

REPORT DATE

Mar 20, 2026

OVERALL SCORE

64/100

BIOMARKERS ANALYZED

296

ZONE

Early Disruption

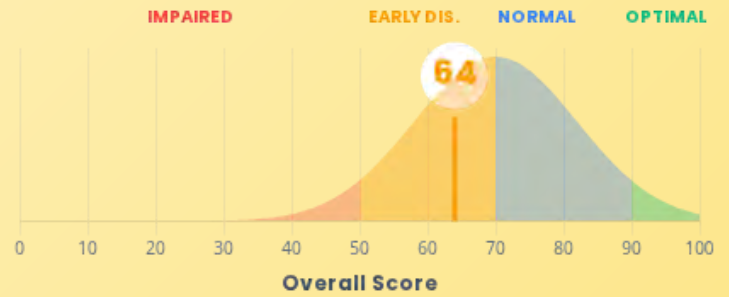
64

Overall Status Score

Early Disruption

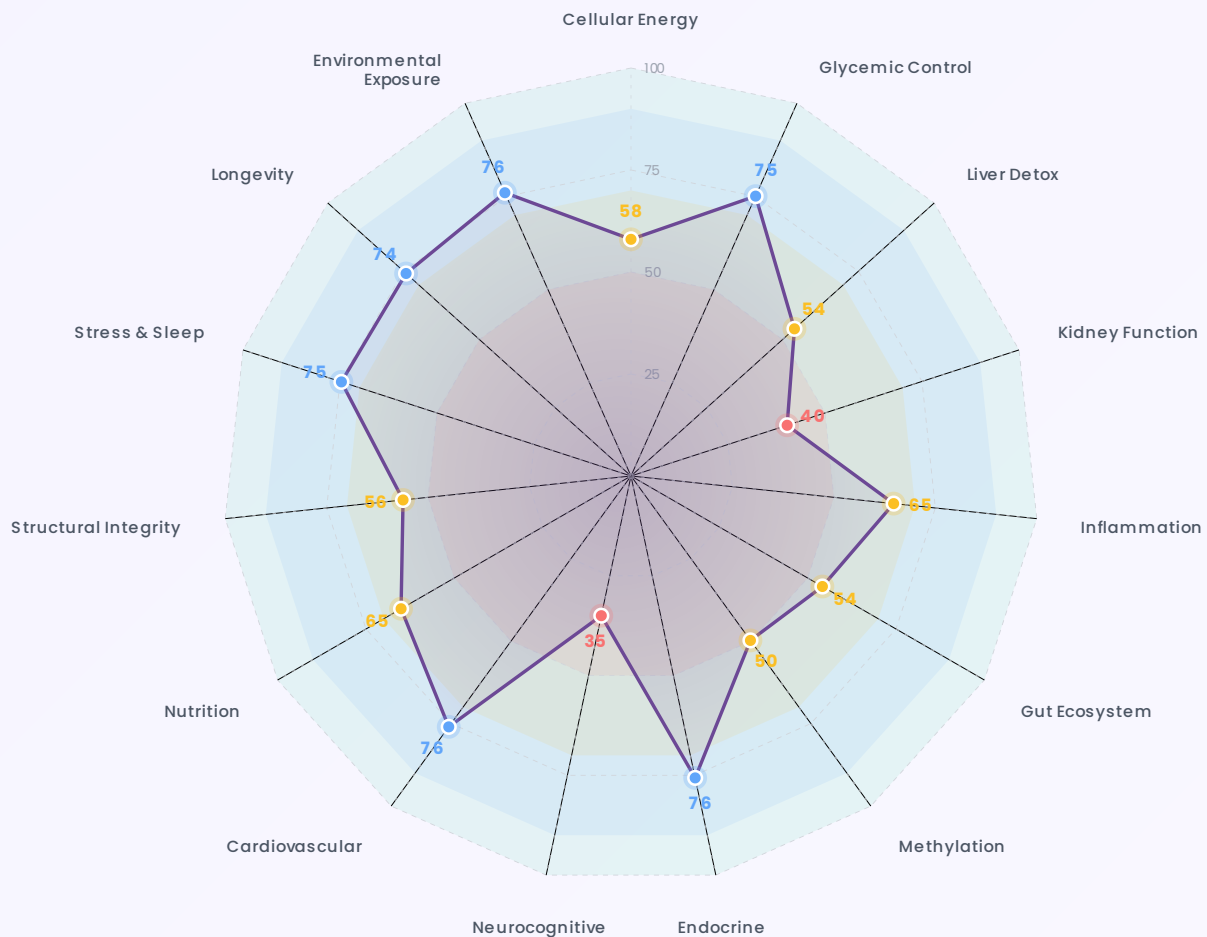
Overall metabolic health assessment based on 15 domains.

Score Distribution vs Reference Cohort (n=513)



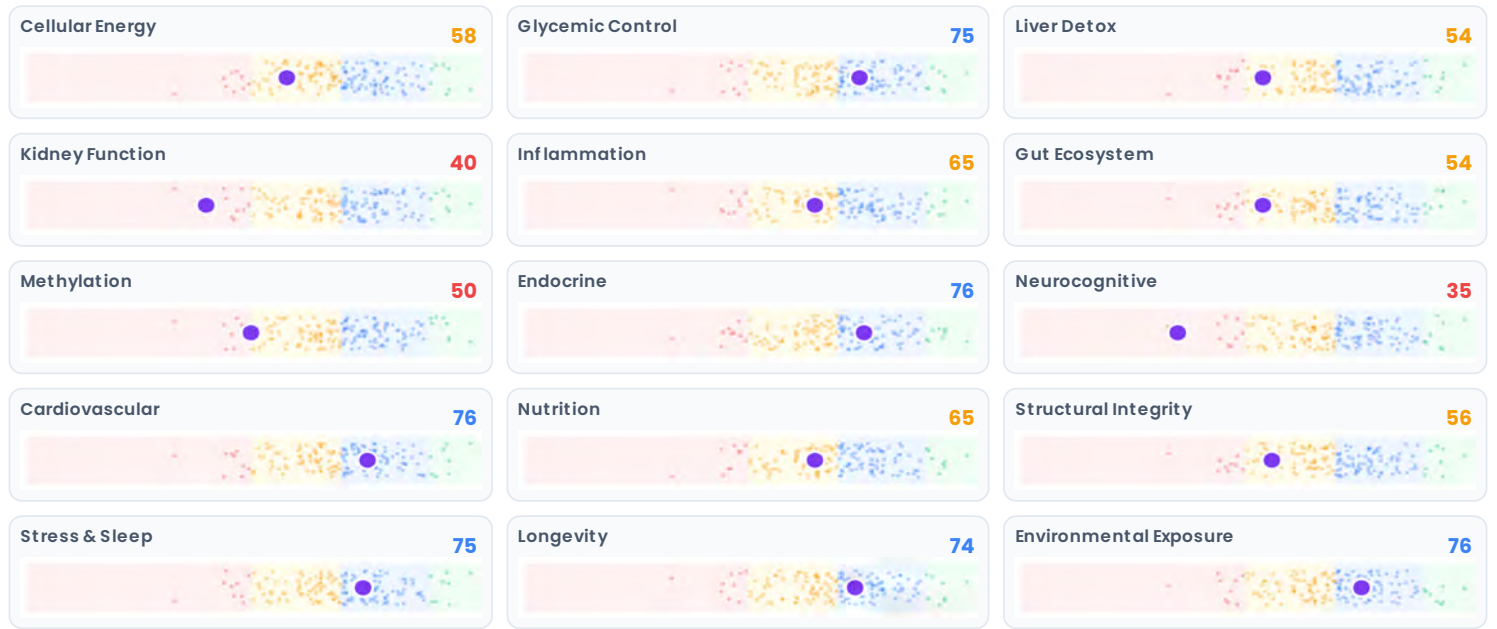
Metabolomic Domain Profile

15-domain radar view — each axis represents one operational domain scored 0-100



● Optimal (90-100) ● Normative (70-89) ● Early Disruption (50-69) ● Impaired (0-49)

Domain Scores Breakdown



Subdomain Zone Distribution



● Impaired (0-49) ● Early (50-69) ● Normative (70-89) ● Optimal (90-100)

Total subdomains: **124** (Impaired: 49, Early: 50, Normative: 21, Optimized: 4).
 Coverage ensures 1 recommendation for every flagged subdomain.

Sample Quality

99

Quality Score

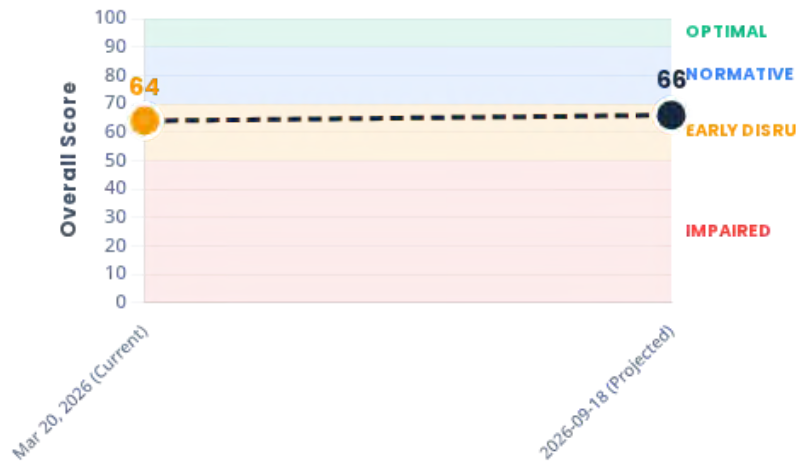
Score: 99/100 — Incomplete

HOLD <70	CAUTION 70-84	PASS 85-100
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Sample meets all quality thresholds.

Fasting Yes	Integrity Incomplete
Coverage 293/296	QC Flags None
Circadian AM (7-9)	Exertion None 12h

Historical & Projected Trajectory



Projected trajectory: Current to Digital Twin projection (26 weeks)
 ■ Projected score (66) reflects personalized recommendations from Digital Twin modeling
 ↑ Higher scores indicate improved metabolic function

Key Clinical Insights

Dysfunction Category	Priority	Key Biomarkers / Pathways	Clinical Objective
Myelin/Membrane Integrity Compromise	#1	Choline, Serine, Acetylcholine	Elevated choline (z=2.34), acetylcholine (z=3.31), and serine (z=2.15) indicate disrupted phospholipid metabolism and membrane turnover critical for myelin maintenance and neural signal transduction in the context of significant neurocognitive impairment.
Reduced Glomerular Filtration Reserve	#2	Urate, Asymmetric dimethylarginine, Ornithine	Elevated ADMA (z=2.28), urate (z=2.16), and ornithine (z=2.26) indicate impaired renal microvascular tone and NOS inhibition compromising glomerular filtration efficiency in this patient with significant kidney dysfunction.
Nucleotide Synthesis Impairment (One-Carbon)	#3	dTMP, dUTP	Markedly elevated dTMP (z=3.56) and dUTP (z=2.32) indicate folate-dependent thymidylate synthesis dysregulation with potential DNA misincorporation risk, consistent with impaired methylation domain status.
Ammonia Clearance Impairment (Urea Cycle Stress)	#4	Ornithine, Glutamine, Aspartate	Elevated ornithine (z=2.26), glutamine (z=2.31), and aspartate (z=2.31) indicate urea cycle strain from excess nitrogen load, consistent with early hepatic detoxification disruption and kidney impairment.
Yeast/Fungal Overgrowth Signature	#5	L-Arabitol, Adonitol	Significantly elevated L-arabitol (z=3.16) and adonitol (z=3.23) are characteristic sugar alcohols consistent with Candida or fungal overgrowth in the GI tract, aligning with early gut ecosystem disruption.

Key Clinical Insights (continued)

Dysfunction Category	Priority	Key Biomarkers / Pathways	Clinical Objective
Glycosylation / Sialylation Defect	#6	N-Acetylneuraminic acid, Glucosamine	Extremely elevated glucosamine (z=12.03) and N-acetylneuraminic acid (z=4.40) indicate significant glycosylation pathway disruption affecting cell signaling, immune recognition, and structural protein function.
Polyamine-Driven Immune Proliferation	#7	Spermidine, Ornithine	Elevated spermidine (z=3.50) and ornithine (z=2.26) suggest increased polyamine synthesis indicating immune cell proliferation and altered autophagy regulation in the context of early inflammatory disruption.
Glutathione Depletion & Conjugation Failure	#8	Pyroglutamic acid, Glutamine	Elevated pyroglutamic acid (z=2.43) suggests gamma-glutamyl cycle stress and potential glutathione depletion, compromising Phase II conjugation and systemic antioxidant defense capacity.

