial biogenesis and diminished cellular energy production, highlighting this variant's role in metabolic health through the SIRT1-PGC-1α pathway.
NQO1 **rs1800566**	**GA**	NQO1 encodes an enzyme that reduces quinones to prevent reactive radical formation, detoxifies metabolic and environmental toxins, and regenerates antioxidants including vitamin E and CoQ10. The rs1800566 variant causes a proline to serine change making the protein unstable. GA heterozygotes have reduced NQO1 expression and detoxification capacity, while AA homozygotes have complete absence of functional enzyme, severely limiting quinone detoxification and antioxidant regeneration, making A carriers vulnerable to oxidative stress and increased cancer susceptibility.
GABPB1 **rs7181866**	**AA**	GABPB1 encodes the beta subunit of NRF2 complex, regulating genes for mitochondrial biogenesis, oxidative phosphorylation, and electron transport chain. The rs7181866 variant affects GABPB1 expression or splicing, modifying mitochondrial gene activation. The G allele improves endurance athletic performance but increases obesity risk and metabolic complications, particularly in Type 2 Diabetes. G carriers, especially GG genotype, exhibit higher leptin, TNF-α, IL-6, reduced adiponectin, increased insulin resistance, and greater metabolic dysfunction propensity.

Detoxification

Detoxification describes your body's natural cleaning systems that process and eliminate waste products, environmental toxins, and harmful substances. Your liver and other organs work together using specialized enzymes to transform these substances into forms your body can safely remove. This panel examines genetic variations affecting your body's detox enzymes, antioxidant systems, and protective mechanisms against cellular damage. Understanding your detoxification genetics helps identify how efficiently your body processes everyday exposures from food, environment, and normal metabolism, and whether you may benefit from additional detoxification support.

Products

Selected by your provider

DETOX & ANTIOXIDANT SUPPORT

Our exclusive Detox & Antioxidant Support is a physician-derived blend of ingredients that provide a superior glutathione supplement readily utilized in the body to support the immune system and cellular functioning. Glutathione is a master antioxidant (scavenging free radicals), anti-inflammatory, and immunity powerhouse.

INTRACELLULAR DETOX COMPLEX

Our exclusive Intracellular Detox Complex is a potent combination of well-studied ingredients known to optimize multiple biologic pathways within the cell. This anti-inflammatory powerhouse protects cells from oxidative stressors and damage while combating aging and promoting autophagy.

TOXIN CLEANSE PRO

Our exclusive Toxin Cleanse Pro provides complete support for the complex detoxification processes essential to life. This supplement enhances the elimination of environmental toxins and other substances that may be harmful to the body.

Provider Recommendations

Given your other genetic needs, I don't see a lot of need to focus here at the moment.

Dietary Recommendations

- Scrutinize labels to identify and reduce sources of added sugars, particularly in beverages and processed snacks (e.g., replace soda with sparkling water; choose plain yogurt and add fruit).
- Replace sources of saturated fat with unsaturated fats (e.g., replace butter with olive oil; choose lean poultry over fatty red meat; use low-fat cheese instead of full-fat).
- Focus on achieving the daily goal of fiber: About 25 grams for women and 38 grams for men.
- Incorporate Omega-3 sources: Fatty fish twice weekly (e.g., salmon, herring, mackerel) and plant sources (e.g., walnuts, flaxseed, soybean oil).

Lifestyle Recommendations

- Sleep: Maintain a consistent sleep-wake schedule, aiming for 7-9 hours of quality sleep per night.
- Physical Activity: Engage in regular physical activity (e.g., at least 150 minutes of moderate-intensity aerobic activity per week, plus muscle-strengthening activities on 2 or more days), advised by a professional.
- Environmental Control: Choose natural cleaning products to reduce indoor air pollutants. Increase time spent outdoors in fresh air.
- Therapeutic Practices: Consider using a sauna or taking a hot bath once a week to promote sweating, advised by a professional.

Detoxification Genes

The table below presents each gene and rsID, the genotype for each variant, and a description, all organized by topic.

GSTM1 **rs366631**	**AA**	GSTM1 is a phase II detoxification enzyme that conjugates glutathione to carcinogens, drugs, and pollutants for elimination. The rs366631 is not a true SNP but a marker for GSTM1 gene deletion. GG genotype indicates complete gene deletion (null), AG indicates one copy deleted (intermediate expression), AA indicates both copies present (normal expression). This copy number variation affects detoxification capacity and oxidative stress protection, with population-specific distributions.
GSTP1 **rs1695**	**AA**	GSTP1 catalyzes glutathione conjugation to toxins and carcinogens for detoxification, protects against oxidative damage, and regulates cell signaling affecting survival and inflammation. The rs1695 variant (Ile105Val) G allele reduces enzyme activity and alters kinetics, hindering detoxification of electrophiles and reactive oxygen species. GG homozygotes show elevated lipid peroxidation and increased heart failure risk with higher inflammation markers. The G allele also increases allergic sensitization susceptibility from air pollution, particularly in children.
GPX1 **rs1050450**	**GA**	GPX1 is a selenium-dependent enzyme that converts peroxides to water and oxygen, protecting against oxidative stress. The rs1050450 variant (Pro198Leu) A allele carriers have lower erythrocyte GPX1 activity than GG carriers, resulting in less efficient peroxide detoxification and increased oxidative damage risk. GG homozygotes show increased GPX1 expression with selenium supplementation, suggesting A carriers may need higher dietary selenium for comparable protective effects.
GSR **rs1002149**	**CC**	GSR encodes glutathione-disulfide reductase, crucial for antioxidant defense by maintaining redox equilibrium. The regulatory region rs1002149 variant may modulate transcriptional activity. The A allele is associated with heightened COPD risk among non-smokers, potentially from diminished glutathione recycling capacity increasing pulmonary oxidative injury vulnerability. The A allele was also associated with lower likelihood of reaching advanced age in some populations, suggesting impact on longevity through oxidative stress resilience.
SOD1 **rs4998557**	**GG**	SOD1 encodes copper-zinc superoxide dismutase that converts superoxide anions to oxygen and hydrogen peroxide, protecting against oxidative stress. In the cochlea, SOD1 protects against hearing damage from reactive oxygen species. The intronic rs4998557 A allele is associated with elevated sudden sensorineural hearing loss risk in Japanese individuals compared to GG genotypes, likely from diminished SOD1 function or expression under oxidative stress.

SOD2 **rs4880**	**GG**	SOD2 encodes manganese superoxide dismutase, a mitochondrial antioxidant that converts superoxide radicals to hydrogen peroxide. The rs4880 variant (Ala16Val) G allele demonstrates diminished enzyme activity from compromised mitochondrial targeting. GG homozygotes show reduced superoxide detoxification, elevated reactive oxygen species, and greater cellular damage from oxidative stressors. This increased oxidative stress contributes to heightened End-Stage Renal Disease risk in GG genotypes.
NAT2 **rs1801280**	**TC**	NAT2 is a phase-II enzyme that acetylates drugs and environmental carcinogens for detoxification or activation. The rs1801280 variant's C allele results in the most pronounced decrease in enzymatic activity, characteristic of the slowest acetylator phenotype. Since NAT2-mediated acetylation is the primary detoxification pathway, C allele carriers have elevated adverse drug reaction risk in high-exposure environments.
NAT2 **rs1208**	**AA**	NAT2 encodes an arylamine N-acetyltransferase for phase II drug metabolism, detoxifying or activating xenobiotics including isoniazid, sulfonamides, and hydralazine. The rs1208 variant (803A>G) AA genotype is associated with enhanced endurance athletic performance, possibly through oxidative stress regulation or mitochondrial reactive oxygen species modulation, though this remains speculative beyond NAT2's established xenobiotic metabolism role.
AHCY **rs819147**	**GG**	AHCY encodes S-adenosylhomocysteine hydrolase, which converts S-adenosylhomocysteine to homocysteine and adenosine, maintaining the SAH/SAM ratio essential for cellular methylation, DNA methylation, and neurotransmitter synthesis. The rs819147 variant has the A allele designated as risk and G as non-risk based on limited data. However, insufficient published evidence exists regarding functional impact or clinical associations. Information included for completeness only - future research needed to determine biological and clinical significance.

