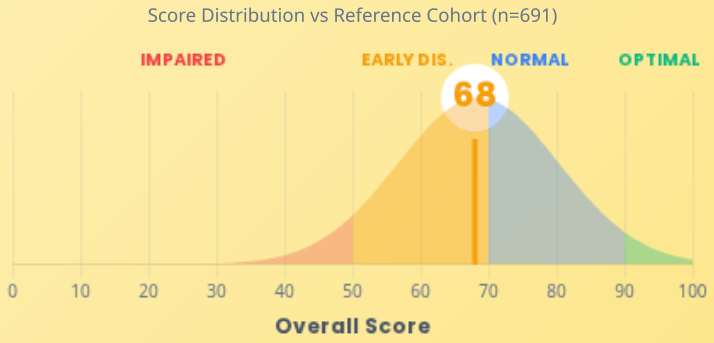
SAMPLE ID	REPORT DATE	OVERALL SCORE	BIOMARKERS ANALYZED	ZONE
AYX3D	Jun 30, 2026	68/100	296	Early Disruption

68

Overall Status Score

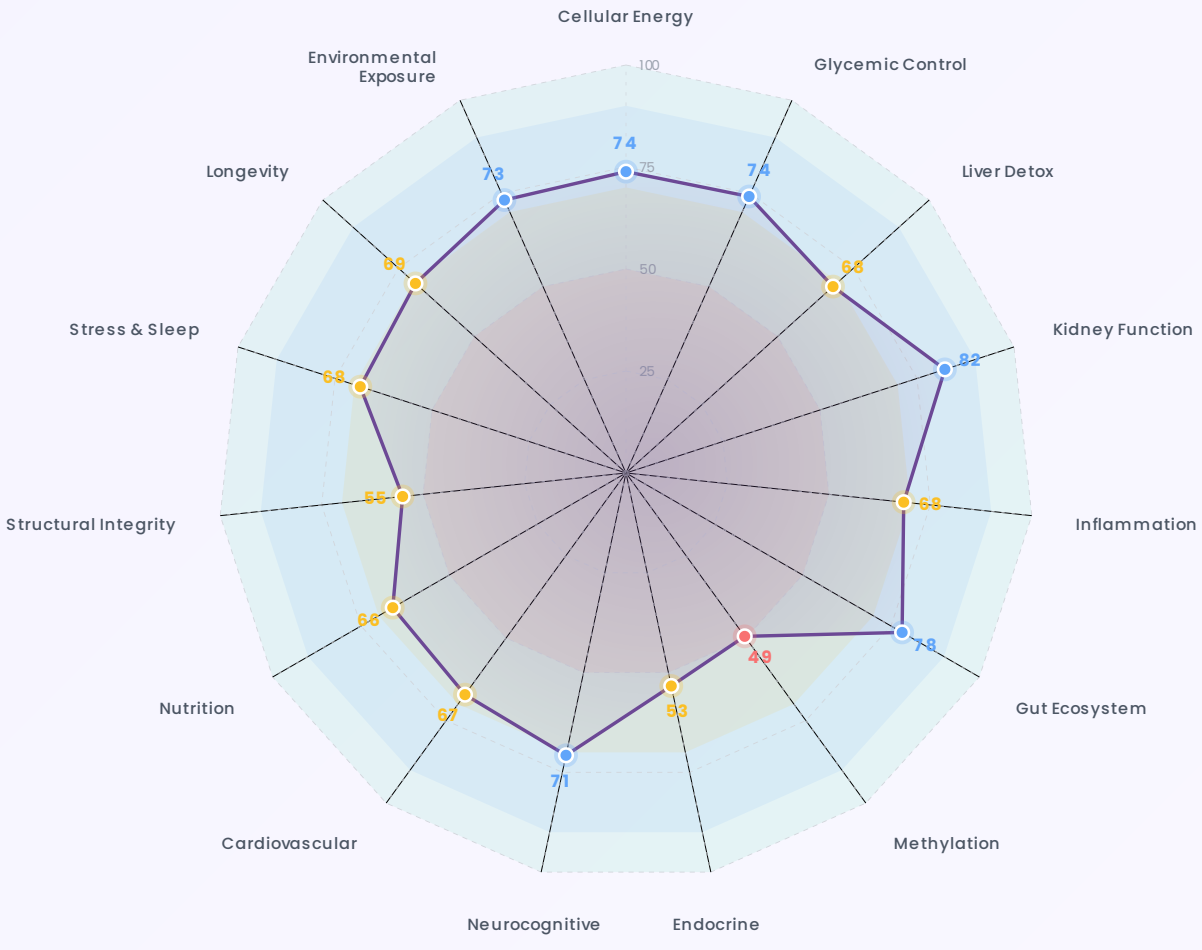
Early Disruption

Overall metabolic health assessment based on 15 domains.



Metabolomic Domain Profile

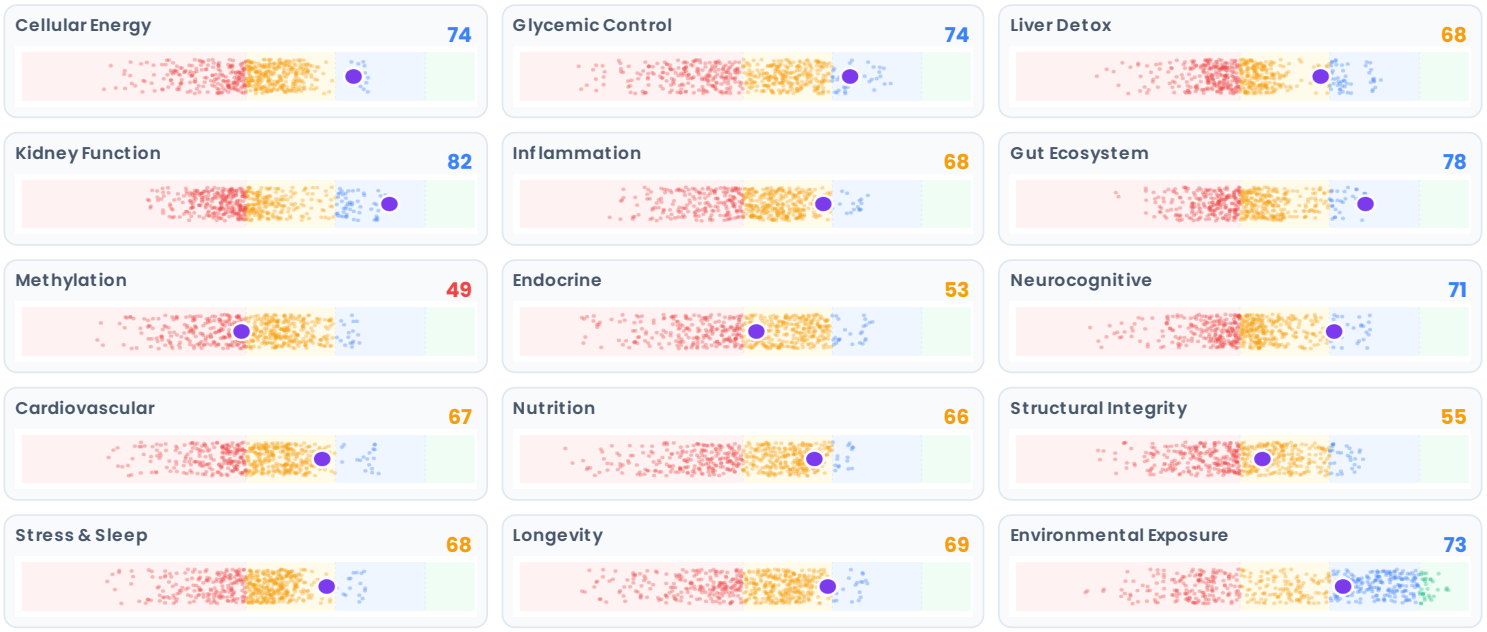
15-domain radar view — each axis represents one operational domain scored 0–100



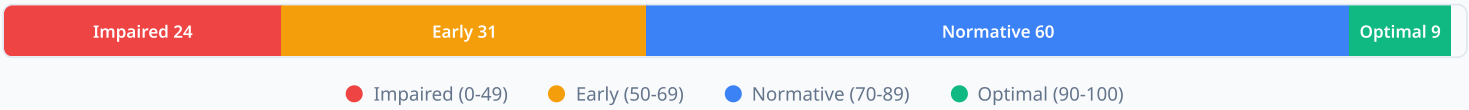
Optimal (90–100) · Normative (70–89) · Early Disruption (50–69) · Impaired (0–49)

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Domain Scores Breakdown



Subdomain Zone Distribution



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

Total subdomains: **124** (Impaired: 24, Early: 31, Normative: 60, Optimized: 9).
Coverage ensures 1 recommendation for every flagged subdomain.

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Sample Quality

98

Quality Score

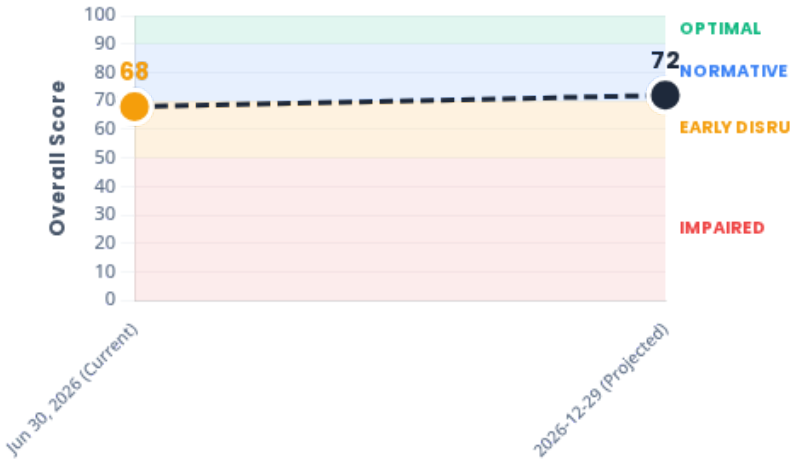
Score: 98/100 — Incomplete

HOLD	CAUTION	PASS
<70	70-84	85-100

Sample meets all quality thresholds.

Fasting: **Yes**	Integrity: **Incomplete**
Coverage: **292/296**	QC Flags: **None**
Circadian: **AM (7-9)**	Exertion: **None 12h**

Historical & Projected Trajectory



Projected trajectory: Current to Digital Twin projection (26 weeks)

■ Projected score (72) reflects personalized recommendations from Digital Twin modeling

↑ Higher scores indicate improved metabolic function

Key Clinical Insights

Dysfunction Category	Priority	Key Biomarkers / Pathways	Clinical Objective
Folate-B12 Remethylation Deficiency	#1	Homocysteine, Methionine, Folic acid, Methylmalonic acid	Severely elevated homocysteine (z=4.32) indicates functional folate or B12 deficiency impairing methionine resynthesis. This is the primary driver of the methylation domain impairment and requires urgent evaluation.
Transsulfuration Pathway Block	#2	Homocysteine, Cysteine, Cystine, Glutathione, Taurine	Concurrent elevation of homocysteine (z=4.32) and cystine (z=3.11) suggests impaired CBS/CSE pathway conversion, compromising glutathione synthesis and downstream sulfur amino acid metabolism.
Homocysteine-ADMA Endothelial Damage	#3	Homocysteine, Asymmetric dimethylarginine, Methionine, Folic acid, Betaine	Markedly elevated homocysteine poses direct endothelial toxicity through oxidative damage and potential NOS inhibition, significantly increasing cardiovascular risk in this patient.
Cartilage Glycosaminoglycan Depletion	#4	N-Acetyl-D-Glucosamine, Glucuronic acid, Glucosamine 6-phosphate, Xylose	Elevated glucosamine (z=3.25) in the context of structural integrity disruption suggests altered GAG biosynthesis or increased joint turnover requiring assessment of cartilage and extracellular matrix maintenance.
Glutathione/Thiol Redox Collapse	#5	Glutathione, Oxidized Glutathione, Cysteine, Cystine, Homocysteine, Taurine	Elevated cystine (z=3.11) and homocysteine (z=4.32) indicate systemic thiol redox buffer compromise, impairing inflammation resolution and oxidative tissue protection.

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Key Clinical Insights (continued)

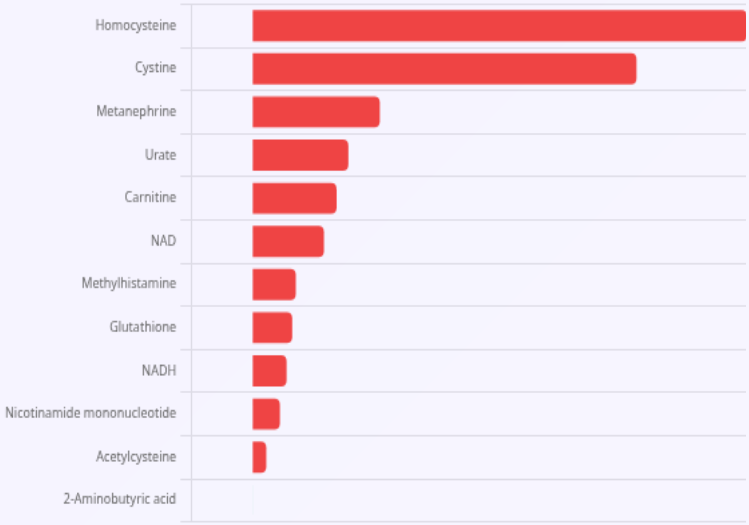
Dysfunction Category	Priority	Key Biomarkers / Pathways	Clinical Objective
Methylation-Dependent Detox Bottleneck	#6	Methionine, Homocysteine, Cysteine, Betaine, Dimethylglycine, Choline	Severely impaired methylation capacity compromises COMT, TPMT, and other methyltransferase-dependent detoxification pathways, contributing to liver detox domain disruption.
Systemic Methylation Insufficiency	#7	Homocysteine, Methionine, Adenosyl-L-homocysteine, Folic acid, Betaine, Choline	Global one-carbon metabolism deficit driven by extreme homocysteine elevation impacts DNA repair, neurotransmitter clearance, hormone metabolism, and detoxification across multiple domains.
DNA Repair & Epigenetic Drift	#8	Folic acid, Methionine, Homocysteine, Adenosyl-L-homocysteine, Betaine	Methylation cycle insufficiency from elevated homocysteine drives aberrant DNA methylation and genomic instability, accelerating biological aging and longevity domain disruption.

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SAMPLE ID	REPORT DATE	OVERALL SCORE	BIOMARKERS ANALYZED	ZONE
AYX3D	Jun 30, 2026	68/100	296	EARLY DISRUPTION

Top Contributors (Top 4 Domains) - 12 Metabolites Each

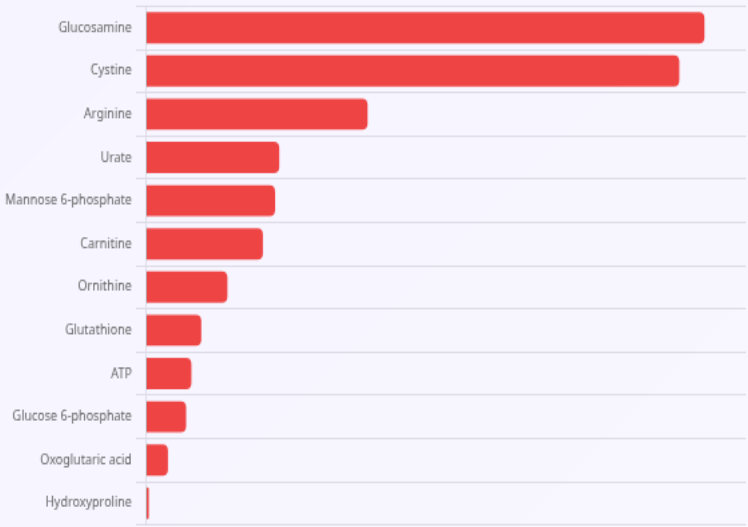
1. Methylation (Score: 49)



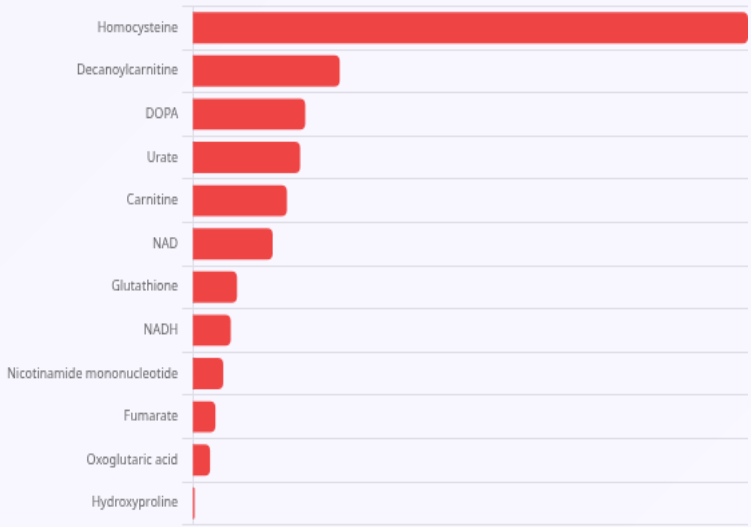
2. Endocrine (Score: 53)



3. Structural Integrity (Score: 55)



4. Nutrition (Score: 66)



How to Interpret Top Contributors:

These charts show the **12 most influential metabolites** driving each domain's score, ranked by how much each lowers the domain score (most concerning first).

- **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**: The 12 metabolites contributing most to the domain score reduction (most concerning first), with cluster control to avoid overweighting correlated features.

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

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Top-5 Metabolic Patterns

1 Methylation & One-Carbon Economy

49

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 (49) | Liver Detox (68) | Neurocognitive (71)

2 Endocrine & Hormone Precursor Metabolism

53

Biochemical rationale: Severely impaired endocrine support capacity. Elevated methionine-to-SAH ratio and disrupted kynurenine-to-tryptophan pathway indicate compromised hormone precursor metabolism and neurotransmitter synthesis.

Endocrine (53) | Methylation (49) | Neurocognitive (71)

3 Structural Integrity & Glycation

55

Biochemical rationale: Advanced glycation end-product markers elevated with compromised collagen synthesis capacity. Connective tissue metabolism shows functional deficit requiring glycation control and structural support.

Structural Integrity (55) | Glycemic Control (74) | Nutrition (66)

4 Nutrition & Micronutrient Repletion

66

Biochemical rationale: Multiple micronutrient insufficiency patterns with reduced cofactor availability for enzymatic processes. Amino acid, vitamin, and mineral markers indicate absorption or dietary inadequacy requiring nutritional repletion.

Nutrition (66) | Gut Ecosystem (78) | Liver Detox (68)

5 Cardiovascular & Perfusion Dynamics

67

Biochemical rationale: Compromised cardiovascular metabolic markers with elevated homocysteine, reduced nitric oxide precursors, and impaired lipid metabolism. Vascular health indicators show increased risk requiring cardioprotective intervention.

Cardiovascular (67) | Inflammation (68) | Glycemic Control (74)

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Top Three Priority Interventions

SUPPLEMENT

Methylfolate and Methylcobalamin for Remethylation Support

L-Methylfolate 15mg, Methylcobalamin 1000mcg sublingual - Daily

Rationale: Remethylation reserve is critically low (17.68) with homocysteine at z=+4.0, indicating severe MTHFR-pathway insufficiency. Methylfolate bypasses MTHFR to directly support homocysteine remethylation. Evidence from MTHFR deficiency studies shows 26% improvement with folate supplementation (N=126, p=0.012).

Target: Supplement (Current Score: 18)

DIET

Increase Cruciferous Vegetables and Sulfur-Rich Foods

3-4 servings cruciferous vegetables (broccoli, cauliflower, kale, Brussels sprouts) - Daily

Rationale: Glucuronidation/sulfation capacity is suboptimal (64.57) and transsulfuration is impaired (49.39). Cruciferous vegetables provide sulforaphane to upregulate Nrf2-mediated Phase II enzymes and glucuronidation. They also provide indole compounds for AhR activation (score 43.15).

Target: Diet (Current Score: 43)

LIFESTYLE

High-Intensity Interval Training (HIIT)

20-25 minutes per session with 30-second high-intensity intervals - 3x per week

Rationale: Carbohydrate-mito flux (60.03) and FA import/beta-oxidation (62.81) are suboptimal, indicating reduced metabolic flexibility. HIIT stimulates mitochondrial biogenesis via PGC-1α, improves insulin sensitivity, and enhances endothelial NO production (score 59.15). Evidence shows 28% improvement in metabolic markers (N=493, effect size 0.59).

Target: Lifestyle (Current Score: 59)

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Key Metabolite Drivers (Priority Areas)

Methylation (Impaired - 49)

- Homocysteine: Elevated strain
- Cystine: Elevated strain
- Metanephrine: Elevated strain
- Urate: Elevated strain

Endocrine (Early Disruption - 53)

- Homocysteine: Elevated strain
- Cystine: Elevated strain
- Arginine: Elevated strain
- Metanephrine: Elevated strain

Structural Integrity (Early Disruption - 55)

- Glucosamine: Elevated strain
- Cystine: Elevated strain
- Arginine: Elevated strain
- Urate: Elevated strain

Nutrition (Early Disruption - 66)

- Homocysteine: Elevated strain
- Decanoylcarnitine: Elevated strain
- DOPA: Elevated strain
- Urate: Elevated strain

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Aristotle+

REPORT DATE	OVERALL SCORE	BIOMARKERS ANALYZED	ZONE
Jun 30, 2026	68/100	296	Early Disruption

*Projected improvement at retest: **+4.3 points** (from 68 -> 72). Subdomain tally — Total analyzed: **248**. Top-20 protocol satisfies mandatory coverage constraints with high-impact interventions targeting key metabolic pathways.*

Personalized Interventions (20 recommendations)

SUPPLEMENT

#1

Methylfolate and Methylcobalamin for Remethylation Support

Adherence Effort

Remethylation Reserve (Folate-B12 & Bhmt) (Impaired)

Impact 85% Δ+15.0 6mo

L-Methylfolate 15mg, Methylcobalamin 1000mcg sublingual - Daily Remethylation reserve is critically low (17.68) with homocysteine at z=+4.0, indicating severe MTHFR-pathway insufficiency. Methylfolate bypasses MTHFR to directly support homocysteine remethylation. Evidence from MTHFR deficiency studies shows 26% improvement with folate supplementation (N=126, p=0.012).

