Datasheet

Version: 1.0.0 Revision date: 04 Aug 2023



Human A disintegrin and metalloproteinase with thrombospondin motifs 15 (ADAMTS15) ELISA Kit

Catalogue No.:abx503216

Human A disintegrin and metalloproteinase with thrombospondin motifs 15 (ADAMTS15) ELISA Kit is an ELISA Kit for the in vitro quantitative measurement of Human A disintegrin and metalloproteinase with thrombospondin motifs 15 (ADAMTS15) concentrations in serum, plasma and other biological fluids.

Target: A disintegrin and metalloproteinase with thrombospondin motifs 15 (ADAMTS15)

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: Q8TE58 (UniProt, ExPASy)

Gene Symbol: ADAMTS15

OMIM: 607509

KEGG: hsa:170689

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

Standard Form: Lyophilized

Detection Method: Colorimetric

Assay Data: Quantitative

Sample Type: Serum, plasma and other biological fluids.

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Note:

This product is for research use only.

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 ELISA and CLIA 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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