lola

TruDiagnostic™ The Epigenetic Company

NAME
Lola

DATE OF BIRTH
14 March 1984

AGE AT COLLECTION
42.5

SEX ASSIGNED AT BIRTH
Female

TEST
TruAge

REPORTS
TruAge · AdvancedTruAge

SAMPLE COLLECTED
2 September 2026

RESULT REPORTED
9 September 2026

RESULT REFERENCE
SAMPLE-REPORT

Your biological age results

Your sample was read for the chemical marks on DNA that change as we age. Statistical models turn that pattern into the estimates in this report, each placed against the laboratory's reference cohort of other people. The pages that follow explain what each one is and how to read it.

Chronological age	OMICm Age	Overall systems age	Pace of ageing
42.5 years	38.9 years	40.1 years	0.87
	3.6 years below your chronological age	2.4 years below your chronological age	

Sample processed and analysed by TruDiagnostic's laboratory. Lola presents the laboratory's estimates and their positions within its balanced reference cohort.

What these are

Estimates read from the methylation pattern of one sample. Where the name is a familiar one, such as a vitamin or a cholesterol fraction, the figure is what that pattern predicts for it.

Who you are compared with

People of the same sex and a similar age, drawn from the laboratory's balanced reference cohort. Each measurement is placed among them separately, so two figures for the same person can sit at opposite ends without disagreeing.

How to read a bar

The shaded span is the laboratory's own range for that marker, or the middle of the cohort where it publishes none. The mark is this sample, and neither end of the scale is a target. The full guide is at the back.

What this report covers

Every section, how many measurements are in it, and how many of those sit outside a range the laboratory published.

SECTION	MEASUREMENTS	WITH A RANGE	OUTSIDE IT
Biological age estimates	3	—	—
Body-system age estimates	11	—	—
Fitness and physical function estimates	4	—	—
Lipids and lipoproteins	3	—	—
Glucose, energy and hormone markers	6	—	—
Amino acids and related metabolites	5	—	—
Inflammation markers	3	—	—
Immune cell profile	14	1	—
Liver, kidney and blood-cell markers	8	—	—
Vitamins, cofactors and antioxidants	1	—	—
Neurological and neurotransmitter markers	1	—	—
Tissue and cellular proteins	4	—	—
Environmental and lifestyle exposure markers	3	—	—

Sample processed and analysed by TruDiagnostic. Lola presents the laboratory's estimates.

Your headline measurements

The measurements this report leads with, each set against your chronological age.

OMICm Age

38.9 years

An age estimate based on DNA methylation patterns linked to several types of biological measurements in the model's training data.

Developed with Brigham and Women's Hospital and Harvard Medical School. Published in Nature Aging, 2026.

37 your age, 42.5 48

3.6 years below your chronological age

PEOPLE OF THE SAME AGE AND SEX **27.8** PERCENTILE

0 middle 60% of the cohort, 20–80 100

Lower than 72% of people the same age and sex

Since your last sample was 40.1 · **−1.2**

Overall systems age

40.1 years

A combined age estimate from methylation patterns associated with several body systems.

Developed by researchers at Yale. Published in Nature Aging, 2025.

38 your age, 42.5 48

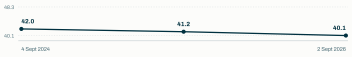
2.4 years below your chronological age

PEOPLE OF THE SAME AGE AND SEX **34.5** PERCENTILE

0 middle 60% of the cohort, 20–80 100

Lower than 66% of people the same age and sex

Since your last sample was 41.2 · **−1.1**



Pace of ageing

0.87

A methylation-based estimate of biological ageing pace, in biological years per calendar year.
A value of 1.0 represents the average pace in the model's training group.

Developed by researchers at Duke University and the University of Otago from the Dunedin Longitudinal Study.