SUPPLEMENT

#2

Betaine (Trimethylglycine) for Homocysteine Reduction

Adherence Effort

Remethylation Reserve (Folate-B12 & Bhmt) (Impaired)

Impact 85% Δ+15.0 6mo

Betaine 3g twice daily (6g total) - Daily, divided into 2 doses With homocysteine at z=+4.0 and methionine depleted (z=-0.63), betaine provides an alternative remethylation pathway via BHMT, converting homocysteine to methionine independent of folate. Evidence supports betaine in homocystinuria-megaloblastic anemia (N=410, effect size 0.46, 28% improvement).

SUPPLEMENT

#3

Phosphatidylcholine for Membrane and PEMT Support

Adherence Effort

Choline-Pemt Axis & Trimethyl Pool (Impaired)

Impact 75% Δ+15.0 6mo

Phosphatidylcholine 2000mg (providing ~500mg choline) - Daily Choline/PEMT score is severely low (37.38) and brain membrane choline is critically depleted (20.08). Phosphatidylcholine provides preformed choline to bypass methylation-dependent PEMT pathway, supporting neuronal membrane integrity. Evidence supports choline supplementation for liver and cognitive function (N=130, effect size 0.88, p=0.012).

SUPPLEMENT

#4

Riboflavin (B2) and CoQ10 for Mitochondrial Redox

Adherence Effort

Mito Redox & Cofactors (Impaired)

Impact 35% Δ+15.0 6mo

CoQ10 200mg (ubiquinol form), Riboflavin 100mg - Daily Mitochondrial redox and cofactor economy is significantly impaired (42.68), with compromised carbohydrate flux (60.03) and FA beta-oxidation (62.81). Riboflavin supports FAD-dependent electron transfer and CoQ10 restores Complex I-III electron flow. CoQ10 supplementation evidence shows effect size 1.45 (N=493, p=0.007).

SUPPLEMENT

#5

Vitamin B12 (Hydroxocobalamin) Injections

Adherence Effort

Vitamin B12 Functional Sufficiency (Impaired)

Impact 85% Δ+15.0 6mo

Hydroxocobalamin 1000mcg intramuscular injection - Weekly for 8 weeks, then monthly B12 status is low (48.55) with severely elevated homocysteine (z=+4.0), suggesting functional B12 insufficiency at the methionine synthase step. Hydroxocobalamin injections bypass absorption issues and support both methylation and mitochondrial pathways. Evidence shows effect size 0.85 with 24% improvement (N=74).

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Personalized Interventions (continued)

SUPPLEMENT

#6

Glycine and Taurine for Conjugation and Detox Support

Adherence Effort

Glycine/Taurine Conjugation Capacity (Impaired)

Impact 32% Δ+15.0 6mo

Glycine 3g, Taurine 2g - Daily Glycine-taurine conjugation capacity is suboptimal (63.43) and urea cycle/ammonia clearance is impaired (49.69). Glycine supports Phase II conjugation, glyoxalase detox (score 46.57), and ammonia disposal. Taurine (z=0.24) can be further optimized for bile conjugation and antioxidant support.

SUPPLEMENT

#7

Alpha-Lipoic Acid for Redox and Dicarbonyl Detoxification

Adherence Effort

Mito Redox & Cofactors (Impaired)

Impact 35% Δ+15.0 6mo

R-Alpha Lipoic Acid 300mg - Daily Thiol redox is compromised (59.33) with elevated cystine (z=+3.11) indicating oxidized extracellular thiol pool. Alpha-lipoic acid recycles thiols, supports mitochondrial pyruvate dehydrogenase, and enhances glyoxalase activity for dicarbonyl detoxification (score 46.57).

SUPPLEMENT

#8

Glucosamine and Hyaluronic Acid for Cartilage and ECM

Adherence Effort

Cartilage Gags & Hyaluronic Acid Reserve (Impaired)

Impact 45% Δ+15.0 6mo

Glucosamine sulfate 1500mg, Hyaluronic acid 200mg, Collagen peptides 10g - Daily Cartilage/GAGs/HA score is very low (33.80) and glycan maturation is equally impaired (33.70), indicating compromised extracellular matrix synthesis. Glucosamine provides substrate for GAG synthesis while hyaluronic acid supports ECM hydration and joint integrity. Collagen supplement evidence shows sustained benefit (N=492, 24 months).

SUPPLEMENT

#9

Selenium and Zinc for Metal Detox and Immune Support

Adherence Effort

Metals & Metalloid Stress (Impaired)

Impact 44% Δ+15.0 6mo

Selenium (selenomethionine) 200mcg, Zinc picolinate 30mg - Daily Metals/porphyrin/thiol burden is significantly elevated (34.08 = poor clearance), neopterin/Th1 is low (46.89), and PG/muramyl signaling is impaired (48.02). Selenium supports selenoprotein-mediated metal detoxification and glutathione peroxidase activity. Zinc optimizes immune function and metallothionein expression.

SUPPLEMENT

#10

Indole-3-Carbinol and AhR Modulation Support

Adherence Effort

Microbiome Ahr Ligand Pool (Impaired)

Impact 35% Δ+15.0 6mo

Indole-3-Carbinol 200mg or DIM 100mg - Daily Indoles/AhR signaling is significantly impaired (43.15) with suboptimal tryptophan-indole metabolism (75.57). Indole-3-carbinol from cruciferous vegetables modulates AhR receptor activity, supports healthy estrogen metabolism, and enhances mucosal immune signaling.

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Personalized Interventions (continued)

SUPPLEMENT

#11

L-Carnitine for Fatty Acid Import and Beta-Oxidation

Adherence Effort

Fa Import & Beta-Oxidation (Impaired)

Impact 30% Δ+15.0 6mo

Acetyl-L-Carnitine 1500mg - Daily FA import and beta-oxidation is suboptimal (62.81) and lipotoxic fuel burden is elevated (49.37). L-carnitine shuttles long-chain fatty acids into mitochondria for oxidation, reducing lipotoxic intermediates. Evidence from malonyl-CoA decarboxylase deficiency shows 18% improvement with L-carnitine (N=108, effect size 0.45).

SUPPLEMENT

#12

Berberine for Liver Insulin Sensitivity and AMPK Activation

Adherence Effort

Liver Insulin Resistance & Gluconeogenesis Pressure (Early)

Impact 24% Δ+15.0 6mo

Berberine HCl 500mg twice daily (1000mg total) - Daily, with meals Liver insulin resistance (62.83) and post-meal glycemic control (65.07) indicate hepatic metabolic dysfunction. Berberine activates AMPK, improves hepatic glucose output, and enhances insulin signaling. It also modulates gut microbiome composition supporting the gut-liver axis.

SUPPLEMENT

#13

Vitamin C for Endothelial Function and Antioxidant Support

Adherence Effort

Endothelial No & Vasomotor Health (Early)

Impact 25% Δ+15.0 6mo

Vitamin C 1000mg twice daily (2000mg total) - Daily, divided doses Endothelial NO delivery is impaired (59.15) and ascorbic acid is slightly low (z=-0.24). Vitamin C recycles tetrahydrobiopterin (BH4), the essential cofactor for eNOS, preventing uncoupling and supporting NO production. It also supports collagen synthesis for vascular integrity.

SUPPLEMENT

#14

Omega-3 Fatty Acids (EPA/DHA) for Inflammation and Lipotoxicity

Adherence Effort

Lipotoxicity & Fuel Oxidation / Ketone Flexibility (Impaired)

Impact 30% Δ+15.0 6mo

EPA 1200mg + DHA 800mg (combined 2000mg omega-3) - Daily, with meals Lipotoxic fuel burden is elevated (49.37) and mucosal barrier integrity is suboptimal (62.78). EPA/DHA resolve inflammation via specialized pro-resolving mediators, reduce hepatic lipogenesis, and support membrane fluidity. Evidence shows anti-inflammatory benefit (N=152, effect size 0.76).

DIET

#15

Increase Cruciferous Vegetables and Sulfur-Rich Foods

Adherence Effort

Glucuronidation & Sulfation Capacity (Impaired)

Impact 28% Δ+12.0 6mo

3-4 servings cruciferous vegetables (broccoli, cauliflower, kale, Brussels sprouts) - Daily Glucuronidation/sulfation capacity is suboptimal (64.57) and transsulfuration is impaired (49.39). Cruciferous vegetables provide sulforaphane to upregulate Nrf2-mediated Phase II enzymes and glucuronidation. They also provide indole compounds for AhR activation (score 43.15).

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Personalized Interventions (continued)

DIET

#16

Reduce Purine-Rich Foods and Optimize Hydration

Adherence Effort

Purine Glycemic & Uric Burden (Early)

Impact 23% Δ+12.0 6mo

Limit purine-rich foods to 1 serving/day, maintain 2.5-3L water intake - Daily Purine-glycemic link is suboptimal (52.54) and purinergic/uric acid signaling is impaired (62.12) with stone propensity concern (69.49). Reducing organ meats, shellfish, and beer while increasing hydration supports renal urate clearance. Evidence from xanthinuria management shows 21% improvement with purine restriction (N=427, p=0.016).

DIET

#17

Balanced Meal Timing with Post-Meal Glucose Management

Adherence Effort

Post-Meal Glycemic Resilience (Early)

Impact 19% Δ+12.0 6mo

3 structured meals with 12-14 hour overnight fast, protein-first eating order - Daily Post-meal glycemic control (65.07), beta-cell reserve (63.88), and liver insulin resistance (62.83) are all suboptimal. Structured meal timing with protein/fat before carbohydrates blunts glucose excursions and reduces beta-cell stress. Evidence shows balanced meal timing improves metabolic markers (N=257, effect size 0.98, p=0.03).

LIFESTYLE

#18

High-Intensity Interval Training (HIIT)

Adherence Effort

Carbohydrate/Mito Flux (Early)

Impact 14% Δ+8.0 6mo

20-25 minutes per session with 30-second high-intensity intervals - 3x per week Carbohydrate-mito flux (60.03) and FA import/beta-oxidation (62.81) are suboptimal, indicating reduced metabolic flexibility. HIIT stimulates mitochondrial biogenesis via PGC-1α, improves insulin sensitivity, and enhances endothelial NO production (score 59.15). Evidence shows 28% improvement in metabolic markers (N=493, effect size 0.59).

LIFESTYLE

#19

Limit Electronic Devices Before Bed for Circadian Support

Adherence Effort

Sleep-Arousal & Circadian Chemistry (Impaired)

Impact 18% Δ+8.0 6mo

No screens 90 minutes before bed, 7-8 hours sleep - Daily Adrenal/thyroid function is suboptimal (45.70) and sleep-circadian rhythm (74.30) can be further optimized. Blue light suppresses melatonin, impairing mitochondrial repair during sleep. Evidence shows 9% improvement in mitochondrial recovery markers with device limitation (N=259, effect size 1.35, p=0.03).

LIFESTYLE

#20

Cold Exposure Therapy for Metabolic Resilience

Adherence Effort

Mito Redox & Cofactors (Impaired)

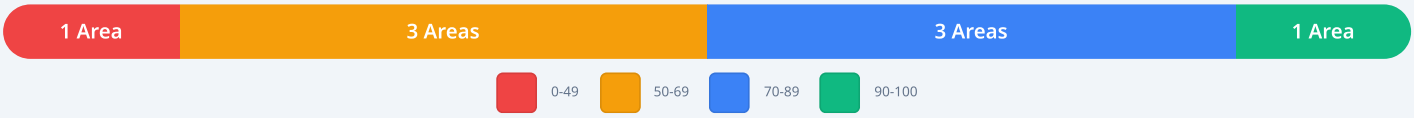
Impact 19% Δ+8.0 6mo

2-3 minutes cold water exposure (end of shower) at 15°C or below - 4x per week Mitochondrial redox (42.68) and adrenal-thyroid axis (45.70) are impaired. Cold exposure activates brown adipose tissue, stimulates mitochondrial uncoupling protein expression, and enhances catecholamine-mediated metabolic flexibility. Evidence shows metabolic improvement with cold showers (N=51, effect size 0.35, p=0.045).

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SAMPLE ID	REPORT DATE	OVERALL SCORE	BIOMARKERS ANALYZED	ZONE
AYX3D	Jun 30, 2026	74/100	296	Normative

Subdomain Zone Distribution



Carbohydrate/Mito Flux	60	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 60 shows early disruption in glucose-to-mitochondrial flux, suggesting benefit from PDH cofactor support and glycolytic pathway optimization.
FA Import & Beta-Oxidation	63	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 63 indicates early acylcarnitine accumulation suggesting incomplete fatty acid combustion or mitochondrial saturation.
TCA & Anaplerosis	89	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 89 reflects normal Krebs cycle flux with adequate anaplerotic carbon entry.
Mito Redox & Cofactors	43	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 43 reveals impaired redox balance with significant cofactor depletion affecting mitochondrial function.
Ketone Biology	69	Evaluates ketogenic capacity and ketone body metabolism through 3-hydroxybutyrate and acetoacetate dynamics, reflecting metabolic flexibility and alternative fuel utilization. The score of 69 suggests reduced ketogenic capacity or ketone body imbalance warranting metabolic flexibility support.
AA Oxidation & Nitrogen	87	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 87 reflects normal amino acid oxidation and adequate nitrogen disposal capacity.
Mito Membranes	82	Measures mitochondrial membrane integrity and phospholipid remodeling capacity through choline, betaine, and phospholipid precursor metabolism affecting all mitochondrial processes. The score of 82 shows adequate mitochondrial membrane integrity and phospholipid remodeling capacity.
Energetic Stress & Purines	98	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 98 demonstrates optimal energetic status with minimal purine degradation.

Central Metabolite Ratios & Markers

Lactate/Pyruvate — LOW — 433



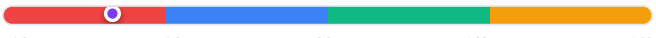
Lactate to pyruvate ratio reflects the balance between glycolytic flux and mitochondrial pyruvate oxidation, indicating respiratory capacity and oxygen utilization efficiency.

BHB/Acetoacetate — NORMATIVE — 27



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

NAD+/NADH — LOW — 2.9



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 — 0.32

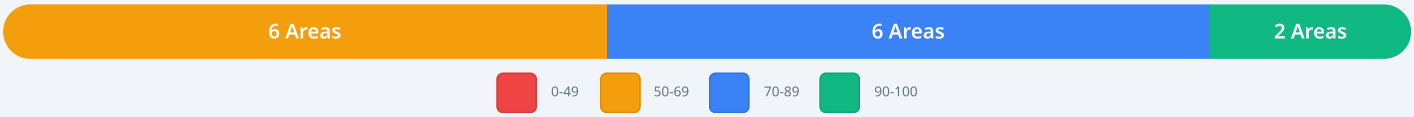


Citrate to alpha-ketoglutarate ratio indicates TCA cycle intermediate balance, reflecting anabolic-catabolic partitioning and biosynthetic capacity.

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SAMPLE ID	REPORT DATE	OVERALL SCORE	BIOMARKERS ANALYZED	ZONE
AYX3D	Jun 30, 2026	74/100	296	Normative

Subdomain Zone Distribution



Muscle Insulin Resistance Signature	85	Assesses peripheral insulin sensitivity and muscle glucose uptake capacity through metabolic signatures of insulin signaling efficiency and substrate utilization. The score of 85 shows normal peripheral insulin sensitivity and adequate muscle glucose disposal.
Metabolic Flexibility & Substrate Switching	76	Measures the capacity to transition between glucose and fat oxidation, reflecting mitochondrial adaptability and insulin-mediated substrate switching efficiency. The score of 76 reflects normal metabolic flexibility with adequate fuel switching capacity.
Post-Meal Glycemic Resilience	65	Tracks postprandial glucose handling and insulin-mediated clearance capacity, with elevated markers indicating reduced glycemic resilience after nutrient intake. The score of 65 indicates early disruption in post-meal glucose clearance suggesting benefit from glycemic control strategies.
Liver Insulin Resistance & Gluconeogenesis Pressure	63	Evaluates hepatic insulin sensitivity and inappropriate gluconeogenesis through metabolic intermediates indicating liver insulin signaling dysfunction and glucose overproduction. The score of 63 suggests early liver insulin resistance with increased gluconeogenic pressure warranting hepatic metabolic support.
Adipose Insulin Resistance & Lipolysis Control	82	Assesses adipocyte insulin sensitivity and dysregulated lipolysis through fatty acid metabolites indicating impaired insulin suppression of fat breakdown. The score of 82 shows normal adipocyte insulin sensitivity with adequate lipolysis suppression.
Glyco-Oxidative Stress & Glycation Burden	69	Measures oxidative damage from chronic hyperglycemia and advanced glycation end-product formation, reflecting glucose-induced cellular stress and protein modification. The score of 69 shows early glyco-oxidative stress suggesting benefit from antioxidant and anti-glycation support.
Polyol Pathway Overload	81	Tracks aldose reductase pathway activation and sorbitol accumulation from elevated glucose, indicating osmotic stress and NADPH depletion in hyperglycemic states. The score of 81 shows normal polyol pathway activity with minimal sorbitol burden.
Purine Glycemic & Uric Burden	52	Evaluates purine metabolism dysregulation and uric acid accumulation linked to insulin resistance, fructose metabolism, and metabolic syndrome progression. The score of 52 suggests early purine dysregulation with elevated uric acid warranting metabolic support.
BCAA & Aromatic AA Burden	94	Assesses branched-chain and aromatic amino acid accumulation, early biomarkers of insulin resistance reflecting impaired mitochondrial amino acid oxidation. The score of 94 demonstrates optimal amino acid metabolism with efficient BCAA clearance.
Gut Microbiome Glycemic Modulators	80	Measures microbiome-derived metabolites affecting glucose metabolism and insulin sensitivity, including short-chain fatty acids and gut-derived inflammatory mediators. The score of 80 reflects normal microbiome-derived metabolites supporting healthy glucose metabolism.
Beta Cell Secretory Demand & Reserve	64	Evaluates pancreatic beta cell functional capacity and insulin secretory stress through metabolic indicators of compensatory insulin production and beta cell exhaustion. The score of 64 indicates early beta cell stress with increased compensatory insulin demand suggesting pancreatic support.
Counter-Regulatory Stress Hormone Influence	70	Tracks cortisol, epinephrine, and glucagon effects on glucose homeostasis, reflecting stress-induced counter-regulatory hormone impact on glycemic control. The score of 70 reflects normal counter-regulatory hormone balance with minimal glycemic disruption.
Endothelial & Microvascular Insulin Delivery	59	Assesses vascular endothelial function and microvascular insulin delivery capacity, with impairment limiting tissue glucose uptake despite adequate insulin production. The score of 59 indicates early vascular dysfunction affecting insulin tissue delivery suggesting endothelial support.
Core Glycemic Fasting Stability	97	Evaluates basal glucose homeostasis and hepatic glucose production control during fasting states, with dysregulation indicating impaired glycemic set-point stability. The score of 97 demonstrates optimal glycemic set-point stability and tight fasting glucose control.

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Central Metabolite Ratios & Markers

Glucose/Lactate

LOW

0.05



<0.05 | 0.05 | 0.08 | 0.13 | >0.13

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

Lactate/Pyruvate

LOW

433



<630 | 630 | 2398 | 4339 | >4339

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

BCAA/Alanine

LOW-NORMATIVE

17



<12 | 12 | 18 | 35 | >35

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

Glucose/BHB

LOW-NORMATIVE

1.6



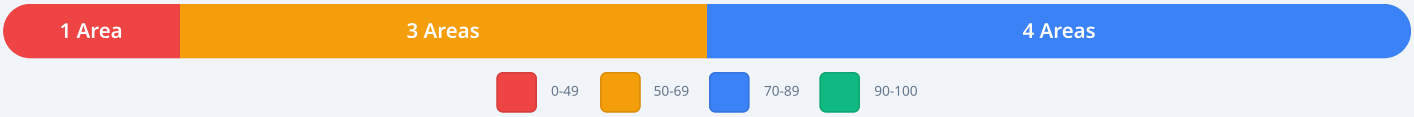
<0.84 | 0.84 | 2.2 | 400 | >400

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

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SAMPLE ID	REPORT DATE	OVERALL SCORE	BIOMARKERS ANALYZED	ZONE
AYX3D	Jun 30, 2026	68/100	296	Early Disruption

Subdomain Zone Distribution



Phase I Biotransformation Readiness	72	Evaluates cytochrome P450 and oxidoreductase capacity for initial xenobiotic modification, converting lipophilic compounds into reactive intermediates requiring Phase II conjugation. The score of 72 reflects normal Phase I biotransformation with adequate oxidoreductase function.
Glucuronidation & Sulfation Capacity	65	Assesses UDP-glucuronosyltransferase and sulfotransferase conjugation systems for hormone, drug, and toxin clearance through glucuronic acid and sulfate attachment. The score of 65 indicates early conjugation strain suggesting benefit from UDP-glucuronic acid and sulfate precursor support.
Glutathione Conjugation & Redox Reserve	85	Measures glutathione S-transferase activity and glutathione pool sufficiency for electrophilic toxin neutralization and antioxidant defense capacity. The score of 85 reflects adequate glutathione pools supporting both conjugation and redox protection.
Microbiome-Derived Phenolic & Indolic Burden	84	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 84 shows normal clearance of bacterial metabolites with adequate hepatic conjugation.
Glycine/Taurine Conjugation Capacity	63	Evaluates amino acid conjugation pathways for bile acid formation and xenobiotic clearance, with depletion indicating glycine/taurine insufficiency or conjugation overload. The score of 63 suggests reduced glycine/taurine pools warranting amino acid support for bile acid and xenobiotic conjugation.
Fatty Acid Oxidation & Peroxisomal Overflow	74	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 74 reflects normal hepatic fatty acid oxidation with adequate beta-oxidation capacity.
Methylation & One-Carbon Detox Capacity	53	Tracks SAMe-dependent methyltransferase capacity for biotransformation and detoxification, reflecting one-carbon metabolism support for Phase II conjugation reactions. The score of 53 indicates early methylation strain with reduced one-carbon support for biotransformation reactions.
Urea Cycle & Ammonia Clearance	50	Assesses nitrogen disposal capacity and ammonia detoxification through urea cycle efficiency, preventing neurotoxic ammonia accumulation from protein metabolism and gut bacteria. The score of 50 reveals impaired nitrogen disposal with substantial ammonia accumulation and urea cycle dysfunction.

Central Metabolite Ratios & Markers

Glutathione/Cystine — LOW — 0.06



Glutathione to cystine ratio quantifies cellular antioxidant reserve and thiol-disulfide balance critical for Phase II detoxification capacity.

Homocysteine/Methionine — ELEVATED — 11



Homocysteine to methionine ratio reflects methylation cycle efficiency and transsulfuration pathway flux for hepatic detoxification.

