

Abbexa Ltd, Innovation Centre, Cambridge Science Park, Cambridge, CB4 0EY, UK
Telephone: +44 (0) 1223 755950 - Fax: +44 (0) 1223 755951 - E-Mail: info@abbexa.com

Human X-Ray Repair Cross Complementing 5 (XRCC5) CLIA Kit

Catalogue No.: abx494044



Human X-Ray Repair Cross Complementing 5 (XRCC5) CLIA Kit is a Sandwich CLIA Kit for use with Tissue homogenates and other biological fluids.

Please note that this kit is also available as an ELISA Kit [abx153525](#).

Target: X-Ray Repair Cross Complementing 5

Reactivity: Human

Tested Applications: CLIA

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

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

Sensitivity: < 0.057 ng/ml

Validity: The validity for this kit is 6 months.

Storage: Store at 2°C to 8°C upon receipt.

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.

Standard Form: Lyophilized

ELISA Detection: Fluorometric

ELISA Type: Sandwich

Abbexa Ltd, Innovation Centre, Cambridge Science Park, Cambridge, CB4 0EY, UK
Telephone: +44 (0) 1223 755950 - Fax: +44 (0) 1223 755951 - E-Mail: info@abbexa.com

ELISA Data: Quantitative

Sample Type: Tissue homogenates and other biological fluids.

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.