HURDLE

Epigenetic Health

The Future of Preventative Healthcare

Preventative healthcare benefits everyone

People want to live healthier lives for longer.

But they need an **objective and scientifically-validated way** to quantify if their prevention efforts are working.

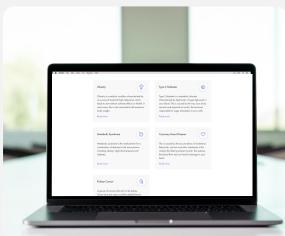
With **clear recommendations** and actions on the next steps in their journey.



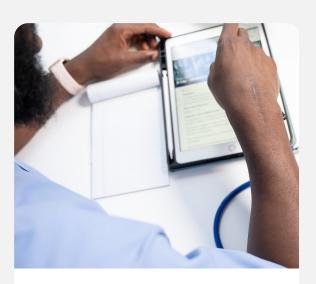
We have designed a platform suited for the prevention journey



Accessibility. A simple saliva test that can be done from the comfort of your own home, accessing this information has never been easier.



Technology. A comprehensive view of health with all risk factors in one place. Using thousands of biomarkers that reflect your genetics and lifestyle, allowing for a personalised multi-disease prevention platform.



Actionability. A powerful tool to promote positive behavioral change based on results. Employers and doctors can use this technology to personalise and effectively engage with patients, maximising better health outcomes.

Epigenetics: The Platform for Preventative Healthcare

Epigenetics is like the operating system of our genes. It controls how our DNA is read and expressed, determining which genes are turned on or off, and ultimately influencing our risk of developing age-related and chronic diseases.

Unlike genetics, epigenetics can ...





Change over time, so patients can see progress.



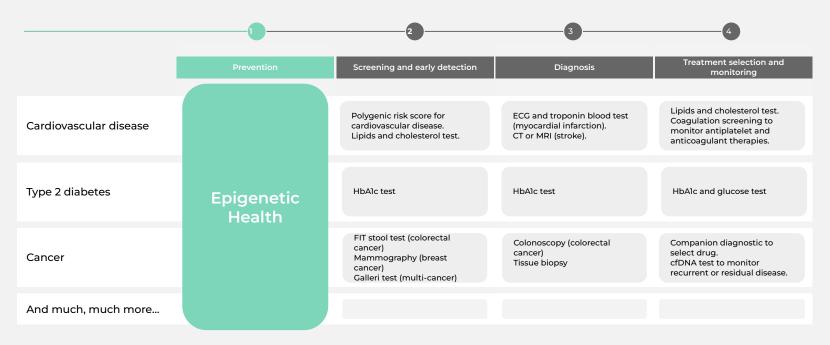
Integrate the effects of **both genetics** and lifestyle/environmental factors.



Actionable

It is the most accurate way to simultaneously quantify the risk of developing many age-related diseases.

The Entry point for personalised preventative care



State-of-the-art experience







Biological Age Test Result

Sample collection date / 24.06.2022, 10:52 am

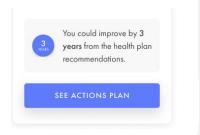
We've analysed thousands of sites on your DNA to determine how old you are on the inside – biological age is a much more accurate picture of your health than your calendar age. Ready to take a look?



Test1, based on your DNA test result, your biological age is:





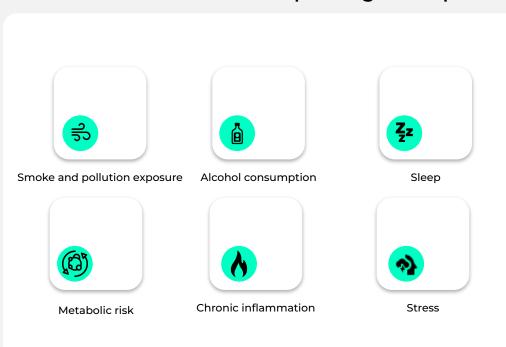


Epigenetic Health Advancements



BioAge - Unlocking today's potential

The Future Biomarkers - Expanding our impact



Proven Innovation



Founded in science

Founded by esteemed scientists and the leading experts from Oxford and Cambridge University

Peer-reviewed publications

10+ publications on epigenetics of ageing, computational biology and novel omics technologies

Patents

Novel age calculation method Novel reprogramming method Epigenetic platform for ML

Novel biomarkers & IVDs Created

First saliva-based NGS epigenetic biomarker for biological age First CF-marked saliva-based COVID-19 PCR test



Making epigenetics more accessible since 2017

We have reduced the cost to 1/5th (from ~1000 GBP to ~200 GBP at low





HIPAA









Security and Quality. Built right in. We design our hardware and software products with global standards at the forefront.

#1

Unrivaled Usability, Unbeatable Price. Scientifically-backed innovations, we deliver unparalleled accessibility, user-friendly experiences and cost-effective solutions for all.

HURDLE

Epigenetic health.
Join the revolution
that is creating a
healthier tomorrow.