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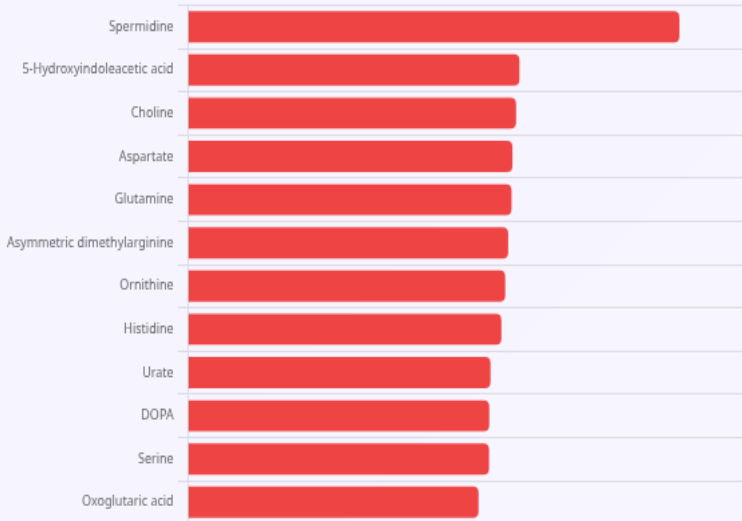
296

ZONE

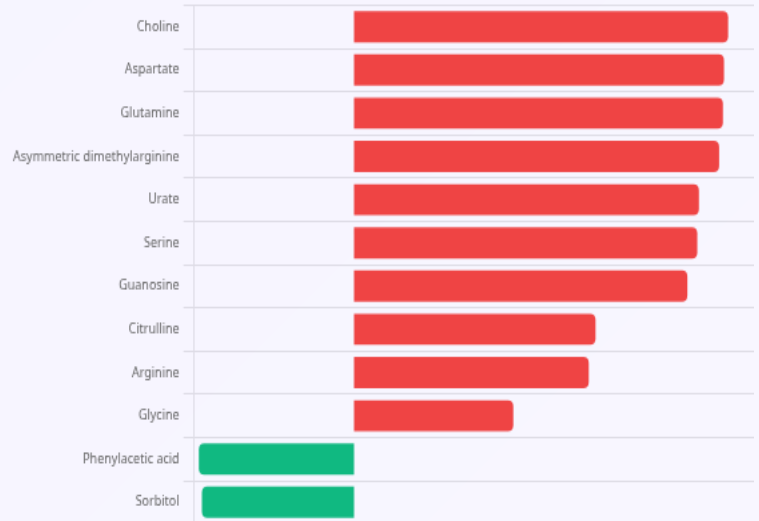
EARLY DISRUPTION

Top Contributors (Top 4 Domains) - 12 Metabolites Each

1. Neurocognitive (Score: 35)



2. Kidney Function (Score: 40)



3. Methylation (Score: 50)



4. Liver Detox (Score: 54)



How to Interpret Top Contributors:

These charts show the 12 most influential metabolites driving each domain's score, ranked by absolute contribution magnitude.

- **Red bars (Strain):** Metabolites that are elevated, depleted, or imbalanced in ways that *increase* metabolic strain in this domain (positive contribution).
- **Green bars (Optimized):** Metabolites in protective or beneficial ranges, or depleted factors whose low levels indicate dysfunction (negative contribution, but still highlighting the problem).
- **Values shown:** Weighted contribution scores (not raw concentrations) combining the metabolite's z-score deviation, pathway importance, and confidence weighting.
- **Larger bars** = greater impact on the domain's overall score.
- **Selection criteria:** Top 12 metabolites by absolute contribution value using cluster control to avoid overweighting correlated features.

These contributors directly map to the clinical hypotheses on Page 4 and inform targeted intervention strategies.

Top-5 Metabolic Patterns

1 Neurocognitive & Cognitive Reserve

35

Biochemical rationale: Impaired neurotransmitter precursor availability with reduced tryptophan-to-serotonin conversion and elevated kynurenine pathway activation. Cognitive reserve markers show functional deficit requiring neuroprotective support.

Neurocognitive (35)

Methylation (50)

Endocrine (76)

2 Kidney Filtration & Renal Resilience

40

Biochemical rationale: Impaired renal filtration efficiency with elevated urea cycle intermediates and reduced creatinine clearance markers. Nitrogen handling capacity shows functional limitation requiring renal support and reduced protein load.

Kidney Function (40)

Inflammation (65)

3 Methylation & One-Carbon Economy

50

Biochemical rationale: Suboptimal SAME/SAH ratio with impaired folate cycle function and homocysteine elevation. Methylation capacity shows functional limitation affecting DNA repair, neurotransmitter synthesis, and detoxification pathways.

Methylation (50)

Liver Detox (54)

Neurocognitive (35)

4 Liver Detoxification & Conjugation Capacity

54

Biochemical rationale: Phase I and Phase II conjugation pathways showing significant functional stress. Reduced glutathione conjugation capacity and impaired amino acid metabolism limiting detoxification of inflammatory mediators. Sulfation capacity borderline, glycine availability reduced.

Liver Detox (54)

Methylation (50)

Nutrition (65)

5 Gut Microbiome & Intestinal Health

54

Biochemical rationale: Dysbiotic microbiome metabolite patterns with reduced short-chain fatty acids, elevated putrefaction markers, and compromised intestinal barrier function. Microbial metabolism shows inflammatory signature requiring gut restoration.

Gut Ecosystem (54)

Inflammation (65)

Liver Detox (54)

DIET

Beetroot and Nitrate-Rich Vegetable Protocol

250ml beetroot juice or 2 servings nitrate-rich vegetables (arugula, spinach, beets) - Daily

Rationale: With ENDO_NO at 35 and arginine-NO bioavailability critically depleted, dietary nitrate provides an alternative NO generation pathway via the enterosalivary nitrate-nitrite-NO cycle independent of eNOS. Evidence supports natural nitrate sources (ES=1.23, p=0.0495, N=383) with 16.38% improvement and sustained effects over 21 months. This complements L-citrulline by activating the nitrate reductase pathway.

Target: Diet (Current Score: 76)

LIFESTYLE

Targeted Exercise Protocol: Strength Training and Zone 2 Cardio

30-45 min Zone 2 cardio; 2 sessions/week resistance training - 5x per week (3 Zone 2 cardio + 2 strength sessions)

Rationale: TCA capacity (35), AA oxidation (35), and bioenergetic-oxidative (35) scores indicate profound mitochondrial underperformance. Zone 2 aerobic training stimulates mitochondrial biogenesis via PGC-1 α while resistance training improves insulin sensitivity and BCAA catabolism in skeletal muscle. Evidence supports strength training (ES=0.78, N=478) for preserving metabolic capacity.

Target: Lifestyle (Current Score: 76)

SUPPLEMENT

N-Acetylcysteine (NAC) for Glutathione and Transsulfuration Support

600mg twice daily (1200mg total) - Daily

Rationale: Multiple subdomains are critically low at 35: glutathione conjugation/redox reserve, transsulfuration-glutathione redox, and thiol redox reserve (47.52). NAC is the rate-limiting precursor for glutathione synthesis via the transsulfuration pathway, directly replenishing hepatic and systemic GSH pools. This addresses the convergent deficits in detoxification Phase II conjugation, neuroinflammatory redox defense, and carbonyl detox capacity.

Target: Supplement (Current Score: 76)

Key Metabolite Drivers (Priority Areas)

Neurocognitive (Impaired - 35)

- Spermidine: Elevated strain
- 5-Hydroxyindoleacetic acid: Elevated strain
- Choline: Elevated strain
- Aspartate: Elevated strain

Kidney Function (Impaired - 40)

- Choline: Elevated strain
- Aspartate: Elevated strain
- Glutamine: Elevated strain
- Asymmetric dimethylarginine: Elevated strain

Methylation (Impaired - 50)

- dTMP: Elevated strain
- Spermidine: Elevated strain
- Pyroglutamic acid: Elevated strain
- Choline: Elevated strain

Liver Detox (Early Disruption - 54)

- Decanoylcarnitine: Elevated strain
- Pyroglutamic acid: Elevated strain
- Choline: Elevated strain
- Aspartate: Elevated strain

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ZONE

Normative

Projected improvement at retest: **+4.3 points** (from 76 -> 66). Subdomain tally — Total analyzed: **196**. Top-20 protocol satisfies mandatory coverage constraints with high-impact interventions targeting key metabolic pathways.

Personalized Interventions (20 recommendations)

#1

N-Acetylcysteine (NAC) for Glutathione and Transsulfuration Support

Adherence Effort |||

Glutathione Conjugation & Redox Reserve (Normative)

Impact 21% Δ+15.0 6mo

600mg twice daily (1200mg total) - Daily Multiple subdomains are critically low at 35: glutathione conjugation/redox reserve, transsulfuration-glutathione redox, and thiol redox reserve (47.52). NAC is the rate-limiting precursor for glutathione synthesis via the transsulfuration pathway, directly replenishing hepatic and systemic GSH pools. This addresses the convergent deficits in detoxification Phase II conjugation, neuroinflammatory redox defense, and carbonyl detox capacity.

#2

Methylfolate and Methylcobalamin for Remethylation Reserve

Adherence Effort |||

Fermentation Load & Fodmap Intolerance (Normative)

Impact 21% Δ+15.0 6mo

L-methylfolate 1mg + methylcobalamin 1000mcg sublingual - Daily Remethylation reserve is critically depleted (35.45) alongside genomic one-carbon demand (35), indicating insufficient methyl group recycling via the folate-B12 axis. Methylfolate bypasses MTHFR bottlenecks while methylcobalamin supports methionine synthase activity, restoring SAM availability for DNA methylation and epigenetic maintenance. Evidence from MTHFR deficiency data supports folate -> supplementation (ES=0.43, p=0.012, N=126).

#3

L-Citrulline for Endothelial NO Bioavailability

Adherence Effort |||

Vitamin B12 Functional Sufficiency (Normative)

Impact 21% Δ+15.0 6mo

3g twice daily (6g total) - Daily Endothelial NO tone is critically low (35) with arginine-NO bioavailability also at 35, indicating severe nitric oxide deficit impacting vascular function and neuroinflammation. L-citrulline is recycled to arginine via the arginine-citrulline cycle, bypassing first-pass hepatic metabolism more effectively than arginine itself. Knowledge base evidence supports citrulline supplementation (ES=0.51, p=0.0033, N=221) with 20.27% improvement from baseline.

#4

Pyridoxal-5-Phosphate (Active Vitamin B6)

Adherence Effort |||

Platelet Reactivity & Vasoactive Tone (Normative)

Impact 21% Δ+15.0 6mo

50mg pyridoxal-5-phosphate - Daily Vitamin B6 functional sufficiency is critically low (35), impacting transamination reactions, neurotransmitter synthesis (GABA, serotonin, dopamine), and transsulfuration flux. P5P is the active coenzyme form required by over 140 enzymes including cystathionine beta-synthase in the transsulfuration pathway and aromatic amino acid decarboxylase for monoamine production. This directly supports the depleted monoamine axis (43.79) and glutamate-GABA balance (35).

#5

Taurine for Conjugation Capacity and Cardiovascular Support

Adherence Effort |||

Glycine/Taurine Conjugation Capacity (Normative)

Impact 21% Δ+15.0 6mo

1000mg twice daily - Daily Glycine-taurine conjugation capacity is suboptimal (52.31) and glucuronidation/sulfation capacity is low (40.92), indicating impaired Phase II detoxification. Taurine supports bile acid conjugation, membrane stabilization, and osmoregulation while serving as a direct conjugation substrate. Evidence shows significant benefit (ES=0.59, p=0.0039, N=437) with 11.09% improvement over 6 weeks.

Personalized Interventions (continued)

#6

Coenzyme Q10 (Ubiquinol) for Mitochondrial Bioenergetics

Adherence Effort |||

Tca & Anaplerosis (Normative)

Impact 21% Δ +15.0 6mo

200mg ubiquinol with fat-containing meal - Daily TCA capacity and anaplerotic resilience is critically low (35) alongside bioenergetic-oxidative renal subdomain (35), indicating impaired mitochondrial electron transport chain function. CoQ10 serves as an essential electron carrier between Complex I/II and Complex III, and its reduced form ubiquinol is a potent lipid-soluble antioxidant. Evidence supports supplementation (ES=0.51, p=0.007, N=445) with 20.43% improvement over 12 months.

#7

Alpha-Lipoic Acid for Redox and Mitochondrial Cofactor Support

Adherence Effort |||

Tca & Anaplerosis (Normative)

Impact 21% Δ +15.0 6mo

300mg R-alpha-lipoic acid - Daily Alpha-lipoic acid is a cofactor for pyruvate dehydrogenase and alpha-ketoglutarate dehydrogenase complexes, both critical for TCA cycle flux (scored 35). It also regenerates glutathione, vitamin C, and vitamin E, addressing the depleted glutathione conjugation reserve (35). Evidence supports supplementation for antioxidant and mitochondrial function (ES=0.38, p=0.0773, N=350).