0.60 average pace, 1.00 1.40

PEOPLE OF THE SAME AGE AND SEX **22.1** PERCENTILE

0 middle 60% of the cohort, 20–80 100

Lower than 78% of people the same age and sex

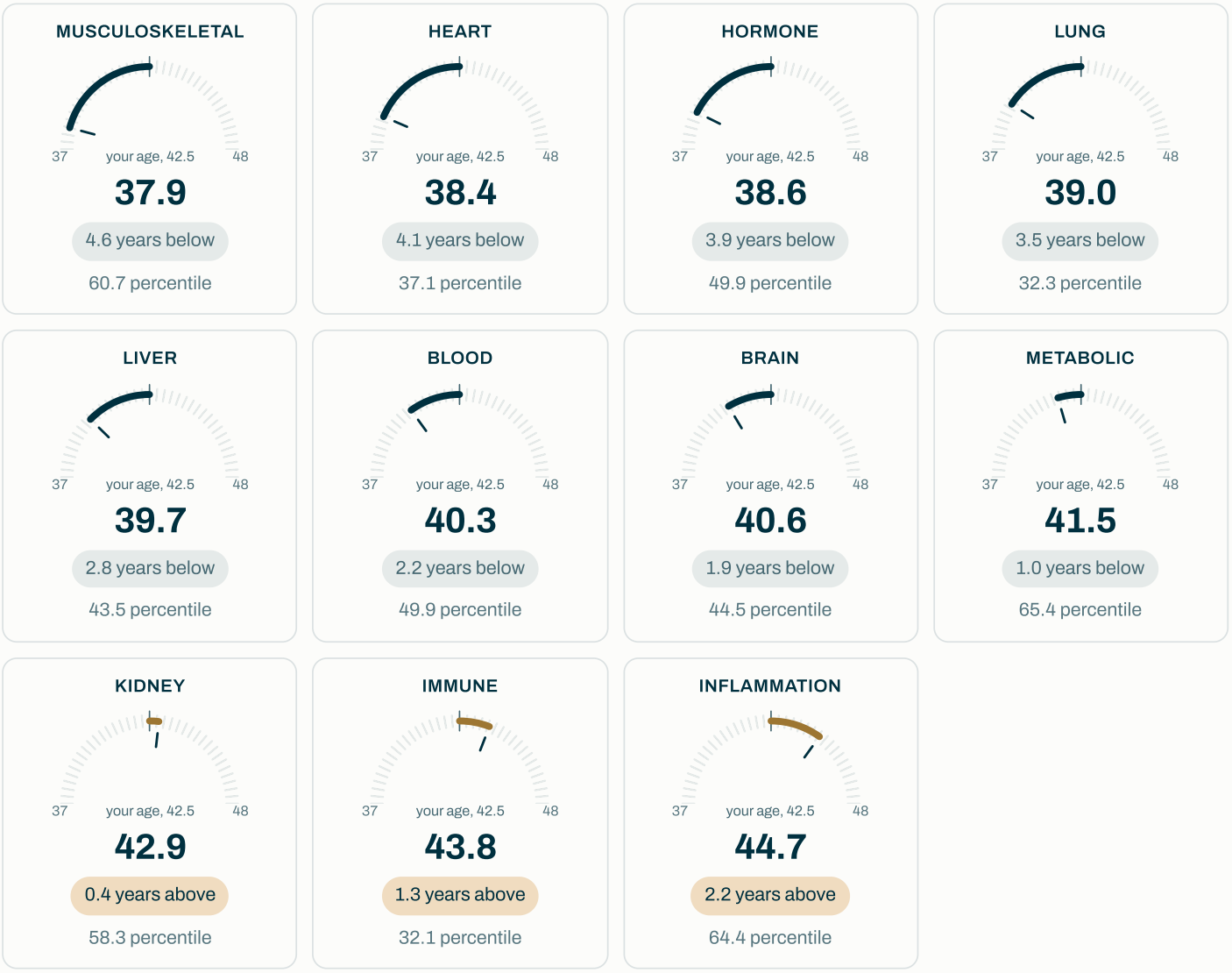
Since your last sample was 0.91 · **−0.04**

Sample processed and analysed by TruDiagnostic. Lola presents the laboratory's estimates.

