

# The immunostaining method is ideal for hydroxy methylation of DNA.

## Is it true or false?

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Is identifying DNA hydroxy methylation best achieved by immunostaining? Yes, this method is adaptable and popular but calling it the "perfect" approach is not ideal. Let's see why it is so. Here are 3 key points which support this statement as false-

<b>Measurement:</b>	It can detect the presence of 5-hydroxymethylcytosine (5hmC) in a material. But research has shown that it falls short in measuring DNA hydroxy methylation. Furthermore, it is not that good at providing the quantitative measurements of 5hmC levels accurately.
<b>Image Resolution:</b>	It shows the presence of 5hmC, but it falls short in providing the resolution which is required for performing genome-wide analysis. So sophisticated methods such as TET-assisted bisulfite sequencing (TAB-Seq) and Oxidative bisulfite sequencing (oxBS-seq) are superior to immunostaining. These methods provide a mapping of the 5hmC at single-base resolution across the genome. Hence, they can provide a detailed and precise which gives them an advantage over immunostaining.
<b>Antibody specificity:</b>	Antibody specificity is another part which determines the value of these types of techniques because it determines how 'reliable' this technique is. Factors such as cross-reactivity and DNA changes, such as 5-methylcytosine (5mC) can mislead the results attained. Since these are major factors, fully relying on immunostaining can be concerning and produce wrong results

As a conclusion it can be noted that though immunostaining is a valuable and useful method in the epigenetic toolbox, it cannot be called a perfect method for the analysis of DNA hydroxy methylation. Techniques such as mass spectrometry, genome-wide profiling and more are required to be used in combination to characterise the landscape of DNA hydroxy methylation mainly due to its limited ability in quantification, resolution and antibody specification.