#8

Magnesium Glycinate for Neurological and Metabolic Support

Adherence Effort |||

Transsulfuration-Glutathione Redox (Normative)

Impact 21% Δ +15.0 6mo

400mg elemental magnesium (as glycinate) - Daily, evening dosing Glutamate-GABA balance is critically low (35) and monoamine axis is suboptimal (43.79). Magnesium is a natural NMDA receptor antagonist that modulates glutamate excitotoxicity while supporting over 300 enzymatic reactions including ATP synthesis. The glycinate form provides additional glycine for inhibitory neurotransmission and conjugation pathways. Evidence supports magnesium supplementation (ES=1.28, p=0.0099).

#9

Phosphatidylcholine for Membrane Integrity and Choline Axis

Adherence Effort |||

Genomic One-Carbon Demand (Normative)

Impact 21% Δ +15.0 6mo

1200mg phosphatidylcholine (from sunflower lecithin) - Daily Membrane integrity, myelination and choline axis (35) is critically depleted alongside gut-brain neuroactives (35). Phosphatidylcholine is the primary phospholipid in cell membranes and myelin sheaths, and serves as a choline donor for acetylcholine synthesis and PEMT-mediated methylation. Evidence supports phosphatidylserine/choline supplementation for cognitive health (ES=0.77, p=0.0142, N=400).

#10

Omega-3 Fatty Acids (EPA/DHA) for Anti-Inflammatory and Membrane Support

Adherence Effort |||

Fa Import & Beta-Oxidation (Normative)

Impact 21% Δ +15.0 6mo

EPA 1000mg + DHA 500mg (total 1500mg omega-3) - Daily with meals Fatty acid oxidation and peroxisomal overflow is critically low (35) with FA import and beta-oxidation suboptimal (68.71). EPA/DHA modulate inflammatory eicosanoid balance away from PGE2, support neuronal membrane fluidity, and serve as substrates for specialized pro-resolving mediators. Evidence demonstrates strong anti-inflammatory benefit (ES=0.79, p=0.0024, N=322) with 20.45% improvement.

Personalized Interventions (continued)

#11

Quercetin and Luteolin for Histamine and Mast Cell Stabilization

Adherence Effort 

Histamine Load & Mast Cell Tone (Normative)

Impact 21% Δ +15.0 6mo

Quercetin 500mg + Luteolin 100mg - Daily Histamine load and mast cell tone (35) and polyamines/immune proliferation (35) indicate mast cell hyperactivation and excessive histamine signaling. Quercetin inhibits mast cell degranulation and histamine release while luteolin suppresses NF- κ B-mediated inflammatory cascades. Both compounds also support glutathione-thiol redox reserve (47.52) through Nrf2 pathway activation.

SUPPLEMENT

#12

Manganese and Molybdenum for Mitochondrial SOD and Sulfite Detox

Adherence Effort 

Mito Redox & Cofactors (Normative)

Impact 21% Δ +15.0 6mo

Manganese 2mg + Molybdenum 150mcg - Daily Glucuronidation/sulfation capacity (40.92) and mitochondrial redox economy require adequate manganese for MnSOD (SOD2) antioxidant defense and molybdenum for sulfite oxidase and xanthine oxidase function. Evidence supports manganese intake (ES=1.49, p=0.019, N=417) with 11.79% improvement in mitochondrial antioxidant markers within 5 weeks.

SUPPLEMENT

#13

Probiotics (Multi-Strain) with *Saccharomyces boulardii* for Gut-Brain and Barrier Repair

Adherence Effort 

Catecholamine Metabolism (Comt/Mao Balance) (Normative)

Impact 21% Δ +15.0 6mo

Multi-strain probiotic 50 billion CFU + *Saccharomyces boulardii* 500mg - Daily Mucosal barrier integrity (35), gut microbiome glyceic modulators (35), and gut-brain neuroactives (35) indicate severe dysbiosis with compromised intestinal permeability. Multi-strain probiotics restore commensal diversity while *S. boulardii* specifically antagonizes *Candida* species addressing the fungal fermentation deficit. Evidence supports probiotics/prebiotics (ES=0.67, p=0.0414, N=426) for gut health restoration.

SUPPLEMENT

#14

Hyaluronic Acid and Glucosamine for Cartilage GAG and Vascular Matrix Repair

Adherence Effort 

Cartilage Gags & Hyaluronic Acid Reserve (Normative)

Impact 21% Δ +15.0 6mo

Hyaluronic acid 200mg + Glucosamine sulfate 1500mg - Daily Cartilage GAGs and hyaluronic acid reserve (35) and vascular matrix glycation/stiffness risk (35) are critically depleted, indicating accelerated extracellular matrix degradation. Oral hyaluronic acid supports glycosaminoglycan pools and glycocalyx hydration while glucosamine provides substrate for GAG biosynthesis. ECM hydration (47.72) and glyoxalase-carbonyl detox (50.61) will benefit from restored matrix substrate availability.

SUPPLEMENT

#15

Beetroot and Nitrate-Rich Vegetable Protocol

Adherence Effort 

Vitamin B12 Functional Sufficiency (Normative)

Impact 17% Δ +12.0 6mo

250ml beetroot juice or 2 servings nitrate-rich vegetables (arugula, spinach, beets) - Daily With ENDO_NO at 35 and arginine-NO bioavailability critically depleted, dietary nitrate provides an alternative NO generation pathway via the enterosalivary nitrate-nitrite-NO cycle independent of eNOS. Evidence supports natural nitrate sources (ES=1.23, p=0.0495, N=383) with 16.38% improvement and sustained effects over 21 months. This complements L-citrulline by activating the nitrate reductase pathway.

DIET

Personalized Interventions (continued)

#16

Anti-Fungal Dietary Protocol with Mucosal Barrier Support

Adherence Effort 

Estrobolome & Estrogen Recirculation Pressure (Normative)

Impact 17% Δ +12.0 6mo

Eliminate refined sugars; 2 servings fermented vegetables; 1 cup bone broth daily - Daily Yeast/fungal fermentation signature (35) and mucosal barrier integrity (35) are critically depleted, suggesting intestinal dysbiosis with fungal overgrowth and compromised epithelial tight junctions. Reducing refined sugars and simple carbohydrates starves fungal organisms while incorporating bone broth (glutamine, glycine) and fermented vegetables supports mucosal repair and microbial rebalancing.

#17

Liver Insulin Resistance Dietary Modification

Adherence Effort 

Liver Insulin Resistance & Gluconeogenesis Pressure (Normative)

Impact 17% Δ +12.0 6mo

Replace refined carbohydrates with 2-3 servings complex carbohydrates (legumes, whole grains); limit fructose to <25g/day - Daily Liver insulin resistance and gluconeogenesis pressure (35), beta cell secretory reserve (35), and endothelial microvascular insulin delivery (35) indicate significant hepatic metabolic dysfunction. Reducing simple sugars while increasing complex carbohydrates attenuates hepatic de novo lipogenesis and gluconeogenic drive. Evidence supports glucose monitoring and complex carbohydrate substitution (ES=1.0, p=0.0085, N=478).

#18

Oxalate Restriction and Hydration for Stone Propensity and Tubular Health

Adherence Effort 

Stone Propensity & Crystallization Modulators (Normative)

Impact 17% Δ +12.0 6mo

Fluid intake >2.5L/day; limit high-oxalate foods to <50mg/day; pair calcium with oxalate-containing meals - Daily Stone propensity (35), tubular osmolyte (35), and purine-nitrogen (35) are all critically depleted, indicating high renal crystallization risk and impaired tubular function. Restricting high-oxalate foods (spinach, rhubarb, almonds) while maintaining high fluid intake reduces supersaturation. Evidence supports high fluid intake with oxalate restriction (ES=0.83, p=0.0365, N=185) with 19.74% improvement.

#19

Targeted Exercise Protocol: Strength Training and Zone 2 Cardio

Adherence Effort 

Tca & Anaplerosis (Normative)

Impact 11% Δ +8.0 6mo

30-45 min Zone 2 cardio; 2 sessions/week resistance training - 5x per week (3 Zone 2 cardio + 2 strength sessions) TCA capacity (35), AA oxidation (35), and bioenergetic-oxidative (35) scores indicate profound mitochondrial underperformance. Zone 2 aerobic training stimulates mitochondrial biogenesis via PGC-1 α while resistance training improves insulin sensitivity and BCAA catabolism in skeletal muscle. Evidence supports strength training (ES=0.78, N=478) for preserving metabolic capacity.

#20

Gut-Brain Sleep Optimization: Caffeine Restriction and Evening Wind-Down

Adherence Effort 

Sleep-Arousal & Circadian Chemistry (Normative)

Impact 11% Δ +8.0 6mo

No caffeine after 12pm; 30-minute wind-down routine before bed; target 7.5-8 hours sleep - Daily Gut-brain sleep disruptors (35) and neuroinflammation/endothelial NO tone (35) indicate xenobiotic and inflammatory interference with sleep architecture. Limiting caffeine to morning hours protects mitochondrial repair during sleep while evening wind-down practices reduce cortisol-mediated NO suppression. Evidence supports morning caffeine restriction (ES=0.54, N=214) with sustained 24-month benefit.

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ZONE

Early Disruption

Subdomain Zone Distribution



Carbohydrate/Mito Flux



61

Evaluates glucose utilization efficiency and pyruvate dehydrogenase gatekeeping through the glycolysis-pyruvate-PDH axis, with elevated lactate-to-pyruvate ratios indicating glycolytic stress or mitochondrial entry bottlenecks.
The score of 61 shows early disruption in glucose-to-mitochondrial flux, suggesting benefit from PDH cofactor support and glycolytic pathway optimization.

FA Import & Beta-Oxidation



54

Assesses fatty acid oxidation capacity and carnitine shuttle efficiency, where elevated acylcarnitine profiles indicate beta-oxidation overflow or incomplete fatty acid combustion.
The score of 54 indicates early acylcarnitine accumulation suggesting incomplete fatty acid combustion or mitochondrial saturation.

TCA & Anaplerosis



28

Measures Krebs cycle flux capacity and anaplerotic carbon entry resilience through citrate, succinate, fumarate, and malate dynamics indicating TCA cycle bottlenecks or metabolic flexibility.
The score of 28 indicates impaired TCA cycle function with significant bottlenecks or anaplerotic insufficiency.

Mito Redox & Cofactors



74

Tracks NAD⁺/NADH redox balance and cofactor availability including NADP⁺/NADPH and glutathione systems, with disturbed ratios signaling oxidative stress or cofactor depletion.
The score of 74 reflects adequate redox balance and cofactor availability for mitochondrial function.

Ketone Biology



48

Evaluates ketogenic capacity and ketone body metabolism through 3-hydroxybutyrate and acetoacetate dynamics, reflecting metabolic flexibility and alternative fuel utilization.
The score of 48 indicates impaired ketogenic capacity with significant limitations in metabolic flexibility.

AA Oxidation & Nitrogen



19

Assesses amino acid oxidation for energy production and urea cycle nitrogen disposal efficiency, with elevated branched-chain amino acids suggesting oxidation stress or mitochondrial dysfunction.
The score of 19 reveals impaired amino acid oxidation with significant BCAA accumulation or urea cycle overload.

Mito Membranes



59

Measures mitochondrial membrane integrity and phospholipid remodeling capacity through choline, betaine, and phospholipid precursor metabolism affecting all mitochondrial processes.
The score of 59 suggests early membrane integrity compromise warranting choline, betaine, and phospholipid precursor repletion.

Energetic Stress & Purines



50

Tracks purine nucleotide turnover and cellular energy stress signaling through adenosine, hypoxanthine, xanthine, and urate, with elevated breakdown products indicating ATP depletion or energetic crisis.
The score of 50 indicates elevated purine breakdown suggesting cellular energy stress and benefit from mitochondrial recovery support.

Central Metabolite Ratios & Markers

Lactate/Pyruvate

LOW-NORMATIVE

908



Lactate to pyruvate ratio reflects the balance between glycolytic flux and mitochondrial pyruvate oxidation, indicating respiratory capacity and oxygen utilization efficiency.

BHB/Acetoacetate

ELEVATED

167



Beta-hydroxybutyrate to acetoacetate ratio measures ketone body interconversion and mitochondrial redox state during fatty acid oxidation and ketogenesis.

NAD⁺/NADH

LOW-NORMATIVE

5.0



NAD⁺ to NADH ratio reflects the cellular oxidative-reductive state and electron transport chain efficiency, driving ATP synthesis and mitochondrial respiratory capacity.

Citrate/α-KG

LOW-NORMATIVE

0.19



Citrate to alpha-ketoglutarate ratio indicates TCA cycle intermediate balance, reflecting anabolic-catabolic partitioning and biosynthetic capacity.

