

Explore the exciting role of epigenetics through accessing our proprietary Nucleosomics™ platform, Nu.Q® Discover.

- Nu.Q® Discover gives you access to a range of 13 state-of-the-art assays, built on our proprietary Nucleosomics™ platform, for rapid epigenetic profiling in disease model development, preclinical testing and clinical trials.

Our H3.1 assay is also available for purchase as a Research Use Only kit.

- **What are the benefits?** You can use our assays to answer your clinical questions, such as measuring treatment efficacy, or on-target and off-target effects in drug development.

Applications include biomarker discovery in oncology, inflammatory conditions, diabetes and more.

- **Who can benefit?** If you are a pharmaceutical company or academic research institution, we can work with you to support your development needs and help you execute your vision.

- **What does it cost?** To purchase our H3.1 assay or receive a quote for any of the assays within our Nu.Q® Discover portfolio, please contact our commercial team today by emailing sales@volition.com.

- **Where are the assays processed?**

Our Silver One site in Belgium offers cutting edge, purpose-built manufacturing and processing facilities. We manufacture our own plates and large scale batches of our antibodies on beads.

Our expert team will be on hand throughout, to offer guidance and support and to fulfil your needs. Volition's objective is to establish long-term mutually beneficial commercial relationships (subject to IP).

- **How can I find out more?** If you would like more information about Nu.Q® Discover, get in touch with our commercial team by emailing sales@volition.com



Assay Target List

A complete solution to profiling nucleosomes.

Nu.Q® V

H3.1

The nucleosome core particle is composed of an octamer of histone proteins comprising a tetramer of histone H3 and H4 and two dimers H2A-H2B, around which 147bp of DNA is wrapped. In addition to the post-translational modifications occurring on the N-terminal tails of the histone, histone variants (for histone H3, H2A and H2B but not H4) could be incorporated. The canonical H3.1 histone variant, incorporated during S-phase, is maintained at high levels in cells dividing at a high rate but is massively evicted in cells undergoing their last cell cycle before exit to differentiation.

Our H3.1 assay is available for purchase as a Research Use Only kit. For more details, please contact our commercial team.

Nu.Q® Mutation

H3K27M

Mutation in the Histone 3 (H3) on the lysine 27 replaced by a Methionine and is found in aggressive pediatric gliomas.

Nu.Q® M - Methylation

H3K4Me2

Epigenetic modification on the Histone 3 (H3). This mark indicates the di-methylation of lysine 4 on H3 protein and is enriched in cis-regulatory regions in particular, promoters of transcriptionally active genes.

H3K9Me3

Epigenetic modification on the Histone 3 (H3). This epigenetic mark indicates the tri-methylation of lysine 9 on H3 protein and is associated with gene repression and silent hetero- chromatin. H3K9me3 plays a major role in the cell integrity, genomic stability, and heterochromatin maintenance.

H3K27Me3

Epigenetic modification on the Histone 3 (H3). This epigenetic mark indicates the tri-methylation of lysine 27 on H3 protein. This modification is mainly associated with genes repression and often found in heterochromatin regions. H3K27Me3 is regulated by Enhancer of Zeste (EZH2) of Polycomb Repressive Complex PRC2. H3K27me3 has been implicated in numerous of diseases including cancer and it has also been linked to the repair of DNA damage.

H3K36Me3

Epigenetic modification on the Histone 3 (H3). This epigenetic mark indicates the tri-methylation of lysine 36 on H3 protein. This modification is often found in gene body of transcriptionally active genes. The trimethylation is mainly catalysed by SETD2 methyltransferase.

Nu.Q® M - Acetylation

H3K9Ac

Epigenetic modification on the Histone 3 (H3). This mark indicates the acetylation of lysine 9 on H3 protein. This mark, as H3K14Ac, is linked to gene activation and active promoters.

Our H3.1 assay is available for purchase as a Research Use Only kit. For more details, please contact our commercial team.

H3K14Ac

Epigenetic modification on the Histone 3 (H3). This mark indicates the acetylation of lysine 14 on H3 protein. As H3K9Ac, H3K14Ac has been shown to be linked to active promoter state.

H3K27Ac

Epigenetic modification on the Histone 3 (H3). This mark indicates the acetylation of lysine 27 on H3 protein. This mark is associated with the higher activation of transcription, and primarily defined as an active enhancer mark. H3K27Ac is also found surrounding transcriptional start sites (TSS).

H4PanAc

Epigenetic modification on the Histone 4 (H4). These marks indicate the acetylation of some lysine (5, 8, 12 and 16) on H4 protein. H4 acetylation blocks interaction between the H4 tail and the acidic patch on adjacent nucleosomes, decreasing inter-nucleosomal interactions and creating open chromatin.

Nu.Q® M - Other PTMS

pH2AX

Epigenetic modification on the isoform X of Histone 2A (H2AX). This mark indicates the phosphorylation of serine 139 on H2AX protein. This modification correlates with double-strand DNA damage.

H3R8Cit

Epigenetic modification on the Histone 3 (H3). This mark indicates the citrullination of arginine 8 on H3 protein. Protein arginine deiminase 4 (PAD4) mediates citrullination of histone tail residues.

H3S10Ph

Epigenetic modification of Nucleosome on the Histone 3 (H3). This mark indicates the phosphorylation of serine 10 on H3 protein. This modification, done by Aurora kinase, plays a role in mitosis.

For more information:

- email sales@volition.com
- go to volition.com

