Science: Frequently Asked Questions

DNA is the hardware. Epigenetics is the software.

Epigenetic regulation helps influence how genes are activated or expressed in different cells and contexts without changing the underlying DNA sequence.

Epigenetics

Epigenetics is the layer of gene regulation that influences how strongly genes are activated and expressed (made into proteins), without changing the DNA sequence itself.

How is epigenetics different from genetics?

Genetics is the sequence you inherit. Epigenetics is the layer of regulation that influences which genes are more active or less active in different cells and contexts. Unlike genetic sequence, epigenetic patterns can shift over time in response to aging, environment, exposures, and lifestyle-related factors.

DNA Methylation (DNAm)

One of the most extensively studied epigenetic mechanisms. It involves chemical modifications at specific sites across the genome that help regulate gene activity.

1. DNAm patterns can shift with aging, environment, exposures, lifestyle, and underlying biological processes.
2. DNAm is foundational to many modern aging clocks and system-based epigenetic health insights.

Does methylation mean a gene is “on” or “off”?

In many contexts, methylation is associated with reduced gene expression, but biology is nuanced. DNAm is best understood as one part of a larger regulatory system that influences gene activity, rather than a simple on/off switch.

Is methylation 'good' or 'bad'?

Methylation is not inherently good or bad. It is a normal regulatory mechanism that helps maintain healthy cellular function.

1. Some methylation patterns support normal development, stable cell identity, and healthy regulation.
2. Other patterns may be associated with aging, inflammation, environmental exposures, or physiologic stress.

The clinical relevance comes from the pattern across many sites and how those patterns relate to validated biological signals, not from “more” or “less” methylation in isolation.

Clinical Insights: Epigenetic Biomarkers

Epigenetic Biomarkers

Epigenetic biomarkers are statistical model-derived estimates that are generated from DNA methylation (DNAm) patterns associated with specific biologic pathways and health risks. They are longitudinal biologic signals, meaning that they typically reflect the status of an organ or a specific biological process (e.g. mitochondrial function) over periods of months or even years. They are not direct serum or urine measurements of the analytes or molecules.

What types of biological signals can epigenetic biomarkers provide?

Unlike static genetic tests, epigenetic biomarkers may provide dynamic insight into biological patterns associated with current or recent physiological state. They may offer insights into:

1. Inflammation & immune signaling
2. Metabolic & glycemic signaling (including mitochondrial function)
3. Toxicology / exposures: patterns associated with pollutant or heavy metal exposure signals.
4. Lipids/vascular signaling

These results are intended to support clinical context, patient education, lifestyle targeting, and longitudinal tracking, not to diagnose disease independently.

Why does epigenetics matter in clinical care?

Because DNAm patterns may shift in response to factors such as aging, exposures, sleep, exercise, stress, and nutrition, they can provide a complementary view of biological change over time. When interpreted alongside clinical history, physical examination, conventional labs, and patient goals, epigenetic insights may help support earlier lifestyle focus, personalized intervention planning, and longitudinal monitoring.

For additional clinical education or implementation support, contact your Epigenetic Healthcare Consultant or email providers@trudiagnostic.com

TruDiagnostic™
The Epigenetic Company

How do epigenetic biomarkers differ from traditional lab biomarkers?

Traditional blood biomarkers and epigenetic biomarkers provide different types of biological information. Many blood-based biomarkers reflect circulating analytes that can fluctuate with near-term factors such as meals, hydration, acute stress, illness, medications, or time of day.
Epigenetic biomarkers are not intended to replace conventional labs. They provide a complementary layer of biological insight that may support longitudinal tracking, lifestyle targeting, and clinical follow-up.

ATTRIBUTE	TRADITIONAL LABS	EPIGENETIC BIOMARKERS
Timeframe	Near-term snapshot	Longer-horizon pattern
Variability	May be influenced by meals, hydration, stress, illness, Rx, and timing	May reflect more sustained biological patterns
Nature	Direct measurement of circulating analytes	Model-derived estimates from DNAm patterns
Clinical Role	Core diagnostic and monitoring tools	Expanded insights and longitudinal tracking

Biological Aging & Epigenetic Clocks

What is "biological age" and how is it measured?

Biological age is a model-derived estimate intended to characterize aging-related biological patterns that may differ from chronological age. In epigenetic testing, biological age is commonly estimated using statistical models, often called "clocks," that analyze DNA methylation patterns.

OMICmAge™ is a composite, whole-body epigenetic aging estimate derived from DNAm patterns associated with aging-related health phenotypes. It is designed to summarize overall biological aging burden and support longitudinal tracking over time.

SYMPHONYAge™ is a set of organ system-specific epigenetic aging models designed to estimate aging-related patterns across different biological systems based on DNAm signatures.

DunedinPACE™ is a DNA methylation-based measure of the pace of aging. Rather than estimating biological age at a single point in time, it estimates the rate at which aging-related biological change is occurring.

System-based Health Insights

How can DNAm patterns inform system-based health insights?

DNA methylation can be used not only to estimate biological aging, but also to generate epigenetic biomarker estimates.

1. These outputs are designed to help characterize longer-horizon biological patterns tied to multi-system physiology.
2. Instead of focusing primarily on how old a person may appear biologically, system-based epigenetic insights may help identify which biological domains warrant additional clinical context, lifestyle focus, or longitudinal monitoring.
3. Common categories include nutrition-related patterns, metabolic function, inflammation and immune signaling, and exposure-related signatures.

Evidence & Methodology

What is this built on?

TruDiagnostic's epigenetic outputs are based on peer-reviewed DNA methylation science, published algorithms, and validated analytical methods, including work and collaborations with institutions such as Harvard, Yale, and Duke.

Where applicable, individual biomarkers and clocks should be interpreted according to their specific validation evidence, intended use, limitations, and report-level context.

Are epigenetic results diagnostic?

No. Epigenetic results are not diagnostic and are intended to provide adjunctive biological insight. They should be interpreted in context and are best used as an adjunct to clinical evaluation, history, conventional labs, and medical guidance.