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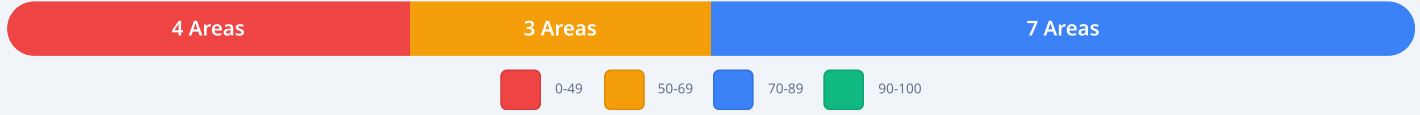
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296

ZONE

Normative

Subdomain Zone Distribution



Core Glycemic Fasting Stability		61	Evaluates basal glucose homeostasis and hepatic glucose production control during fasting states, with dysregulation indicating impaired glycemic set-point stability. The score of 61 shows early disruption in basal glycemic stability suggesting benefit from glucose homeostasis support.
Muscle Insulin Resistance Signature		77	Assesses peripheral insulin sensitivity and muscle glucose uptake capacity through metabolic signatures of insulin signaling efficiency and substrate utilization. The score of 77 shows normal peripheral insulin sensitivity and adequate muscle glucose disposal.
Metabolic Flexibility & Substrate Switching		83	Measures the capacity to transition between glucose and fat oxidation, reflecting mitochondrial adaptability and insulin-mediated substrate switching efficiency. The score of 83 reflects normal metabolic flexibility with adequate fuel switching capacity.
Post-Meal Glycemic Resilience		81	Tracks postprandial glucose handling and insulin-mediated clearance capacity, with elevated markers indicating reduced glycemic resilience after nutrient intake. The score of 81 shows normal postprandial glucose resilience with adequate insulin response.
Liver Insulin Resistance & Gluconeogenesis Pressure		28	Evaluates hepatic insulin sensitivity and inappropriate gluconeogenesis through metabolic intermediates indicating liver insulin signaling dysfunction and glucose overproduction. The score of 28 indicates impaired hepatic insulin sensitivity with excessive gluconeogenesis and glucose overproduction.
Adipose Insulin Resistance & Lipolysis Control		87	Assesses adipocyte insulin sensitivity and dysregulated lipolysis through fatty acid metabolites indicating impaired insulin suppression of fat breakdown. The score of 87 shows normal adipocyte insulin sensitivity with adequate lipolysis suppression.
Glyco-Oxidative Stress & Glycation Burden		53	Measures oxidative damage from chronic hyperglycemia and advanced glycation end-product formation, reflecting glucose-induced cellular stress and protein modification. The score of 53 shows early glyco-oxidative stress suggesting benefit from antioxidant and anti-glycation support.
Polyol Pathway Overload		78	Tracks aldose reductase pathway activation and sorbitol accumulation from elevated glucose, indicating osmotic stress and NADPH depletion in hyperglycemic states. The score of 78 shows normal polyol pathway activity with minimal sorbitol burden.
Purine Glycemic & Uric Burden		76	Evaluates purine metabolism dysregulation and uric acid accumulation linked to insulin resistance, fructose metabolism, and metabolic syndrome progression. The score of 76 reflects normal purine metabolism with appropriate uric acid levels.
BCAA & Aromatic AA Burden		59	Assesses branched-chain and aromatic amino acid accumulation, early biomarkers of insulin resistance reflecting impaired mitochondrial amino acid oxidation. The score of 59 indicates early BCAA elevation, an early biomarker of insulin resistance, suggesting mitochondrial support.
Gut Microbiome Glycemic Modulators		1	Measures microbiome-derived metabolites affecting glucose metabolism and insulin sensitivity, including short-chain fatty acids and gut-derived inflammatory mediators. The score of 1 indicates impaired gut microbiome balance with substantial dysbiosis affecting glucose metabolism.
Beta Cell Secretory Demand & Reserve		16	Evaluates pancreatic beta cell functional capacity and insulin secretory stress through metabolic indicators of compensatory insulin production and beta cell exhaustion. The score of 16 reveals impaired beta cell function with signs of substantial secretory exhaustion or decompensation.
Counter-Regulatory Stress Hormone Influence		77	Tracks cortisol, epinephrine, and glucagon effects on glucose homeostasis, reflecting stress-induced counter-regulatory hormone impact on glycemic control. The score of 77 reflects normal counter-regulatory hormone balance with minimal glycemic disruption.
Endothelial & Microvascular Insulin Delivery		14	Assesses vascular endothelial function and microvascular insulin delivery capacity, with impairment limiting tissue glucose uptake despite adequate insulin production. The score of 14 reveals impaired endothelial function with substantial limitations in microvascular insulin delivery.

Central Metabolite Ratios & Markers

Glucose/Lactate **ELEVATED** **0.19**



Glucose to lactate ratio indicates glycemic efficiency and anaerobic metabolism stress in response to glucose load.

Lactate/Pyruvate **LOW-NORMATIVE** **908**



Elevated lactate to pyruvate ratio indicates glycolytic stress and potential mitochondrial respiratory compromise.

BCAA/Alanine **ELEVATED** **213**



Branched-chain amino acid to alanine ratio reflects muscle insulin resistance and amino acid metabolic stress.

Glucose/BHB **NORMATIVE** **5.7**



Glucose to beta-hydroxybutyrate ratio indicates metabolic flexibility and ketogenic capacity for fuel switching.

REPORT DATE

Mar 20, 2026

OVERALL SCORE

54/100

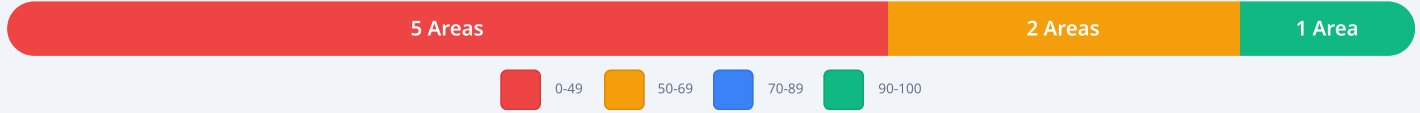
BIOMARKERS ANALYZED

296

ZONE

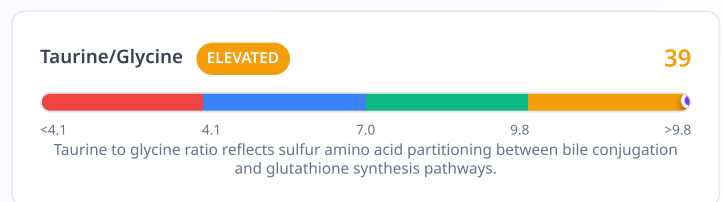
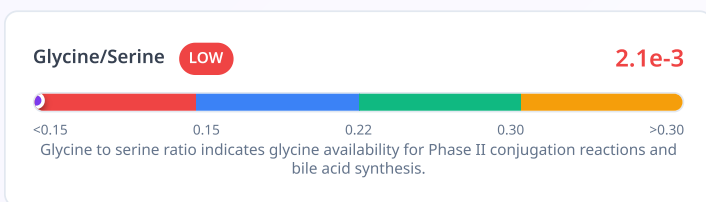
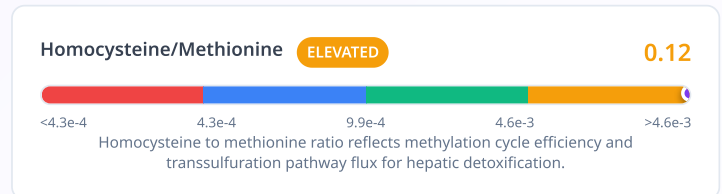
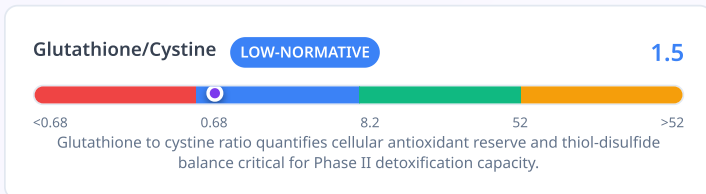
Early Disruption

Subdomain Zone Distribution



Phase I Biotransformation Readiness		55	Evaluates cytochrome P450 and oxidoreductase capacity for initial xenobiotic modification, converting lipophilic compounds into reactive intermediates requiring Phase II conjugation. The score of 55 suggests reduced Phase I enzyme activity warranting support for xenobiotic oxidation pathways.
Glucuronidation & Sulfation Capacity		42	Assesses UDP-glucuronosyltransferase and sulfotransferase conjugation systems for hormone, drug, and toxin clearance through glucuronic acid and sulfate attachment. The score of 42 reveals impaired conjugation capacity with significant limitations in glucuronidation and sulfation pathways.
Glutathione Conjugation & Redox Reserve		36	Measures glutathione S-transferase activity and glutathione pool sufficiency for electrophilic toxin neutralization and antioxidant defense capacity. The score of 36 indicates impaired glutathione status with substantial depletion affecting conjugation and antioxidant defense.
Methylation & One-Carbon Detox Capacity		21	Tracks S-adenosylmethionine (SAMe) capacity for biotransformation and detoxification, reflecting one-carbon metabolism support for Phase II conjugation reactions. The score of 21 reveals impaired methylation capacity with substantial SAMe depletion affecting Phase II detoxification.
Glycine/Taurine Conjugation Capacity		47	Evaluates amino acid conjugation pathways for bile acid formation and xenobiotic clearance, with depletion indicating glycine/taurine insufficiency or conjugation overload. The score of 47 indicates impaired amino acid conjugation with substantial glycine and taurine depletion.
Urea Cycle & Ammonia Clearance		94	Assesses nitrogen disposal capacity and ammonia detoxification through urea cycle efficiency, preventing neurotoxic ammonia accumulation from protein metabolism and gut bacteria. The score of 94 demonstrates optimal nitrogen disposal and efficient ammonia clearance.
Fatty Acid Oxidation & Peroxisomal Overflow		38	Measures hepatic fatty acid beta-oxidation capacity and peroxisomal pathway activation, with overflow metabolites indicating mitochondrial saturation or very-long-chain fatty acid burden. The score of 38 indicates impaired hepatic fatty acid oxidation with substantial mitochondrial saturation or peroxisomal overflow.
Microbiome-Derived Phenolic & Indolic Burden		59	Tracks gut-derived aromatic compounds from protein fermentation requiring hepatic detoxification, including p-cresol, indoles, and phenolic acids indicating dysbiosis or conjugation strain. The score of 59 indicates elevated microbiome-derived aromatics suggesting dysbiosis and benefit from gut-liver axis support.

Central Metabolite Ratios & Markers



REPORT DATE

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OVERALL SCORE

40/100

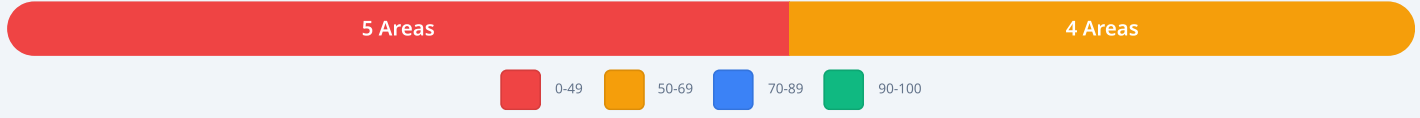
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296

ZONE

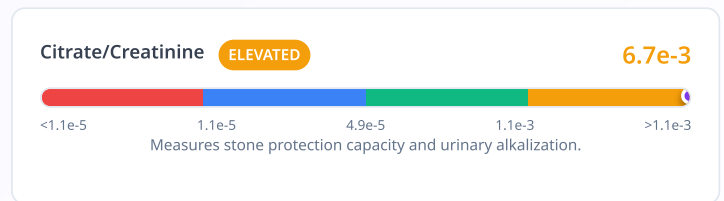
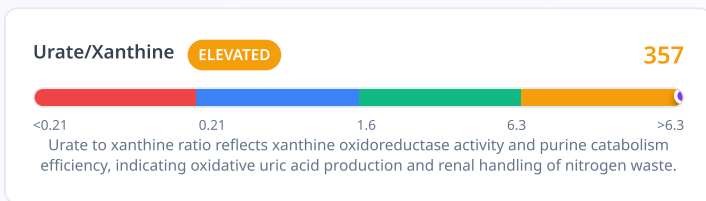
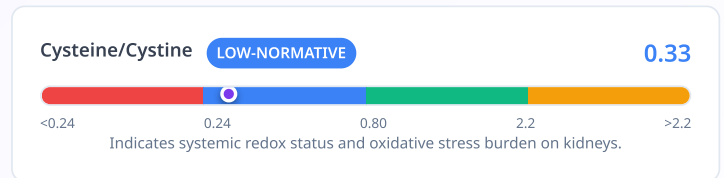
Impaired