Glycine/Serine — ELEVATED — 0.71



Glycine to serine ratio indicates glycine availability for Phase II conjugation reactions and bile acid synthesis.

Taurine/Glycine — LOW — 2.3

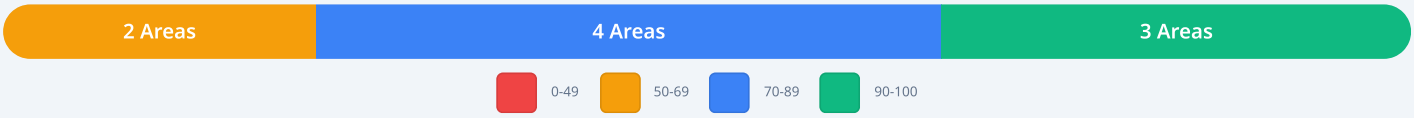


Taurine to glycine ratio reflects sulfur amino acid partitioning between bile conjugation and glutathione synthesis pathways.

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SAMPLE ID	REPORT DATE	OVERALL SCORE	BIOMARKERS ANALYZED	ZONE
AYX3D	Jun 30, 2026	82/100	296	Normative

Subdomain Zone Distribution



Stone Propensity & Crystallization Modulators	70	Assesses metabolic risk factors for kidney stone formation including oxalate, citrate, and mineral balance indicating crystallization risk and lithogenic burden. The score of 70 indicates elevated lithogenic risk suggesting benefit from citrate support and oxalate management.
Nephrotoxicant & Drug Clearance Load	76	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 76 reflects normal renal detoxification with adequate drug and toxin clearance.
Glomerular Filtration Reserve & Microvascular Tone	79	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 79 reflects normal glomerular filtration rate with adequate renal microvascular function.
Tubular Transport Capacity & Osmolyte Defense	82	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 82 shows normal tubular transport with adequate osmolyte reserves and reabsorption capacity.
Acid-Base Balance & Ammonia Excretion	91	Measures renal acid-base regulation and ammonia production for hydrogen ion buffering, with dysregulation indicating impaired renal acidification or alkalinization capacity. The score of 91 demonstrates optimal acid-base regulation and efficient renal pH buffering.
Nitrogenous Waste & Purine Burden	92	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 92 demonstrates optimal renal clearance of uric acid and purine metabolites.
Gut-Renal Uremic Toxin Load	93	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 93 demonstrates optimal detoxification of gut-renal axis metabolites.
Tubulointerstitial Injury & Fibrosis Activity	68	Measures markers of tubular damage and interstitial fibrosis progression reflecting chronic kidney disease activity and structural renal injury beyond glomerular changes. The score of 68 suggests early tubular injury markers warranting renal protective strategies to prevent fibrosis progression.
Renal Bioenergetic Reserve & Oxidative Stress	88	Tracks mitochondrial function and oxidative damage in kidney tissue through metabolic indicators of renal energetic capacity and antioxidant defense status. The score of 88 shows adequate renal energetics with normal oxidative stress management.

Central Metabolite Ratios & Markers

Creatinine/Creatine — LOW — 0.39



Reflects kidney filtration efficiency and muscle metabolism.

Cysteine/Cystine — LOW — 0.02



Indicates systemic redox status and oxidative stress burden on kidneys.

Urate/Xanthine — ELEVATED — 419



Urate to xanthine ratio reflects xanthine oxidoreductase activity and purine catabolism efficiency, indicating oxidative uric acid production and renal handling of nitrogen waste.

Citrate/Creatinine — ELEVATED — 9.2e-3

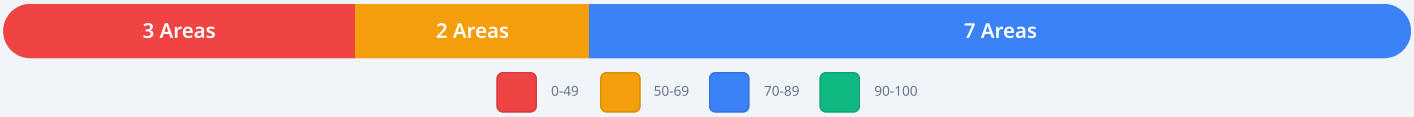


Measures stone protection capacity and urinary alkalization.

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SAMPLE ID	REPORT DATE	OVERALL SCORE	BIOMARKERS ANALYZED	ZONE
AYX3D	Jun 30, 2026	68/100	55	Early Disruption

Subdomain Zone Distribution



IDO & Kynurenine Immune Tolerance	83	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 83 reflects normal tryptophan-kynurenine balance with appropriate immune tolerance mechanisms.
Histamine Load & Mast Cell Tone	72	Assesses histamine production, degradation capacity, and mast cell activation status through histamine metabolites indicating allergic inflammation, MCAS, or histamine intolerance. The score of 72 shows normal histamine metabolism with adequate degradation capacity.
Arginine-NO Bioavailability	80	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 80 reflects normal arginine-citrulline-NO cycle with adequate nitric oxide bioavailability.
Nitrosative Stress Burden	81	Tracks peroxynitrite formation and protein nitration from excessive nitric oxide production, indicating oxidative-nitrosative damage in chronic inflammation and mitochondrial dysfunction. The score of 81 shows normal nitric oxide metabolism with minimal nitrosative damage.
Glutathione & Thiol Redox Reserve	59	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 59 suggests reduced thiol reserves warranting glutathione and cysteine support for immune resilience.
Polyamines & Immune Proliferation	74	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 74 shows normal polyamine levels supporting adequate immune proliferation and healing.
Inflammasome & Macrophage Activation	89	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 89 reflects normal innate immune activation with appropriate inflammasome function.
Purinergic Danger Signaling	62	Evaluates extracellular ATP, adenosine, and uric acid acting as damage-associated molecular patterns (DAMPs) triggering sterile inflammation and innate immune activation. The score of 62 suggests elevated extracellular ATP and uric acid warranting purinergic modulation support.
Microbiome AhR Ligand Pool	43	Assesses gut microbiome-derived aryl hydrocarbon receptor ligands including indoles and tryptophan metabolites modulating immune tolerance, barrier function, and inflammatory tone. The score of 43 reveals impaired aryl hydrocarbon receptor signaling with substantial loss of microbiome-derived immunomodulatory compounds.
Bacterial Cell Wall Burden	48	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 48 indicates impaired gut barrier with substantial bacterial translocation and endotoxin burden.
Neopterin Th1 Immune Activation	47	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 47 reveals impaired immune regulation with substantial Th1 skew and excessive IFN-gamma-driven activation.
Eicosanoid Bias PGE2 Axis	83	Tracks prostaglandin E2 pathway activity and cyclooxygenase-driven eicosanoid production reflecting inflammatory lipid mediator balance and resolution capacity. The score of 83 shows normal eicosanoid balance with adequate inflammatory resolution capacity.

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Central Metabolite Ratios & Markers

Kynurenine/Tryptophan — LOW — 2.1e-3



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

Citrulline/Arginine — LOW — 0.08



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

Glutathione/Cystine — LOW — 0.06



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

Putrescine/Spermidine — LOW-NORMATIVE — 2.4

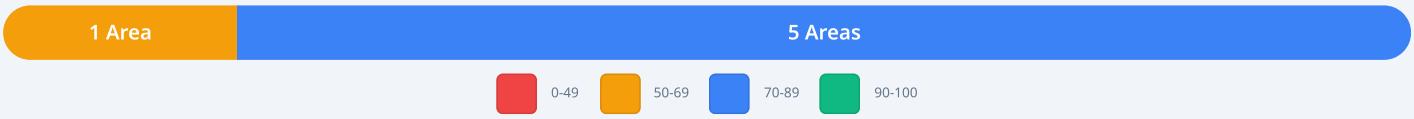


Reflects polyamine metabolism balance affecting immune cell proliferation, autophagy regulation, and inflammatory signaling.

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SAMPLE ID	REPORT DATE	OVERALL SCORE	BIOMARKERS ANALYZED	ZONE
AYX3D	Jun 30, 2026	78/100	39	Normative

Subdomain Zone Distribution



Fermentation Load & FODMAP Intolerance	88	Evaluates carbohydrate fermentation byproducts including short-chain fatty acids, lactate, and gas-producing metabolites indicating FODMAP sensitivity, SIBO, or carbohydrate malabsorption. The score of 88 reflects normal fermentation balance with appropriate short-chain fatty acid production.
Protein Putrefaction & Histamine/Biogenic Amines	86	Assesses bacterial protein fermentation producing putrescine, cadaverine, tyramine, and histamine reflecting colonic dysbiosis, proteolytic bacterial overgrowth, and histamine intolerance. The score of 86 shows normal protein metabolism with adequate bacterial balance and minimal histamine production.
Tryptophan-Indole-Serotonin Axis	76	Measures tryptophan metabolism into serotonin, indoles, and kynurenine by gut microbiota and enterochromaffin cells, affecting mood, GI motility, and immune signaling. The score of 76 reflects normal tryptophan metabolism with balanced serotonin and indole production.
Microbial Phenolics & Beta-Glucuronidase	73	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 73 shows normal microbial phenolic production with appropriate glucuronidase activity.
Yeast/Fungal Fermentation Signature	84	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 84 reflects normal fungal-bacterial balance with minimal yeast overgrowth.
Mucosal Barrier Integrity & Microbial Translocation	63	Assesses intestinal permeability and tight junction integrity through markers of bacterial endotoxin, lipopolysaccharide, and bacterial metabolite translocation into systemic circulation. The score of 63 indicates early barrier compromise with elevated LPS and bacterial metabolite leakage warranting barrier repair.

Central Metabolite Ratios & Markers

Lactate/Pyruvate — LOW — 433



Lactate to pyruvate ratio in the gut reflects microbial fermentation efficiency and bacterial NADH/NAD+ redox cycling, indicating anaerobic metabolism load and potential small intestinal bacterial overgrowth.

Indole-3-acetic acid/Tryptophan — ELEVATED — 0.04



Indole-3-acetic acid to tryptophan ratio reflects bacterial indole-pyruvate pathway activity converting tryptophan to indolic compounds, indicating gut microbial metabolic diversity and auxin-like signaling affecting intestinal motility.

Hippuric acid/Benzoic acid — ELEVATED — 0.45



Hippuric acid to benzoic acid ratio measures Phase II glycine conjugation capacity for microbially-derived benzoate, indicating liver conjugation efficiency and gut-liver axis function in aromatic compound clearance.

Putrescine/Histamine — LOW-NORMATIVE — 1.6

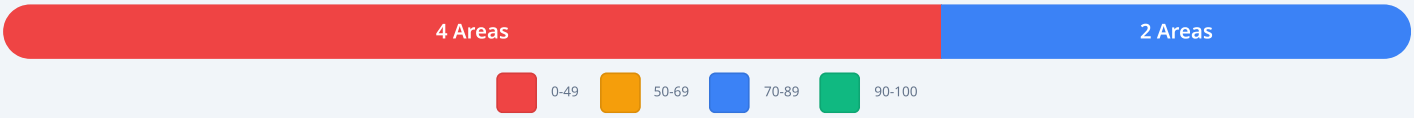


Putrescine to histamine ratio reflects the balance between bacterial polyamine production from protein fermentation versus histamine accumulation, indicating dysbiosis pattern and intestinal amine handling capacity.

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SAMPLE ID	REPORT DATE	OVERALL SCORE	BIOMARKERS ANALYZED	ZONE
AYX3D	Jun 30, 2026	49/100	55	Impaired

Subdomain Zone Distribution



Remethylation Reserve (Folate-B12 & BHMT)	18	Evaluates folate-dependent and betaine-dependent remethylation capacity for converting homocysteine to methionine, supporting SAMe regeneration and methylation reactions. The score of 18 indicates impaired remethylation capacity with substantial homocysteine elevation and SAMe depletion.
Transsulfuration-Glutathione Redox	49	Assesses homocysteine conversion to cysteine and glutathione through the transsulfuration pathway, providing antioxidant defense and sulfur amino acid sufficiency. The score of 49 reveals impaired transsulfuration with substantial glutathione depletion and compromised antioxidant defense.
Niacin-NAD Resilience	74	Measures NAD+ biosynthesis from niacin (vitamin B3) and tryptophan supporting cellular energy, DNA repair, and sirtuin-dependent longevity pathways. The score of 74 reflects normal NAD+ metabolism with adequate niacin pathway capacity.
Methylation Drain Load	46	Tracks excessive methylation demand from detoxification, neurotransmitter synthesis, and creatine production depleting SAMe pools and creating methyl donor insufficiency. The score of 46 reveals impaired methylation capacity with substantial SAMe depletion from excessive detoxification and neurotransmitter demands.
Choline-PEMT Axis & Trimethyl Pool	37	Evaluates choline availability and phosphatidylethanolamine N-methyltransferase activity for phospholipid synthesis, betaine production, and maintaining the trimethylglycine methylation reserve. The score of 37 indicates impaired choline metabolism with substantial limitations in phospholipid synthesis and betaine production.
Genomic One-Carbon Demand	73	Assesses one-carbon metabolism supporting DNA synthesis, purine and pyrimidine nucleotide production, and genomic methylation for epigenetic regulation and cell proliferation. The score of 73 shows normal one-carbon metabolism supporting adequate DNA synthesis and epigenetic regulation.

Central Metabolite Ratios & Markers

Methionine/Homocysteine — LOW — 0.09



Reflects remethylation pathway efficiency and methyl donor availability.

GSH/GSSG — ELEVATED — 162



Measures transsulfuration pathway output and cellular redox buffering capacity.

Homocysteine — ELEVATED — 4511



Indicates critical methylation cycle branch point reflecting B-vitamin status.

Betaine/Choline — LOW — 0.18

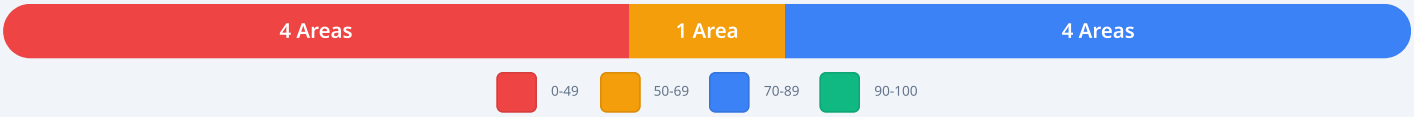


Indicates choline oxidation providing alternative methyl donors via BHMT pathway.

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SAMPLE ID	REPORT DATE	OVERALL SCORE	BIOMARKERS ANALYZED	ZONE
AYX3D	Jun 30, 2026	53/100	50	Early Disruption

Subdomain Zone Distribution



Adrenal Stress & Recovery Capacity	30	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 30 reveals impaired HPA axis function with substantial adrenal reserve depletion and cortisol dysregulation.
Catecholamine Metabolism (COMT/MAO Balance)	28	Assesses catechol-O-methyltransferase and monoamine oxidase activity for dopamine, epinephrine, and norepinephrine degradation, requiring SAMe and managing neurotransmitter-hormone clearance. The score of 28 reveals impaired catecholamine clearance with substantial COMT or MAO dysfunction affecting neurotransmitter balance.
Estrobolome & Estrogen Recirculation Pressure	73	Evaluates gut bacterial beta-glucuronidase activity and estrogen deconjugation driving enterohepatic recirculation and estrogen reabsorption, elevating systemic estrogen burden. The score of 73 reflects normal estrobolome function with appropriate estrogen deconjugation and clearance.
Histamine Clearance & Hormone Cross Talk	43	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 43 reveals impaired histamine clearance with substantial HNMT-DAO dysfunction affecting hormone-histamine cross talk.
Insulin Axis Mirror (Metabolic–Hormonal Coupling)	74	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 74 reflects normal insulin-endocrine crosstalk with adequate SHBG and hormone balance.
Sex Steroid Detox & Clearance Readiness	24	Tracks Phase I and Phase II conjugation capacity for estrogen, testosterone, and progesterone metabolite clearance preventing hormone accumulation and receptor overstimulation. The score of 24 reveals impaired sex steroid clearance with substantial hormone metabolite accumulation.
Steroidogenesis Cofactor Reserve	73	Measures cofactor availability for steroid hormone synthesis including cholesterol, vitamin C, B5 (pantothenic acid), and mitochondrial support for pregnenolone production. The score of 73 reflects normal steroidogenesis cofactor availability with adequate hormone precursor production.
Thyroid Activation & Conversion Support	57	Evaluates metabolic support for thyroid hormone synthesis, T4-to-T3 conversion, and deiodinase cofactor availability including selenium, zinc, and tyrosine sufficiency. The score of 57 suggests reduced deiodinase activity warranting selenium, zinc, and tyrosine support for thyroid hormone activation.
Tryptophan Pathways: Serotonin–Melatonin vs Kynurenine Tilt	78	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 78 reflects balanced tryptophan partitioning with adequate serotonin-melatonin and kynurenine metabolism.

Central Metabolite Ratios & Markers

Methionine/SAH — LOW — 0.27



Reflects COMT methylation capacity for hormone detoxification.

Kynurenine/Tryptophan — LOW — 2.1e-3



Indicates IDO activity and inflammation impact on HPA axis.

Methylhistamine/Histamine — ELEVATED — 3.7



Measures HNMT clearance activity in estrogen-histamine axis.

2-Hydroxybutyric acid — NORMATIVE — 1009

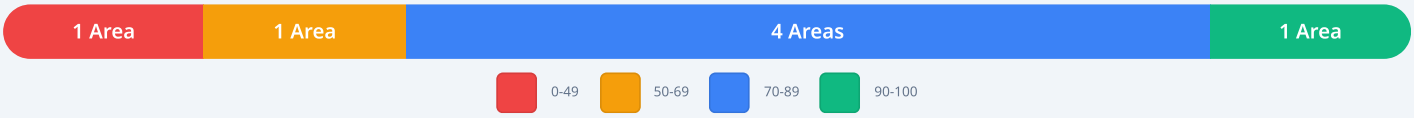


Indicates oxidative stress in steroidogenic tissues.

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SAMPLE ID	REPORT DATE	OVERALL SCORE	BIOMARKERS ANALYZED	ZONE
AYX3D	Jun 30, 2026	71/100	81	Normative

Subdomain Zone Distribution



Brain Bioenergetics & NAD+ Reserve	63	Evaluates neuronal energy metabolism, mitochondrial function, and NAD+ availability supporting synaptic activity, neurotransmitter synthesis, and cognitive processing demands. The score of 63 suggests reduced brain bioenergetic capacity warranting NAD+ precursor and mitochondrial support.
Glutamate-GABA Excitation-Inhibition Balance	88	Assesses excitatory glutamate and inhibitory GABA neurotransmitter balance critical for cognitive function, anxiety regulation, and preventing excitotoxicity or excessive neural inhibition. The score of 88 shows normal glutamate-GABA balance with adequate excitatory-inhibitory regulation.
Gut-Brain Neuroactives & Ammonia Handling	94	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 94 demonstrates optimal gut-brain axis with beneficial microbiome neuroactive production and efficient ammonia handling.
Membrane Integrity, Myelination & Choline Axis	20	Assesses phosphatidylcholine, phosphatidylserine, and omega-3 fatty acid availability for neuronal membrane fluidity, myelin maintenance, and acetylcholine neurotransmitter synthesis. The score of 20 reveals impaired neuronal membrane integrity with substantial phospholipid depletion affecting myelin and acetylcholine synthesis.
Monoamine Mood & Motivation Axis	78	Evaluates dopamine, serotonin, and norepinephrine synthesis and metabolism affecting mood regulation, motivation, reward processing, and emotional resilience through neurotransmitter precursor availability. The score of 78 reflects normal monoamine metabolism with adequate neurotransmitter synthesis for mood and motivation.
Neuroinflammation & Nitrosative Stress Signature	77	Tracks kynurenine pathway activation, quinolinic acid neurotoxicity, and nitric oxide-related neuroinflammation indicating microglial activation and blood-brain barrier disruption. The score of 77 shows normal neuroinflammatory balance with minimal kynurenine pathway excess.
Sleep-Arousal & Circadian Chemistry	74	Measures melatonin, adenosine, and circadian rhythm metabolites regulating sleep-wake cycles, sleep pressure accumulation, and restorative sleep quality. The score of 74 reflects normal circadian chemistry with adequate sleep pressure and melatonin production.

Central Metabolite Ratios & Markers

5-HIAA/Serotonin — LOW-NORMATIVE — 0.07



<0.06 | 0.06 | 0.23 | 0.82 | >0.82

Reflects serotonin turnover rate and monoamine oxidase activity.

Glycine/Glutamate — ELEVATED — 2.5



<0.09 | 0.09 | 0.13 | 0.38 | >0.38

Assesses inhibitory-excitatory neurotransmitter balance.

NADPH/NADP+ — LOW — 0.06



<3.5 | 3.5 | 11 | 31 | >31

Reflects neuronal antioxidant capacity and redox homeostasis.

HVA/Dopamine — ELEVATED — 4.6



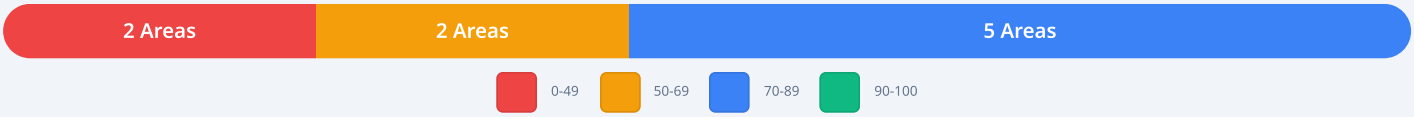
<0.10 | 0.10 | 0.35 | 1.1 | >1.1

Measures dopamine turnover via COMT and MAO pathways.

