abcam

Product datasheet

Human Histone H4 (glcnac S47) peptide ab166696

Description

Product name Human Histone H4 (glcnac S47) peptide

Purity > 70 % HPLC.

70 - 90% purity determined by HPLC

Accession P62805

Animal free No

Nature Synthetic

Species Human

Modifications glenae S47

Specifications

Our $\underline{\textbf{Abpromise guarantee}}$ covers the use of $\underline{\textbf{ab166696}}$ in the following tested applications.

The application notes include recommended starting dilutions; optimal dilutions/concentrations should be determined by the end user.

Form

Lyophilized

Additional notes

- First try to dissolve a small amount of peptide in either water or buffer. The more charged residues on a peptide, the more soluble it is in aqueous solutions.
- If the peptide doesn't dissolve try an organic solvent e.g. DMSO, then dilute using water or buffer.
- Consider that any solvent used must be compatible with your assay. If a peptide does not dissolve and you need to recover it, lyophilise to remove the solvent.
- Gentle warming and sonication can effectively aid peptide solubilisation. If the solution is cloudy or has gelled the peptide may be in suspension rather than solubilised.
- Peptides containing cysteine are easily oxidised, so should be prepared in solution just prior to use.

Preparation and Storage

Stability and Storage

Shipped at 4° C. Upon delivery aliquot and store at -20°C or -80°C. Avoid repeated freeze / thaw

cycles.

Information available upon request.

General Info

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Function Core component of nucleosome. Nucleosomes wrap and compact DNA into chromatin, limiting

DNA accessibility to the cellular machineries which require DNA as a template. Histones thereby play a central role in transcription regulation, DNA repair, DNA replication and chromosomal stability. DNA accessibility is regulated via a complex set of post-translational modifications of

histones, also called histone code, and nucleosome remodeling.

Sequence similaritiesBelongs to the histone H4 family.

Post-translational modifications

 $Acetylation\ at\ Lys-6\ (H4K5ac),\ Lys-9\ (H4K8ac),\ Lys-13\ (H4K12ac)\ and\ Lys-17\ (H4K16ac)\ occurs$

in coding regions of the genome but not in heterochromatin.

Citrullination at Arg-4 (H4R3ci) by PADI4 impairs methylation.

Monomethylation and asymmetric dimethylation at Arg-4 (H4R3me1 and H4R3me2a, respectively) by PRMT1 favors acetylation at Lys-9 (H4K8ac) and Lys-13 (H4K12ac).

Demethylation is performed by JMJD6. Symmetric dimethylation on Arg-4 (H4R3me2s) by the

PRDM1/PRMT5 complex may play a crucial role in the germ-cell lineage.

 $Monomethylated, dimethylated or trimethylated at Lys-21 \ (H4K20me1, H4K20me2, H4K20me3).$

Monomethylation is performed by SET8. Trimethylation is performed by SUV420H1 and

SUV420H2 and induces gene silencing.

Ubiquitinated by the CUL4-DDB-RBX1 complex in response to ultraviolet irradiation. This may weaken the interaction between histones and DNA and facilitate DNA accessibility to repair proteins. Monoubiquitinated at Lys-92 of histone H4 (H4K91ub1) in response to DNA damage. The exact role of H4K91ub1 in DNA damage response is still unclear but it may function as a licensing signal for additional histone H4 post-translational modifications such as H4 Lys-21

methylation (H4K20me).

Sumoylated, which is associated with transcriptional repression.

Cellular localization Nucleus. Chromosome.

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