Vitamins and Minerals

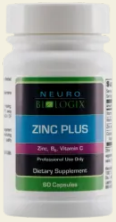
Vitamins and Minerals describes how your genes influence your body's ability to absorb, transport, and use essential nutrients from your diet. Your genetic makeup affects how efficiently you process different vitamins like A, D, E, C, and B12, as well as important minerals like zinc, iron, and iodine. This panel analyzes variations in genes controlling nutrient transporters, storage proteins, and enzymes that activate vitamins and minerals in your body. Understanding your nutrient genetics helps identify which vitamins and minerals you may need more of, how well you absorb supplements, and your unique nutritional requirements for optimal health.

Products

Selected by your provider

LONGEVITY MULTI

Longevity Multi is a high-potency, professional-grade, iron-free multivitamin and mineral formula for optimalwellness.*



ZINC PLUS

Zinc Plus provides ultimate zinc delivery for enhanced immune system and metabolism function. For optimal assimilation and pH balance, our Zinc Plus formulation uses zinc citrate, the form of zinc found naturally in human milk. Including B6 and C vitamins facilitates zinc metabolism and delivery.

BIOTIN

Biotin provides ultimate supplementation potency for those with significant metabolic needs. As a B vitamin, biotin is essential to many metabolic processes and supports healthy glucose metabolism. This supplement especially benefits those with compromised absorption, bariatric procedures, or a higher need for this B vitamin.

D3 5000 + K1&K2

D3 5000 + K1&K2 contains the most bioavailable and bioactive version of vitamin K2 available (K2VITAL® MK7), paired with 5000 IUs of vitamin D3 (cholecalciferol), and available in a liquid capsule with olive oil for improved absorption.* The vitamin D3 in D3 5000 + K1&K2 helps transport calcium from the intestines into the bloodstream as the Vitamin K2 directs the calcium into the bones while also supporting the minimization of calcium buildup in the arteries.*

MAGNESIUM GLYCINATE COMPLEX

Magnesium Glycinate Complex is an easy-to-digest source of magnesium, a critical nutrient that facilitates multiple essential life processes. Magnesium helps convert carbohydrates, protein, and fats to energy and catalyzes thousands of enzymatic processes.

METHYLATION COMPLETE™

Methylation Complete™ allows maximum delivery of B12, B6 and 5-MTHF to the nervous and immune systems. Fast-dissolving tablets allow for quick release into the bloodstream and may be especially beneficial for persons who are vegetarian or have gastrointestinal issues due to aging, illness, surgery, or a methylation deficiency. Improved methylation has many benefits for the immune and nervous systems.

Provider Recommendations

The Longevity Multi should cover most of your needs but we will focus on sunlight primarily for vitamin D. We may consider the D3/K1+K2 in winter months.

Vitamins and Minerals Genes

The table below presents each gene and rsID, the genotype for each variant, and a description, all organized by topic.

TTPA **rs6994076**	**AA**	TTPA encodes α-tocopherol transfer protein, which selectively binds vitamin E and facilitates its distribution throughout the body via lipoproteins. The regulatory region rs6994076 variant affects gene expression. Males with TT genotype show reduced baseline serum vitamin E compared to AA genotype. T allele carriers demonstrate less pronounced vitamin E increase following supplementation, likely from reduced TTPA expression limiting vitamin E loading into lipoproteins. T allele carriers may require increased or personalized vitamin E supplementation with serum monitoring.
BCO1 **rs7501331**	**CT**	BCO1 converts dietary β-carotene into vitamin A, ensuring sufficient vitamin A from plant sources. The rs7501331 variant (A379V) T allele causes inefficient β-carotene to vitamin A conversion, leading to elevated β-carotene levels and decreased vitamin A bioavailability. This increases clinical or subclinical vitamin A deficiency risk when preformed vitamin A intake is insufficient. Carrying both T risk alleles (rs7501331 and rs12934922) significantly diminishes conversion, requiring emphasis on preformed vitamin A sources rather than plant carotenoids.
BCO1 **rs12934922**	**AA**	BCO1 converts β-carotene into vitamin A from plant sources. The rs12934922 variant (R267S) T allele compromises vitamin A conversion, increasing deficiency risk especially with insufficient dietary vitamin A. Carrying both T risk alleles (rs7501331 and rs12934922) significantly diminishes β-carotene conversion, necessitating monitoring and guidance emphasizing preformed vitamin A sources over plant-derived carotenoids.
BCO1 **rs6564851**	**TG**	BCO1 converts β-carotene to vitamin A from plant sources. The promoter rs6564851 G allele reduces BCO1 activity, causing inefficient conversion and increased β-carotene levels. G carriers have higher total and non-HDL cholesterol, indicating altered lipid metabolism, and show smaller serum lycopene increases with supplementation than TT homozygotes. In men only, T allele links to higher triglycerides compared to GG, suggesting sex-specific effects on triglyceride metabolism.
SLC30A8 **rs11558471**	**GA**	SLC30A8 encodes ZnT8 for zinc transport into pancreatic β-cells, aiding insulin storage and secretion. The rs11558471 A allele increases fasting glucose through impaired zinc transport, elevating type 2 diabetes risk, particularly with lower zinc intake. Higher dietary or supplemental zinc mitigates this risk by attenuating the glucose-raising effect. AA genotype shows significantly greater diabetes risk than GG. Adequate zinc is potentially protective for A allele carriers.