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SAMPLE ID	REPORT DATE	OVERALL SCORE	BIOMARKERS ANALYZED	ZONE
AYX3D	Jun 30, 2026	67/100	35	Early Disruption

Subdomain Zone Distribution



Cardiorenal Toxin Load & Acid–Base Impact	63	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 63 suggests elevated cardiorenal stress warranting renal support, uremic toxin clearance, and acid-base optimization.
Diet–Microbiome Atherothrombotic Signals	72	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 72 shows normal microbiome cardiovascular profile with adequate TMAO regulation and controlled atherothrombotic signals.
Endothelial NO & Vasomotor Health	59	Quantifies endothelial nitric oxide bioavailability and vasomotor signaling through arginine-ADMA balance, eNOS coupling, antioxidant cofactors, and cGMP-mediated vasodilation pathways. The score of 59 suggests reduced eNOS coupling and NO synthesis efficiency warranting arginine, antioxidant cofactor, and endothelial support.
Insulin Resistance Cardiometabolic Signature	73	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 73 reflects normal insulin sensitivity with adequate amino acid oxidation and glycolytic-oxidative balance.
Lipotoxicity & Fuel Oxidation / Ketone Flexibility	49	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 49 reveals impaired fatty acid metabolism with substantial lipotoxic burden, acylcarnitine overflow, and reduced ketogenic flexibility.
Methylation–Homocysteine/ADMA Endothelial Risk	45	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 45 indicates impaired methylation with substantial homocysteine and ADMA elevation increasing endothelial injury and nitric oxide inhibition.
Platelet Reactivity & Vasoactive Tone	87	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 87 shows normal platelet reactivity with adequate vasoactive balance and thrombotic protection.
Purine–Urate Oxidative Burden	73	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 73 reflects normal purine catabolism with adequate urate handling and controlled oxidative burden.
Vascular Glycation & Matrix Integrity	83	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 83 shows normal vascular glycation control with adequate matrix integrity and carbonyl detoxification.

Central Metabolite Ratios & Markers

Arginine/ADMA — LOW-NORMATIVE — 9.7



Reflects endothelial function and nitric oxide synthesis capacity through arginine availability.

Citrulline/Arginine — LOW — 0.08



Citrulline to arginine ratio measures nitric oxide synthase cycling efficiency and arginine recycling for vascular endothelial function.

Homocysteine/Methionine — ELEVATED — 11



Homocysteine to methionine ratio reflects methylation efficiency and homocysteine clearance affecting thrombotic risk and vascular injury.

Lactate/Pyruvate — LOW — 433

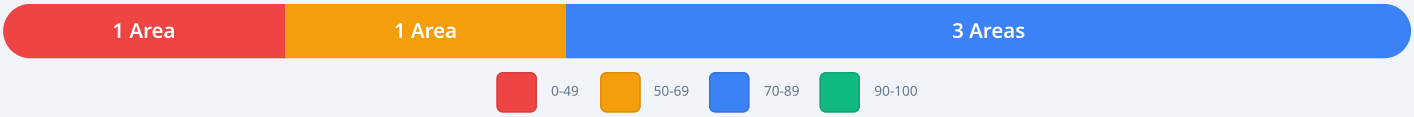


Reflects tissue perfusion and cellular oxygenation status.

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SAMPLE ID	REPORT DATE	OVERALL SCORE	BIOMARKERS ANALYZED	ZONE
AYX3D	Jun 30, 2026	66/100	55	Early Disruption

Subdomain Zone Distribution



Niacin-NAD Currency & Repair Reserve	71	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 71 reflects normal niacin-NAD metabolism with adequate energy production and genomic maintenance.
Pantothenate-CoA (Adrenal) Reserve	63	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 63 indicates reduced pantothenic acid availability suggesting benefit from B5 support for adrenal function.
Vitamin B12 Functional Sufficiency	49	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 49 indicates impaired B12 function with substantial methylmalonic acid elevation and homocysteine accumulation.
Vitamin B6 Functional Sufficiency	72	Assesses pyridoxal-5-phosphate functional status through kynurenine pathway metabolites, neurotransmitter synthesis markers, and amino acid metabolism reflecting B6 enzymatic activity. The score of 72 shows normal vitamin B6 status with adequate kynurenine pathway and neurotransmitter regulation.
Vitamin C-Collagen Repair Readiness	75	Assesses ascorbic acid functional status supporting collagen synthesis, antioxidant defense, carnitine production, and immune function through vitamin C-dependent enzymatic reactions. The score of 75 reflects normal vitamin C status with adequate collagen synthesis and antioxidant capacity.

Central Metabolite Ratios & Markers

MMA/Methionine — ELEVATED — 0.97



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

Xanthurenic/Kynurenine — ELEVATED — 0.93



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

4-Pyridoxic Acid/Pyridoxine — LOW — 6.1



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

Ascorbate — ELEVATED — 72

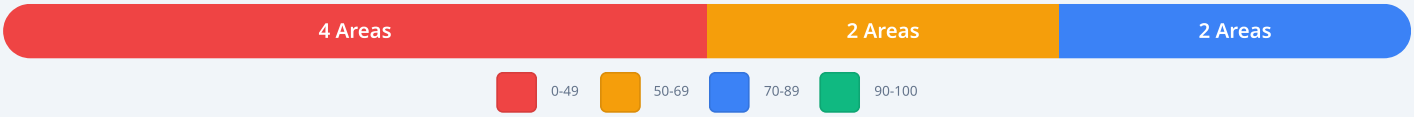


Ascorbate (vitamin C) levels reflect antioxidant reserves and cofactor availability for prolyl and lysyl hydroxylases.

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SAMPLE ID	REPORT DATE	OVERALL SCORE	BIOMARKERS ANALYZED	ZONE
AYX3D	Jun 30, 2026	55/100	62	Early Disruption

Subdomain Zone Distribution



AGE Burden & Dicarbonyl Pressure	74	Evaluates advanced glycation end-product formation and reactive dicarbonyl stress from glucose and fructose metabolism causing protein crosslinking and cellular dysfunction. The score of 74 reflects normal AGE defense with adequate protection from reactive dicarbonyl compounds.
Cartilage GAGs & Hyaluronic Acid Reserve	34	Assesses glycosaminoglycan and hyaluronic acid synthesis capacity for cartilage matrix integrity, joint lubrication, and tissue hydration supporting musculoskeletal resilience. The score of 34 reveals impaired glycosaminoglycan synthesis with substantial depletion affecting cartilage matrix and joint integrity.
Collagen & Elastin Matrix Integrity	49	Measures collagen and elastin precursor availability, crosslinking quality, and degradation markers affecting skin, vascular, and connective tissue structural integrity. The score of 49 indicates impaired collagen-elastin synthesis with substantial structural integrity compromise.
ECM Hydration & Glycocalyx Osmolyte Balance	65	Tracks osmolyte balance including taurine, betaine, and myo-inositol supporting extracellular matrix hydration, cell volume regulation, and glycocalyx structural integrity. The score of 65 indicates reduced taurine, betaine, and myo-inositol warranting osmolyte support for tissue hydration.
Glycan Maturation (Glycosylation, Sulfation & Sialylation)	34	Evaluates protein and lipid glycosylation pathways including N-glycan branching, sulfation, and sialylation affecting receptor function, cell signaling, and immune recognition. The score of 34 indicates impaired glycosylation with substantial limitations in N-glycan branching and sialylation capacity.
Glyoxalase–Carbonyl Detox Capacity	47	Assesses glyoxalase enzyme activity and glutathione availability for detoxifying methylglyoxal and other reactive carbonyls preventing AGE formation and dicarbonyl stress. The score of 47 reveals impaired glyoxalase function with substantial methylglyoxal accumulation and AGE formation.
Matrix Repair Energetics & Antioxidant Reserve	78	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 78 reflects normal extracellular matrix repair with adequate biosynthetic capacity.
Vascular Matrix Glycation & Stiffness Risk	60	Tracks vascular-specific glycation burden and elastin-collagen crosslinking affecting arterial stiffness, pulse wave velocity, and cardiovascular aging acceleration. The score of 60 indicates elevated vascular glycation suggesting benefit from arterial anti-aging and flexibility support.

Central Metabolite Ratios & Markers

Ascorbic Acid/Glucose — ELEVATED — 0.04



Ascorbic acid to glucose ratio reflects vitamin C antioxidant reserve relative to glycation pressure, supporting prolyl hydroxylase cofactor availability for collagen synthesis.

Carnosine/Glucose — ELEVATED — 0.30



Carnosine to glucose ratio measures histidine-dipeptide anti-glycation capacity, providing cellular defense against advanced glycation end product (AGE) formation.

Taurine/Glycine — LOW — 2.3



Taurine to glycine ratio indicates osmolyte balance for extracellular matrix hydration and glycocalyx maintenance, supporting structural protein stability.

Glucosamine/Glucose — ELEVATED — 6.8

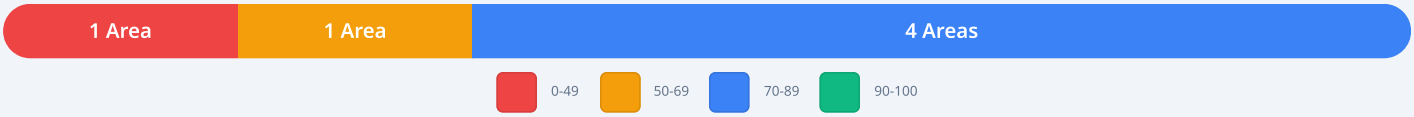


Glucosamine to glucose ratio reflects hexosamine pathway flux converting glucose to glycosaminoglycan (GAG) precursors essential for cartilage and proteoglycan biosynthesis.

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SAMPLE ID	REPORT DATE	OVERALL SCORE	BIOMARKERS ANALYZED	ZONE
AYX3D	Jun 30, 2026	68/100	58	Early Disruption

Subdomain Zone Distribution



Adenosine Sleep Pressure (Purine Turnover)	72	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 72 reflects normal homeostatic sleep pressure with adequate ATP conservation and restorative sleep.
Adrenal Stress Resilience & Thyroid Support	46	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 46 reveals impaired HPA-thyroid axis function with substantial adrenal exhaustion and metabolic-endocrine dysregulation.
Gut–Brain Sleep Disruptors & Stimulant Xenobiotic Load	83	Tracks caffeine metabolites, gut-derived stimulatory compounds, and xenobiotic burden disrupting sleep architecture, circadian rhythm, and parasympathetic nervous system recovery. The score of 83 reflects normal xenobiotic metabolism with minimal sleep-disrupting compound burden.
Mitochondrial Recovery & NAD⁺ Repletion	72	Measures mitochondrial repair capacity and NAD+ regeneration during rest supporting cellular energy restoration, autophagy activation, and metabolic recovery from daily stress. The score of 72 shows normal mitochondrial recovery with adequate NAD+ regeneration and autophagy activation during sleep.
Neuroinflammation & Endothelial NO Tone	55	Evaluates kynurenine pathway neuroinflammation and nitric oxide bioavailability affecting sleep quality, vascular relaxation, and restorative parasympathetic nervous system activity. The score of 55 suggests elevated neuroinflammation warranting NO support and microglial modulation for restorative sleep.
Sleep Neurotransmitters & Melatonin Axis	83	Assesses melatonin synthesis from serotonin, GABA production, and glycine availability supporting sleep initiation, sleep architecture, and circadian rhythm entrainment. The score of 83 shows normal sleep neurotransmitter production with adequate melatonin synthesis and circadian entrainment.

Central Metabolite Ratios & Markers

Glycine/Histamine — ELEVATED — 95



Glycine to histamine ratio reflects the balance between inhibitory neurotransmitter reserve and histaminergic arousal signaling, modulating sleep-wake transitions and stress reactivity.

Tryptophan/Kynurenine — ELEVATED — 470



Tryptophan to kynurenine ratio indicates substrate partitioning between serotonin-melatonin synthesis pathway and inflammatory kynurenine degradation route, affecting sleep quality and mood.

Lactate/Pyruvate — LOW — 433



Lactate to pyruvate ratio measures anaerobic glycolytic burden and cellular stress response, reflecting metabolic adaptation to physiological or psychological stressors.

3-Hydroxybutyric acid/Glucose — NORMATIVE — 0.61

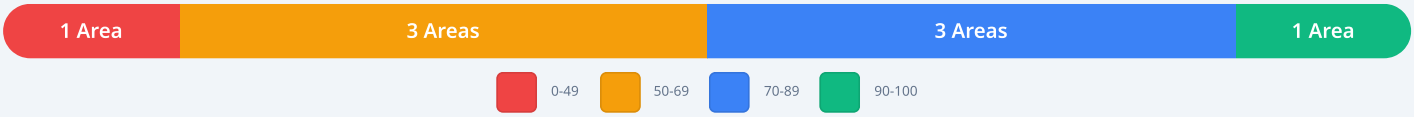


Beta-hydroxybutyrate to glucose ratio assesses metabolic flexibility and ketogenic capacity, supporting mitochondrial recovery and circadian metabolic adaptation during sleep-fast cycles.

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SAMPLE ID	REPORT DATE	OVERALL SCORE	BIOMARKERS ANALYZED	ZONE
AYX3D	Jun 30, 2026	69/100	68	Early Disruption

Subdomain Zone Distribution



Autophagy–Mitophagy & Cellular Cleanup	65	Evaluates cellular self-digestion and damaged organelle clearance through spermidine, leucine signaling, and mitochondrial quality control supporting cellular rejuvenation and longevity. The score of 65 suggests reduced mitophagy efficiency warranting spermidine, leucine, and mitochondrial quality control support.
Collagen/ECM Renewal & Anti-Glycation	41	Assesses extracellular matrix turnover, collagen synthesis, and glycation resistance through hydroxyproline, glycine, and anti-glycation defenses maintaining tissue youthfulness. The score of 41 reveals impaired extracellular matrix turnover with substantial glycation burden affecting tissue youthfulness.
DNA Repair, Methylation & Epigenetic Balance	78	Measures DNA repair capacity, genomic methylation maintenance, and epigenetic stability through one-carbon metabolism, PARP activity, and base excision repair support. The score of 78 reflects normal DNA repair capacity with adequate genomic methylation maintenance.
Glutathione & Redox Defense	58	Tracks glutathione biosynthesis and redox buffering capacity protecting against oxidative damage, supporting detoxification, and maintaining cellular reducing environment for longevity. The score of 58 indicates reduced GSH biosynthesis suggesting benefit from cysteine, glycine, and glutamate precursor support.
Gut–Longevity Crosstalk	76	Evaluates microbiome-derived longevity metabolites including butyrate, urolithins, and postbiotics supporting gut barrier integrity, immune tolerance, and healthy aging. The score of 76 reflects normal microbiome-derived longevity metabolites with adequate gut barrier and immune tolerance.
Inflammaging & Immunometabolic Load	83	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 83 shows normal age-related inflammatory balance with minimal immunometabolic dysfunction.
Mitochondrial Repair & Bioenergetics	64	Measures mitochondrial biogenesis, respiratory chain efficiency, and energetic capacity supporting cellular vitality, stress resistance, and metabolic health span extension. The score of 64 suggests reduced energetic capacity warranting mitochondrial biogenesis support and stress resistance optimization.
NAD⁺ & Sirtuin Repair Axis	91	Evaluates NAD+ biosynthesis and sirtuin activation supporting DNA repair, mitochondrial function, circadian rhythm, and metabolic resilience as central longevity regulators. The score of 91 demonstrates optimal NAD+ reserves with robust sirtuin activation supporting central longevity regulation.

Central Metabolite Ratios & Markers

Carnitine/Acylcarnitines — LOW — 1.1



Free carnitine to acylcarnitine ratio reflects mitochondrial fatty acid oxidation flux and efficiency of beta-oxidation for cellular energy production.

Ornithine/Arginine — NORMATIVE — 2.0



Ornithine to arginine ratio measures polyamine biosynthetic capacity via arginase activity, supporting autophagy and cellular proliferation pathways.

Cysteine/Homocysteine — LOW — 0.12



Cysteine to homocysteine ratio indicates transsulfuration pathway efficiency for glutathione synthesis and sulfur-based redox defense systems.

Nicotinamide/Tryptophan — LOW-NORMATIVE — 1.7

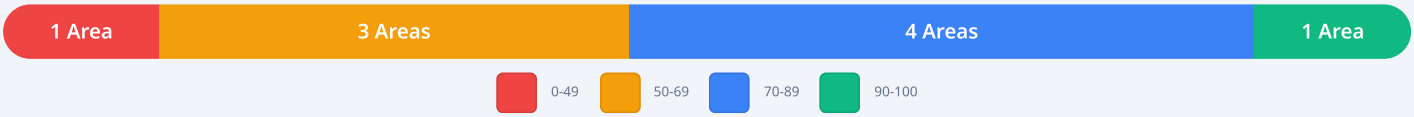


Nicotinamide to tryptophan ratio reflects NAD+ salvage pathway activity versus de novo synthesis through the kynurenine pathway.

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SAMPLE ID	REPORT DATE	OVERALL SCORE	BIOMARKERS ANALYZED	ZONE
AYX3D	Jun 30, 2026	73/100	296	Normative

Subdomain Zone Distribution



Plastics, Parabens & Phthalates	82	Assesses endocrine disruptor burden from plasticizers, parabens, and phthalates found in personal care products and food packaging.	The score of 82 reflects normal plasticizer clearance with minimal endocrine-disrupting compound burden.
VOC & Solvent Burden (BTEX–Styrene)	69	Tracks volatile organic compound (VOC) exposure from solvents, styrene, and petrochemical sources including paints, adhesives, and industrial emissions.	The score of 69 suggests elevated VOC metabolites warranting Phase II detoxification support and exposure source reduction.
Reactive Carbonyls & Aldehydes	65	Tracks aldehyde and dicarbonyl electrophiles from oxidative stress and dietary advanced glycation end products (AGEs).	The score of 65 indicates elevated aldehyde metabolites suggesting benefit from glutathione and aldehyde dehydrogenase support.
Aryl Phenols & Benzenoid Load	69	Measures aromatic xenobiotic load from environmental phenols requiring Phase II conjugation for clearance.	The score of 69 indicates elevated benzenoid metabolites suggesting benefit from glucuronidation and sulfation pathway support.
Air Pollution & Oxidant Gas	83	Measures oxidative stress from nitrogen oxides (NOx) and ozone (O_3) exposure typical of air pollution.	The score of 83 reflects normal oxidative stress management with adequate protection from environmental air pollutants.
Metals & Metalloid Stress	34	Assesses heavy metal burden (mercury, lead, cadmium, arsenic) affecting porphyrin synthesis and thiol antioxidant systems.	The score of 34 indicates impaired heavy metal clearance with substantial mercury, lead, cadmium, or arsenic burden.
Mold & Mycotoxin Exposure	87	Evaluates mycotoxin and fungal VOC exposure from water-damaged buildings and contaminated foods.	The score of 87 shows normal mycotoxin metabolism with minimal mold or water damage exposure.
Pesticide & Herbicide Exposure	92	Measures glyphosate and organophosphate pesticide exposure disrupting the shikimate pathway and cholinergic function.	The score of 92 demonstrates optimal pesticide detoxification with negligible herbicide or insecticide burden.
Combustion & Tobacco Smoke (PAH)	77	Evaluates polycyclic aromatic hydrocarbon (PAH) exposure from combustion sources including tobacco smoke, grilled foods, and vehicle exhaust.	The score of 77 shows normal PAH clearance with minimal combustion source exposure.

Central Metabolite Ratios & Markers

Mandelic acid — LOW-NORMATIVE — 311



Mandelic acid is the primary urinary metabolite of styrene and ethylbenzene, indicating recent exposure to volatile organic compounds (VOCs) from plastics, paints, adhesives, and industrial solvents.

Phthalic acid — NORMATIVE — 6574



Phthalic acid reflects exposure to phthalate plasticizers from food packaging, personal care products, and PVC materials, indicating body burden of endocrine-disrupting xenobiotics.

Hippuric acid/Benzoic acid — ELEVATED — 0.45



Hippuric acid to benzoic acid ratio measures Phase II glycine conjugation efficiency for xenobiotic detoxification, reflecting hepatic conjugation capacity and glycine reserve for aromatic compound clearance.

GSH/GSSG — ELEVATED — 162



Reduced to oxidized glutathione ratio indicates cellular antioxidant reserve under toxicant stress, reflecting Phase II conjugation capacity and redox buffering against environmental oxidative insults.

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Metabolite Atlas

Complete metabolomic profile showing all 296 measured metabolites grouped by chemical class. Each card displays the patient value against the reference population distribution (n=513 healthy adults).

How to Read Each Card

Left border color indicates how far the patient deviates from the reference population:

Normal	Deviation	Extreme
Within 1 SD	1–2 SD	Beyond 2 SD

Bell curve: Reference population distribution with colored zone bands. The **purple marker** shows the patient's value.

