Datasheet

Version: 3.0.0 Revision date: 26 Mar 2025



Human Bromodomain adjacent to zinc finger domain protein 2A (BAZ2A) ELISA Kit

Catalogue No.:abx503570

Human Bromodomain adjacent to zinc finger domain protein 2A (BAZ2A) ELISA Kit is an ELISA Kit for the in vitro quantitative measurement of Human Bromodomain adjacent to zinc finger domain protein 2A (BAZ2A) concentrations in tissue homogenates, cell lysates and other biological fluids.

Target: Bromodomain adjacent to zinc finger domain protein 2A (BAZ2A)

Reactivity: Human

Tested Applications: ELISA

Recommended dilutions: Optimal dilutions/concentrations should be determined by the end user.

Storage: Shipped at 4 °C. Upon receipt, store the kit according to the storage instruction in the kit's manual.

Validity: The validity for this kit is 6 months.

Stability: The stability of the kit is determined by the rate of activity loss. The loss rate is less than 5% within

the expiration date under appropriate storage conditions. To minimize performance fluctuations, operation procedures and lab conditions should be strictly controlled. It is also strongly suggested

that the whole assay is performed by the same user throughout.

UniProt Primary AC: Q9UIF9 (UniProt, ExPASy)

Gene Symbol: BAZ2A

KEGG: hsa:11176

Test Range: 0.156 ng/ml - 10 ng/ml

Standard Form: Lyophilized

Detection Method: Colorimetric

Assay Data: Quantitative

Sample Type: Tissue homogenates, cell lysates and other biological fluids.

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Note:

THIS PRODUCT IS FOR RESEARCH USE ONLY. NOT FOR USE IN DIAGNOSTIC OR THERAPEUTIC PROCEDURES.

The range and sensitivity is subject to change. Please contact us for the latest product information. For accurate results, sample concentrations must be diluted to mid-range of the kit. If you require a specific range, please contact us in advance or write your request in your order comments. Please note that our kits are optimised for detection of native samples, rather than recombinant proteins. We are unable to guarantee detection of recombinant proteins, as they may have different sequences or tertiary structures to the native protein.



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