SLC23A1 rs33972313	**CC**	SLC23A1 encodes SVCT1, which transports dietary vitamin C from intestine into bloodstream and reabsorbs it in kidney, maintaining systemic levels. The rs33972313 variant substitutes valine (C) with methionine (T). The T allele impairs ascorbate transport, leading to lower plasma vitamin C and reduced antioxidant defense, particularly in oxidative-damage susceptible tissues like the lens, elevating cortical and posterior subcapsular cataract risk.
SLC5A6 rs1395	**GA**	SLC5A6 encodes the sodium-dependent multivitamin transporter for pantothenate and biotin uptake. The rs1395 A allele reduces intestinal absorption, cellular delivery, and transplacental transport of these vitamins. A allele carriers may be predisposed to inadequate biotin and pantothenate absorption, potentially requiring dietary modification.
VDR rs2228570	**GG**	VDR encodes the vitamin D receptor mediating biological effects of active vitamin D. The rs2228570 (FokI) variant at the translation start site affects receptor activity. GG genotype (producing more active receptor) responds better to vitamin D supplementation with higher serum 25(OH)D increases than AA genotype. A allele carriers may have weaker calcium absorption, lower bone mineral density, and increased osteoporosis and fracture risk.
GC rs2282679	**TT**	GC encodes vitamin D-binding protein (DBP), synthesized in liver, that transports vitamin D and its metabolites. The rs2282679 T allele leads to reduced DBP and lower serum vitamin D concentrations, increasing clinical vitamin D deficiency risk, helping guide preventive strategies in at-risk populations.
CYP2R1 rs10741657	**AG**	CYP2R1 encodes vitamin D 25-hydroxylase, which converts vitamin D to 25-hydroxyvitamin D in the liver. The regulatory region rs10741657 G allele may reduce enzyme activity, causing inefficient conversion. G allele carriers, particularly GG homozygotes, are prone to lower 25(OH)D levels and increased vitamin D insufficiency or deficiency risk.
NADSYN1 rs12785878	**TT**	The NADSYN1/DHCR7 locus rs12785878 primarily affects DHCR7, which converts 7-dehydrocholesterol to cholesterol, regulating substrate for UVB-dependent vitamin D3 synthesis in skin. The T allele may enhance cholesterol conversion, reducing substrate for vitamin D3 synthesis. T carriers often have lower 25-hydroxyvitamin D levels and reduced response to vitamin D supplements.
TCN2 rs1801198	**CG**	TCN2 encodes transcobalamin II, which transports vitamin B12 from gut to cells. After intestinal absorption, B12 binds to TCII forming holotranscobalamin (active B12) for cellular delivery. The rs1801198 variant (Arg259Pro) affects this transport system. The GG genotype is associated with lower holotranscobalamin levels, reducing vitamin B12 availability for cellular uptake. Individuals with GG genotype have increased risk of subclinical but functionally relevant B12 deficiency, potentially requiring monitoring or supplementation.

FUT2 **rs492602**	**AG**	FUT2 encodes α(1,2) fucosyltransferase, determining secretor status and ABO antigen expression on epithelial cells and body fluids. The rs492602 G allele is linked to elevated Crohn's disease vulnerability, possibly due to enzyme function loss, absence of ABO(H) antigens in secretions, and dysbiosis that disrupts mucosal immune homeostasis.
FOXE1 **rs1867277**	**GG**	FOXE1 encodes a thyroid transcription factor regulating thyroglobulin and thyroid peroxidase expression for thyroid hormone synthesis. The promoter rs1867277 A allele modifies transcription factor binding, potentially altering gene expression. The A allele is linked to thyroid hormone dysregulation, particularly decreased TSH levels, which can mask early thyroid disease.
TMPRSS6 **rs855791**	**GG**	TMPRSS6 encodes matriptase-2, a liver protease that reduces hepcidin, the key iron-regulating hormone. Hepcidin decreases iron absorption and release by affecting ferroportin. TMPRSS6 cleaves hemojuvelin, lowering hepcidin and increasing blood iron. The rs855791 variant (Val736Ala) substitutes valine with alanine. The A allele impairs TMPRSS6's ability to suppress hepcidin, resulting in elevated hepcidin expression that reduces iron absorption and release, lowering serum iron levels. A allele carriers have increased iron deficiency and anemia risk, which may influence supplementation strategies.

NeuroBalance

Neurobalance describes the genetic factors that influence your brain's chemical messengers and how they work together to support mood, focus, and emotional wellbeing. Your genes affect how your body makes, uses, and breaks down important brain chemicals like serotonin, dopamine, GABA, and others that regulate everything from stress response to sleep patterns. This panel analyzes variations in genes controlling neurotransmitter production, breakdown processes, receptors, and brain growth factors. Understanding your neurobalance genetics helps identify your unique patterns for managing stress, maintaining positive mood, and supporting optimal brain function.

Products

Selected by your provider

FULL FOCUS™

Our exclusive Full Focus™ is a unique formula that consists of nine carefully selected ingredients that work together to optimize dopamine production and improve overall brain function. Full Focus™ consists of the exact vitamins and amino acids needed to produce the natural compounds essential for optimal brain function.

BLISSFUL MOOD

Our exclusive Blissful Mood provides enhanced neurological and nervous system support recommended for mood support, sleep disturbances, poor libido, and maintaining a healthy stress level. Blissful Mood features a carefully formulated combination of nutrients that function as neurotransmitters to support the overall nervous system and promote a healthy mood.

NEURO CALM & REBALANCE

Our exclusive Neuro Calm & Rebalance provides five critical ingredients needed to help support and maintain a healthy nervous system, regulate muscle relaxation, improve digestive health, reduce stress, and promote relaxation. This best-in-class supplement provides more beneficial and effective support than traditional GABA and other natural relaxation sources.

NIGHTTIME CALMING COMPLEX

Nighttime Calming Complex is a physician-formulated blend of seven ingredients designed to promote healthy sleep, support normal nocturnal rhythms during stress, and assist with occasional sleeplessness.

NIGHT NIGHT (LIPOSOMAL SPRAY)

Night Night is an oral spray that supports healthy sleep cycles. This restorative sleep formula utilizes serotonin, gamma-aminobutyric acid (GABA), and melatonin. The unique liposomal delivery system protects nutrients for targeted delivery and improved absorption into the body.

L-THEANINE

L-Theanine reduces stress and relaxes your brain by increasing alpha wave activity. L-Theanine provides stress-reducing effects without causing drowsiness and can increase relaxation and stimulate neuron and dopamine production.

MAGNESIUM GLYCINATE COMPLEX

Magnesium Glycinate Complex is an easy-to-digest source of magnesium, a critical nutrient that facilitates multiple essential life processes. Magnesium helps convert carbohydrates, protein, and fats to energy and catalyzes thousands of enzymatic processes.

Provider Recommendations

As mentioned, let's focus on your sleep quality and stress with our systemic Magnesium support. We may return here and look at mood support if more support is needed.

Dietary Recommendations

- Adopt a good dietary pattern: Focus on a Mediterranean or DASH-style diet (fruits, vegetables, whole grains, lean proteins).
- Set an adequate hydration (approximately 8 glasses, approximately 2 liters or 64 oz, of fluid per day), prioritizing beverages with no added sugar (e.g., water, herbal tea).
- Increase consumption of soluble fiber (e.g., oatmeal, beans, lentils).
- Incorporate fermented foods (e.g., kombucha, tempeh, miso) and probiotics (e.g., yogurt with live cultures, kefir, kombucha) to improve your digestion, reduce inflammation, boost your immune system, and support a healthy gut microbiome.
- Strict elimination of added sugars and refined carbohydrates is a primary therapeutic goal.
- Consider a daily blend a green smoothie (e.g., base of leafy greens, berries, and a healthy fat like avocado or walnuts) with adaptogens, such as ashwagandha.

Lifestyle Recommendations

- Sleep: Maintain a consistent sleep-wake schedule, aiming for 7-9 hours of quality sleep per night.
- Stress Management: Incorporate basic stress management techniques into your daily routine (e.g., diaphragmatic breathing exercises, short walks in nature).
- Sleep Hygiene: Establish strictly consistent sleep-wake times, even on weekends. Limit screen time for at least 60-90 minutes before bed.
- Mindfulness Practice: Practice 10 minutes of daily meditation.
- Medical Collaboration: discuss light therapy or other forms of chronotherapy with a qualified healthcare provider.

NeuroBalance Genes

The table below presents each gene and rsID, the genotype for each variant, and a description, all organized by topic.