Arrows: ↑ higher is better | ↓ lower is better | ↔ neutral • **Mean:** population average • **IQR:** 25th–75th percentile range

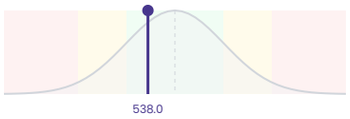
Chemical Classes (296 metabolites across 15 classes)

Amine	12 metabolites
Amino Acid	42 metabolites
Carbohydrate	36 metabolites
Fatty Acid	13 metabolites
Indole	17 metabolites
Lipid	9 metabolites
Nucleotide	39 metabolites
Organic Acid	64 metabolites
Other	4 metabolites
Peptide	7 metabolites
Pharmaceutical	8 metabolites
Phenolic	28 metabolites
Polyamine	4 metabolites
Steroid	1 metabolites
Vitamin	12 metabolites

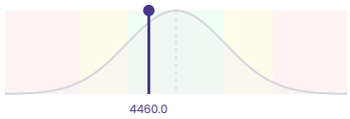
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Amine

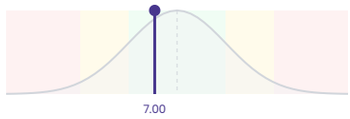
12 metabolites

4-Imidazoleacetic acid
538.0
HMDB0002024
Amine


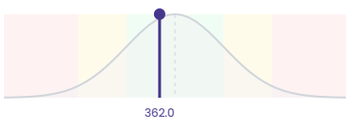
z=-0.55 ↔ 29th percentile
Mean: 11697.6 Range: 0-72323.5

Acetylcholine
4460.0
HMDB0000895
Amine


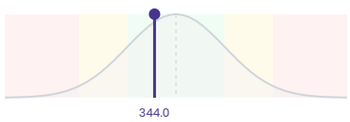
z=-0.56 ↔ 29th percentile
Mean: 19677.3 Range: 0-101770.2

Cystamine
7.00
HMDB0250701
Amine


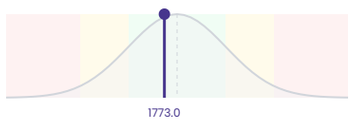
z=-0.46 ↔ 32th percentile
Mean: 158.7 Range: 0-1152.5

Dopamine
362.0
HMDB0000073
Amine


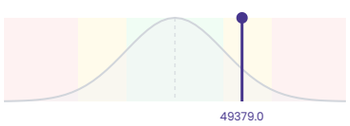
z=-0.31 ↔ 38th percentile
Mean: 1955.6 Range: 0-17216.2

Epinephrine
344.0
HMDB0000068
Amine


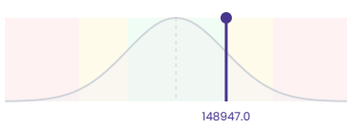
z=-0.44 ↔ 33th percentile
Mean: 1343.7 Range: 0-8173.2

Histamine
1773.0
HMDB0000870
Amine


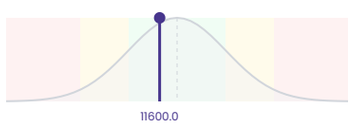
z=-0.26 ↔ 40th percentile
Mean: 13777.4 Range: 0-152590.3

Imidazole
49379.0
HMDB0001525
Amine


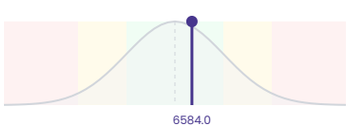
z=+1.37 ↔ 92th percentile
Mean: 19428.2 Range: 0-84821.4

Metanephrine
148947.0
HMDB0004063
Amine


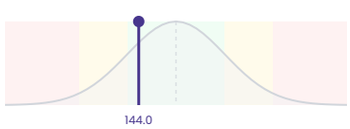
z=+1.03 ↔ 85th percentile
Mean: 42223.2 Range: 0-353585.4

Methylguanidine
11600.0
HMDB0001522
Amine


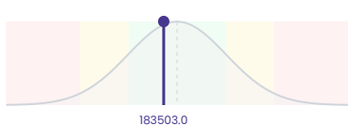
z=-0.36 ↔ 36th percentile
Mean: 18018.1 Range: 0-71973.5

Methylhistamine
6584.0
HMDB0000898
Amine


z=+0.35 ↔ 64th percentile
Mean: 5230.6 Range: 0-16891.0

Normetanephrine
144.0
HMDB0000819
Amine


z=-0.76 ↔ 22th percentile
Mean: 1200.4 Range: 0-5354.9

TMAO
183503.0
HMDB0000925
Amine


z=-0.27 ↔ 39th percentile
Mean: 674599.9 Range: 0-6055805.9

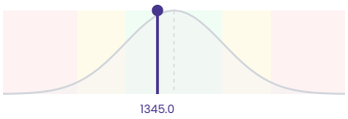
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Amino Acid

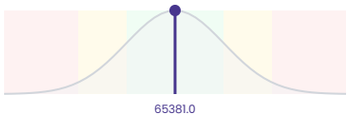
42 metabolites

1-Methylhistidine
1181998.0
HMDB0000001
Amino Acid

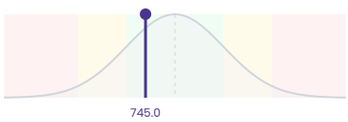

z=+0.95 ↔ 83th percentile
Mean: 502819.4 Range: 0–2649181.3

2-Aminoadipic acid
1345.0
HMDB0302754
Amino Acid


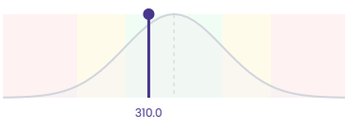
z=-0.34 ↔ 37th percentile
Mean: 17024.6 Range: 0–156371.4

2-Aminobutyric acid
65381.0
HMDB0000452
Amino Acid


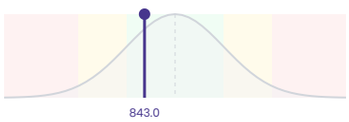
z=-0.00 ↔ 50th percentile
Mean: 65421.2 Range: 0–356212.6

3-Aminobutyric acid
745.0
HMDB0031654
Amino Acid


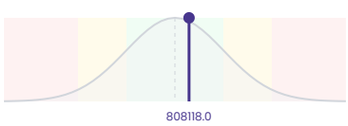
z=-0.60 ↔ 27th percentile
Mean: 5447.1 Range: 0–28895.5

3-Nitrotyrosine
310.0
HMDB0001904
Amino Acid


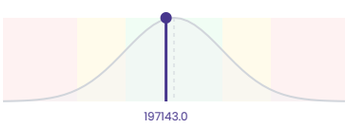
z=-0.52 ↔ 30th percentile
Mean: 786.2 Range: 0–3549.5

4-Aminobutyric acid
843.0
HMDB0000112
Amino Acid


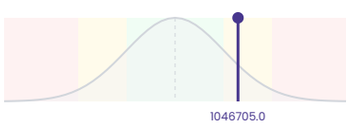
z=-0.63 ↔ 27th percentile
Mean: 8141.9 Range: 0–43171.3

5-Aminolevulinic acid
808118.0
HMDB0001149
Amino Acid


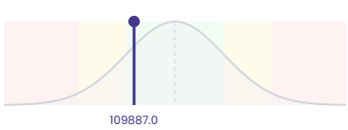
z=+0.29 ↔ 61th percentile
Mean: 659090.1 Range: 0–2203624.0

Alanine
197143.0
HMDB0000161
Amino Acid


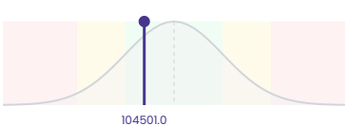
z=-0.16 ↔ 44th percentile
Mean: 290234.4 Range: 0–2005204.5

Arginine
1046705.0
HMDB0000517
Amino Acid


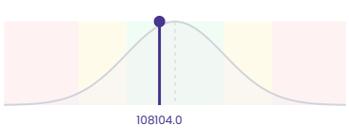
z=+1.29 ↔ 90th percentile
Mean: 399536.8 Range: 0–1906403.0

Asparagine
109887.0
HMDB0000168
Amino Acid


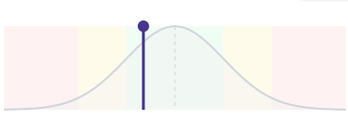
z=-0.84 ↔ 20th percentile
Mean: 352168.1 Range: 0–1221581.4

Aspartate
104501.0
HMDB0000191
Amino Acid


z=-0.61 ↔ 27th percentile
Mean: 374901.3 Range: 0–1707918.6

Asymmetric dimethylarginine
108104.0
HMDB0001539
Amino Acid


z=-0.32 ↔ 38th percentile
Mean: 187751.0 Range: 0–937001.5

Betaine
45528.0
HMDB0000043
Amino Acid


z=-0.64 ↔ 26th percentile
Mean: 11905466.8 Range: 0–67077608.2

Citrulline
81827.0
HMDB0000904
Amino Acid


z=-1.07 ↔ 14th percentile
Mean: 751919.6 Range: 0–2627237.9

Cysteine
531.0
HMDB0000574
Amino Acid


z=-0.23 ↔ 41th percentile
Mean: 3131.4 Range: 0–37028.1

Cystine
30364.0
HMDB0250712
Amino Acid


z=+3.11 ↔ 100th percentile
Mean: 6235.5 Range: 0–29543.2

Dimethylglycine
65970.0
HMDB0000092
Amino Acid

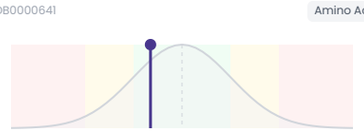

z=-0.24 ↔ 40th percentile
Mean: 98339.2 Range: 0–498917.7

DOPA
1117.0
HMDB0000181
Amino Acid

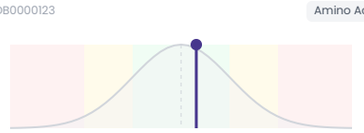

z=+0.81 ↔ 79th percentile
Mean: 609.3 Range: 0–2488.1

Glutamic acid
68292.0
HMDB0000148
Amino Acid

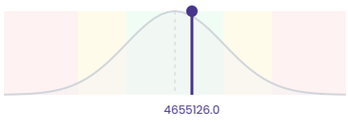

z=-0.84 ↔ 20th percentile
Mean: 782809.8 Range: 0–3336997.6

Glutamine
3934547.0
HMDB0000641
Amino Acid


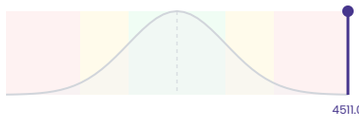
z=-0.64 ↔ 26th percentile
Mean: 7756222.5 Range: 0–25544811.4

Glycine
168197.0
HMDB0000123
Amino Acid


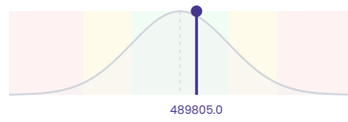
z=+0.31 ↑ 62th percentile
Mean: 104463.8 Range: 0–718388.7

Histidine
4655126.0
HMDB0000177
Amino Acid


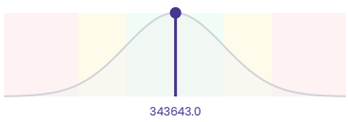
z=+0.35 ↔ 64th percentile
Mean: 3468981.3 Range: 0–13678063.7

Homocysteine
4511.0
HMDB0000742
Amino Acid


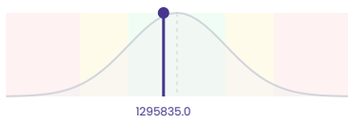
z=+4.00 ↓ 100th percentile
Mean: 495.9 Range: 0–3285.4

Homoserine
489805.0
HMDB0000719
Amino Acid


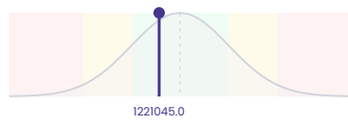
z=+0.34 ↔ 63th percentile
Mean: 327744.8 Range: 0–1771742.2

Hydroxyproline
343643.0
HMDB0000725
Amino Acid


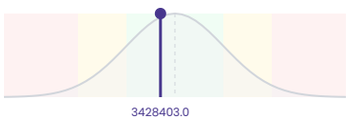
z=+0.01 ↔ 51th percentile
Mean: 336803.0 Range: 0–1890781.2

Isoleucine
1295835.0
HMDB0000172
Amino Acid


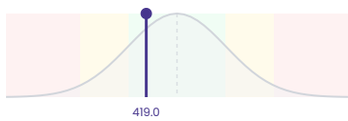
z=-0.28 ↔ 39th percentile
Mean: 1541381.7 Range: 0–4213329.8

Leucine
1221045.0
HMDB0000687
Amino Acid


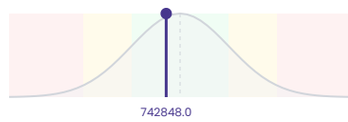
z=-0.43 ↔ 33th percentile
Mean: 1621927.5 Range: 0–4429659.6

Lysine
3428403.0
HMDB0000182
Amino Acid


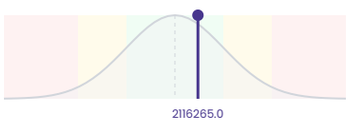
z=-0.30 ↔ 38th percentile
Mean: 5202367.5 Range: 0–23226088.3

Methionine
419.0
HMDB0000696
Amino Acid


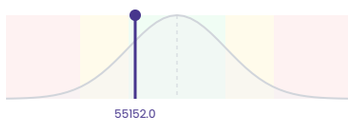
z=-0.63 ↔ 27th percentile
Mean: 38077.4 Range: 0–217648.3

Norvaline
742848.0
HMDB0013716
Amino Acid


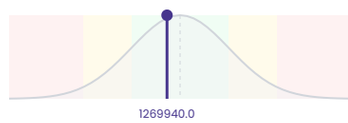
z=-0.28 ↔ 39th percentile
Mean: 1034692.4 Range: 0–4113847.5

Ornithine
2116265.0
HMDB0000214
Amino Acid


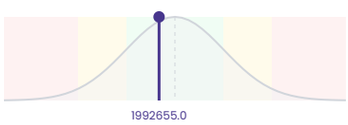
z=+0.47 ↔ 68th percentile
Mean: 1419139.8 Range: 0–5855317.9

Phenylalanine
55152.0
HMDB0000159
Amino Acid


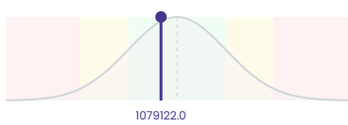
z=-0.86 ↔ 20th percentile
Mean: 456535.0 Range: 0–1863848.9

Pipecolinic acid
1269940.0
HMDB0000070
Amino Acid


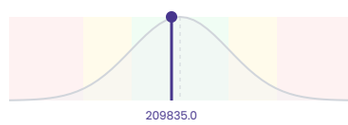
z=-0.27 ↔ 40th percentile
Mean: 1828968.9 Range: 0–8101792.6

Proline
1992655.0
HMDB0000162
Amino Acid


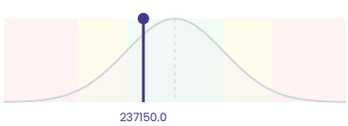
z=-0.32 ↔ 37th percentile
Mean: 3481417.7 Range: 0–17253315.3

Pyroglutamic acid
1079122.0
HMDB0000267
Amino Acid


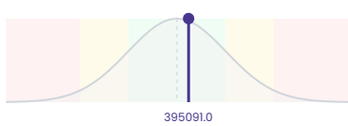
z=-0.33 ↔ 37th percentile
Mean: 1660705.7 Range: 0–6994985.7

Sarcosine
209835.0
HMDB0000271
Amino Acid


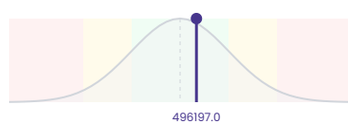
z=-0.17 ↔ 43th percentile
Mean: 314881.9 Range: 0–2119015.8

Serine
237150.0
HMDB0000187
Amino Acid


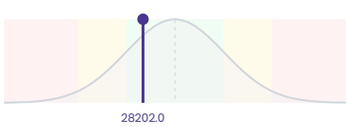
z=-0.64 ↔ 26th percentile
Mean: 996762.6 Range: 0–4531391.1

Taurine
395091.0
HMDB0000251
Amino Acid


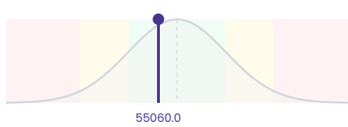
z=+0.24 ↑ 59th percentile
Mean: 351631.7 Range: 0–900517.5

Threonine
496197.0
HMDB0000167
Amino Acid


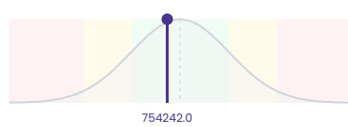
z=+0.33 ↔ 63th percentile
Mean: 333362.0 Range: 0–1792373.2

Tryptophan
28202.0
HMDB0000929
Amino Acid


z=-0.65 ↔ 26th percentile
Mean: 88196.2 Range: 0–363773.8

Tyrosine
55060.0
HMDB0000158
Amino Acid


z=-0.38 ↔ 35th percentile
Mean: 126571.0 Range: 0–690744.0

Valine
754242.0
HMDB0000883
Amino Acid


z=-0.26 ↔ 40th percentile
Mean: 1022224.9 Range: 0–4078455.5

Carbohydrate

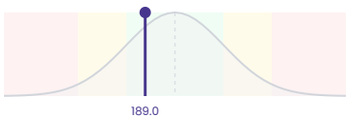
36 metabolites

Adonitol

189.0

HMDB0000508

Carbohydrate



z=-0.61 ↔ 27th percentile

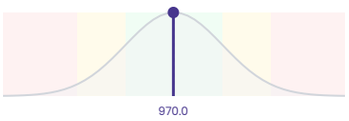
Mean: 1041.8 Range: 0-5246.2

Cellobiose

970.0

HMDB0000055

Carbohydrate



z=-0.01 ↔ 50th percentile

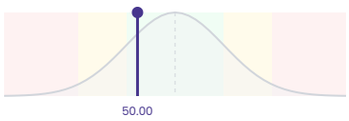
Mean: 1004.3 Range: 0-9254.6

D-Mannitol

50.00

HMDB0000765

Carbohydrate



z=-0.77 ↔ 22th percentile

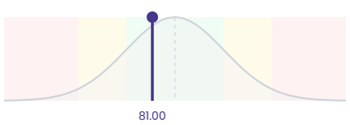
Mean: 551.0 Range: 0-2505.3

D-Ribose 5-phosphate

81.00

HMDB0001548

Carbohydrate



z=-0.46 ↔ 32th percentile

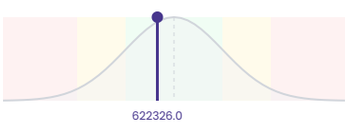
Mean: 259.5 Range: 0-1418.9

Dihydroxyacetone

622326.0

HMDB0001882

Carbohydrate



z=-0.34 ↔ 37th percentile

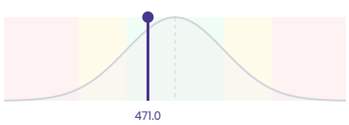
Mean: 1368973.4 Range: 0-7951155.7

Dulcitol

471.0

HMDB0000107

Carbohydrate



z=-0.56 ↔ 29th percentile

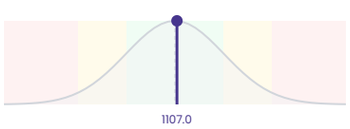
Mean: 1234.4 Range: 0-5357.4

Erythrose

1107.0

HMDB0002649

Carbohydrate



z=+0.04 ↔ 52th percentile

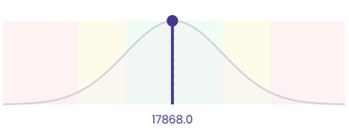
Mean: 1058.4 Range: 0-4554.1

Fructose

17868.0

HMDB0000660

Carbohydrate



z=-0.03 ↔ 49th percentile

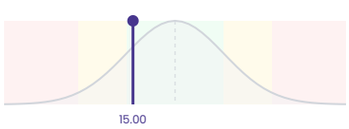
Mean: 18291.2 Range: 0-57046.1

Fructose 1,6-bisphosphate

15.00

HMDB0001058

Carbohydrate



z=-0.86 ↔ 19th percentile

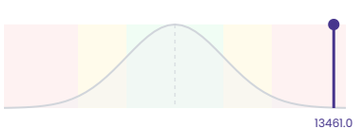
Mean: 784.9 Range: 0-3464.6

Glucosamine

13461.0

HMDB0001514

Carbohydrate



z=+3.25 ↔ 100th percentile

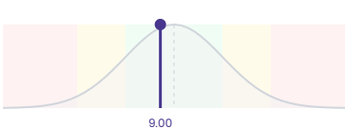
Mean: 2560.7 Range: 0-12616.0

Glucosamine 6-phosphate

9.00

HMDB0001254

Carbohydrate



z=-0.28 ↔ 39th percentile

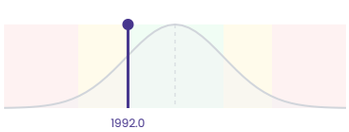
Mean: 46.80 Range: 0-453.5

Glucose

1992.0

HMDB0000122

Carbohydrate



z=-0.96 ↓ 17th percentile

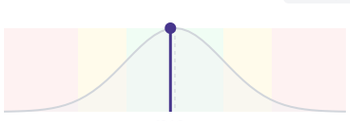
Mean: 13103.5 Range: 0-47709.3

Glucose 1-phosphate

104.0

HMDB0001586

Carbohydrate



z=-0.09 ↔ 46th percentile

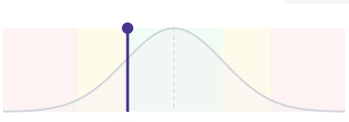
Mean: 114.4 Range: 0-456.2

Glucose 1,6-bisphosphate

31.00

HMDB0003514

Carbohydrate



z=-0.95 ↔ 17th percentile

Mean: 375.2 Range: 0-1462.4

Glucose 6-phosphate

368.0

HMDB0001401

Carbohydrate



z=+0.23 ↔ 59th percentile

Mean: 283.9 Range: 0-1377.1

Glyceraldehyde 3-phosphate

224.0

HMDB0001112

Carbohydrate



z=-0.45 ↔ 33th percentile

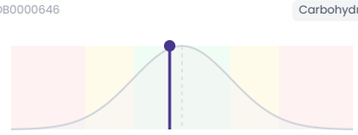
Mean: 2027.8 Range: 0-13929.5

L-(+)-Arabinose

867.0

HMDB0000646

Carbohydrate



z=-0.25 ↔ 40th percentile

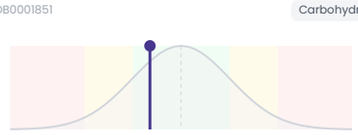
Mean: 1195.3 Range: 0-5097.0

L-Arabitol

94.00

HMDB0001851

Carbohydrate



z=-0.64 ↔ 26th percentile

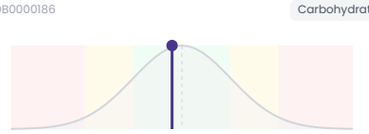
Mean: 1665.2 Range: 0-9061.7

Lactose

760.0

HMDB0000186

Carbohydrate



z=-0.20 ↔ 42th percentile

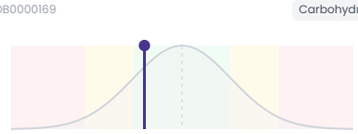
Mean: 1365.7 Range: 0-10368.5

Mannose

2741.0

HMDB0000169

Carbohydrate



z=-0.77 ↔ 22th percentile

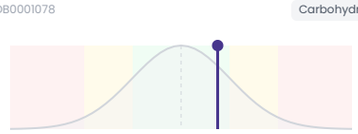
Mean: 9008.0 Range: 0-33453.6

Mannose 6-phosphate

3668.0

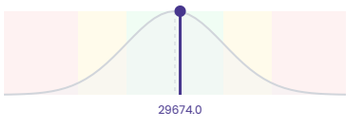
HMDB0001078

Carbohydrate

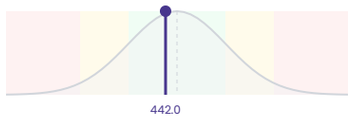


z=+0.75 ↔ 77th percentile

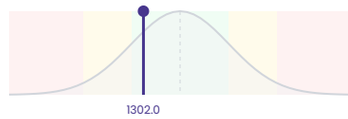
Mean: 1723.4 Range: 0-9511.0

Methyl alpha-D-galactopyranoside
29674.0
HMDB0246173
Carbohydrate


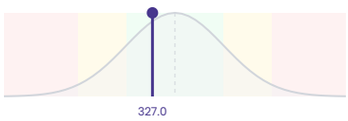
z=+0.11 ↔ 54th percentile
Mean: 26437.4 Range: 0–116312.4

Myoinositol
442.0
HMDB0000211
Carbohydrate


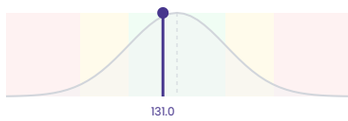
z=-0.23 ↔ 41th percentile
Mean: 1736.3 Range: 0–18335.0