Body-system ages against your chronological age

Ageing is not one process on one timetable. The same sample carries separate estimates for eleven body systems, each trained against the measurements clinicians use for that system, so they can and routinely do disagree with one another and with the headline figure.

The eleven dials are drawn to one scale, with your calendar age at the top of each. A needle further from the top is further from your age, and that distance can be compared across the set. Read it for its spread rather than for any one number.



Measurements outside the laboratory's range

The laboratory publishes its own range for 1 of the measurements in this report, and this sample sits inside every one of them.

Sample processed and analysed by TruDiagnostic. Lola presents the laboratory's estimates.

Living with your results

General guidance that applies to everybody, whatever your figures say.

SLEEP

Most adults settle between seven and nine hours a night. Regularity counts for as much as the total: a bedtime and a waking time that stay put across the week.

MOVEMENT

World Health Organization guidance for adults is at least 150 minutes of moderate activity a week, or 75 minutes of vigorous activity, alongside muscle-strengthening work on at least two days. Its own summary of the evidence is short: some is good, more is better.

FOOD

Dietary guidance the world over converges on the same few points: at least five portions of a variety of fruit and vegetables a day, plenty of fibre, and fish twice a week, one of them oily. The Mediterranean pattern of vegetables, pulses, whole grains, olive oil and fish is the most studied of the named eating patterns.

ALCOHOL AND TOBACCO

Both leave methylation signatures the laboratory reads directly, which is why this report carries a measure of each. Less of either is the direction every national guideline points in.

STRESS AND CONNECTION

Published work on methylation patterns includes measures of long-term stress and of social connection, alongside the behaviours above. What people find workable varies; the common thread in the research is regularity rather than intensity.

KEEPING A RECORD

Writing down what you changed and when is what makes the next result readable. Two samples six months apart say a great deal more when you can name what sat between them.

WHAT NEXT

Testing again

One sample is a position. Two are a direction, and the interval between them is what makes the second one readable.

THREE TO SIX MONTHS

Methylation patterns move slowly. Three to six months between samples is long enough for a change to mean something; a fortnight is not. For this sample, that is any time from December 2026.

SIMILAR CONDITIONS

Time of day, a recent illness and a recent vaccination can all move methylation readings on their own. Sampling under similar conditions each time keeps the comparison about you rather than about the week.

READ THEM TOGETHER

Comparing two results is a different conversation from reading one. Where a measurement has moved, this report prints what it was alongside what it is.

Biological age estimates

Whole-body age estimates calculated from DNA methylation patterns. Different models use different training data and can give different ages for the same sample.

Bars run 0–100, a percentile among people of the same age and sex · the shaded span is the middle 60% of the cohort, 20–80

MEASUREMENT	VALUE	COHORT POSITION	POSITION
Fitness age estimate	**39.2** years	3.3 years below your chronological age	
An age estimate combining methylation-based predictions related to fitness, expressed in years.			
Telomere age estimate	**40.8** years	1.7 years below your chronological age	
An age estimate based on a methylation pattern associated with telomere length. *Since your last sample: was 38.0 · **+2.8***			
PC telomere length	**63.4** percentile		higher than 63%
A DNA methylation-based estimate related to telomere length. Telomeres are protective structures at chromosome ends.			

Body-system age estimates

Age estimates based on methylation patterns associated with different body systems, plus a combined estimate. They are grouped by the measurements used to train each model.

The same estimates plotted above, each with its position in the cohort · Bars run 0–100, a percentile among people of the same age and sex · the shaded span is the middle 60% of the cohort, 20–80

MEASUREMENT	VALUE	COHORT POSITION	POSITION	SINCE LAST SAMPLE
Heart system age	**38.4** years		lower than 63%	was 34.9 · **+3.5**
The heart and blood vessels move blood around the body. This estimate comes from methylation patterns associated with markers of cardiac and vascular tissue.				
Lung system age	**39.0** years		lower than 68%	
The lungs move air and exchange oxygen for carbon dioxide. This estimate comes from methylation patterns associated with markers of breathing capacity.				