COMT **rs4680**	**GA**	COMT inactivates dopamine, norepinephrine, and epinephrine through methylation, particularly crucial in the prefrontal cortex, where dopamine transporters are scarce. The rs4680 variant (Val158Met) creates three genotypes: GG (Val/Val) with high enzyme activity and faster dopamine breakdown, GA (Val/Met) with intermediate activity, and AA (Met/Met) with low activity, resulting in elevated dopamine. The Met allele (A) is associated with increased obsessive-compulsive disorder risk (particularly in males), altered personality traits including lower extraversion and higher neuroticism (especially in women), and variations in cognitive function and stress response, highlighting the importance of COMT in mental health treatment.
MAO-A **rs6323**	**TT**	MAO-A catalyzes oxidative deamination of serotonin, norepinephrine, and dopamine, regulating synaptic neurotransmitter levels. The rs6323 variant affects enzyme activity - G allele produces higher activity increasing neurotransmitter degradation, T allele results in lower activity. The low-activity T allele is associated with increased impulsive aggression and antisocial traits especially with adverse environmental factors. The high-activity G allele shows reduced placebo response in depression treatment due to increased monoamine catabolism.
MAOB **rs1799836**	**TT**	MAO-B catalyzes oxidative deamination of dopamine and other monoamines, producing reactive oxygen species that can induce oxidative stress. The intronic rs1799836 variant affects enzyme activity - TT genotype confers higher MAO-B activity with increased dopamine turnover and oxidative stress, C allele associates with lower activity. TT genotype individuals face increased risk for levodopa-induced dyskinesia in Parkinson's disease and greater Alzheimer's risk especially with APOE ε4, while C carriers show lower risk.
DRD2 **rs1076560**	**CC**	DRD2 encodes dopamine receptor D2, vital for reward, motivation, and motor control. Two isoforms exist: D2S (presynaptic autoreceptor) and D2L (postsynaptic receptor). The intronic rs1076560 variant affects isoform production - the A allele reduces D2S expression, potentially leading to diminishing presynaptic autoinhibition and increasing dopamine release. The A allele is associated with modestly increased susceptibility to schizophrenia and alcohol dependence.
ADRA2A **rs1800544**	**CC**	ADRA2A encodes the alpha-2A adrenergic receptor, an inhibitory autoreceptor that creates negative feedback for norepinephrine release. The promoter rs1800544 G allele results in lower receptor expression, reducing presynaptic inhibition and elevating norepinephrine. G allele carriers show increased motion sickness susceptibility due to reduced noradrenergic feedback, while ADHD children with G allele demonstrate improved methylphenidate response due to altered noradrenergic tone enhancing medication effects.

GAD1 **rs3749034**	**CG**	GAD1 encodes GAD67, the principal enzyme synthesizing GABA, the brain's chief inhibitory neurotransmitter. The promoter rs3749034 variant affects transcription factor binding and methylation. The G allele causes altered splicing patterns, increased fetal-type transcripts instead of mature GAD67, and distinct methylation patterns. G allele carriers show increased schizophrenia risk with persistent "immature" GABAergic state and greater prevalence in treatment-resistant schizophrenia, particularly among females.
GAD1 **rs3791878**	**TG**	GAD1 encodes GAD67 for GABA synthesis, vital for inhibitory neurotransmission and brain development. The promoter rs3791878 variant involves loss of transcription factor binding sites with the G allele. GG genotype individuals show reduced GAD67 expression and lower GABA synthesis, reducing inhibitory neurotransmission and increasing neural excitability. This results in significantly elevated risk for post-traumatic seizures following traumatic brain injury, while GT or TT genotypes appear protective.
HTR2A **rs6313**	**GA**	HTR2A encodes the serotonin receptor 5-HT2A, involved in neurotransmission, cognition, and mood. Many antipsychotics target this receptor. The rs6313 variant's A allele creates methylation-susceptible CpG sites, leading to lower HTR2A expression and reduced receptor density. The A allele is associated with lower receptor expression, increased schizophrenia susceptibility, and potentially diminished antipsychotic drug efficacy due to reduced available target receptors.
SLC6A4 **rs1042173**	**AA**	SLC6A4 encodes the serotonin transporter facilitating serotonin reuptake, regulating mood and reward behaviors, and serving as the SSRI target. The 3'UTR rs1042173 variant's A allele results in lower transporter expression compared to C allele, elevating synaptic serotonin. AA genotype individuals show neuroadaptive changes including enhanced dopaminergic output in reward circuits, resulting in greater alcohol consumption severity and dependence risk in Caucasians, though AA genotype (with 5'-HTTLPR LL) predicts better ondansetron response for alcohol treatment.
TPH2 **rs4570625**	**TG**	TPH2 is the rate-limiting enzyme for brain serotonin synthesis in raphe nuclei neurons. The promoter rs4570625 variant modulates expression - T allele correlates with enhanced TPH2 expression and increased serotonin, G allele with reduced expression. TT genotype demonstrates protective benefits including lower neuroticism, anxiety, aggressiveness, and resilience against depression, while GG or GT genotypes lack these protective effects and show increased mood disorder vulnerability.

DBH **rs1108580**	**GA**	DBH converts dopamine to norepinephrine in sympathetic neurons. The rs1108580 variant's A allele causes substantially reduced DBH expression in an allele-dose dependent manner, decreasing norepinephrine and elevating dopamine. This altered catecholamine balance leads to orthostatic hypotension, hypoglycemia, and autonomic dysfunction. The A allele is associated with increased hypertension, cardiovascular disease, addiction susceptibility, ADHD, and schizophrenia risk.
BDNF **rs6265**	**CC**	BDNF is crucial for neuronal growth, survival, and synaptic plasticity. Mature BDNF binds TrkB receptors to support neuronal survival, learning, and memory. The rs6265 (Val66Met) variant causes a valine-to-methionine change that impairs BDNF trafficking and activity-dependent release, reducing BDNF availability for neuronal plasticity. Met (T) allele carriers exhibit dose-dependent reductions in BDNF secretion affecting synaptic plasticity and hippocampal volume, leading to increased risk for depression, schizophrenia, Alzheimer's, Parkinson's, and other neuropsychiatric disorders, with each additional Met allele incrementally increasing disease susceptibility.
NGF **rs6330**	**AA**	NGF is a neurotrophic factor essential for neuronal development, survival, and plasticity, regulating synaptic plasticity, neurogenesis, and stress response particularly in hippocampus and amygdala through TrkA and p75NTR receptors. The rs6330 variant produces Ala35Val substitution - the G allele codes for alanine affecting NGF trafficking and stability, while the A allele codes for valine influencing protein processing and secretion. The A allele (Val) is significantly more prevalent in migraine with aura patients, enhancing vulnerability to cortical spreading depression, while the G allele (Ala) appears protective against migraine aura.
PER3 **rs10462020**	**TT**	PER3 is crucial for the circadian system, regulating sleep-wake cycles and circadian timing. The rs10462020 variant causes Val647Gly amino acid substitution in the PER3 protein. The T allele alters protein stability or function, leading to extreme morningness chronotype and increased bipolar disorder susceptibility. This manifests as advanced sleep phase, early morning awakening, and inflexible circadian timing. The G allele is associated with more adaptable circadian rhythm regulation.
PER3 **rs228697**	**CC**	PER3 regulates sleep-wake cycles and circadian timing. The rs228697 variant causes Pro864Ala substitution that disrupts protein binding domains, altering phosphorylation patterns and interactions with regulatory proteins like Casein Kinase 1, affecting PER3 stability within the molecular clock. The G allele is strongly associated with evening chronotype, delayed sleep phase, and increased free-running circadian rhythm disorder susceptibility. CC genotype may increase vulnerability to SSRI-induced sleep disturbances. The C allele associates with stable circadian regulation and normal to morning-type sleep patterns.