N-Acetyl-D-galactosamine
1302.0
HMDB0000212
Carbohydrate


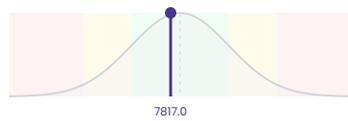
z=-0.75 ↔ 23th percentile
Mean: 5619.5 Range: 0–22890.1

N-Acetyl-D-Glucosamine
327.0
HMDB0000215
Carbohydrate


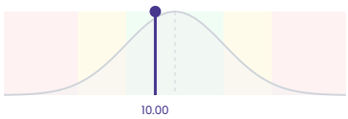
z=-0.46 ↔ 32th percentile
Mean: 8745.6 Range: 0–63674.4

N-Acetylmuramic Acid
131.0
HMDB0060493
Carbohydrate


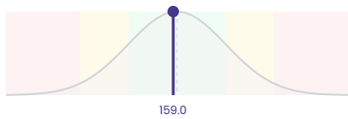
z=-0.29 ↔ 39th percentile
Mean: 663.4 Range: 0–6214.1

N-Acetylneuraminic acid
7817.0
HMDB0000230
Carbohydrate


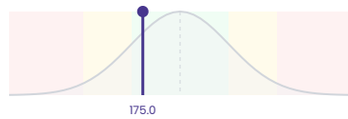
z=-0.19 ↔ 42th percentile
Mean: 9933.4 Range: 0–42794.0

Raffinose
10.00
HMDB0003213
Carbohydrate


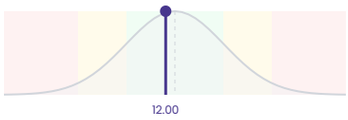
z=-0.40 ↔ 34th percentile
Mean: 62.03 Range: 0–451.1

Ribose
159.0
HMDB0000283
Carbohydrate


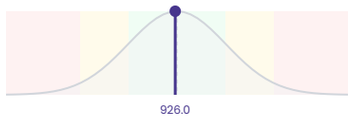
z=-0.08 ↔ 47th percentile
Mean: 221.8 Range: 0–2661.1

Sorbitol
175.0
HMDB0000247
Carbohydrate


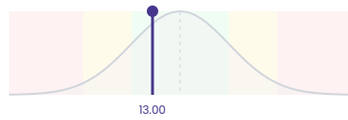
z=-0.76 ↔ 22th percentile
Mean: 827.3 Range: 0–3392.2

Sucrose
12.00
HMDB0000258
Carbohydrate


z=-0.19 ↔ 43th percentile
Mean: 853.6 Range: 0–14214.2

Trehalose
926.0
HMDB0000975
Carbohydrate


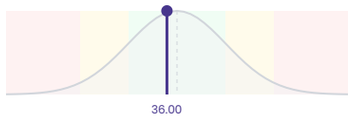
z=-0.04 ↔ 49th percentile
Mean: 1095.2 Range: 0–15136.2

UDP-GlcNAc
13.00
HMDB0000290
Carbohydrate


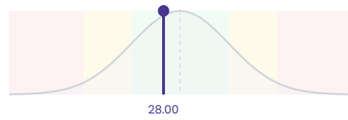
z=-0.56 ↔ 29th percentile
Mean: 526.1 Range: 0–3253.5

Xylitol
14.00
HMDB0242149
Carbohydrate


z=-0.71 ↔ 24th percentile
Mean: 1291.8 Range: 0–6653.5

Xylose
36.00
HMDB0000098
Carbohydrate


z=-0.21 ↔ 42th percentile
Mean: 205.1 Range: 0–2668.8

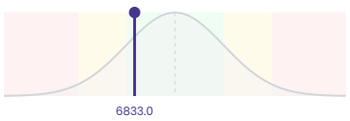
Xylulose-5-phosphate
28.00
HMDB0000868
Carbohydrate


z=-0.34 ↔ 37th percentile
Mean: 15803.6 Range: 0–155656.4

Fatty Acid

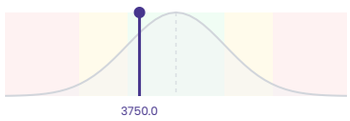
13 metabolites

Capric acid
HMDB0000511 — Fatty Acid — **6833.0**



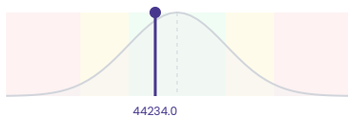
z=-0.83 ↔ 21th percentile
Mean: 88920.5 Range: 0-387338.9

Caprylic acid
HMDB0000482 — Fatty Acid — **3750.0**



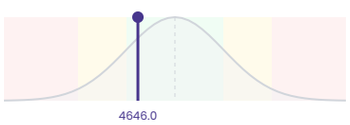
z=-0.75 ↔ 23th percentile
Mean: 108388.8 Range: 0-528637.3

Heptadecanoic acid
HMDB0002259 — Fatty Acid — **44234.0**



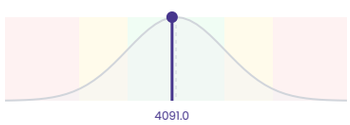
z=-0.45 ↔ 33th percentile
Mean: 79094.9 Range: 0-313027.1

Hexanoic acid
HMDB0000535 — Fatty Acid — **4646.0**



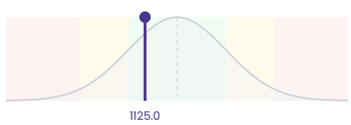
z=-0.76 ↔ 22th percentile
Mean: 51345.3 Range: 0-236264.5

Isobutyric acid
HMDB0001873 — Fatty Acid — **4091.0**



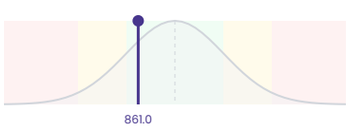
z=-0.08 ↔ 47th percentile
Mean: 4449.6 Range: 0-17820.5

Isovaleric acid
HMDB0000718 — Fatty Acid — **1125.0**



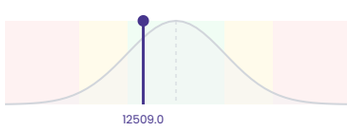
z=-0.66 ↔ 26th percentile
Mean: 2606.0 Range: 0-9374.7

Lauric acid
HMDB0000638 — Fatty Acid — **861.0**



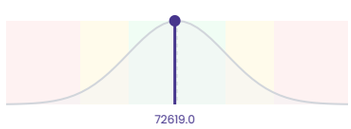
z=-0.75 ↔ 23th percentile
Mean: 325354.4 Range: 0-1621069.7

Myristic acid
HMDB0000806 — Fatty Acid — **12509.0**



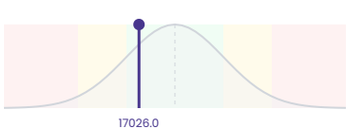
z=-0.67 ↔ 25th percentile
Mean: 166716.2 Range: 0-857434.0

Nonadecanoic acid
HMDB0000772 — Fatty Acid — **72619.0**



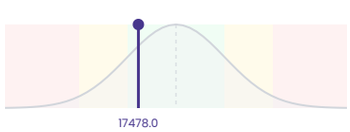
z=-0.05 ↔ 48th percentile
Mean: 75186.3 Range: 0-243192.6

Palmitic acid
HMDB0000220 — Fatty Acid — **17026.0**



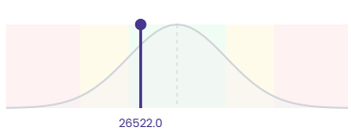
z=-0.73 ↔ 23th percentile
Mean: 3858001.0 Range: 0-19534396.4

Pentadecanoic acid
HMDB0000826 — Fatty Acid — **17478.0**



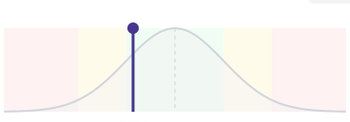
z=-0.77 ↔ 22th percentile
Mean: 102850.5 Range: 0-435586.4

Stearic acid
HMDB0000827 — Fatty Acid — **26522.0**



z=-0.75 ↔ 23th percentile
Mean: 1421829.4 Range: 0-7039089.9

Valeric acid
HMDB0000892 — Fatty Acid — **1502.0**

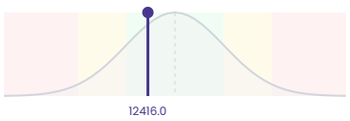


z=-0.86 ↔ 20th percentile
Mean: 6678.6 Range: 0-24809.8

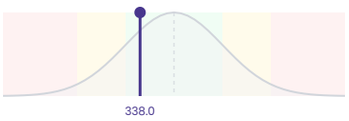
This report is for informational purposes only and does not constitute medical advice. Consult a qualified healthcare provider for clinical decisions.

Indole

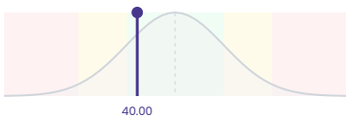
17 metabolites

3-hydroxyanthranilic acid
12416.0
HMDB0001476
Indole


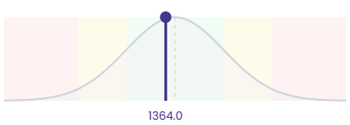
z=-0.55 ↔ 29th percentile
Mean: 59451.8 Range: 0-314640.1

3-hydroxykynurenine
338.0
HMDB0000732
Indole


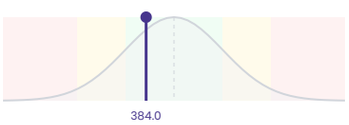
z=-0.69 ↔ 24th percentile
Mean: 17039.3 Range: 0-89191.5

3-Indolepropionic acid
40.00
HMDB0002302
Indole


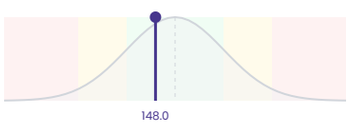
z=-0.77 ↔ 22th percentile
Mean: 1175.6 Range: 0-5573.9

5-Hydroxyindoleacetic acid
1364.0
HMDB0000763
Indole


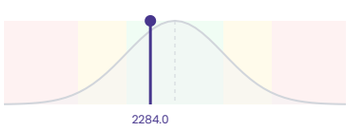
z=-0.19 ↔ 43th percentile
Mean: 2184.1 Range: 0-15246.3

5-Hydroxytryptophan
384.0
HMDB0000472
Indole


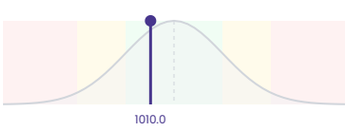
z=-0.57 ↔ 28th percentile
Mean: 3782.2 Range: 0-21643.7

Anthranilic acid
148.0
HMDB0001123
Indole


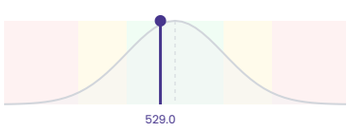
z=-0.40 ↔ 34th percentile
Mean: 1214.5 Range: 0-9197.6

Indole
2284.0
HMDB0000738
Indole


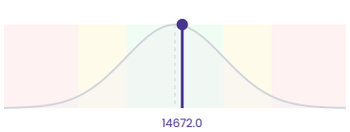
z=-0.50 ↔ 31th percentile
Mean: 33872.7 Range: 0-222708.0

Indole-3-acetic acid
1010.0
HMDB0000197
Indole


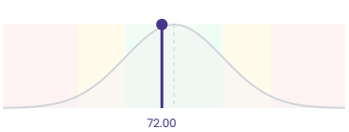
z=-0.48 ↔ 32th percentile
Mean: 6994.2 Range: 0-44417.9

Indole-3-lactic acid
529.0
HMDB0000671
Indole


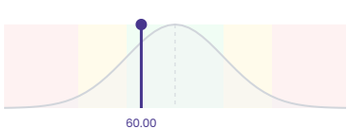
z=-0.30 ↔ 38th percentile
Mean: 3638.3 Range: 0-34753.6

Indole-3-pyruvic acid
14672.0
HMDB0060484
Indole


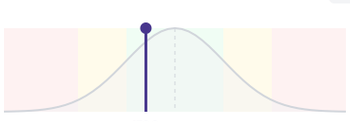
z=+0.15 ↔ 56th percentile
Mean: 11161.4 Range: 0-81209.9

Kynurenic acid
72.00
HMDB0000715
Indole


z=-0.25 ↔ 40th percentile
Mean: 206.4 Range: 0-1834.0

Kynurenine
60.00
HMDB0000684
Indole


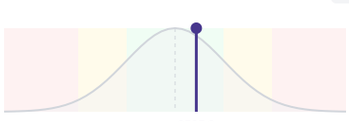
z=-0.69 ↓ 24th percentile
Mean: 2995.6 Range: 0-15722.5

Melatonin
172.0
HMDB0001389
Indole


z=-0.59 ↔ 28th percentile
Mean: 966.4 Range: 0-4976.0

Serotonin
19255.0
HMDB0000259
Indole


z=-0.47 ↔ 32th percentile
Mean: 36014.8 Range: 0-144059.7

Tryptamine
3535.0
HMDB0000303
Indole


z=+0.43 ↔ 67th percentile
Mean: 2318.1 Range: 0-10718.5

Urocanic acid
2807.0
HMDB0000301
Indole


z=-0.44 ↔ 33th percentile
Mean: 177517.6 Range: 0-1374196.6

Xanthurenic acid
56.00
HMDB0000881
Indole

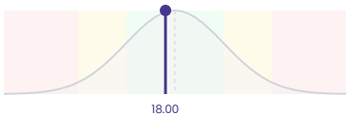

z=-0.37 ↔ 36th percentile
Mean: 252.3 Range: 0-1844.3

This report is for informational purposes only and does not constitute medical advice. Consult a qualified healthcare provider for clinical decisions.

Lipid

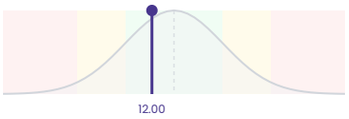
9 metabolites

3-Hydroxybutyryl-CoA
18.00
HMDB0001166 | Lipid



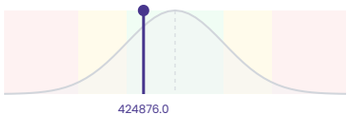
z=-0.19 ↔ 42th percentile
Mean: 21.31 Range: 0-72.67

Acetyl-CoA
12.00
HMDB0001206 | Lipid



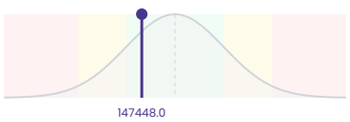
z=-0.45 ↔ 33th percentile
Mean: 86.41 Range: 0-580.4

Acetylcarnitine
424876.0
HMDB0000201 | Lipid



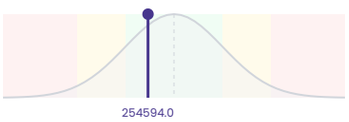
z=-0.65 ↔ 26th percentile
Mean: 8914813.6 Range: 0-48383102.2

Carnitine
147448.0
HMDB0000062 | Lipid



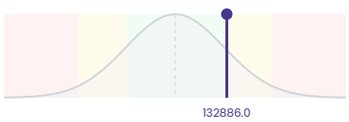
z=-0.68 ↑ 25th percentile
Mean: 2941759.6 Range: 0-15304248.7

Choline
254594.0
HMDB0000097 | Lipid



z=-0.53 ↔ 30th percentile
Mean: 944350.5 Range: 0-4834129.3

Decanoylcarnitine
132886.0
HMDB0000651 | Lipid



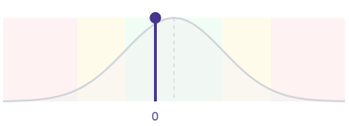
z=+1.06 ↔ 86th percentile
Mean: 60071.6 Range: 0-266387.2

Isobutyryl-CoA
4.00
HMDB0001243 | Lipid



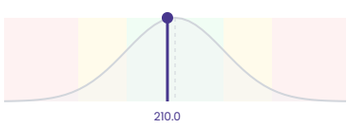
z=-0.60 ↔ 27th percentile
Mean: 45.76 Range: 0-253.4

Malonyl-CoA
0
HMDB0001175 | Lipid



z=-0.38 ↔ 35th percentile
Mean: 61.85 Range: 0-549.2

PGE2
210.0
HMDB0001220 | Lipid

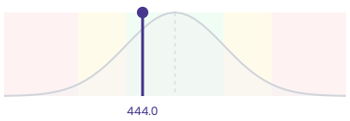


z=-0.16 ↔ 44th percentile
Mean: 567.2 Range: 0-7418.0

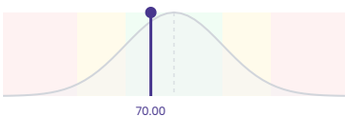
This report is for informational purposes only and does not constitute medical advice. Consult a qualified healthcare provider for clinical decisions.

Nucleotide

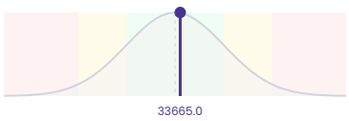
39 metabolites

1-Methyladenosine
444.0
HMDB0003331
Nucleotide


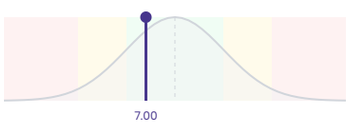
z=-0.66 ↔ 25th percentile
Mean: 7460.2 Range: 0-39280.2

2-Deoxyadenosine
70.00
HMDB0000101
Nucleotide


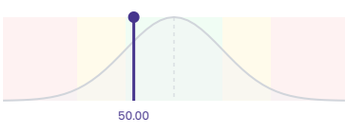
z=-0.47 ↔ 32th percentile
Mean: 1065.7 Range: 0-7365.2

2-deoxyguanosine
33665.0
HMDB0000085
Nucleotide


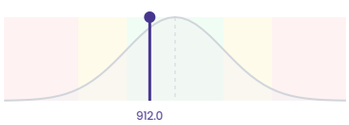
z=+0.10 ↔ 54th percentile
Mean: 23408.7 Range: 0-316686.9

2-Deoxyuridine
7.00
HMDB0000012
Nucleotide


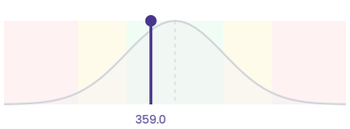
z=-0.59 ↔ 28th percentile
Mean: 238.9 Range: 0-1411.5

5-Methylcytidine
50.00
HMDB0000982
Nucleotide


z=-0.82 ↔ 21th percentile
Mean: 529.6 Range: 0-2277.2

Adenine
912.0
HMDB0000034
Nucleotide


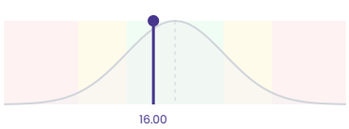
z=-0.52 ↔ 30th percentile
Mean: 26772.6 Range: 0-176443.0

Adenosine
359.0
HMDB0000050
Nucleotide


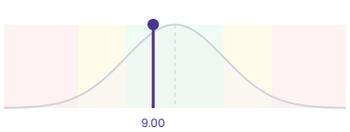
z=-0.49 ↔ 31th percentile
Mean: 6731.5 Range: 0-45633.2

Adenosyl-L-homocysteine
1545.0
HMDB0000939
Nucleotide

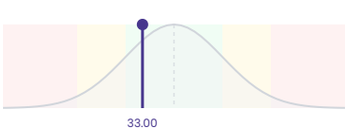

z=-0.48 ↔ 31th percentile
Mean: 3967.2 Range: 0-19001.3

Adenylosuccinate
16.00
HMDB0000536
Nucleotide


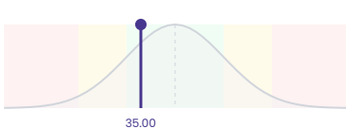
z=-0.44 ↔ 33th percentile
Mean: 59.56 Range: 0-354.1

ADP
9.00
HMDB0001341
Nucleotide


z=-0.44 ↔ 33th percentile
Mean: 1151.8 Range: 0-8864.4

ADP ribose
33.00
HMDB0248024
Nucleotide


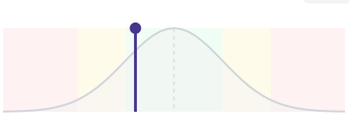
z=-0.64 ↔ 26th percentile
Mean: 138.5 Range: 0-629.7

AMP
35.00
HMDB0000045
Nucleotide


z=-0.70 ↔ 24th percentile
Mean: 48364.8 Range: 0-255360.6

ATP
133.0
HMDB0000538
Nucleotide


z=-0.26 ↑ 40th percentile
Mean: 212.2 Range: 0-1120.8

cADPR
0
HMDB0249529
Nucleotide


z=-0.79 ↔ 22th percentile
Mean: 15.97 Range: 0-76.63

cGMP
11.00
HMDB0001314
Nucleotide


z=-0.14 ↔ 44th percentile
Mean: 177.3 Range: 0-3646.6

Cytidine
89.00
HMDB0000089
Nucleotide


z=-0.42 ↔ 34th percentile
Mean: 1650.8 Range: 0-12782.1

Cytosine
289.0
HMDB0000630
Nucleotide

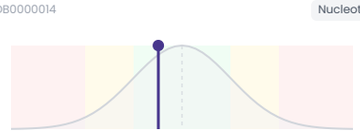

z=-0.28 ↔ 39th percentile
Mean: 10849.3 Range: 0-125579.5

DCDP
14.00
HMDB0001245
Nucleotide

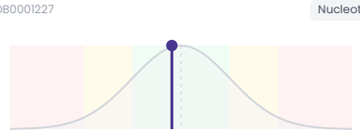

z=-0.26 ↔ 40th percentile
Mean: 29.57 Range: 0-207.5

DCTP
10.00
HMDB0000998
Nucleotide


z=-0.57 ↔ 28th percentile
Mean: 39.36 Range: 0-194.0

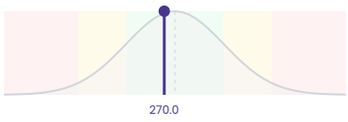
Deoxycytidine
6.00
HMDB0000014
Nucleotide


z=-0.48 ↔ 31th percentile
Mean: 441.3 Range: 0-3137.2

dTMP
1846.0
HMDB0001227
Nucleotide


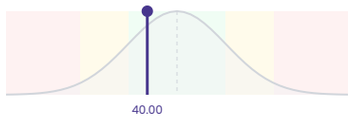
z=-0.19 ↔ 43th percentile
Mean: 2924.1 Range: 0-20046.6

DUMP
HMDB0001409 — Nucleotide — **270.0**



z=-0.22 ↔ 41th percentile
Mean: 589.6 Range: 0-4988.8

dUTP
HMDB0001191 — Nucleotide — **40.00**



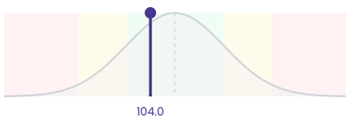
z=-0.61 ↔ 27th percentile
Mean: 894.8 Range: 0-5112.1