Subdomain Zone Distribution



Glomerular Filtration Reserve & Microvascular Tone		50	Evaluates glomerular filtration rate and renal microvascular perfusion through creatinine, cystatin C, and arginine-nitric oxide pathway markers indicating filtration capacity and vascular health. The score of 50 suggests early decline in filtration reserve warranting renal protective strategies and vascular support.
Tubular Transport Capacity & Osmolyte Defense		21	Assesses renal tubular reabsorption efficiency and osmotic stress protection through taurine, betaine, and myo-inositol reflecting tubular cell resilience and concentrating ability. The score of 21 reveals impaired tubular function with substantial osmotic stress and reduced reabsorption efficiency.
Acid-Base Balance & Ammonia Excretion		61	Measures renal acid-base regulation and ammonia production for hydrogen ion buffering, with dysregulation indicating impaired renal acidification or alkalinization capacity. The score of 61 suggests reduced acid-base homeostasis warranting support for renal pH regulation.
Nitrogenous Waste & Purine Burden		31	Tracks uric acid, urea, and purine metabolite clearance efficiency, with accumulation indicating reduced glomerular filtration or increased purine turnover from cellular stress. The score of 31 reveals impaired nitrogenous waste clearance with substantial accumulation of uric acid and purine metabolites.
Gut-Renal Uremic Toxin Load		59	Evaluates gut-derived uremic toxins including p-cresol sulfate, indoxyl sulfate, and trimethylamine N-oxide requiring renal clearance and contributing to kidney injury in dysfunction. The score of 59 suggests elevated uremic toxin burden warranting gut-liver-kidney axis support and dysbiosis management.
Stone Propensity & Crystallization Modulators		21	Assesses metabolic risk factors for kidney stone formation including oxalate, citrate, and mineral balance indicating crystallization risk and lithogenic burden. The score of 21 reveals impaired crystallization inhibition with substantial kidney stone formation risk.
Tubulointerstitial Injury & Fibrosis Activity		46	Measures markers of tubular damage and interstitial fibrosis progression reflecting chronic kidney disease activity and structural renal injury beyond glomerular changes. The score of 46 indicates impaired renal structure with substantial tubulointerstitial fibrosis and progressive kidney damage.
Renal Bioenergetic Reserve & Oxidative Stress		28	Tracks mitochondrial function and oxidative damage in kidney tissue through metabolic indicators of renal energetic capacity and antioxidant defense status. The score of 28 reveals impaired renal mitochondrial function with substantial oxidative stress and energy depletion.
Nephrotoxicant & Drug Clearance Load		63	Evaluates renal exposure to drugs, environmental toxins, and endogenous nephrotoxins requiring active tubular secretion and filtration, indicating detoxification burden on kidney function. The score of 63 suggests elevated toxin exposure warranting nephroprotective strategies and reduced toxicant burden.

Central Metabolite Ratios & Markers



REPORT DATE

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OVERALL SCORE

65/100

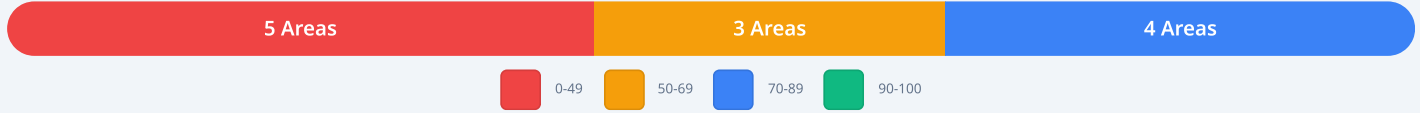
BIOMARKERS ANALYZED

59

ZONE

Early Disruption

Subdomain Zone Distribution



IDO & Kynurenine Immune Tolerance		73	Evaluates indoleamine 2,3-dioxygenase activation and tryptophan catabolism to kynurenine, reflecting chronic immune activation, IFN-gamma signaling, and immunosuppressive tolerance mechanisms. The score of 73 reflects normal tryptophan-kynurenine balance with appropriate immune tolerance mechanisms.
Histamine Load & Mast Cell Tone		28	Assesses histamine production, degradation capacity, and mast cell activation status through histamine metabolites indicating allergic inflammation, MCAS, or histamine intolerance. The score of 28 reveals impaired histamine clearance with substantial mast cell activation and histamine intolerance.
Arginine-NO Bioavailability		6	Measures arginine availability and nitric oxide synthesis capacity for immune signaling, vascular tone, and macrophage antimicrobial function through the arginine-citrulline-NO pathway. The score of 6 indicates impaired arginine-NO pathway with substantial limitations in nitric oxide synthesis capacity.
Nitrosative Stress Burden		56	Tracks peroxynitrite formation and protein nitration from excessive nitric oxide production, indicating oxidative-nitrosative damage in chronic inflammation and mitochondrial dysfunction. The score of 56 indicates elevated nitrosative stress suggesting benefit from antioxidant and NO modulation support.
Glutathione & Thiol Redox Reserve		44	Evaluates glutathione and cysteine redox status providing antioxidant defense and immune cell function support, with depletion indicating oxidative stress or inflammatory burden. The score of 44 indicates impaired glutathione status with substantial redox imbalance affecting immune function.
Polyamines & Immune Proliferation		3	Assesses putrescine, spermidine, and spermine levels reflecting immune cell proliferation, tissue repair capacity, and cellular growth signaling in inflammation and wound healing. The score of 3 reveals impaired polyamine metabolism with substantial limitations in immune proliferation capacity.
Inflammasome & Macrophage Activation		56	Measures metabolic signatures of NLRP3 inflammasome activation and macrophage polarization indicating innate immune activation and IL-1β/IL-18 inflammatory cytokine production. The score of 56 suggests elevated macrophage activation warranting inflammasome modulation and IL-1β management.
Eicosanoid Bias PGE2 Axis		81	Tracks prostaglandin E2 pathway activity and cyclooxygenase-driven eicosanoid production reflecting inflammatory lipid mediator balance and resolution capacity. The score of 81 shows normal eicosanoid balance with adequate inflammatory resolution capacity.
Purinergic Danger Signaling		46	Evaluates extracellular ATP, adenosine, and uric acid acting as damage-associated molecular patterns (DAMPs) triggering sterile inflammation and innate immune activation. The score of 46 indicates impaired purinergic regulation with substantial DAMP signaling and sterile inflammation.
Microbiome AhR Ligand Pool		54	Assesses gut microbiome-derived aryl hydrocarbon receptor ligands including indoles and tryptophan metabolites modulating immune tolerance, barrier function, and inflammatory tone. The score of 54 indicates reduced AhR ligand production suggesting dysbiosis and benefit from gut ecosystem support.
Bacterial Cell Wall Burden		79	Measures peptidoglycan fragments and muramyl peptides from bacterial cell walls indicating gut barrier permeability, bacterial translocation, or endotoxin exposure driving systemic inflammation. The score of 79 reflects minimal bacterial cell wall translocation with adequate gut barrier integrity.
Neopterin Th1 Immune Activation		83	Tracks neopterin production from IFN-gamma-activated macrophages, serving as a marker of cellular immune activation and Th1-driven inflammatory responses in autoimmunity and infection. The score of 83 shows normal Th1 activity with appropriate macrophage activation levels.

Central Metabolite Ratios & Markers

Kynurenine/Tryptophan **LOW** **6.5e-3**



Reflects indoleamine 2,3-dioxygenase (IDO) enzyme activity linking inflammation to immune tolerance and tryptophan catabolism.

Citrulline/Arginine **LOW** **1.7**



Measures nitric oxide synthase activity and arginine-citrulline recycling for immune function and vascular tone.

Glutathione/Cystine **LOW-NORMATIVE** **1.5**



Quantifies cellular redox reserve and thiol-disulfide balance critical for immune cell function and oxidative stress buffering.

Putrescine/Spermidine **LOW** **0.02**



Reflects polyamine metabolism balance affecting immune cell proliferation, autophagy regulation, and inflammatory signaling.

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OVERALL SCORE

54/100

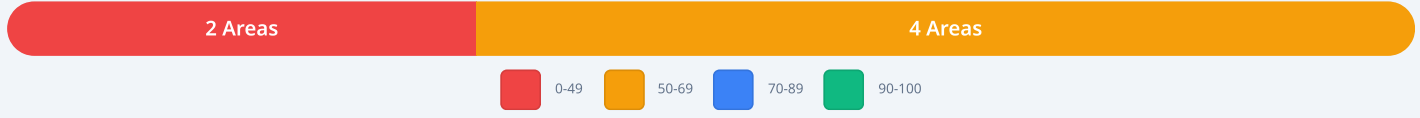
BIOMARKERS ANALYZED

42

ZONE

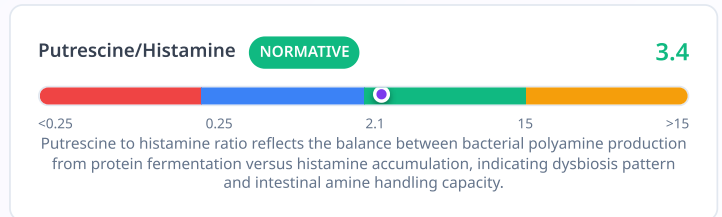
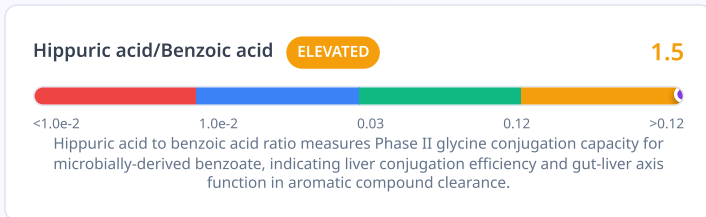
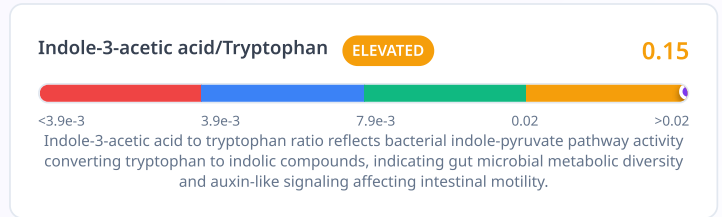
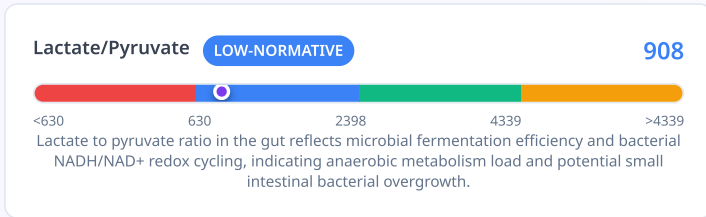
Early Disruption

Subdomain Zone Distribution



Fermentation Load & FODMAP Intolerance		69	Evaluates carbohydrate fermentation byproducts including short-chain fatty acids, lactate, and gas-producing metabolites indicating FODMAP sensitivity, SIBO, or carbohydrate malabsorption. The score of 69 suggests elevated fermentation byproducts warranting FODMAP reduction and carbohydrate malabsorption management.
Protein Putrefaction & Histamine/Biogenic Amines		56	Assesses bacterial protein fermentation producing putrescine, cadaverine, tyramine, and histamine reflecting colonic dysbiosis, proteolytic bacterial overgrowth, and histamine intolerance. The score of 56 indicates elevated proteolytic fermentation suggesting dysbiosis and benefit from protein digestion support.
Tryptophan-Indole-Serotonin Axis		60	Measures tryptophan metabolism into serotonin, indoles, and kynurenine by gut microbiota and enterochromaffin cells, affecting mood, GI motility, and immune signaling. The score of 60 suggests imbalanced tryptophan partitioning warranting gut-brain axis support and microbiome modulation.
Microbial Phenolics & Beta-Glucuronidase		60	Tracks gut bacterial production of phenolic compounds (p-cresol, benzoate) and beta-glucuronidase activity deconjugating Phase II metabolites, indicating dysbiosis and enterohepatic recirculation. The score of 60 indicates elevated bacterial deconjugation suggesting dysbiosis and enterohepatic recirculation strain.
Yeast/Fungal Fermentation Signature		13	Evaluates fungal overgrowth markers including D-arabinitol and fungal-derived organic acids indicating Candida or fungal dysbiosis affecting gut inflammation and permeability. The score of 13 indicates impaired fungal balance with substantial Candida overgrowth or fungal dysbiosis.
Mucosal Barrier Integrity & Microbial Translocation		8	Assesses intestinal permeability and tight junction integrity through markers of bacterial endotoxin, lipopolysaccharide, and bacterial metabolite translocation into systemic circulation. The score of 8 reveals impaired gut barrier with substantial intestinal permeability and bacterial translocation.