CLOCK

rs1801260

AG

CLOCK is a core circadian clock component that pairs with BMAL1 to regulate genes controlling sleep cycles, hormone levels, temperature, feeding, metabolism, and neurotransmitter systems affecting mood. The 3'UTR rs1801260 variant's G allele increases CLOCK mRNA levels by reducing microRNA binding, enhancing transcript stability. This shifts timing and amplitude of circadian gene regulation, causing phase delays. The G allele is associated with evening chronotype, delayed sleep onset, reduced sleep duration, and disrupted sleep-wake patterns, while the A allele associates with typical sleep patterns.

Metabolic Health

Metabolic Health is a cornerstone of any holistic wellness plan. Genetics plays a key role in how well the body processes nutrients and maintains metabolic balance. Utilizing personalized wellness tests provides unrivaled information to help achieve optimal health outcomes. The Metabolic Health panel includes information that helps inform decisions about lactose tolerance, caffeine metabolism, chromium utilization, and salt sensitivity, providing insights into how genetic variations influence nutrient processing and metabolic efficiency.

Products

Selected by your provider

WEIGHT MANAGEMENT SUPPORT

Our NBX Wellness Weight Management formula incorporates a wide array of 10 natural ingredients shown to support potential weight loss, improve cognitive performance, and aid in appetite suppression.*

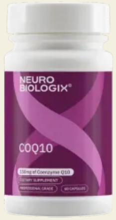
Designed to deliver a wide range of nutrients, this formula includes Green Tea Extract, Green Coffee Bean Extract, Raspberry Ketones, Olive Leaf, Bacopa Monnieri, Garcinia, CLA, and Forskolin along with nutrient cofactors for maximum

METABOLIC STIMULATOR PRO

Our exclusive formula, Metabolic Stimulator Pro, provides the ultimate metabolism support for your body. Crafted by Kendal Stewart, MD, this formula combines D-Chiro-Inositol with three other nutrient cofactors for optimal delivery. Metabolic Stimulator Pro enhances vital biochemical steps needed for cellular energy and may assist with fatigue, memory support, hormone regularity, weight control, as well as offering other health benefits.

OMEGACELL 1600 TG

A clean, sustainably-sourced Omega-3 formulawith 1600mg of EPA and DHA in an equal, 1:1 ratio to support cardiovascular, brain, and cellular health.

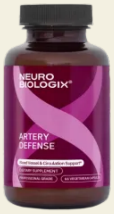


COQ10

CoQ10 (Coenzyme Q10) is a naturally occurring nutrient essential for cell growth and maintenance. Aging decreases the body's ability to process and produce ubiquinol, the biologically functioning form of CoQ10. Illness, poor nutrient intake, and certain medications can result in inadequate internal production of CoQ10 to sustain optimal organ function.

BLISSFUL MOOD

Our exclusive Blissful Mood provides enhanced neurological and nervous system support recommended for mood support, sleep disturbances, poor libido, and maintaining a healthy stress level. Blissful Mood features a carefully formulated combination of nutrients that function as neurotransmitters to support the overall nervous system and promote a healthy mood.



ARTERY DEFENSE

Artery & Circulation Supplement Formula for Enhanced Blood Flow & Blood and Vascular Support.*

With 8 key ingredients, including Equol, this formula was designed to improve the overall health of your blood vessels and provide enhanced circulation. Artery Defense protects blood vessels from damage: Equol, Grape Seed Extract, and Gotu Kola protect the health of your blood vessels through a powerful antioxidant effect

L-ARGININE PLUS

L-Arginine is a conditionally essential amino acid critical to health and wellness during increased physical stress or illness. L-Arginine supports growth hormone metabolism, tissue integrity, energy metabolism, and immune function. It also supports the synthesis of nitric oxide, a molecule produced in all body tissues that serve an essential role in the body's cardiovascular, immune, endocrine, and nervous systems.*

BERBERINE COMPLEX

Berberine Complex supports cardiometabolic health with a powerful, synergistic combination, featuring 400 mg of berberine per capsule enhanced with alpha-lipoic acid (ALA) and supported by biotin and chromium. This specialized formulation is designed to help optimize glucose and insulin metabolism, hemoglobin A1c (HbA1c) levels, cardiovascular health, and weight management.*

New Improved Formula!

Provider Recommendations

Berberine can help with your weight loss goals as you're seeing an increased risk of insulin resistance. This can manifest as the symptoms you described when managing your weight.

Metabolic Health Genes

The table below presents each gene and rsID, the genotype for each variant, and a description, all organized by topic.

ADIPOQ **rs17300539**	**GG**	ADIPOQ encodes adiponectin, a hormone crucial for glucose and lipid metabolism regulation. The promoter rs17300539 variant affects transcriptional activity through PPARγ response elements. The G allele is associated with decreased adiponectin expression, reduced insulin sensitivity, and increased metabolic syndrome susceptibility. The A allele associates with enhanced adiponectin production, improved insulin sensitivity, and better metabolic regulation. G allele carriers have increased risk for obesity-related metabolic dysfunction, while A carriers show protective effects against metabolic syndrome.
LEPR **rs1137101**	**GG**	LEPR encodes the leptin receptor, critical for energy balance and appetite control. The rs1137101 variant (Gln223Arg) results from A>G substitution, altering glutamine to arginine. This disrupts JAK2 signaling, potentially causing leptin resistance, impaired satiety, and energy imbalance. G allele carriers, particularly GG homozygotes, show increased BMI, waist circumference, elevated fasting insulin and glucose, adverse lipid profiles, and higher obesity and metabolic disorder risk. High saturated fat intake further amplifies these effects.
GHRL **rs696217**	**GG**	GHRL encodes preproghrelin, processed into ghrelin - the only circulating hormone that promotes food intake, fat storage, and glucose/insulin balance. The rs696217 variant (Leu72Met) doesn't alter mature ghrelin structure but may affect processing, secretion, or stability of preproghrelin, influencing transport and hormone interactions. The T allele is associated with increased obesity and metabolic syndrome susceptibility.
FTO **rs9939609**	**TT**	FTO is highly expressed in hypothalamus, adipose tissue, and muscle, affecting body weight through energy intake and food preferences. The intronic rs9939609 variant (T>A) makes the A allele a common genetic obesity risk factor through increased energy intake and adiposity. Lifestyle factors significantly modify risk - physical activity and low-fat hypocaloric diets may reduce or reverse the increased risk, with more pronounced effects in adulthood.