Sample processed and analysed by TruDiagnostic. Lola presents the laboratory's estimates.

Brain system age

40.6 years

lower than 56%

was 43.3 · **−2.7**

The brain and nervous system carry signalling between the body and the brain. This estimate comes from methylation patterns associated with markers of nerve tissue.

Liver system age

39.7 years

lower than 57%

The liver processes nutrients, clears substances from blood and makes many circulating proteins. This estimate comes from methylation patterns associated with liver enzymes and proteins.

Kidney system age

42.9 years

higher than 58%

was 42.6 · **+0.3**

The kidneys filter blood and regulate fluid and salt balance. This estimate comes from methylation patterns associated with markers of filtration.

Blood system age

40.3 years

lower than 50%

The blood system carries oxygen, nutrients and clotting factors. This estimate comes from methylation patterns associated with blood cell counts and haemoglobin.

Immune system age

43.8 years

lower than 68%

was 46.8 · **−3.0**

The immune system responds to infection and injury. This estimate comes from methylation patterns associated with the proportions of immune cell populations in the sample.

Inflammation system age

44.7 years

higher than 64%

was 42.3 · **+2.4**

Inflammation is part of how the body responds to injury and infection. This estimate comes from methylation patterns associated with inflammatory signalling markers.

Hormone system age

38.6 years

lower than 50%

was 39.5 · **−0.9**

Hormones are chemical messengers regulating growth, metabolism and reproduction. This estimate comes from methylation patterns associated with hormone-signalling markers.

Metabolic system age

41.5 years

higher than 65%

Metabolism converts food into energy and stores what is not used. This estimate comes from methylation patterns associated with glucose and lipid handling.

Musculoskeletal system age

37.9 years

higher than 61%

was 39.8 · **−1.9**

Muscles, bones and connective tissue give the body structure and movement. This estimate comes from methylation patterns associated with markers of muscle and bone.

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Fitness and physical function estimates

Methylation-based estimates related to breathing volume, walking speed, grip strength and aerobic capacity.

Bars run 0–100, a percentile among people of the same age and sex · the shaded span is the middle 60% of the cohort, 20–80

MEASUREMENT	VALUE	COHORT POSITION	POSITION
VO2 max estimate A methylation-based estimate related to maximal oxygen uptake (VO2 max), a measure of aerobic capacity. *Since your last sample: was 67.3 · **+4.0***	**71.3** percentile		higher than 71%
Grip strength estimate A methylation-based estimate related to hand-grip force.	**58.2** percentile		higher than 58%
Gait speed estimate A methylation-based estimate related to walking speed.	**66.0** percentile		higher than 66%
FEV1 estimate A methylation-based estimate related to forced expiratory volume in one second (FEV1): the air a person can forcefully breathe out in the first second.	**54.4** percentile		higher than 54%

Lipids and lipoproteins

Cholesterol is carried through blood in particles called lipoproteins; other lipids help form cell membranes. These rows group methylation-based estimates of those substances and particles.

Bars run 0–100, a percentile among people of the same age and sex · the shaded span is the middle 60% of the cohort, 20–80

MEASUREMENT	VALUE	COHORT POSITION	POSITION	SINCE LAST SAMPLE
Paraoxonase 1 (PON1) An enzyme carried on HDL particles with antioxidant activity.	**44.5** percentile		lower than 56%	
1-stearoyl-2-adrenoyl-GPC A phosphatidylcholine, one of the fats that help form cell membranes, containing stearic and adrenic fatty-acid chains.	**70.8** percentile		higher than 71%	 was 67.7 · **+3.1**

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1-margaroyl glycerophospholipid — 44.7 percentile — lower than 55% — was 43.9 · +0.8

A member of the phospholipid family, the fats that help form cell membranes. It contains a 17-carbon fatty-acid chain.

Glucose, energy and hormone markers

Glucose, ketones and related compounds help supply energy; hormones help coordinate how that energy is used and stored. These rows describe methylation-based estimates associated with those processes.