Selected Scientific Publications - Management Team

<u>Single cell DNA methylation ageing in mouse blood.</u> Bonder MJ, Clark SJ, Krueger F, Luo S, de Sousa JA, Hashtroud AM, <u>Stubbs TM</u>, Stark A, Rulands S, Stegle O, Reik W, von Meyenn F, bioRxiv 2023.01.30.526343 https://doi.org/10.1101/2023.01.30.526343

Multi-omic rejuvenation of naturally aged tissues by a single cycle of transient reprogramming. Chondronasiou D, Gill D, Mosteiro L, Urdinguio RG, Berenguer A, Aguilera M, Durand S, Aprahamian F, Nirmalathasan N, Abad M, Martin-Herranz DE, Stephan Otto-Attolini C, Prats N, Kroemer G, Fraga MF, Reik W, Serrano M. Aging Cell 2022 21, e13578; doi: https://doi.org/10.1111/acel.13578

Multi-omic rejuvenation of human cells by maturation phase transient reprogramming.

Gill D, Parry A, Santos F, Hernando-Herraez I, Stubbs TM, Milagre I, Reik W. eLife 2022

11:e71624: doi: https://doi.org/10.7554/eLife.71624

Remote Consultations Handbook Edition 2: Strategies to ensure a safe and effective consultation via video or telephone. Abbs A, Hyams A, Ahmed Z. Independent 2020 2nd ed., pp.0–72

https://www.amazon.co.uk/Remote-Consultations-Handbook-Strategies-consultation-ebook/dp/B09NP9VJC9

Ageing affects DNA methylation drift and transcriptional cell-to-cell variability in mouse muscle stem cells. Hernando-Herraez I, Evano B, <u>Stubbs TM</u>, Commere PH, Jan Bonder M, Clark S, Andrews S, Tajbakhsh S, Reik W. Nat Commun 10, 4361.2019. https://doi.org/10.1038/s41467-019-12293-4

Screening for genes that accelerate the epigenetic aging clock in humans reveals a role for the H3K36 methyltransferase NSDI. Martin-Herranz DE, Aref-Eshghi E, Bonder MJ, Stubbs TM, Choufani S, Weksberg R, Stegle O, Sadikovic B, Reik W, Thornton JM. Genome Biol. 2019 Aug 14:20(1):146. doi: 10.1186/s13059-019-1753-9.

Hepatic gene body hypermethylation is a shared epigenetic signature of murine longevity. Hahn O, Stubbs TM, Reik W, Grönke S, Beyer A, Partridge L. PLoS Genet. 2018 Nov 21;14(11):e1007766. doi: 10.1371/journal.pgen.1007766. eCollection 2018 Nov.

scNMT-seq enables joint profiling of chromatin accessibility DNA methylation and transcription in single cells, Clark SJ, Argelaguet R, Kapourani CA, Stubbs TM, Lee HJ, Alda-Catalinas C, Krueger F, Sanguinetti G, Kelsey G, Marioni JC, Stegle O, Reik W. Nat Commun. 2018 Feb 22;9(1):781. doi: 10.1038/s41467-018-03149-4.

cuRRBS: simple and robust evaluation of enzyme combinations for reduced representation approaches. Martin-Herranz DE, Ribeiro AJM, Krueger F, Thornton JM, Reik W, Stubbs TM. Nucleic Acids Res. 2017 Nov 16;45(20):11559-11569. doi: 10.1093/nar/gkx814.

Multi-tissue DNA methylation age predictor in mouse. Stubbs TM, Bonder MJ, Stark AK, Krueger F; BI Ageing Clock Team, von Meyenn F, Stegle O, Reik W. Genome Biol. 2017 Apr 11;18(1):68. doi: 10.1186/s13059-017-1203-5.

<u>Dietary restriction protects from age-associated DNA methylation and induces epigenetic reprogramming of lipid metabolism.</u> Hahn O, Grönke S, <u>Stubbs TM</u>, Ficz G, Hendrich O, Krueger F, Andrews S, Zhang Q, Wakelam MJ, Beyer A, Reik W, Partridge L. Genome Biol. 2017 Mar 28;18(1):56. doi: 10.1186/s13059-017-1187-1.

Gender Differences in Global but Not Targeted Demethylation in iPSC Reprogramming. Milagre I, Stubbs TM, King MR, Spindel J, Santos F, Krueger F, Bachman M, Segonds-Pichon A, Balasubramanian S, Andrews SR, Dean W, Reik W. Cell Rep. 2017 Jan 31;18(5):1079-1089. doi: 10.1016/j.celrep.2017.01.008.

MERVL/Zscan4 Network Activation Results in Transient Genome-wide DNA Demethylation of mESCs. Eckersley-Maslin MA, Svensson V, Krueger C, <u>Stubbs TM</u>, Giehr P, Krueger F, Miragaia RJ, Kyriakopoulos C, Berrens RV, Milagre I, Walter J, Teichmann SA, Reik W. Cell Rep. 2016 Sep 27;17(1):179-192. doi: 10.1016/j.celrep.2016.08.087.

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