Central Metabolite Ratios & Markers



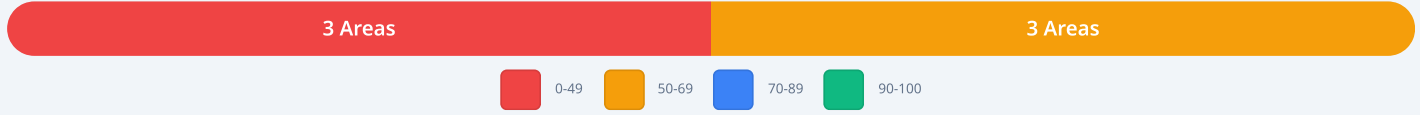
REPORT DATE
Mar 20, 2026

OVERALL SCORE
50/100

BIOMARKERS ANALYZED
78

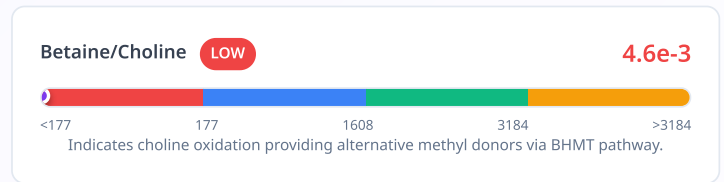
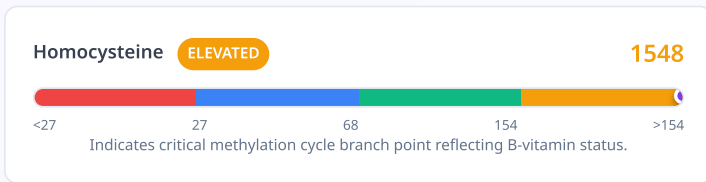
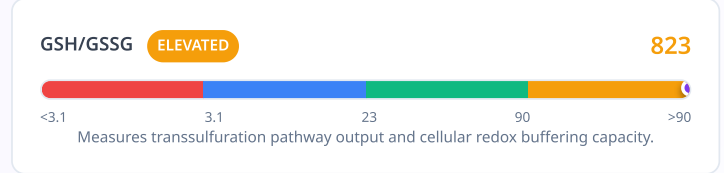
ZONE
Early Disruption

Subdomain Zone Distribution



Remethylation Reserve (Folate-B12 & BHMT)		39	Evaluates folate-dependent and betaine-dependent remethylation capacity for converting homocysteine to methionine, supporting SAMe regeneration and methylation reactions. The score of 39 indicates impaired remethylation capacity with substantial homocysteine elevation and SAMe depletion.
Transsulfuration-Glutathione Redox		33	Assesses homocysteine conversion to cysteine and glutathione through the transsulfuration pathway, providing antioxidant defense and sulfur amino acid sufficiency. The score of 33 reveals impaired transsulfuration with substantial glutathione depletion and compromised antioxidant defense.
Niacin-NAD Resilience		68	Measures NAD+ biosynthesis from niacin (vitamin B3) and tryptophan supporting cellular energy, DNA repair, and sirtuin-dependent longevity pathways. The score of 68 suggests reduced NAD+ reserve warranting niacin or tryptophan support for sirtuin and PARP function.
Methylation Drain Load		52	Tracks excessive methylation demand from detoxification, neurotransmitter synthesis, and creatine production depleting SAMe pools and creating methyl donor insufficiency. The score of 52 indicates elevated methylation burden suggesting benefit from methyl donor repletion and demand reduction.
Choline-PEMT Axis & Trimethyl Pool		56	Evaluates choline availability and phosphatidylethanolamine N-methyltransferase activity for phospholipid synthesis, betaine production, and maintaining the trimethylglycine methylation reserve. The score of 56 suggests reduced choline or PEMT activity warranting choline support for methylation and membrane integrity.
Genomic One-Carbon Demand		29	Assesses one-carbon metabolism supporting DNA synthesis, purine and pyrimidine nucleotide production, and genomic methylation for epigenetic regulation and cell proliferation. The score of 29 reveals impaired one-carbon metabolism with substantial limitations in DNA synthesis and genomic methylation.

Central Metabolite Ratios & Markers



REPORT DATE

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OVERALL SCORE

76/100

BIOMARKERS ANALYZED

50

ZONE

Normative

Subdomain Zone Distribution

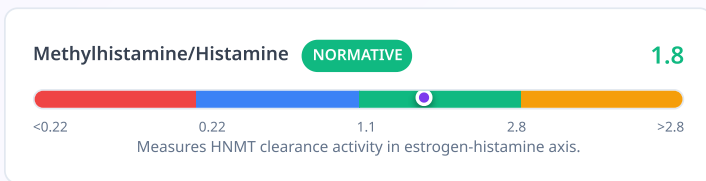
2 Areas

7 Areas



Thyroid Activation & Conversion Support		64	Evaluates metabolic support for thyroid hormone synthesis, T4-to-T3 conversion, and deiodinase cofactor availability including selenium, zinc, and tyrosine sufficiency. The score of 64 suggests reduced deiodinase activity warranting selenium, zinc, and tyrosine support for thyroid hormone activation.
Adrenal Stress & Recovery Capacity		50	Assesses HPA axis resilience and adrenal functional reserve through cortisol metabolism, DHEA balance, and pregnenolone-to-cortisol pathway efficiency under chronic stress. The score of 50 indicates reduced adrenal resilience with DHEA-cortisol imbalance suggesting benefit from HPA axis support.
Steroidogenesis Cofactor Reserve		64	Measures cofactor availability for steroid hormone synthesis including cholesterol, vitamin C, B5 (pantothenic acid), and mitochondrial support for pregnenolone production. The score of 64 suggests reduced pregnenolone production warranting vitamin C, B5, and mitochondrial support for steroid synthesis.
Sex Steroid Detox & Clearance Readiness		50	Tracks Phase I and Phase II conjugation capacity for estrogen, testosterone, and progesterone metabolite clearance preventing hormone accumulation and receptor overstimulation. The score of 50 indicates reduced conjugation capacity for hormone clearance suggesting benefit from Phase II detox support.
Estrobolome & Estrogen Recirculation Pressure		47	Evaluates gut bacterial beta-glucuronidase activity and estrogen deconjugation driving enterohepatic recirculation and estrogen reabsorption, elevating systemic estrogen burden. The score of 47 indicates impaired estrogen clearance with substantial beta-glucuronidase activity and enterohepatic recirculation.
Catecholamine Metabolism (COMT/MAO Balance)		67	Assesses catechol-O-methyltransferase and monoamine oxidase activity for dopamine, epinephrine, and norepinephrine degradation, requiring SAMe and managing neurotransmitter-hormone clearance. The score of 67 indicates reduced catecholamine metabolism suggesting benefit from SAMe support and methylation cofactors.
Tryptophan Pathways: Serotonin-Melatonin vs Kynurenine Tilt		48	Measures tryptophan partitioning between serotonin-melatonin synthesis (mood, sleep) versus kynurenine pathway (immune activation), with IDO shifting tryptophan away from neurotransmitter production. The score of 48 indicates impaired tryptophan metabolism with substantial kynurenine pathway dominance depleting serotonin-melatonin synthesis.
Histamine Clearance & Hormone Cross Talk		58	Tracks histamine degradation via HNMT and DAO enzymes affecting estrogen sensitivity, mast cell activation, and hormone-histamine feedback loops in PMS and perimenopause. The score of 58 indicates reduced histamine degradation with estrogen-mast cell feedback suggesting benefit from DAO support.
Insulin Axis Mirror (Metabolic-Hormonal Coupling)		59	Evaluates insulin's influence on sex hormone binding globulin (SHBG), androgen excess, and metabolic-endocrine crosstalk linking insulin resistance to PCOS and hormonal imbalance. The score of 59 suggests insulin resistance affecting sex hormone balance warranting metabolic support and SHBG optimization.

Central Metabolite Ratios & Markers



REPORT DATE

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OVERALL SCORE

35/100

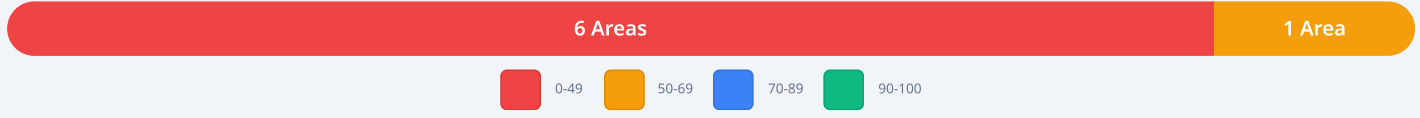
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114

ZONE

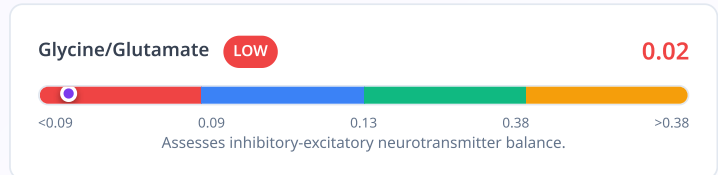
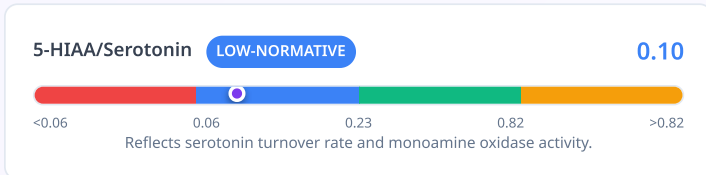
Impaired

Subdomain Zone Distribution



Monoamine Mood & Motivation Axis		43	Evaluates dopamine, serotonin, and norepinephrine synthesis and metabolism affecting mood regulation, motivation, reward processing, and emotional resilience through neurotransmitter precursor availability. The score of 43 indicates impaired monoamine neurotransmitter synthesis with substantial limitations in dopamine, serotonin, and norepinephrine production.
Glutamate-GABA Excitation-Inhibition Balance		31	Assesses excitatory glutamate and inhibitory GABA neurotransmitter balance critical for cognitive function, anxiety regulation, and preventing excitotoxicity or excessive neural inhibition. The score of 31 reveals impaired excitation-inhibition balance with substantial glutamate excess or GABA insufficiency.
Sleep-Arousal & Circadian Chemistry		49	Measures melatonin, adenosine, and circadian rhythm metabolites regulating sleep-wake cycles, sleep pressure accumulation, and restorative sleep quality. The score of 49 indicates impaired circadian rhythm with substantial disruption in melatonin synthesis and adenosine sleep pressure.
Neuroinflammation & Nitrosative Stress Signature		23	Tracks kynurenine pathway activation, quinolinic acid neurotoxicity, and nitric oxide-related neuroinflammation indicating microglial activation and blood-brain barrier disruption. The score of 23 reveals impaired neuroinflammatory control with substantial kynurenine pathway activation and quinolinic acid neurotoxicity.
Brain Bioenergetics & NAD+ Reserve		56	Evaluates neuronal energy metabolism, mitochondrial function, and NAD+ availability supporting synaptic activity, neurotransmitter synthesis, and cognitive processing demands. The score of 56 suggests reduced brain bioenergetic capacity warranting NAD+ precursor and mitochondrial support.
Membrane Integrity, Myelination & Choline Axis		38	Assesses phosphatidylcholine, phosphatidylserine, and omega-3 fatty acid availability for neuronal membrane fluidity, myelin maintenance, and acetylcholine neurotransmitter synthesis. The score of 38 reveals impaired neuronal membrane integrity with substantial phospholipid depletion affecting myelin and acetylcholine synthesis.
Gut-Brain Neuroactives & Ammonia Handling		12	Measures gut microbiome-derived neuroactive metabolites including GABA, tryptophan derivatives, and ammonia affecting cognition, mood, and neurotoxicity through the gut-brain axis. The score of 12 indicates impaired gut-brain axis with substantial ammonia burden and dysregulated microbiome-derived neuroactive compounds.