Bars run 0–100, a percentile among people of the same age and sex · the shaded span is the middle 60% of the cohort, 20–80

MEASUREMENT	VALUE	COHORT POSITION	POSITION	SINCE LAST SAMPLE
HbA1c	55.4 percentile		higher than 55%	was 55.7 · −0.3
HbA1c is haemoglobin with glucose attached. A conventional HbA1c test reflects blood sugar over preceding months; this row instead contains a methylation-based estimate associated with that measurement.				
Fasting glucose	44.1 percentile		lower than 56%	was 47.8 · −3.7
Glucose is the sugar carried in blood for energy. This is a methylation-based estimate associated with fasting glucose.				
IGF-binding protein 2	41.3 percentile		lower than 59%	was 43.2 · −1.9
A carrier protein that regulates how much IGF is available to tissues.				
Androsterone sulfate	60.2 percentile		higher than 60%	was 59.1 · +1.1
A sulfated metabolite downstream of testosterone.				
Gluconate	59.9 percentile		higher than 60%	was 62.6 · −2.7
An oxidised form of glucose involved in carbohydrate handling.				
Ribitol	61.0 percentile		higher than 61%	
A five-carbon sugar alcohol related to ribose, the sugar used in RNA.				

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Amino acids and related metabolites

Amino acids are building blocks of proteins. Related compounds are made as the body and gut microbes process them; this section also groups related products of cellular metabolism.

Bars run 0–100, a percentile among people of the same age and sex · the shaded span is the middle 60% of the cohort, 20–80

MEASUREMENT	VALUE	COHORT POSITION	POSITION
Phenylacetylglutamine A metabolite formed when gut bacteria process phenylalanine. *Since your last sample: was 31.7 · **–0.1***	**31.6** percentile		lower than 68%
4-hydroxyphenylacetylglutamine A gut-microbial metabolite of aromatic amino acids.	**48.6** percentile		lower than 51%
Uridine A nucleoside used in RNA synthesis and cellular energy pathways.	**50.4** percentile		higher than 50%
3-ureidopropionate An intermediate in the breakdown of pyrimidines.	**54.3** percentile		higher than 54%
N-acetyl-isoputreanine A downstream product of polyamine breakdown.	**49.9** percentile		lower than 50%

Inflammation markers

Inflammation is part of the body's response to injury and infection. This group contains methylation-based estimates associated with proteins involved in that response.

Bars run 0–100, a percentile among people of the same age and sex · the shaded span is the middle 60% of the cohort, 20–80

MEASUREMENT	VALUE	COHORT POSITION	POSITION
CRP A methylation-based estimate associated with C-reactive protein, an inflammation-related protein produced by the liver.	**61.9** percentile		higher than 62%
IL-6 A methylation-based estimate associated with interleukin-6, a signalling protein involved in inflammation. *Since your last sample: was 45.3 · **–2.4***	**42.9** percentile		lower than 57%

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Inter-alpha-trypsin inhibitor H3 — 43.5 percentile — lower than 57%

A plasma protein involved in the inflammatory response and tissue repair.

Immune cell profile

White blood cells have different roles in recognising and responding to threats. These rows contain methylation-based estimates related to cell populations, counts and ratios. Two kinds of row sit together here: a share of the white-cell population, and an estimated count of one cell type. They answer different questions, so the same cell type can sit high on one and low on the other.

Bars run 0–100, a percentile among people of the same age and sex · the shaded span is the middle 60% of the cohort, 20–80, unless a row states the laboratory's own range for that marker