FTO rs1558902	TT	FTO encodes an enzyme involved in energy homeostasis and adipocyte biology, affecting appetite and fat cell development. The rs1558902 A allele is within the FTO linkage block and associates with elevated BMI through regulatory effects on gene expression and pathways governing food consumption and adipocyte differentiation. The A allele links to increased obesity risk, including early-onset obesity in children and adolescents.
DIO1 rs2235544	CC	DIO1 encodes type 1 deiodinase, which converts T4 to active T3 thyroid hormone in peripheral tissues like liver and kidneys, vital for metabolic rate regulation. The rs2235544 variant (C785T) T allele carriers exhibit lower DIO1 activity, causing less efficient T4-to-T3 conversion and lower fT3/fT4 ratio. These thyroid hormone alterations are associated with increased metabolic syndrome susceptibility.
CYP1A2 rs762551	AA	CYP1A2 is a cytochrome P450 enzyme crucial for metabolizing compounds including caffeine. The rs762551 variant (-163C>A) affects enzyme activity - A allele increases activity for faster caffeine metabolism, C allele slows it. AA genotype individuals clear caffeine quickly (rapid metabolizers), while CC genotype retain caffeine longer (slow metabolizers). C allele carriers show elevated myocardial infarction and obesity risk with high coffee consumption due to slower caffeine metabolism, which intensifies cardiovascular stimulation and diminishes appetite suppression.
ACE rs4343	GG	ACE encodes an enzyme crucial to the renin-angiotensin-aldosterone system, converting angiotensin I to vasoconstrictor angiotensin II and degrading vasodilator bradykinin, regulating vascular tone and blood pressure. The exon 17 rs4343 variant is a silent mutation (2350A>G). The G allele correlates with upregulated ACE expression and elevated activity, increasing angiotensin II and decreasing bradykinin. This promotes vasoconstriction, sodium retention, and vascular remodeling, amplifying hypertension and cardiometabolic disease risk.
AGT rs699	AA	AGT encodes angiotensinogen, a liver-produced protein that's the sole renin substrate. It's converted to angiotensin I then angiotensin II, regulating blood pressure and salt-water balance. The rs699 variant (M235T) involves G>A substitution in exon 2. The A allele encodes a threonine variant raising circulating angiotensinogen levels, increasing angiotensin II production, enhancing vasoconstriction and sodium retention. This elevates blood pressure and heightens hypertension and preeclampsia risk.
MC4R rs17782313	TT	MC4R encodes the melanocortin 4 receptor regulating appetite, energy expenditure, and food preference in the central nervous system. The rs17782313 variant (T>C) C allele is associated with increased total energy and fat consumption, significant long-term weight and waist circumference gain, elevated obesity risk (most prominent in homozygotes), and increased type 2 diabetes risk independent of BMI.

TFAP2B **rs987237**	**AA**	TFAP2B encodes transcription factor AP-2β, expressed in adipose tissue, regulating adipocyte function. The rs987237 G allele is the obesity risk allele associated with higher waist circumference and adiposity. G carriers show greater weight reduction on high-fat versus low-fat energy-restricted diets compared to AA homozygotes, and more pronounced weight regain on high-protein versus low-protein diets.
UCP1 **rs1800592**	**AA**	UCP1 encodes mitochondrial uncoupling protein 1, facilitating non-shivering thermogenesis in brown adipose tissue. The rs1800592 variant (-3826A>G) G allele carriers exhibit diminished UCP1 expression in intraperitoneal adipose tissue, suggesting decreased thermogenic activity and heat production, predicting lower energy expenditure and increased fat storage.
PPARG **rs1801282**	**CG**	PPARG encodes PPARγ, a master regulator of adipogenesis, lipid/glucose metabolism, and insulin sensitivity. The rs1801282 variant (Pro12Ala, C>G) G allele produces reduced transcriptional activity PPARγ protein. The G allele is the risk allele for obesity and adverse lipid profiles, associated with higher BMI, increased waist circumference, and elevated total cholesterol.
TCF7L2 **rs7903146**	**CT**	TCF7L2 encodes a Wnt pathway transcription factor crucial for pancreatic beta-cell function and GLP-1 biology, affecting insulin secretion. The rs7903146 T allele associates with higher HbA1c and type 2 diabetes susceptibility via altered GLP-1 and reduced insulin responses. TT homozygotes often show smaller weight, fat, and waist losses and less insulin resistance improvement on high-fat versus low-fat diets.
PLIN1 **rs894160**	**AA**	PLIN1 encodes perilipin, the predominant adipocyte lipid droplet protein regulating lipase access and lipolysis. The rs894160 A allele shows heterogeneous effects: some studies suggest greater initial weight loss with better maintenance, others show less waist reduction but more lipid oxidation. The A allele shows diet-dependent effects - associated with reduced waist/hip circumferences with high complex carbohydrate intake (≥144g/d) but increased waist circumference with low intake (<144g/d).
MTNR1B **rs10830963**	**CC**	MTNR1B encodes melatonin receptor MT2, expressed in circadian pacemaker and pancreatic islets, affecting circadian rhythm and insulin secretion. The rs10830963 G allele associates with higher fasting glucose and type 2 diabetes risk via impaired insulin secretion. G allele correlates with increased pancreatic MTNR1B expression, enhancing melatonin signaling that suppresses insulin release. CC genotypes achieve greater weight loss and metabolic improvements than G carriers on hypocaloric diets.

Gastrointestinal Health

Gastrointestinal Health describes how your genes affect your digestive system's ability to break down foods, absorb nutrients, and maintain a healthy gut environment. Your genetic makeup influences whether you can digest certain foods like dairy products containing lactose, and how your immune system responds to proteins like gluten found in wheat, barley, and rye. This panel analyzes genes controlling digestive enzyme production and immune responses in your gut. Understanding your gastrointestinal genetics helps identify which foods work best for your body, potential food sensitivities, and how to optimize your digestive health through personalized dietary choices.

Products

Selected by your provider

BIOTIC SUPREME 50

Biotic Supreme 50 is a next-generation probiotic (NGP) formula that creates a powerful synergistic effect on GI ecology. It delivers over 50 billion CFU of Bifidobacterium, Lactobacillus, and Saccharomyces boulardii to support gut health, immune function, and normal bowel movements. It also includes 500 million AFU of the keystone probiotic Akkermansia muciniphila along with Clostridium butyricum and Bifidobacterium infantis to strengthen the structure and diversity of the entire gut ecosystem.* In addition to being formulated with an overage, Biotic Supreme 50 also uses a moisture-resistant, desiccant-lined package to ensure survival and

Provider Recommendations

We will focus on these other wellness areas as you seem to be genetic sufficient here.

Gastrointestinal Health Genes

The table below presents each gene and rsID, the genotype for each variant, and a description, all organized by topic.

MCM6 **rs4988235**	**AA**	MCM6 regulates the adjacent LCT (lactase) gene. The rs4988235 variant is positioned ~13,910 base pairs upstream from LCT. The A allele acts as an enhancer, disrupting a transcription factor binding site to allow sustained lactase expression post-weaning (lactase persistence). GG genotype leads to lactase downregulation and non-persistence. A allele carriers show higher overweight/obesity risk and increased adiposity but lower total, LDL, and HDL cholesterol compared to non-carriers.
MCM6 **rs182549**	**TT**	MCM6 regulates the adjacent lactase gene. The rs182549 variant is located ~22,018 base pairs upstream of LCT. CC genotype causes LCT downregulation in adulthood, resulting in lactose intolerance with gastrointestinal symptoms after dairy consumption. The T allele associates with lactose tolerance - carriers continue expressing lactase beyond childhood, enabling lactose digestion.
HLA-DQA7 **rs4639334**	**GG**	HLA-DQA7 encodes the alpha chain of HLA-DQ7, participating in gluten peptide presentation to T cells in intestinal mucosa. The rs4639334 variant serves as a genetic marker for HLA-DQ7 haplotype. The A allele indicates DQ7 carriage and may increase celiac disease susceptibility when found with DQ2.2 or DQ2.5 haplotypes, due to formation of high-affinity gluten-presenting heterodimers.
HLA-DQA8 **rs7454108**	**TT**	HLA-DQA8 refers to HLA-DQA1 carrying the DQA1*03 variant that forms HLA-DQ8 heterodimer. The rs7454108 is a tag SNP for the HLA-DQ8 haplotype. The C allele marks DQ8 molecules that present gluten peptides to T cells, triggering aberrant immune activation and increased celiac disease susceptibility.
HLA-DQA1 **rs2187668**	**CC**	HLA-DQA1 encodes the alpha-chain of HLA-DQ, crucial for presenting gluten peptides to T cells in intestinal mucosa, central to celiac disease pathogenesis. The intronic rs2187668 variant serves as a precise marker for the HLA-DQ2.5cis haplotype, the predominant celiac disease genetic risk factor. The T allele indicates significantly elevated celiac disease risk, making this SNP valuable for clinical diagnostics and population screening.
HLA-DQA2 **rs2858331**	**AG**	HLA-DQA2 encodes the alpha-chain of HLA-DQ class II heterodimer for antigen presentation. The intronic rs2858331 between HLA-DQB1 and HLA-DQA2 shows strong linkage with HLA-DQ2.2 and HLA-DQ2.5 haplotypes. The G allele is associated with elevated IgE levels.