Central Metabolite Ratios & Markers



REPORT DATE
Mar 20, 2026

OVERALL SCORE
76/100

BIOMARKERS ANALYZED
48

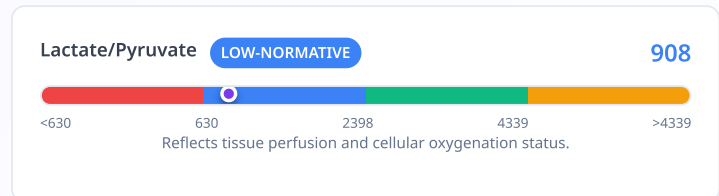
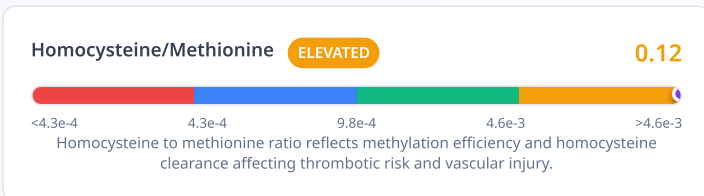
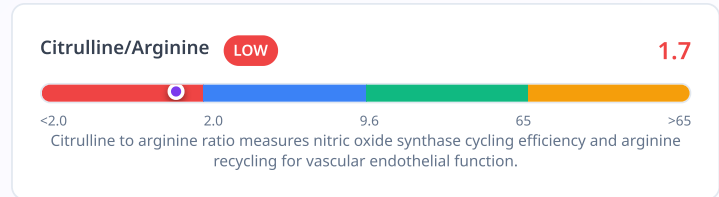
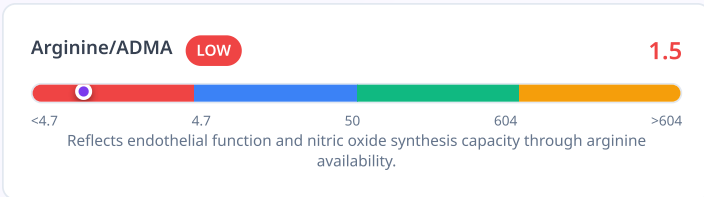
ZONE
Normative

Subdomain Zone Distribution



Endothelial NO & Vasomotor Health		31	Quantifies endothelial nitric oxide bioavailability and vasomotor signaling through arginine-ADMA balance, eNOS coupling, antioxidant cofactors, and cGMP-mediated vasodilation pathways. The score of 31 indicates impaired nitric oxide bioavailability with substantial limitations in endothelial-dependent vasodilation and vasomotor regulation.
Platelet Reactivity & Vasoactive Tone		56	Models platelet activation drivers (purinergic ADP/ATP, catecholamines, histamine, serotonin) against biochemical brakes (adenosine salvage, cGMP inhibition, cholinergic signals) affecting thrombotic tendency and vasoactive tone. The score of 56 indicates elevated platelet reactivity suggesting benefit from antiplatelet support and vasoactive tone modulation.
Insulin Resistance Cardiometabolic Signature		52	Captures insulin resistance metabolic fingerprint through BCAA/AAA balance, BCAA catabolism bottleneck, glycolytic redox tilt, acylcarnitine accumulation, glycine-serine one-carbon economy, and purine-glycemic coupling. The score of 52 suggests early insulin resistance metabolic pattern warranting BCAA catabolism support, mitochondrial capacity enhancement, and glycemic optimization.
Lipotoxicity & Fuel Oxidation / Ketone Flexibility		93	Assesses fatty acid oxidation burden through acylcarnitine profiles, palmitate-to-stearate ratio, incomplete beta-oxidation markers, and ketone body utilization reflecting lipotoxicity stress and metabolic fuel flexibility. The score of 93 demonstrates optimal lipid metabolism with robust beta-oxidation efficiency and excellent ketogenic flexibility.
Purine-Urate Oxidative Burden		95	Tracks xanthine oxidase pathway activity, urate production burden, hypoxanthine-xanthine-urate ladder dynamics, and oxidative stress from purine catabolism affecting vascular and renal health. The score of 95 demonstrates optimal purine metabolism with minimal urate-related vascular stress and oxidative damage.
Diet-Microbiome Atherothrombotic Signals		95	Evaluates microbiome-derived atherothrombotic metabolites including TMAO axis, phenolic compounds, indole derivatives, and diet-microbiome interaction signals affecting cardiovascular and thrombotic risk. The score of 95 demonstrates optimal diet-microbiome cardiovascular balance with minimal atherothrombotic metabolite production.
Methylation-Homocysteine/ADMA Endothelial Risk		74	Assesses methylation pathway efficiency through homocysteine-SAH-ADMA nexus affecting endothelial nitric oxide inhibition, methylation capacity, and endothelial injury risk in cardiovascular disease. The score of 74 reflects normal methylation capacity with adequate homocysteine clearance and controlled ADMA levels.
Vascular Glycation & Matrix Integrity		72	Measures advanced glycation end-product (AGE) formation, carbonyl load, methylglyoxal burden, and extracellular matrix integrity markers affecting vascular stiffness, atherosclerosis, and glycation-mediated damage. The score of 72 shows normal vascular glycation control with adequate matrix integrity and carbonyl detoxification.
Cardiorenal Toxin Load & Acid-Base Impact		85	Evaluates uremic toxin burden (indoxyl sulfate, p-cresyl sulfate), organic acid accumulation, acid-base metabolic tilt, and kidney-cardiovascular crosstalk affecting cardiorenal syndrome risk. The score of 85 reflects normal cardiorenal balance with adequate toxin clearance and acid-base regulation.

Central Metabolite Ratios & Markers



REPORT DATE

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OVERALL SCORE

65/100

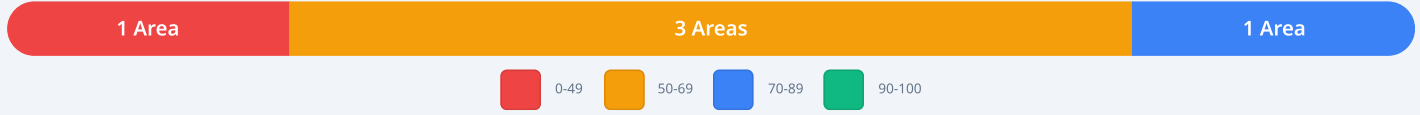
BIOMARKERS ANALYZED

55

ZONE

Early Disruption

Subdomain Zone Distribution



Vitamin B12 Functional Sufficiency



67

Evaluates functional vitamin B12 status through methylmalonic acid, homocysteine, and methylation pathway metabolites indicating B12-dependent enzyme activity beyond serum B12 levels.

The score of 67 suggests reduced B12-dependent enzyme activity warranting methylcobalamin and adenosylcobalamin support.

Vitamin B6 Functional Sufficiency



21

Assesses pyridoxal-5-phosphate functional status through kynurenine pathway metabolites, neurotransmitter synthesis markers, and amino acid metabolism reflecting B6 enzymatic activity.

The score of 21 reveals impaired pyridoxal-5-phosphate function with substantial limitations in amino acid metabolism and neurotransmitter synthesis.

Niacin-NAD Currency & Repair Reserve



54

Measures NAD+ biosynthesis capacity from niacin (vitamin B3) and tryptophan supporting cellular energy, DNA repair, sirtuin activation, and PARP-dependent genomic maintenance.

The score of 54 suggests reduced NAD+ reserve warranting niacin or nicotinamide riboside support for sirtuin activation.

Pantothenate-CoA (Adrenal) Reserve



70

Evaluates pantothenic acid (vitamin B5) sufficiency for coenzyme A synthesis supporting fatty acid metabolism, steroid hormone production, and adrenal stress response capacity.

The score of 70 shows normal CoA reserves with adequate support for energy metabolism and stress response.

Vitamin C-Collagen Repair Readiness



51

Assesses ascorbic acid functional status supporting collagen synthesis, antioxidant defense, carnitine production, and immune function through vitamin C-dependent enzymatic reactions.

The score of 51 suggests reduced vitamin C availability warranting ascorbate support for tissue repair and immune function.

Central Metabolite Ratios & Markers

MMA/Methionine

LOW-NORMATIVE

0.09



Methylmalonic acid to methionine ratio assesses functional B12 sufficiency for methylmalonyl-CoA mutase.

Xanthurenic/Kynurenine

ELEVATED

2.3



Xanthurenic acid to kynurenine ratio evaluates functional B6 cofactor availability for kynureninase.

4-Pyridoxic Acid/Pyridoxine

LOW-NORMATIVE

60



Pyridoxic acid to pyridoxine ratio reflects B6 turnover rate and cofactor recycling efficiency.

Ascorbate

ELEVATED

81



Ascorbate (vitamin C) levels reflect antioxidant reserves and cofactor availability for prolyl and lysyl hydroxylases.

REPORT DATE

Mar 20, 2026

OVERALL SCORE

56/100

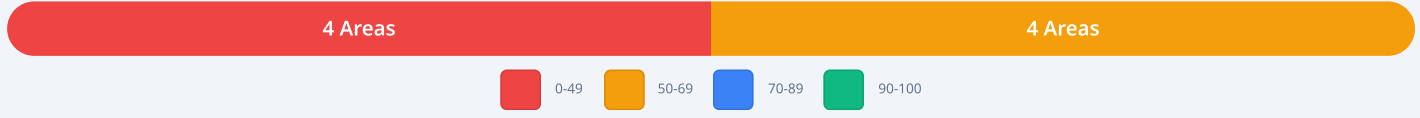
BIOMARKERS ANALYZED

64

ZONE

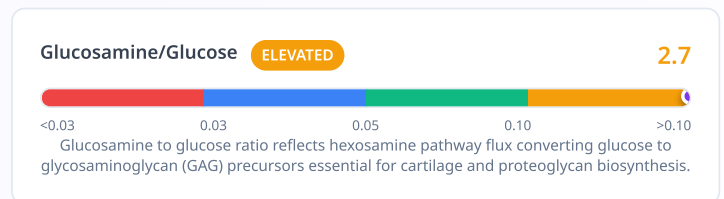
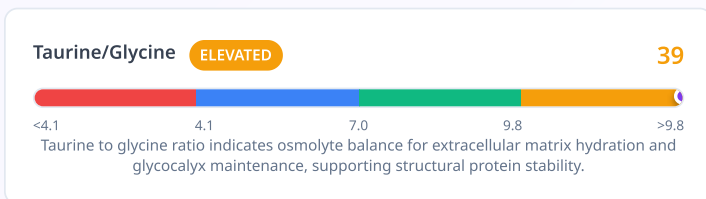
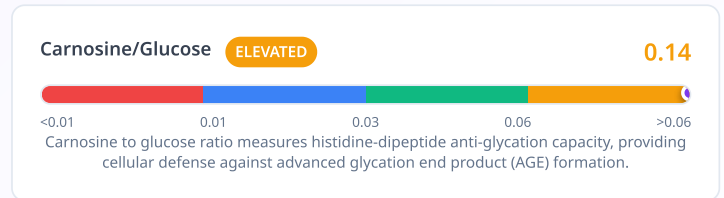
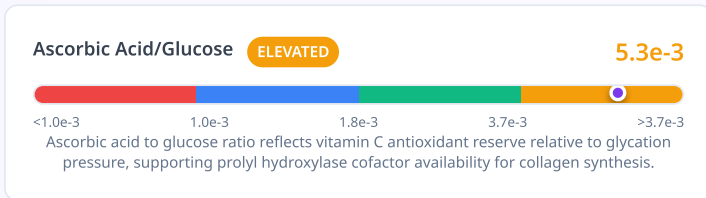
Early Disruption

Subdomain Zone Distribution



AGE Burden & Dicarbonyl Pressure		68	Evaluates advanced glycation end-product formation and reactive dicarbonyl stress from glucose and fructose metabolism causing protein crosslinking and cellular dysfunction. The score of 68 suggests elevated dicarbonyl stress warranting anti-glycation support and glucose-fructose management.
Cartilage GAGs & Hyaluronic Acid Reserve		24	Assesses glycosaminoglycan and hyaluronic acid synthesis capacity for cartilage matrix integrity, joint lubrication, and tissue hydration supporting musculoskeletal resilience. The score of 24 reveals impaired glycosaminoglycan synthesis with substantial depletion affecting cartilage matrix and joint integrity.
Collagen & Elastin Matrix Integrity		53	Measures collagen and elastin precursor availability, crosslinking quality, and degradation markers affecting skin, vascular, and connective tissue structural integrity. The score of 53 suggests reduced extracellular matrix precursor availability warranting glycine, proline, and vitamin C support.
ECM Hydration & Glycocalyx Osmolyte Balance		45	Tracks osmolyte balance including taurine, betaine, and myo-inositol supporting extracellular matrix hydration, cell volume regulation, and glycocalyx structural integrity. The score of 45 reveals impaired osmolyte status with substantial extracellular matrix dehydration and glycocalyx disruption.
Glycan Maturation (Glycosylation, Sulfation & Sialylation)		55	Evaluates protein and lipid glycosylation pathways including N-glycan branching, sulfation, and sialylation affecting receptor function, cell signaling, and immune recognition. The score of 55 suggests reduced glycan maturation warranting support for protein glycosylation and receptor function.
Glyoxalase-Carbonyl Detox Capacity		46	Assesses glyoxalase enzyme activity and glutathione availability for detoxifying methylglyoxal and other reactive carbonyls preventing AGE formation and dicarbonyl stress. The score of 46 reveals impaired glyoxalase function with substantial methylglyoxal accumulation and AGE formation.
Matrix Repair Energetics & Antioxidant Reserve		69	Measures metabolic and antioxidant support for extracellular matrix synthesis and repair including vitamin C, proline, glycine, and energy cofactors for tissue regeneration. The score of 69 suggests reduced matrix synthesis support warranting vitamin C, glycine, proline, and energy cofactor replenition.
Vascular Matrix Glycation & Stiffness Risk		21	Tracks vascular-specific glycation burden and elastin-collagen crosslinking affecting arterial stiffness, pulse wave velocity, and cardiovascular aging acceleration. The score of 21 reveals impaired vascular elasticity with substantial glycation-induced arterial stiffness and collagen crosslinking.