MEASUREMENT	VALUE	COHORT POSITION	POSITION
Neutrophils (share of white cells)	58.6 percentile		higher than 59%
The estimated share of white blood cells that are neutrophils, the most abundant circulating type, as a share of all white cells.			
Monocytes (share of white cells)	60.5 percentile		higher than 61%
The estimated share of white blood cells that are monocytes, which mature into tissue macrophages, as a share of all white cells.			
*Since your last sample: was 57.5 · **+3.0***			
Eosinophils (share of white cells)	63.1 percentile		higher than 63%
The estimated share of white blood cells that are eosinophils, a granulocyte population, as a share of all white cells.			
*Since your last sample: was 66.1 · **−3.0***			
Basophils (share of white cells)	33.3 percentile		lower than 67%
The estimated share of white blood cells that are basophils, a granulocyte population, as a share of all white cells.			
*Since your last sample: was 33.7 · **−0.4***			
Natural killer cells	49.7 percentile		lower than 50%
Part of the innate immune response, acting without needing prior exposure.			
Naive CD4 T cells	43.4 percentile		lower than 57%
Have not yet met their target; they coordinate rather than kill.			
Memory CD4 T cells	69.4 percentile		higher than 69%
Retain a record of a previous immune exposure and coordinate the response to it.			

Sample processed and analysed by TruDiagnostic. Lola presents the laboratory's estimates.

Naive CD8 T cells Have not yet met their target; they act on cells rather than coordinate.	**47.6** percentile		lower than 52%
Memory CD8 T cells Retain a record of a previous immune exposure and act on cells carrying it. *Since your last sample: was 61.7 · **+2.8***	**64.5** percentile		higher than 65%
Regulatory T cells Moderate the activity of other immune cells, keeping a response proportionate. *Since your last sample: was 43.8 · **+3.2***	**47.0** percentile		lower than 53%
Naive B cells Have not yet met the target they are made to recognise. *Since your last sample: was 50.3 · **+1.9***	**52.2** percentile		higher than 52%
Memory B cells Retain a record of a previous immune exposure, so a later response to it is faster.	**47.4** percentile		lower than 53%
Neutrophil to lymphocyte ratio Compares two white-cell populations estimated from the same sample.	**43.1** percentile		lower than 57%
CD4/CD8 T cell ratio Compares two T cell populations estimated from the same sample.	**52.3** percentile	 laboratory's range: 30–80	higher than 52%

Liver, kidney and blood-cell markers

This group brings together substances processed by the liver and kidneys, along with red-blood-cell characteristics. The values are methylation-based estimates associated with those measurements.

Bars run 0–100, a percentile among people of the same age and sex · the shaded span is the middle 60% of the cohort, 20–80

MEASUREMENT	VALUE	COHORT POSITION	POSITION
Haemoglobin The protein in red blood cells that carries oxygen.	**48.6** percentile		lower than 51%
Haematocrit The proportion of blood volume made up of red blood cells. *Since your last sample: was 50.0 · **–2.1***	**47.9** percentile		lower than 52%

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Red blood cell distribution width

56.0 percentile — higher than 56%

The variation in size between red blood cells.

Creatinine

55.4 percentile — higher than 55%

A by-product of normal muscle metabolism, cleared by the kidneys.

Blood urea nitrogen

49.6 percentile — lower than 50%

The nitrogen component of urea, a waste product formed during protein breakdown and cleared by the kidneys.

*Since your last sample: was 48.0 · **+1.6***

Albumin

61.7 percentile — higher than 62%

A protein carried in blood that helps maintain fluid balance and transport other substances.

Alkaline phosphatase

60.5 percentile — higher than 61%

An enzyme found in liver, bone and other tissues.

*Since your last sample: was 63.5 · **–3.0***

Carboxypeptidase B2

56.4 percentile — higher than 56%

An enzyme involved in the balance between clotting and its breakdown.

Vitamins, cofactors and antioxidants

Vitamins and cofactors help enzymes work; antioxidants participate in reactions that manage oxidation. These rows contain methylation-based estimates associated with those compounds and their breakdown products.

Bars run 0–100, a percentile among people of the same age and sex · the shaded span is the middle 60% of the cohort, 20–80 · Related foods name sources of the substance, never a change to make

MEASUREMENT	VALUE	COHORT POSITION	POSITION
Carotene diol A carotenoid found in the diet and carried in the blood.	**53.4** percentile		higher than 53%

RELATED FOODS: Kale · Spinach · Sweetcorn · Egg yolk

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Neurological and neurotransmitter markers

This group contains compounds involved in nerve-cell signalling and related metabolic pathways. The values are methylation-based estimates.