NOD2 **rs2066845**	**GG**	NOD2 encodes an intracellular receptor sensing bacterial peptidoglycan and regulating NF-κB activation. The rs2066845 variant (G908R) in the leucine-rich repeat domain reduces NOD2-dependent NF-κB activation, representing partial loss-of-function. The C allele associates with altered gut microbiome with inflammation-associated bacteria expansion and increased Crohn's disease risk with severe phenotypes including stricturing and penetrating disease. C carriers may benefit from targeted probiotic supplementation.
FUT2 **rs492602**	**AG**	FUT2 encodes α(1,2) fucosyltransferase, determining secretor status and ABO antigen expression on epithelial cells and body fluids. The rs492602 G allele is linked to elevated Crohn's disease vulnerability, possibly due to enzyme function loss, absence of ABO(H) antigens in secretions, and dysbiosis that disrupts mucosal immune homeostasis.

⚥ Women's Health

Women's Health describes how your genes influence hormonal balance, reproductive health, and wellness factors unique to women throughout different life stages. Your genetic makeup affects how your body produces, uses, and clears hormones like estrogen, how your ovaries respond to hormonal signals, and your individual risks for conditions that particularly impact women. This panel analyzes genes controlling hormone metabolism, thyroid function, vitamin D usage for bone health, and cardiovascular factors important for women's health. Understanding your women's health genetics helps identify your hormonal patterns, nutritional needs, and personalized approaches to support optimal wellness through all phases of life.

Products

Selected by your provider

DCI CELL RECOVERY

Our exclusive DCI Cell Recovery provides crucial support for essential chemical processes in the body. This insulin messenger can positively affect symptoms associated with unbalanced blood sugar, cellular function, immune system health, and mood stability.

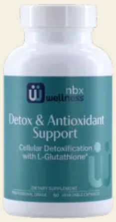
BERBERINE COMPLEX

Berberine Complex supports cardiometabolic health with a powerful, synergistic combination, featuring 400 mg of berberine per capsule enhanced with alpha-lipoic acid (ALA) and supported by biotin and chromium. This specialized formulation is designed to help optimize glucose and insulin metabolism, hemoglobin A1c (HbA1c) levels, cardiovascular health, and weight management.*

New Improved Formula!

ESTRO ZEN

Our exclusive Estro Zen formula helps address estrogen dominance. Our formulation helps improve healthy estrogen metabolism and eliminates harmful forms of estrogen from the body. This supplement benefits those with genetic mutations that increase damaging forms of estrogen.



DETOX & ANTIOXIDANT SUPPORT

Our exclusive Detox & Antioxidant Support is a physician-derived blend of ingredients that provide a superior glutathione supplement readily utilized in the body to support the immune system and cellular functioning. Glutathione is a master antioxidant (scavenging free radicals), anti-inflammatory, and immunity powerhouse.

WEIGHT MANAGEMENT SUPPORT

Our NBX Wellness Weight Management formula incorporates a wide array of 10 natural ingredients shown to support potential weight loss, improve cognitive performance, and aid in appetite suppression.*

Designed to deliver a wide range of nutrients, this formula includes Green Tea Extract, Green Coffee Bean Extract, Raspberry Ketones, Olive Leaf, Bacopa Monnieri, Garcinia, CLA, and Forskolin along with nutrient cofactors for maximum

BLISSFUL MOOD

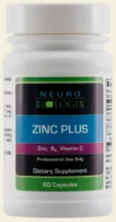
Our exclusive Blissful Mood provides enhanced neurological and nervous system support recommended for mood support, sleep disturbances, poor libido, and maintaining a healthy stress level. Blissful Mood features a carefully formulated combination of nutrients that function as neurotransmitters to support the overall nervous system and promote a healthy mood.

L-THEANINE

L-Theanine reduces stress and relaxes your brain by increasing alpha wave activity. L-Theanine provides stress-reducing effects without causing drowsiness and can increase relaxation and stimulate neuron and dopamine production.

T3/T4 SUPPORT

T3/T4 Support is a targeted nutritional formula designed to promote healthy thyroid function by supporting the balanced production, conversion, and activity of thyroxine (T4) and triiodothyronine (T3). This comprehensive blend includes key bioactive compounds such as forskolin, zinc citrate, and bovine-derived glands, each contributing distinct support for thyroid physiology.

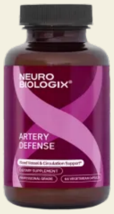


ZINC PLUS

Zinc Plus provides ultimate zinc delivery for enhanced immune system and metabolism function. For optimal assimilation and pH balance, our Zinc Plus formulation uses zinc citrate, the form of zinc found naturally in human milk. Including B6 and C vitamins facilitates zinc metabolism and delivery.

MAGNESIUM GLYCINATE COMPLEX

Magnesium Glycinate Complex is an easy-to-digest source of magnesium, a critical nutrient that facilitates multiple essential life processes. Magnesium helps convert carbohydrates, protein, and fats to energy and catalyzes thousands of enzymatic processes.



ARTERY DEFENSE

Artery & Circulation Supplement Formula for Enhanced Blood Flow & Blood and Vascular Support.*

With 8 key ingredients, including Equol, this formula was designed to improve the overall health of your blood vessels and provide enhanced circulation. Artery Defense protects blood vessels from damage: Equol, Grape Seed Extract, and Gotu Kola protect the health of your blood vessels through a powerful antioxidant effect

Provider Recommendations

Berberine and this systemic Magnesium product should help with some of your hormonal issues as they deal and interact with your body composition goals.

Women's Health Genes

The table below presents each gene and rsID, the genotype for each variant, and a description, all organized by topic.