Central Metabolite Ratios & Markers



REPORT DATE

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OVERALL SCORE

75/100

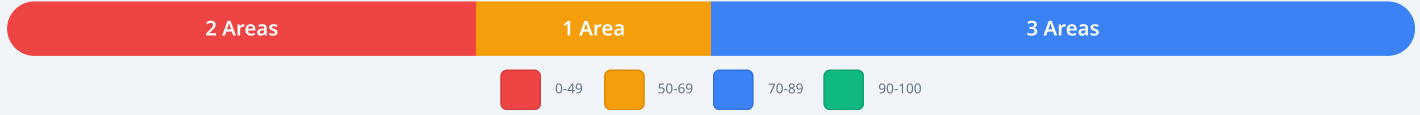
BIOMARKERS ANALYZED

91

ZONE

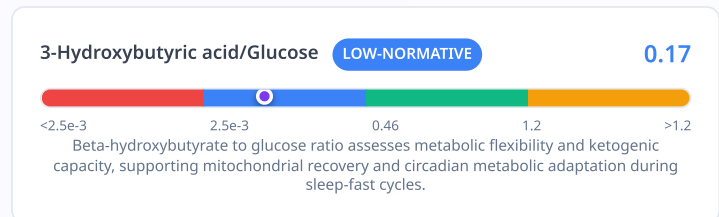
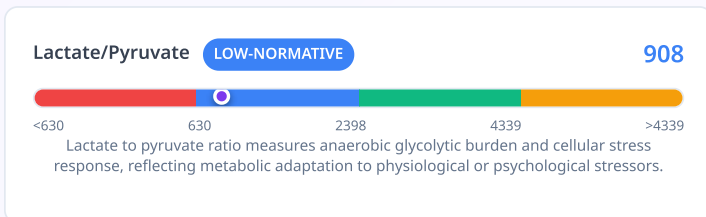
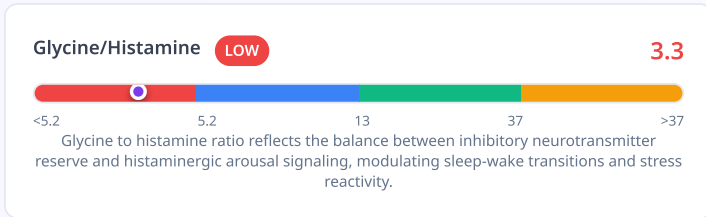
Normative

Subdomain Zone Distribution



Adenosine Sleep Pressure (Purine Turnover)		73	Evaluates adenosine accumulation from ATP breakdown driving homeostatic sleep pressure, with elevated purine metabolites indicating insufficient sleep recovery or cellular energy depletion. The score of 73 reflects normal homeostatic sleep pressure with adequate ATP conservation and restorative sleep.
Adrenal Stress Resilience & Thyroid Support		82	Assesses HPA axis function, cortisol rhythm, DHEA reserve, and thyroid hormone metabolism reflecting stress adaptation capacity and metabolic-endocrine recovery from chronic stress. The score of 82 shows normal HPA axis function with adequate adrenal reserve and thyroid metabolism.
Gut-Brain Sleep Disruptors & Stimulant_Xenobiotic Load		31	Evaluates Gut-Brain Sleep Disruptors & Stimulant_Xenobiotic Load function and metabolic capacity. The score of 31 indicates current functional status in this pathway.
Mitochondrial Recovery & NAD+ Repletion		75	Measures mitochondrial repair capacity and NAD+ regeneration during rest supporting cellular energy restoration, autophagy activation, and metabolic recovery from daily stress. The score of 75 shows normal mitochondrial recovery with adequate NAD+ regeneration and autophagy activation during sleep.
Neuroinflammation & Endothelial NO Tone		18	Evaluates kynurenine pathway neuroinflammation and nitric oxide bioavailability affecting sleep quality, vascular relaxation, and restorative parasympathetic nervous system activity. The score of 18 indicates impaired neuroinflammatory control with substantial kynurenine activation and nitric oxide insufficiency affecting sleep quality.
Sleep Neurotransmitters & Melatonin Axis		63	Assesses melatonin synthesis from serotonin, GABA production, and glycine availability supporting sleep initiation, sleep architecture, and circadian rhythm entrainment. The score of 63 indicates reduced serotonin-to-melatonin conversion suggesting benefit from tryptophan, GABA, and glycine support.

Central Metabolite Ratios & Markers



REPORT DATE

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OVERALL SCORE

74/100

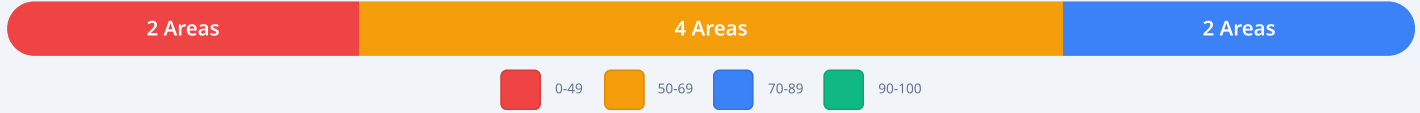
BIOMARKERS ANALYZED

114

ZONE

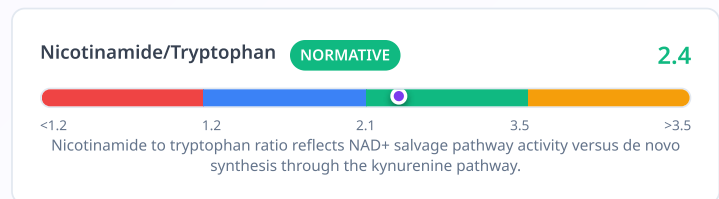
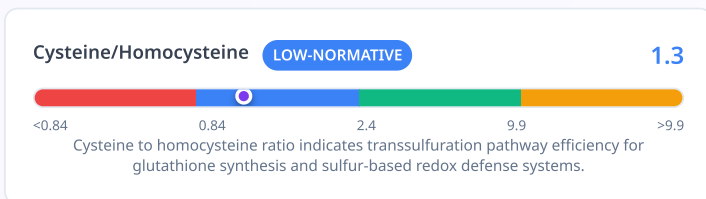
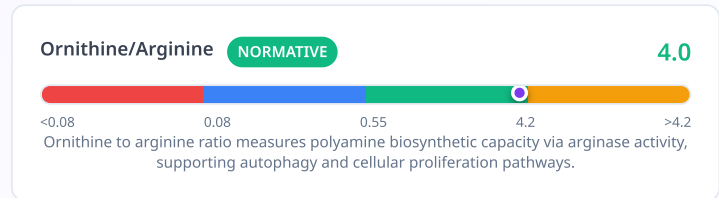
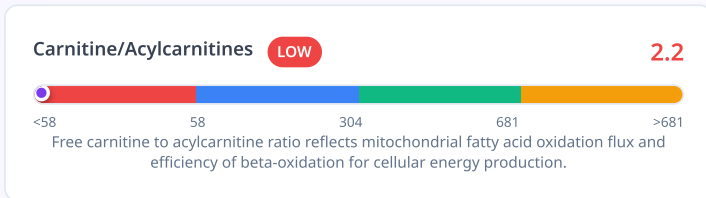
Normative

Subdomain Zone Distribution



Autophagy-Mitophagy & Cellular Cleanup		74	Evaluates cellular self-digestion and damaged organelle clearance through spermidine, leucine signaling, and mitochondrial quality control supporting cellular rejuvenation and longevity. The score of 74 reflects normal cellular self-digestion with adequate autophagy and damaged mitochondria clearance.
Collagen/ECM Renewal & Anti-Glycation		29	Assesses extracellular matrix turnover, collagen synthesis, and glycation resistance through hydroxyproline, glycine, and anti-glycation defenses maintaining tissue youthfulness. The score of 29 reveals impaired extracellular matrix turnover with substantial glycation burden affecting tissue youthfulness.
DNA Repair, Methylation & Epigenetic Balance		19	Measures DNA repair capacity, genomic methylation maintenance, and epigenetic stability through one-carbon metabolism, PARP activity, and base excision repair support. The score of 19 indicates impaired DNA repair with substantial genomic methylation dysregulation and epigenetic instability.
Glutathione & Redox Defense		60	Tracks glutathione biosynthesis and redox buffering capacity protecting against oxidative damage, supporting detoxification, and maintaining cellular reducing environment for longevity. The score of 60 indicates reduced GSH biosynthesis suggesting benefit from cysteine, glycine, and glutamate precursor support.
Gut-Longevity Crosstalk		58	Evaluates microbiome-derived longevity metabolites including butyrate, urolithins, and postbiotics supporting gut barrier integrity, immune tolerance, and healthy aging. The score of 58 suggests reduced beneficial metabolite production warranting gut ecosystem support for healthy aging.
Inflammaging & Immunometabolic Load		66	Assesses chronic low-grade inflammation and immune senescence markers including pro-inflammatory metabolites, senescence-associated secretory phenotype, and age-related immune dysregulation. The score of 66 indicates elevated inflammaging suggesting benefit from immune senescence modulation and inflammatory metabolite clearance.
Mitochondrial Repair & Bioenergetics		71	Measures mitochondrial biogenesis, respiratory chain efficiency, and energetic capacity supporting cellular vitality, stress resistance, and metabolic health span extension. The score of 71 reflects normal mitochondrial health with adequate bioenergetic capacity and cellular vitality.
NAD ⁺ & Sirtuin Repair Axis		69	Evaluates NAD ⁺ biosynthesis and sirtuin activation supporting DNA repair, mitochondrial function, circadian rhythm, and metabolic resilience as central longevity regulators. The score of 69 indicates reduced NAD⁺ availability suggesting benefit from nicotinamide riboside or niacin support for longevity pathways.

Central Metabolite Ratios & Markers



REPORT DATE

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OVERALL SCORE

76/100

BIOMARKERS ANALYZED

296

ZONE

Normative

Subdomain Zone Distribution



VOC & Solvent Burden (BTEX-Styrene)		60	Tracks volatile organic compound (VOC) exposure from solvents, styrene, and petrochemical sources including paints, adhesives, and industrial emissions. The score of 60 suggests elevated VOC metabolites warranting Phase II detoxification support and exposure source reduction.
Aryl Phenols & Benzenoid Load		64	Measures aromatic xenobiotic load from environmental phenols requiring Phase II conjugation for clearance. The score of 64 indicates elevated benzenoid metabolites suggesting benefit from glucuronidation and sulfation pathway support.
Plastics, Parabens & Phthalates		51	Assesses endocrine disruptor burden from plasticizers, parabens, and phthalates found in personal care products and food packaging. The score of 51 suggests elevated phthalate metabolites warranting exposure reduction and hormonal detoxification support.
Combustion & Tobacco Smoke (PAH)		86	Evaluates polycyclic aromatic hydrocarbon (PAH) exposure from combustion sources including tobacco smoke, grilled foods, and vehicle exhaust. The score of 86 shows normal PAH clearance with minimal combustion source exposure.
Air Pollution & Oxidant Gas		44	Measures oxidative stress from nitrogen oxides (NOx) and ozone (O ₃) exposure typical of air pollution. The score of 44 indicates impaired oxidative defense against air pollution with substantial NOx and ozone damage.
Reactive Carbonyls & Aldehydes		49	Tracks aldehyde and dicarbonyl electrophiles from oxidative stress and dietary advanced glycation end products (AGEs). The score of 49 reveals impaired aldehyde clearance with substantial dicarbonyl and reactive carbonyl burden.
Metals & Metalloid Stress		45	Assesses heavy metal burden (mercury, lead, cadmium, arsenic) affecting porphyrin synthesis and thiol antioxidant systems. The score of 45 indicates impaired heavy metal clearance with substantial mercury, lead, cadmium, or arsenic burden.
Mold & Mycotoxin Exposure		64	Evaluates mycotoxin and fungal VOC exposure from water-damaged buildings and contaminated foods. The score of 64 indicates elevated fungal exposure suggesting environmental remediation and detoxification pathway support.
Pesticide & Herbicide Exposure		68	Measures glyphosate and organophosphate pesticide exposure disrupting the shikimate pathway and cholinergic function. The score of 68 suggests elevated herbicide metabolites warranting organic food choices and cholinergic pathway support.

Central Metabolite Ratios & Markers