Bars run 0–100, a percentile among people of the same age and sex · the shaded span is the middle 60% of the cohort, 20–80

MEASUREMENT	VALUE	COHORT POSITION	POSITION	SINCE LAST SAMPLE
Vanillactic acid	**65.4** percentile		higher than 65%	was 61.4 · **+4.0**
A metabolite of aromatic amino acid breakdown.				

Tissue and cellular proteins

Cells use proteins to make energy, organise DNA, maintain their surroundings and communicate. These rows group methylation-based estimates associated with those proteins.

Bars run 0–100, a percentile among people of the same age and sex · the shaded span is the middle 60% of the cohort, 20–80

MEASUREMENT	VALUE	COHORT POSITION	POSITION	SINCE LAST SAMPLE
Histone H2B type 1-K	**59.9** percentile		higher than 60%	
A histone protein that packages DNA within the cell nucleus.				
Bone morphogenetic protein 1	**56.6** percentile		higher than 57%	was 52.7 · **+3.9**
A protein involved in bone formation and connective tissue remodelling.				
Pancreatic ribonuclease	**25.4** percentile		lower than 75%	was 22.9 · **+2.5**
An enzyme that breaks down RNA.				
Versican core protein	**44.0** percentile		lower than 56%	was 44.6 · **−0.6**
The protein component of versican, a large molecule in the supporting material around cells.				

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Environmental and lifestyle exposure markers

Methylation-based estimates associated with environmental compounds, tobacco and alcohol.

Bars run 0–100, a percentile among people of the same age and sex · the shaded span is the middle 60% of the cohort, 20–80

MEASUREMENT	VALUE	COHORT POSITION	POSITION
Alcohol methylation signature A methylation signature the laboratory associates with alcohol intake. It estimates a pattern associated with intake, not an amount consumed.	**31.2** percentile		lower than 69%
Smoking pack-year estimate A methylation-derived estimate of cumulative tobacco exposure.	**8.9** percentile		lower than 91%
4-methoxyphenol sulfate A sulfated metabolite of dietary and environmental phenols. *Since your last sample: was 72.7 · **+2.7***	**75.4** percentile		higher than 75%

Foods that come up

Polyphenol-rich foods	Berries, dark chocolate, green tea, olive oil, coffee.
Cruciferous vegetables	Broccoli, Brussels sprouts, kale, cauliflower, watercress.
Oily fish	Salmon, mackerel, sardines and anchovies: sources of the long-chain omega-3 fatty acids EPA and DHA.
Fermented foods	Kimchi, sauerkraut, kefir, live yoghurt, miso.
Pulses and whole grains	Lentils, chickpeas, beans, oats, barley, rye.

Compounds discussed in ageing research

Spermidine	A polyamine found in wheat germ, aged cheese, mushrooms and soy products, and sold as a supplement.

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Nicotinamide mononucleotide (NMN) and nicotinamide riboside (NR)	Two forms of vitamin B3 precursor studied in relation to cellular energy metabolism.
Quercetin and related senolytics	A flavonoid found in onions, apples and capers, studied alongside other compounds in the senescent-cell literature.

How these numbers are produced

WHAT DNA METHYLATION IS

Your DNA sequence stays the same throughout your life. Methylation is a chemical tag the body adds on top of it, and the pattern of those tags changes with age, environment and behaviour. The laboratory reads that pattern at around a million positions from one sample.

WHAT AN EPIGENETIC CLOCK IS

A clock is a statistical model. Researchers measured methylation in thousands of people whose ages and laboratory values were already known, then found the combination of positions that best predicted them. Putting your pattern through that model returns its estimate.

WHY TWO CLOCKS GIVE DIFFERENT AGES

Each model was trained on different people against different reference measurements, so each answers a slightly different question. Two estimates from the same sample can differ by several years without either being wrong, which is why this report states each one beside the group it was compared with.