CYP1B1 **rs1800440**	**TT**	CYP1B1 encodes cytochrome P450 1B1, which metabolizes sex hormones by converting estrogens to catecholestrogens. The rs1800440 variant (Asn452Ser) results from T>G substitution changing asparagine to serine, altering enzyme activity. The G allele associates with lower circulating estradiol in healthy women. Effects on vasomotor symptoms are contradictory - one study showed higher hot flash odds, another found less frequent hot flashes in African-American women. Effects may be modified by environmental factors like smoking and race.
FSHR **rs6165**	**CT**	FSHR encodes the granulosa cell receptor facilitating FSH-induced folliculogenesis and estrogen synthesis. The rs6165 variant (Thr307Ala) substitutes threonine with alanine. The T allele associates with higher basal FSH, reduced ovarian responsiveness (fewer oocytes), longer stimulation needs, increased low response risk, and greater PCOS susceptibility when homozygous. The variant may change receptor structure/function, producing clinically relevant differences in controlled ovarian stimulation dosing and PCOS phenotype.
CYP19A1 **rs4646**	**AC**	CYP19A1 encodes aromatase, converting androgens to estrogens - the primary peripheral estrogen source post-menopause. The rs4646 C allele shows dose-dependent impact on estrogen levels - AC genotype shows intermediate increase, CC shows most substantial rise in estradiol/estrone. The C allele functions as a regulatory variant associated with increased estrogen exposure and potential link to female pattern hair loss, especially in younger women.
SHBG **rs12150660**	**GG**	SHBG encodes sex hormone-binding globulin, binding testosterone and estradiol to regulate their bioavailability. The rs12150660 T allele associates with increased circulating SHBG and total testosterone. In women, SHBG restricts hormone bioavailability through high-affinity binding. Diminished SHBG (often in obesity) associates with elevated androgens, menstrual dysfunction, and PCOS-like manifestations. The T allele may represent a genetic variant associated with favorable health outcomes in women.
SHBG **rs6259**	**GG**	SHBG encodes sex hormone-binding globulin regulating hormone transport and bioavailability. The rs6259 variant (D327N) shows inconsistent PCOS associations. Most studies indicate no independent effect on SHBG levels or PCOS risk after adjusting for BMI and insulin resistance. Some populations show modest protective signal with A allele. Hypothesized impact involves modifications to SHBG stability or clearance affecting free testosterone, but clinical significance varies across populations.

SHBG **rs1799941**	**GG**	SHBG encodes sex hormone-binding globulin for hormone transport regulation. The rs1799941 variant marks regulatory haplotypes associated with upstream promoter repeat variability. The A allele links to elevated SHBG levels with additive allele-dose effects. Elevated SHBG protects against metabolic conditions including type 2 diabetes. The G allele links to reduced SHBG, with GG genotype associated with lower HDL and increased coronary heart disease risk compared to A carriers.
FOXE1 **rs1867277**	**GG**	FOXE1 encodes a thyroid transcription factor regulating thyroglobulin and thyroid peroxidase expression for thyroid hormone synthesis. The promoter rs1867277 A allele modifies transcription factor binding, potentially altering gene expression. The A allele is linked to thyroid hormone dysregulation, particularly decreased TSH levels, which can mask early thyroid disease.
DIO2 **rs225014**	**TT**	DIO2 encodes deiodinase type 2, which converts inactive T4 to active T3 thyroid hormone, critical for skeletal development, cartilage maintenance, and metabolism. DIO2 is a selenoprotein requiring selenium for structural integrity and activity - inadequate selenium reduces DIO2 expression and function. The rs225014 variant (Thr92Ala) substitutes threonine (T) with alanine (C), resulting in diminished enzyme functionality unaffected by selenium levels. CC homozygotes are at elevated risk of inadequate T3 synthesis, particularly under selenium deficiency conditions.
VDR **rs2228570**	**GG**	VDR encodes the vitamin D receptor mediating biological effects of active vitamin D. The rs2228570 (FokI) variant at the translation start site affects receptor activity. GG genotype (producing more active receptor) responds better to vitamin D supplementation with higher serum 25(OH)D increases than AA genotype. A allele carriers may have weaker calcium absorption, lower bone mineral density, and increased osteoporosis and fracture risk.
GC **rs2282679**	**TT**	GC encodes vitamin D-binding protein (DBP), synthesized in liver, that transports vitamin D and its metabolites. The rs2282679 T allele leads to reduced DBP and lower serum vitamin D concentrations, increasing clinical vitamin D deficiency risk, helping guide preventive strategies in at-risk populations.
ACE **rs4343**	**GG**	ACE encodes an enzyme crucial to the renin-angiotensin-aldosterone system, converting angiotensin I to vasoconstrictor angiotensin II and degrading vasodilator bradykinin, regulating vascular tone and blood pressure. The exon 17 rs4343 variant is a silent mutation (2350A>G). The G allele correlates with upregulated ACE expression and elevated activity, increasing angiotensin II and decreasing bradykinin. This promotes vasoconstriction, sodium retention, and vascular remodeling, amplifying hypertension and cardiometabolic disease risk.

AGT **rs699**	**AA**	AGT encodes angiotensinogen, a liver-produced protein that's the sole renin substrate. It's converted to angiotensin I then angiotensin II, regulating blood pressure and salt-water balance. The rs699 variant (M235T) involves G>A substitution in exon 2. The A allele encodes a threonine variant raising circulating angiotensinogen levels, increasing angiotensin II production, enhancing vasoconstriction and sodium retention. This elevates blood pressure and heightens hypertension and preeclampsia risk.
F5 **rs6025**	**GG**	F5 encodes coagulation factor V, accelerating thrombin generation in the clotting cascade. The rs6025 variant (Factor V Leiden, G1691A) A allele makes factor V resistant to inactivation by Activated Protein C, creating a hypercoagulable state. This is the most common inherited venous thromboembolism (VTE) risk factor. A carriers show dose-dependent increased VTE risk, compounded by obesity, smoking, age, and in women, pregnancy and postpartum period.

III. References

For a comprehensive overview of the scientific literature used to support the genetic data, recommendations, and SNP-related information presented in this report, please follow the link below. This reference page includes key studies and sources that support the scientific basis of our analysis and recommendations.

Nutrigenomics Test References

Legal Disclaimer

NUTRIGENOMICS GENETIC TEST DISCLAIMER SUMMARY

This summary highlights key terms from the complete disclaimer and informed consent agreement signed during online registration.

TEST INFORMATION

This nutrigenomic test analyzes genetic variations (SNPs) to provide personalized nutrition and wellness recommendations. A CLIA-accredited laboratory performs testing. These are Laboratory Developed Tests validated under CLIA but not FDA cleared or approved.

MEDICAL DISCLAIMER

This test and its recommendations ARE NOT intended to diagnose, treat, cure, or prevent any disease. Results should not replace professional medical care. Consult your healthcare provider before making significant dietary or lifestyle changes based on test results.

LIMITATIONS

- Test results represent probabilities based on current scientific understanding
- Genetic factors are only one component of health outcomes
- Individual responses to nutritional interventions vary and cannot be guaranteed
- Not all genetic variations affecting tested genes will be detected

REGULATORY NOTICE

The FDA has not evaluated statements or products recommended through this service. NBX Wellness does not provide medical advice or supervision.

LIABILITY & RISK

You assume full responsibility for decisions regarding the use of test results and recommendations. NBX Wellness and laboratory partners are not liable for damages arising from use of this service to the fullest extent permitted by law.

PARENTAL CONSENT

Parents/guardians registering minors assume complete responsibility for decisions regarding recommendations for the minor child.

ACCEPTANCE

By completing online registration, you acknowledge reading and accepting all terms in the complete disclaimer. This summary does not replace the whole agreement.

NBX Wellness | Neurobiologix
10921 E Crystal Falls Pkwy STE L901, Leander, TX 78641
866-500-5388 | support@neurobiologix.com

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