GDP
HMDB0001201 — Nucleotide — **18.00**



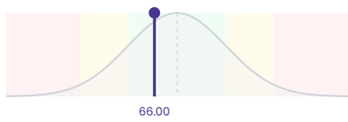
z=-0.47 ↔ 32th percentile
Mean: 42.54 Range: 0-200.7

Guanine
HMDB0000132 — Nucleotide — **104.0**



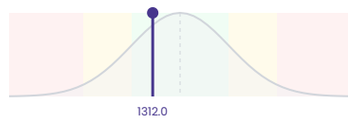
z=-0.50 ↔ 31th percentile
Mean: 4220.3 Range: 0-28845.3

Guanosine
HMDB0000133 — Nucleotide — **66.00**



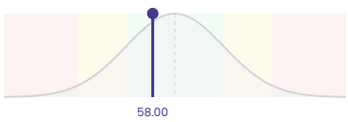
z=-0.46 ↔ 32th percentile
Mean: 7388.7 Range: 0-54968.8

Hypoxanthine
HMDB0000157 — Nucleotide — **1312.0**



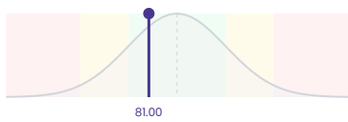
z=-0.56 ↔ 29th percentile
Mean: 174501.0 Range: 0-1101866.4

Inosine
HMDB0000195 — Nucleotide — **58.00**



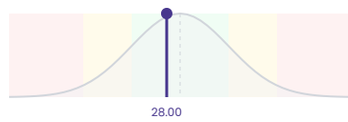
z=-0.45 ↔ 33th percentile
Mean: 41553.8 Range: 0-315800.5

NAD
HMDB0000902 — Nucleotide — **81.00**



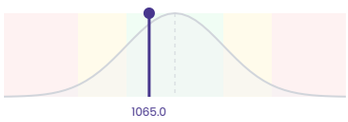
z=-0.58 ↑ 28th percentile
Mean: 1675.6 Range: 0-9983.5

NADH
HMDB0001487 — Nucleotide — **28.00**



z=-0.27 ↑ 39th percentile
Mean: 40.82 Range: 0-181.5

NADP
HMDB0000217 — Nucleotide — **1065.0**



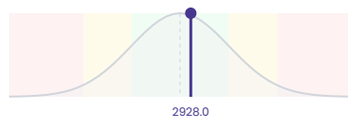
z=-0.53 ↔ 30th percentile
Mean: 20687.5 Range: 0-132403.3

NADPH
HMDB0000221 — Nucleotide — **65.00**



z=-1.17 ↔ 12th percentile
Mean: 1132.6 Range: 0-3874.7

Nicotinamide mononucleotide
HMDB0000229 — Nucleotide — **2928.0**



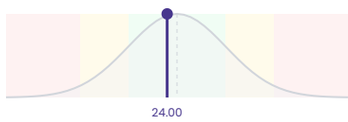
z=+0.22 ↔ 59th percentile
Mean: 2353.9 Range: 0-10204.7

SAICAR
HMDB0000797 — Nucleotide — **119.0**



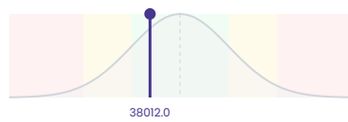
z=-0.81 ↔ 21th percentile
Mean: 783.0 Range: 0-3247.1

UDP
HMDB0000295 — Nucleotide — **24.00**



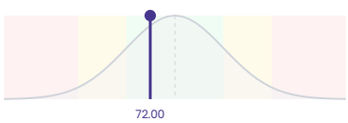
z=-0.20 ↔ 42th percentile
Mean: 488.6 Range: 0-7412.1

Uracil
HMDB0000300 — Nucleotide — **38012.0**



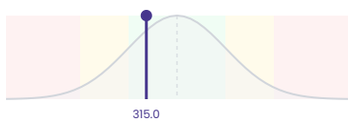
z=-0.62 ↔ 27th percentile
Mean: 156001.6 Range: 0-730925.8

Uridine
HMDB0000296 — Nucleotide — **72.00**



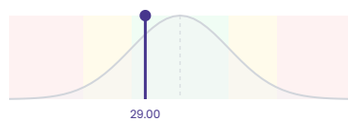
z=-0.51 ↔ 31th percentile
Mean: 944.8 Range: 0-6127.4