How this field arrived

The models behind these estimates were described over little more than a decade.

- **2011** The first age estimate built from DNA methylation is published.
- **2013** The Hannum and Horvath clocks arrive. Horvath's is the first trained across several tissues; Hannum's is built in blood alone.
- **2016** A clock trained on cell division rather than on age alone is described.
- **2018** PhenoAge is trained on clinical laboratory measurements instead of age alone.
- **2019** GrimAge is published, trained on plasma protein markers and smoking history.
- **2020** DunedinPoAm estimates a rate of change rather than a single age.

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- **2021** DunedinPACE refines that rate using repeated samples from the same people.
- **2022** Principal-component clocks improve how closely two runs of one sample agree.
- **2023** OMICmAge is trained on proteomic, metabolomic and clinical measurements together.

What these measurements are

The models behind the headline figures: who built each one, on what data, and what its number is expressed in.

OMICM AGE

An age-scaled estimate computed from selected DNA methylation patterns. Developed by TruDiagnostic with researchers at the Channing Division of Network Medicine, Brigham and Women's Hospital and Harvard Medical School, and published in Nature Aging in 2026. The model uses methylation-based predictions associated with clinical, protein and metabolite measurements, developed on the Mass General Brigham Biobank and validated in two further cohorts.

BODY-SYSTEM AGES

Age-scaled statistical estimates developed by researchers at Yale by linking blood methylation patterns with groups of clinical and functional measurements for each body system. The model combines those predicted patterns into system-level estimates. All eleven come from the one blood sample.

PACE OF AGEING

An estimate of biological ageing pace from one DNA methylation sample, expressed in biological years per calendar year. A value of 1.0 represents the average pace in the training group; below 1.0 is a slower estimated pace than that average and above it is faster. DunedinPACE was developed by researchers including teams at Duke University and the University of Otago, using changes in multiple body-system measurements collected over two decades in the Dunedin Longitudinal Study. The model learns from those repeated observations; your result is a prediction from one sample.

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How to read this report

Reference for the pages above: how these estimates are produced, who each percentile compares you with, and how to read the bar.

WHY THESE ARE NOT BLOOD LEVELS

Many rows carry the name of a substance, such as a vitamin, a cholesterol fraction or an inflammatory protein. Each value is what the methylation pattern predicts for that substance. The pattern moves more slowly than a level in blood, so the figure can differ from a conventional blood test taken the same day.

WHO THIS SAMPLE IS COMPARED WITH

Every percentile here compares your sample with people of the same sex and a similar age, within five years either way, drawn from a reference set the laboratory built from the Mass General Brigham Biobank and TruDiagnostic cohorts and put together to stand in for a population of ordinary health.

HOW TO READ THE PERCENTILE

A percentile places this sample among people of the same age and sex. A percentile of 61 means the measurement is higher than 61 per cent of them and lower than the remaining 39 per cent. It is a position among other people, not a score.

THE SHADED BAND ON EACH BAR

Where the laboratory publishes its own range for a marker, the bar is drawn against that range and prints the numbers it was drawn with. Where it publishes none, the shaded span covers the 20th to 80th percentile instead: the middle 60 per cent of the reference cohort, which describes where most of that group falls rather than a range anyone published. Above the 80th percentile the measurement is higher than 80 per cent of that group; below the 20th it is lower than 80 per cent of them. Neither end of the scale is a target.

A WORKED EXAMPLE

A measurement whose percentile is 61.3 puts the mark just past the middle of the bar, and the position column reads “higher than 61%”, meaning 61 per cent of the cohort measured lower. The same measurement at percentile 8 would put the mark near the left end, and the column would read “lower than 92%”. Both are the same number said in words.

HOW TO READ CHANGE OVER TIME

A change is shown only where an earlier sample exists for the same measurement, and a chart is drawn only for those. A single sample has nothing to compare against, so nothing is shown. Sampling, laboratory variation and model differences all move a number between two runs, so a small change is within what the method itself varies by.