Xanthine
HMDB0000292 — Nucleotide — **315.0**



z=-0.63 ↔ 27th percentile
Mean: 1316.3 Range: 0-6105.9

Xanthosine
HMDB0000299 — Nucleotide — **29.00**



z=-0.71 ↔ 24th percentile
Mean: 434.0 Range: 0-2140.3

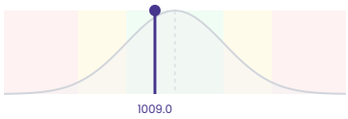
Organic Acid

64 metabolites

2-hydroxybutyric acid

1009.0

HMDB0000008 | Organic Acid



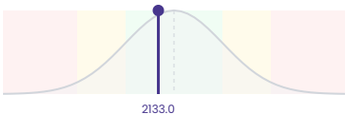
z=-0.41 ↓ 34th percentile

Mean: 3765.2 Range: 0-23975.7

2-Hydroxyglutarate

2133.0

HMDB0059655 | Organic Acid



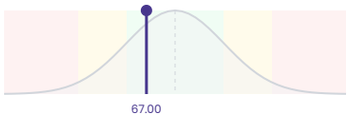
z=-0.32 ↔ 37th percentile

Mean: 3222.6 Range: 0-13423.5

2-Ketobutyric acid

67.00

HMDB0000005 | Organic Acid



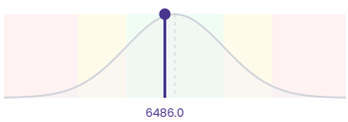
z=-0.59 ↔ 28th percentile

Mean: 230.2 Range: 0-1065.9

2-Methylglutaric acid

6486.0

HMDB0000422 | Organic Acid



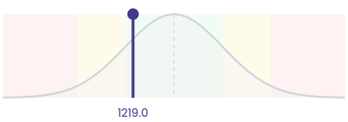
z=-0.21 ↔ 42th percentile

Mean: 12958.2 Range: 0-107103.2

3-hydroxybutyric acid

1219.0

HMDB0000011 | Organic Acid



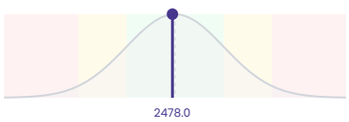
z=-0.84 ↑ 20th percentile

Mean: 6989.2 Range: 0-27635.6

3-Hydroxyisovaleric acid

2478.0

HMDB0000754 | Organic Acid



z=-0.05 ↔ 48th percentile

Mean: 3007.7 Range: 0-32433.2

3-Methyl-2-oxovaleric acid

11806.0

HMDB0000491 | Organic Acid



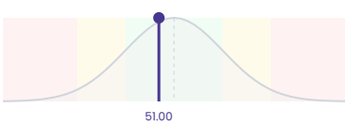
z=-1.29 ↔ 10th percentile

Mean: 57483.1 Range: 0-163314.2

3-Methyladipic acid

51.00

HMDB0000555 | Organic Acid



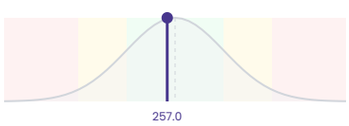
z=-0.31 ↔ 38th percentile

Mean: 80.22 Range: 0-363.9

3-Phosphoglyceric acid

257.0

HMDB0000807 | Organic Acid



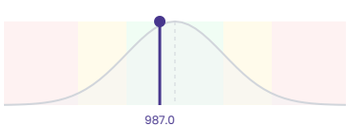
z=-0.16 ↔ 44th percentile

Mean: 379.3 Range: 0-2662.2

4-Hydroxyphenylpyruvic acid

987.0

HMDB0000707 | Organic Acid



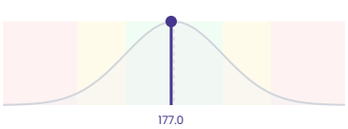
z=-0.31 ↔ 38th percentile

Mean: 18002.5 Range: 0-182716.7

6-Phosphogluconic acid

177.0

HMDB0001316 | Organic Acid



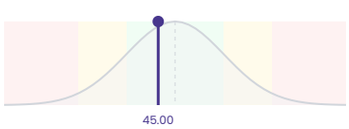
z=-0.06 ↔ 48th percentile

Mean: 220.9 Range: 0-2497.1

Acetoacetate

45.00

HMDB0000060 | Organic Acid



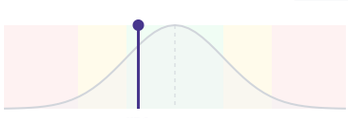
z=-0.35 ↑ 37th percentile

Mean: 494.8 Range: 0-4405.1

Acetylglycine

117.0

HMDB0000532 | Organic Acid



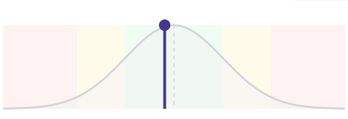
z=-0.75 ↔ 23th percentile

Mean: 894.8 Range: 0-4011.6

Aconitic acid

350.0

HMDB0247961 | Organic Acid



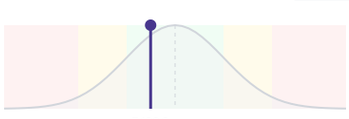
z=-0.19 ↔ 42th percentile

Mean: 610.4 Range: 0-4693.6

Adipic acid

7430.0

HMDB0000448 | Organic Acid



z=-0.50 ↔ 31th percentile

Mean: 15764.8 Range: 0-65708.7

Amino valerate

3397.0

HMDB0003355 | Organic Acid



z=-0.16 ↔ 44th percentile

Mean: 4377.2 Range: 0-23192.8

Azelaic acid

168.0

HMDB0000784 | Organic Acid



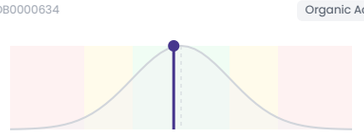
z=-0.36 ↔ 36th percentile

Mean: 1523.8 Range: 0-12712.7

Citraconic acid

4849.0

HMDB0000634 | Organic Acid



z=-0.15 ↔ 44th percentile

Mean: 6052.4 Range: 0-29953.5

Citrate

3951.0

HMDB0000094 | Organic Acid



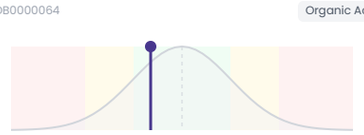
z=+0.02 ↔ 51th percentile

Mean: 3816.5 Range: 0-29948.2

Creatine

1089493.0

HMDB0000064 | Organic Acid



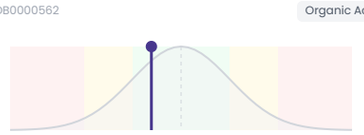
z=-0.64 ↔ 26th percentile

Mean: 5621024.6 Range: 0-26814423.6

Creatinine

427252.0

HMDB0000562 | Organic Acid



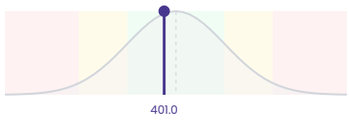
z=-0.61 ↓ 27th percentile

Mean: 3389187.2 Range: 0-18015789.8

D-Galacturonic acid

401.0

HMDB0002545 | Organic Acid



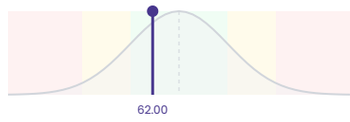
z=-0.24 ↔ 41th percentile

Mean: 636.9 Range: 0-3581.7

Ethylmalonic acid

62.00

HMDB0000622 | Organic Acid



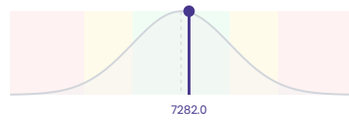
z=-0.54 ↔ 30th percentile

Mean: 611.8 Range: 0-3670.7

Fumarate

7282.0

HMDB0000134 | Organic Acid



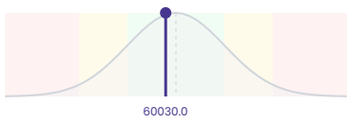
z=+0.16 ↔ 57th percentile

Mean: 5633.6 Range: 0-35943.6

Galactonic acid

60030.0

HMDB0000565 | Organic Acid



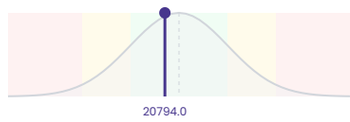
z=-0.21 ↔ 42th percentile

Mean: 80260.4 Range: 0-369725.4

Gluconic acid

20794.0

HMDB0000625 | Organic Acid



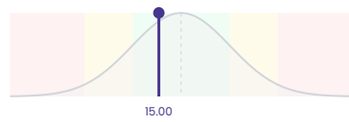
z=-0.29 ↔ 39th percentile

Mean: 32089.2 Range: 0-149468.7

Glucuronic acid

15.00

HMDB0000127 | Organic Acid



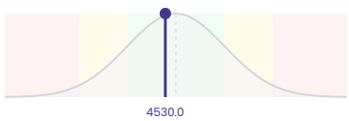
z=-0.46 ↔ 33th percentile

Mean: 121.5 Range: 0-823.9

Glutaconic acid

4530.0

HMDB0000620 | Organic Acid



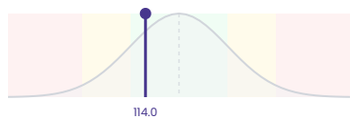
z=-0.22 ↔ 41th percentile

Mean: 17301.8 Range: 0-194217.4

Glutaric acid

114.0

HMDB0000661 | Organic Acid



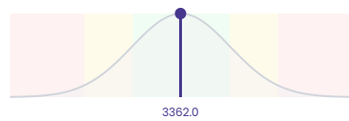
z=-0.69 ↔ 25th percentile

Mean: 716.3 Range: 0-3351.3

Glyceric acid

3362.0

HMDB0000139 | Organic Acid



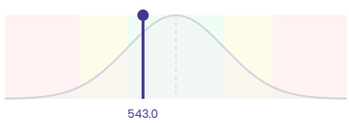
z=-0.01 ↔ 50th percentile

Mean: 3471.6 Range: 0-33146.0

Glycocyamine

543.0

HMDB0000128 | Organic Acid



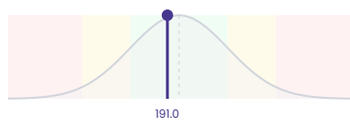
z=-0.67 ↔ 25th percentile

Mean: 94677.2 Range: 0-514248.9

Glycolic acid

191.0

HMDB0000115 | Organic Acid



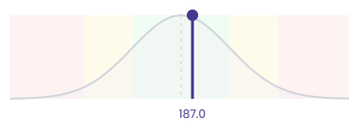
z=-0.24 ↔ 41th percentile

Mean: 366.2 Range: 0-2582.7

Glyoxylic acid

187.0

HMDB0000119 | Organic Acid



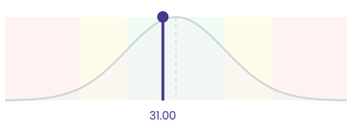
z=+0.23 ↔ 59th percentile

Mean: 146.3 Range: 0-669.3

Homogentisic acid

31.00

HMDB0000130 | Organic Acid



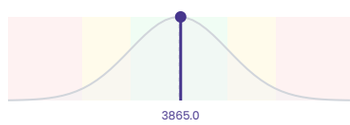
z=-0.27 ↔ 40th percentile

Mean: 87.08 Range: 0-717.4

IsoCitrate

3865.0

HMDB0000193 | Organic Acid



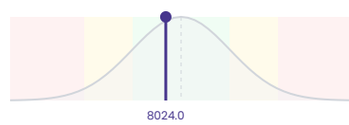
z=+0.03 ↔ 51th percentile

Mean: 3485.2 Range: 0-36524.1

Isovalerylglycine

8024.0

HMDB0000678 | Organic Acid



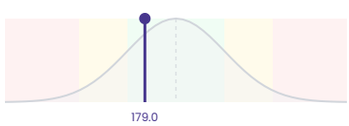
z=-0.31 ↔ 38th percentile

Mean: 26454.5 Range: 0-203148.0

Itaconic acid

179.0

HMDB0002092 | Organic Acid



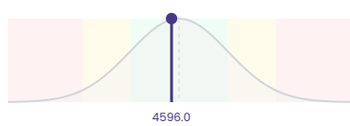
z=-0.64 ↔ 26th percentile

Mean: 5315.5 Range: 0-29575.4

Ketoleucine

4596.0

HMDB0000695 | Organic Acid



z=-0.15 ↔ 44th percentile

Mean: 5547.5 Range: 0-24277.6

L-2-Hydroxyglutaric acid

0

HMDB0000694 | Organic Acid



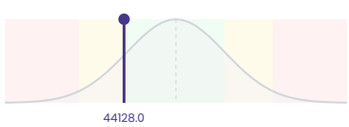
z=-0.87 ↔ 19th percentile

Mean: 788.8 Range: 0-3515.7

Lactate

44128.0

HMDB0000190 | Organic Acid



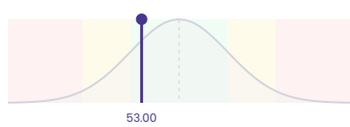
z=-1.06 ↓ 14th percentile

Mean: 135163.5 Range: 0-392389.6

Leucic acid

53.00

HMDB0000624 | Organic Acid



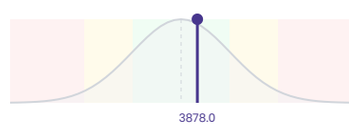
z=-0.76 ↔ 22th percentile

Mean: 903.8 Range: 0-4240.6

Levulinic acid

3878.0

HMDB0000720 | Organic Acid



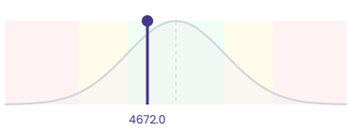
z=+0.33 ↔ 63th percentile

Mean: 2736.3 Range: 0-13019.0

Malate

4672.0

HMDB0000156 | Organic Acid



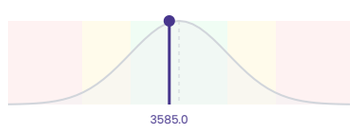
z=-0.58 ↔ 28th percentile

Mean: 11540.7 Range: 0-46862.2

Maleic acid

3585.0

HMDB0000176 | Organic Acid



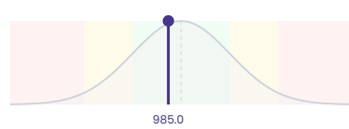
z=-0.20 ↔ 42th percentile

Mean: 4375.8 Range: 0-16333.1

Malonic acid

985.0

HMDB0000691 | Organic Acid



z=-0.26 ↔ 40th percentile

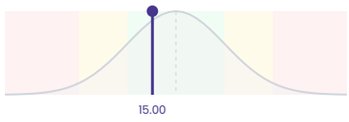
Mean: 6678.2 Range: 0-72343.2

meso-Tartaric acid

15.00

HMDB0062642

Organic Acid



z=-0.48 ↔ 32th percentile

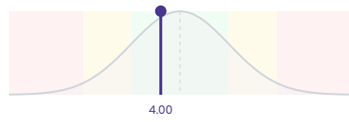
Mean: 40.49 Range: 0-199.5

Methyl succinate

4.00

HMDB0033837

Organic Acid



z=-0.39 ↔ 35th percentile

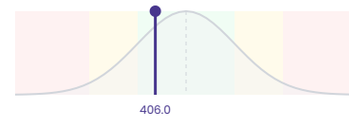
Mean: 67.28 Range: 0-549.7

Methylmalonic acid

406.0

HMDB0000202

Organic Acid



z=-0.63 ↓ 27th percentile

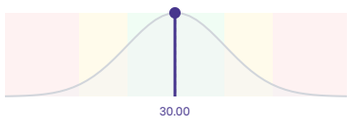
Mean: 4356.3 Range: 0-23184.6

Mucic acid

30.00

HMDB0000639

Organic Acid



z=-0.02 ↔ 49th percentile

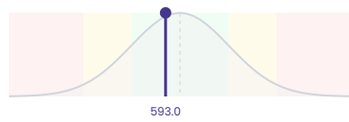
Mean: 32.00 Range: 0-340.3

Muconic acid

593.0

HMDB0000393

Organic Acid



z=-0.29 ↔ 38th percentile

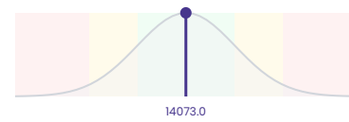
Mean: 806.4 Range: 0-2977.3

Oxaloacetic acid

14073.0

HMDB0000223

Organic Acid



z=-0.00 ↔ 50th percentile

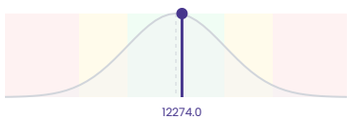
Mean: 14124.7 Range: 0-51533.5

Oxoglutaric acid

12274.0

HMDB0000208

Organic Acid



z=+0.12 ↔ 55th percentile

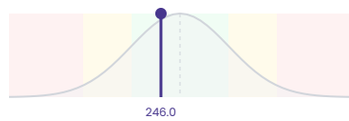
Mean: 10428.5 Range: 0-54829.9

PEP

246.0

HMDB0000263

Organic Acid



z=-0.39 ↔ 35th percentile

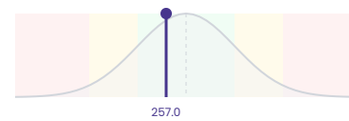
Mean: 1065.6 Range: 0-7373.5

Phenylpyruvic acid

257.0

HMDB0000205

Organic Acid



z=-0.41 ↔ 34th percentile

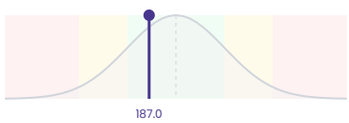
Mean: 587.3 Range: 0-3016.7

Phosphocreatine

187.0

HMDB0001511

Organic Acid



z=-0.55 ↔ 29th percentile

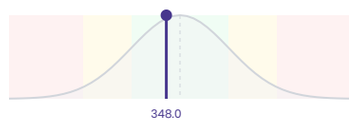
Mean: 56059.6 Range: 0-361776.4

Picolinic acid

348.0

HMDB0002243

Organic Acid



z=-0.28 ↔ 39th percentile

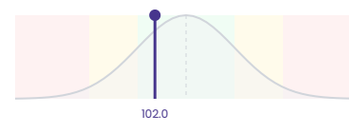
Mean: 468.4 Range: 0-1759.7

Pyruvate

102.0

HMDB0000243

Organic Acid



z=-0.64 ↓ 26th percentile

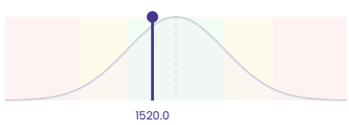
Mean: 495.2 Range: 0-2345.5

Quinolinic acid

1520.0

HMDB0000232

Organic Acid



z=-0.48 ↓ 32th percentile

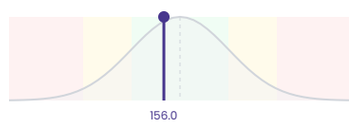
Mean: 16834.8 Range: 0-112546.9

Sebacic acid

156.0

HMDB0000792

Organic Acid



z=-0.33 ↔ 37th percentile

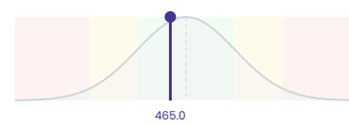
Mean: 361.8 Range: 0-2232.4

Shikimic acid

465.0

HMDB0003070

Organic Acid



z=-0.32 ↔ 37th percentile

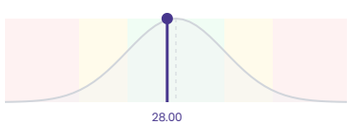
Mean: 3255.1 Range: 0-29238.2

Suberic acid

28.00

HMDB0000893

Organic Acid



z=-0.18 ↔ 43th percentile

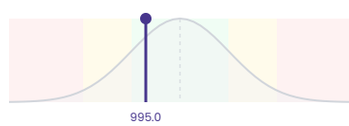
Mean: 609.9 Range: 0-10410.8

Succinate

995.0

HMDB0000254

Organic Acid



z=-0.70 ↔ 24th percentile

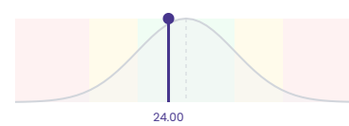
Mean: 9510.3 Range: 0-45999.2

Tartaric acid

24.00

HMDB0000956

Organic Acid



z=-0.36 ↔ 36th percentile

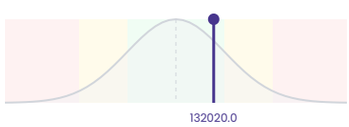
Mean: 41.44 Range: 0-187.1

Urate

132020.0

HMDB0000289

Organic Acid



z=+0.77 ↔ 78th percentile

Mean: 75295.1 Range: 0-295264.7

Other

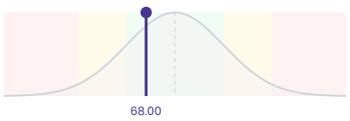
4 metabolites

2-Furoic acid

68.00

HMDB0000617

Other



z=-0.59 ↔ 28th percentile

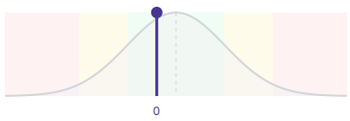
Mean: 169.0 Range: 0-683.4

2-Pyrrolidinone

0

HMDB0002039

Other



z=-0.39 ↔ 35th percentile

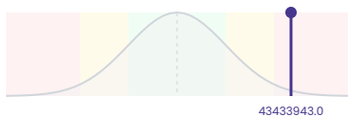
Mean: 11123.9 Range: 0-95885.2

Acetamide

43433943.0

HMDB0031645

Other



z=+2.33 ↔ 99th percentile

Mean: 10077072.5 Range: 0-52973493.8

N,N-Dicyclohexylurea

223.0

HMDB0244166

Other



z=-1.18 ↔ 12th percentile

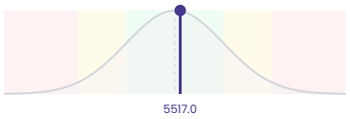
Mean: 1132.5 Range: 0-3452.4

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Peptide

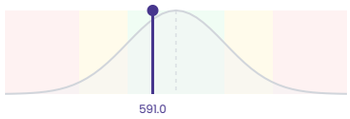
7 metabolites

Acetylcysteine
5517.0
HMDB0001890
Peptide



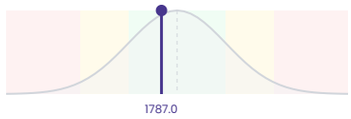
z=+0.11 ↔ 54th percentile
Mean: 4103.5 Range: 0-42952.5

Carnosine
591.0
HMDB0000033
Peptide



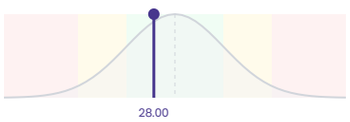
z=-0.48 ↔ 32th percentile
Mean: 2167.3 Range: 0-12097.5

Glutathione
1787.0
HMDB0000125
Peptide



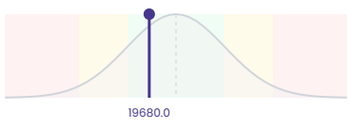
z=-0.32 ↑ 38th percentile
Mean: 9718.2 Range: 0-84314.0

Glycylproline
28.00
HMDB0000721
Peptide



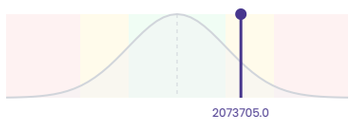
z=-0.43 ↔ 33th percentile
Mean: 287.1 Range: 0-2090.2

N-Acetylglutamine
19680.0
HMDB0006029
Peptide



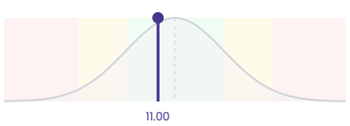
z=-0.55 ↔ 29th percentile
Mean: 134401.3 Range: 0-763123.5

N-Acetylornithine
2073705.0
HMDB0003357
Peptide



z=+1.31 ↔ 90th percentile
Mean: 752840.0 Range: 0-3785182.8

Oxidized Glutathione
11.00
HMDB0003337
Peptide



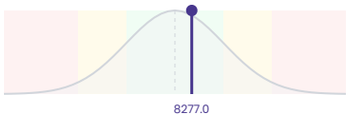
z=-0.35 ↔ 37th percentile
Mean: 144.9 Range: 0-1307.3

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Pharmaceutical

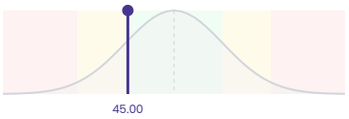
8 metabolites

Acetohydroxamic acid
8277.0
HMDB0014691
Pharmaceutical



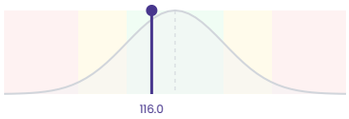
z=+0.34 ↔ 64th percentile
Mean: 5526.8 Range: 0–29455.0

Allopurinol
45.00
HMDB0014581
Pharmaceutical



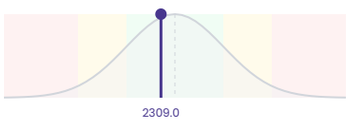
z=-0.94 ↔ 17th percentile
Mean: 835.5 Range: 0–3345.7

Amiloride
116.0
HMDB0014732
Pharmaceutical



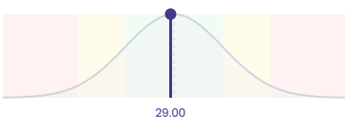
z=-0.48 ↔ 32th percentile
Mean: 1568.5 Range: 0–10670.8

Caffeine
2309.0
HMDB0001847
Pharmaceutical



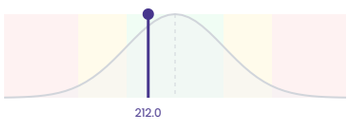
z=-0.29 ↔ 39th percentile
Mean: 4566.7 Range: 0–28289.3

Naproxen
29.00
HMDB0001923
Pharmaceutical



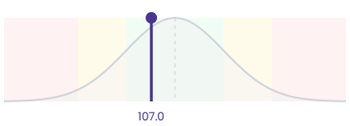
z=-0.07 ↔ 47th percentile
Mean: 424.1 Range: 0–17523.7

Phenylbutazone
212.0
HMDB0014950
Pharmaceutical



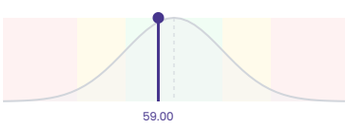
z=-0.55 ↔ 29th percentile
Mean: 1591.4 Range: 0–9125.6

Propranolol
107.0
HMDB0001849
Pharmaceutical



z=-0.48 ↔ 32th percentile
Mean: 195.8 Range: 0–748.0

Tetracaine
59.00
HMDB0258868
Pharmaceutical



z=-0.32 ↔ 37th percentile
Mean: 143.5 Range: 0–933.9

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Phenolic

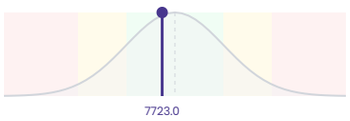
28 metabolites

2-Hydroxybenzoic acid

7723.0

HMDB0001895

Phenolic



z=-0.26 ↔ 40th percentile

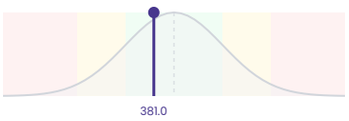
Mean: 22791.5 Range: 0–196016.5

2-Hydroxyphenylacetic acid

381.0

HMDB0000669

Phenolic



z=-0.41 ↔ 34th percentile

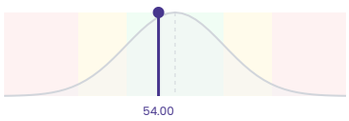
Mean: 8528.6 Range: 0–67754.3

2-Phenylglycinol

54.00

HMDB0245030

Phenolic



z=-0.34 ↔ 37th percentile

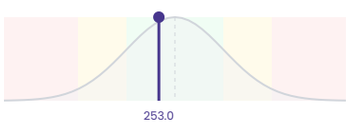
Mean: 122.2 Range: 0–725.5

2,3-Dihydroxybenzoic acid

253.0

HMDB0000397

Phenolic



z=-0.33 ↔ 37th percentile

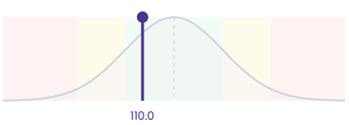
Mean: 3909.9 Range: 0–37331.3

3-Phenyllactic acid

110.0

HMDB0000779

Phenolic



z=-0.64 ↔ 26th percentile

Mean: 824.3 Range: 0–4153.6

4-Aminophenol

12837607.0

HMDB0001169

Phenolic



z=+1.87 ↔ 97th percentile

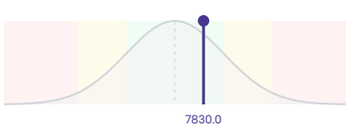
Mean: 2926417.1 Range: 0–18848867.9

4-Ethylbenzoic acid

7830.0

HMDB0002097

Phenolic



z=+0.59 ↔ 72th percentile

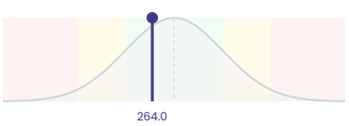
Mean: 6042.7 Range: 0–15195.4

4-Hydroxy-3-methylbenzoic acid

264.0

HMDB0004815

Phenolic



z=-0.44 ↔ 33th percentile

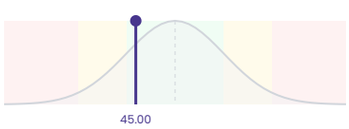
Mean: 6796.2 Range: 0–50888.1

4-Hydroxybenzaldehyde

45.00

HMDB0011718

Phenolic



z=-0.80 ↔ 21th percentile

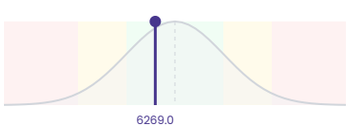
Mean: 32747.4 Range: 0–154713.4

4-Hydroxybenzoic acid

6269.0

HMDB0000500

Phenolic



z=-0.40 ↔ 34th percentile

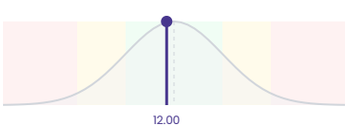
Mean: 29434.0 Range: 0–202424.8

4-Methoxyphenylacetic acid

12.00

HMDB0002072

Phenolic



z=-0.15 ↔ 44th percentile

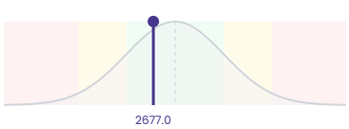
Mean: 13.91 Range: 0–52.00

6-Hydroxynicotinic acid

2677.0

HMDB0002658

Phenolic



z=-0.44 ↔ 33th percentile

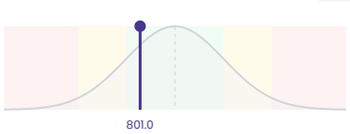
Mean: 13052.8 Range: 0–83017.6

Benzoic acid

801.0

HMDB0001870

Phenolic



z=-0.71 ↔ 24th percentile

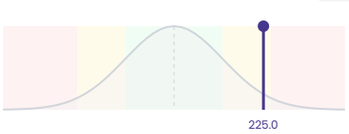
Mean: 21844.4 Range: 0–110514.1

Ferulic acid

225.0

HMDB0000954

Phenolic



z=+1.83 ↔ 97th percentile

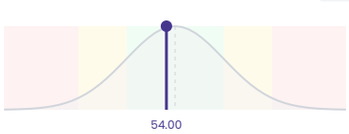
Mean: 43.96 Range: 0–340.6

Gentisic acid

54.00

HMDB0000152

Phenolic



z=-0.18 ↔ 43th percentile

Mean: 69.13 Range: 0–325.5

Gibberellic acid

210.0

HMDB0003559

Phenolic



z=+0.33 ↔ 63th percentile

Mean: 59.46 Range: 0–1425.9

Hippuric acid

362.0

HMDB0000714

Phenolic



z=-0.30 ↔ 38th percentile

Mean: 1487.0 Range: 0–12910.8

Homovanillic acid

1682.0

HMDB0000118

Phenolic



z=-0.42 ↔ 34th percentile

Mean: 14437.6 Range: 0–105510.8

m-Coumaric acid

546.0

HMDB0001713

Phenolic



z=-0.56 ↔ 29th percentile

Mean: 4028.9 Range: 0–22731.7

Mandelic acid

311.0

HMDB0000703

Phenolic



z=-0.45 ↔ 33th percentile

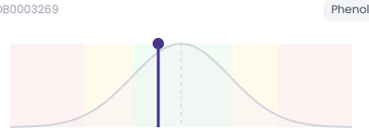
Mean: 2222.9 Range: 0–14909.3

Nicotinuric acid

72.00

HMDB0003269

Phenolic



z=-0.47 ↔ 32th percentile

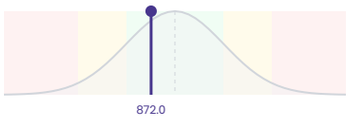
Mean: 358.8 Range: 0–2202.7

p-Coumaric acid

872.0

HMDB0002035

Phenolic



z=-0.49 ↔ 31th percentile

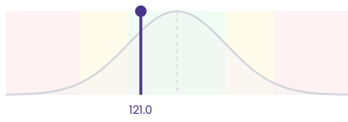
Mean: 3965.0 Range: 0-22997.9

Phenylacetic acid

121.0

HMDB0000209

Phenolic



z=-0.74 ↔ 23th percentile

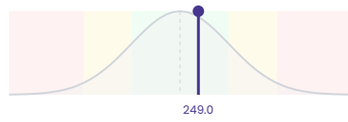
Mean: 5765.4 Range: 0-28624.7

Phenylglyoxylic acid

249.0

HMDB0001587

Phenolic



z=+0.37 ↔ 65th percentile

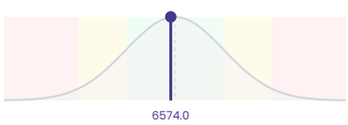
Mean: 196.8 Range: 0-614.5

Phthalic acid

6574.0

HMDB0002107

Phenolic



z=-0.08 ↔ 47th percentile

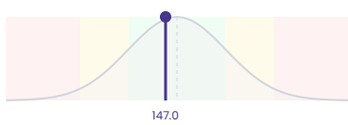
Mean: 7319.6 Range: 0-33776.5

Protocatechuic acid

147.0

HMDB0001856

Phenolic



z=-0.23 ↔ 41th percentile

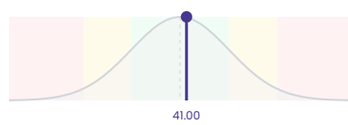
Mean: 3019.9 Range: 0-39876.4

Thymol

41.00

HMDB0001878

Phenolic



z=+0.13 ↔ 55th percentile

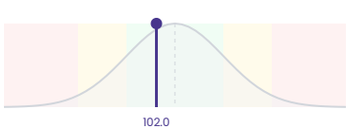
Mean: 35.62 Range: 0-157.9

Vanillic acid

102.0

HMDB0000484

Phenolic



z=-0.38 ↔ 35th percentile

Mean: 230.8 Range: 0-1252.2

Polyamine

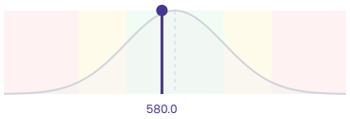
4 metabolites

Agmatine

580.0

HMDB0001432

Polyamine



z=-0.27 ↔ 40th percentile

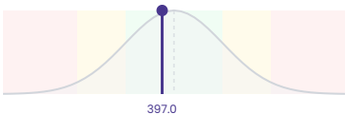
Mean: 3212.6 Range: 0-32938.2

Cadaverine

397.0

HMDB0002322

Polyamine



z=-0.24 ↔ 40th percentile

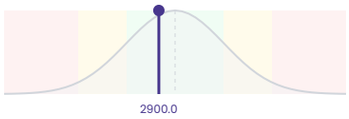
Mean: 2372.3 Range: 0-26820.8

Putrescine

2900.0

HMDB0001414

Polyamine



z=-0.33 ↔ 37th percentile

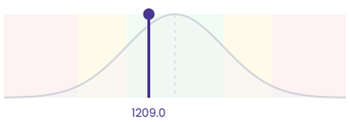
Mean: 90706.4 Range: 0-883793.8

Spermidine

1209.0

HMDB0001257

Polyamine



z=-0.53 ↔ 30th percentile

Mean: 113925.8 Range: 0-747254.2

This report is for informational purposes only and does not constitute medical advice. Consult a qualified healthcare provider for clinical decisions.

Steroid

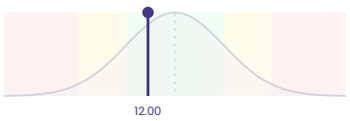
1 metabolite

Pregnenolone sulfate

12.00

HMDB0000774

Steroid



z=-0.55

29th percentile

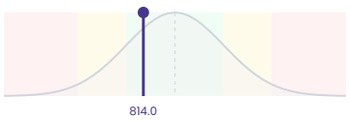
Mean: 658.8

Range: 0-4181.9

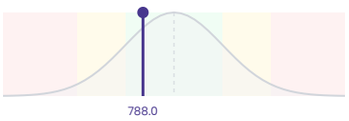
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Vitamin

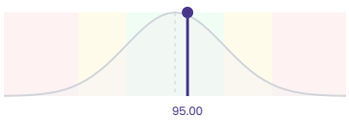
12 metabolites

4-Pyridoxic acid
814.0
HMDB0000017
Vitamin


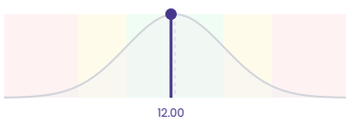
z=-0.65 ↔ 26th percentile
Mean: 15654.5 Range: 0-84596.8

Biotin
788.0
HMDB0000030
Vitamin


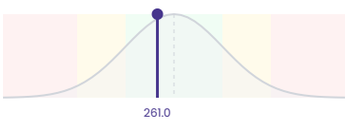
z=-0.64 ↔ 26th percentile
Mean: 14743.0 Range: 0-80675.3

Dihydrofolic acid
95.00
HMDB0001056
Vitamin


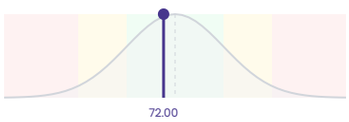
z=+0.26 ↔ 60th percentile
Mean: 65.74 Range: 0-409.3

Folic acid
12.00
HMDB0000121
Vitamin


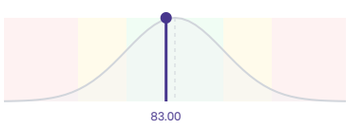
z=-0.08 ↔ 47th percentile
Mean: 153.6 Range: 0-5482.5

Folinic acid
261.0
HMDB0001562
Vitamin


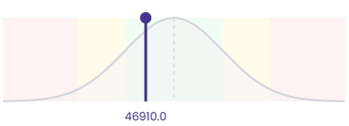
z=-0.34 ↔ 37th percentile
Mean: 746.4 Range: 0-5038.1

L-Ascorbic acid
72.00
HMDB0000044
Vitamin


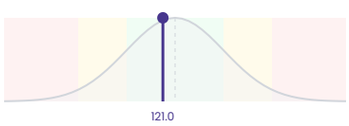
z=-0.24 ↔ 41th percentile
Mean: 101.0 Range: 0-470.1

Neopterin
83.00
HMDB0000845
Vitamin


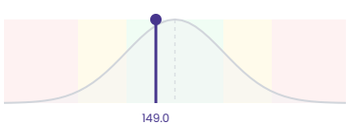
z=-0.18 ↔ 43th percentile
Mean: 101.1 Range: 0-401.2

Nicotinamide
46910.0
HMDB0001406
Vitamin


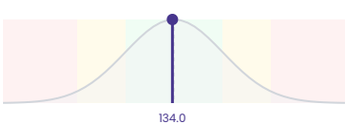
z=-0.58 ↔ 28th percentile
Mean: 191464.0 Range: 0-940627.3

Nicotinic acid
121.0
HMDB0001488
Vitamin


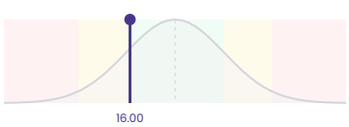
z=-0.25 ↔ 40th percentile
Mean: 334.9 Range: 0-2907.1

Pantothenic acid
149.0
HMDB0000210
Vitamin


z=-0.39 ↔ 35th percentile
Mean: 3567.1 Range: 0-29890.3

Pyridoxine
134.0
HMDB0000239
Vitamin


z=-0.03 ↔ 49th percentile
Mean: 166.6 Range: 0-3213.6

Vitamin D3
16.00
HMDB0000876
Vitamin


z=-0.92 ↔ 18th percentile
Mean: 748.5 Range: 0-3130.1

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