Anti-Human ZNF639, monoclonal

Alternate Names: Zinc finger protein 639

Cat. No. 13-049

FOR RESEARCH USE ONLY NOT FOR USE IN HUMANS

PRODUCT DESCRIPTION

UniProt Summary

UniProt
Primary Accession: Q9UID6

Binds DNA and may function as a transcriptional repressor. Interacts with CTNNA2. Nucleus. Belongs to the krueppel C2H2-type zinc-finger protein family. Contains 8 C2H2-type zinc fingers.

Physical Characteristics

Quantity: 1 ml (culture supernatant) or 100ug at 1mg/ml (purified)

Format: culture supernatant or purified material

Host/Isotype: mouse IgG2a

Clonality: monoclonal; ID R270.2.2B2

Formulation: culture supernatant contains 0.02% NaN3. Purified material contains 30% glycerol, PBS and 0.02% NaN3

Specificity: monospecific for human ZNF639 ; see “Microarray Analysis” below

Reactivity: human; not tested for cross reactivity in other species

Stability/Storage: 12 months long term: -20°C; short term: 4°C; avoid freeze-thaw cycles; aliquot as required

Handling Notes: small volumes of antibody may occasionally become entrapped in the seal of the product vial during shipment and storage; briefly centrifuge the vial on a tabletop centrifuge to dislodge any liquid in the container cap

Tested Research Applications

- **Western Immunoblotting - PASS by SOP**
- **Immunoprecipitation - PASS by SOP**
- **ChIP-Seq - PASS in K562 cell line(s). and did not pass in HepG2 cell line(s).**
  - View raw alignment peaks
  - View MACS peak alignment

Antibody tested as purified IgG. Optimal dilution to be determined by user.

Quality Assurance

Notes:

1. Please refer to the SOP manual (click here) to for detailed explanation of the experimental setup and thresholds used to evaluate the results shown below.
2. Predicted MW of the target protein expressed in the western immunoblotting (WB) and immprecipitation (IP) experiment is **53.46kDa** and the three fusion tags (venus, 3xFLAG, V5) adds another **38.7kDa** to this protein. Therefore the protein is expected to migrate ~**92.16kDa** in a denatured SDS-PAGE gel.
3. See results below for any applicable cautionary notes.

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Lot-specific COA version tracker: v1.0.0

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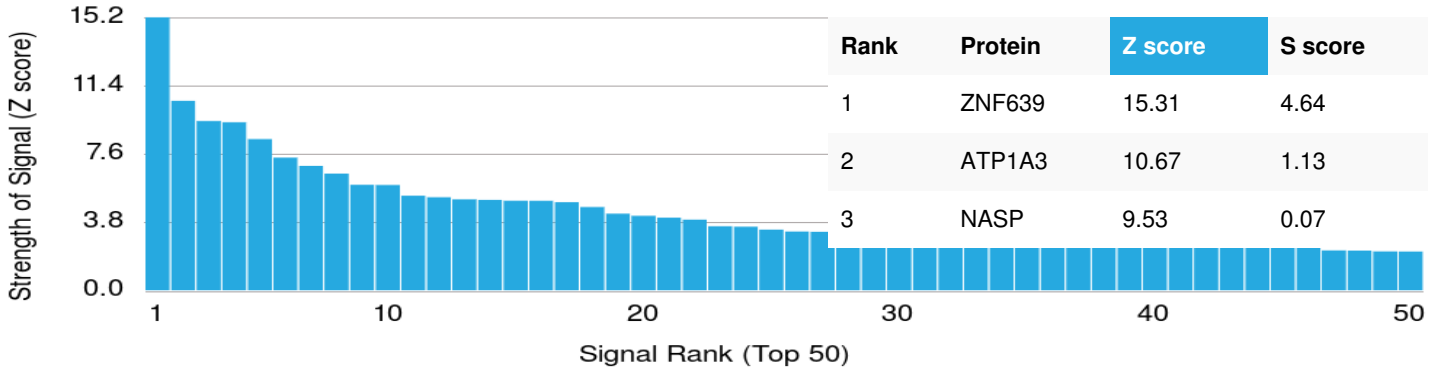
Quality Assurance (HuProt™ Array)



Rank	Protein	Z score	S score
1	ZNF639	15.31	4.64
2	ATP1A3	10.67	1.13
3	NASP	9.53	0.07

About Z and S Scores: The z-score represents the strength of a signal that a mAb (in combination with a fluorescently-tagged anti-IgG secondary antibody) produces when binding to a particular protein on the HuProt™ array. Z-scores are described in units of standard deviations (SDs) above the mean value of all signals generated on that array. To be considered a definite binding event between a mAb and a protein target, the z-score must have a value of at least 2.5 (SDs above the mean). The s-score represents the relative target specificity of a mAb, and is the difference (also in units of SDs) between the z-score a mAb generates upon binding to one protein and the next highest z-score that the mAb generates against another protein. For example, if a mAb binds to protein X with an z-score of 43 and to protein Y with an z-score of 14, then the s-score for the binding of that mAb to protein X is equal to 29.

Affinity Measurements

Binding affinity measure by OIRD

Association constant – K_{on}(1/ms): $1.96 * 10^{4}$

Dissociation constant - K_{off}(1/s): $1.48 * 10^{-8}$

Equilibrium binding constant - K_{d}(M): $5.60 * 10^{-13}$

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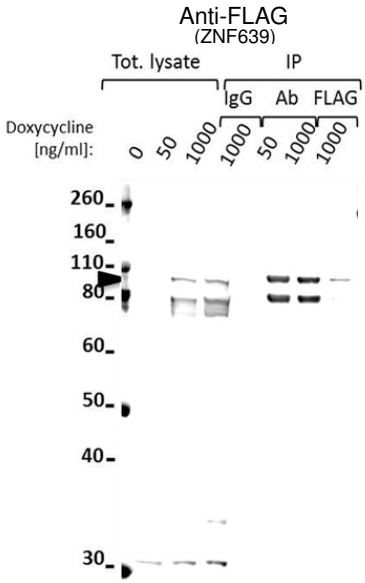
PRODUCT DESCRIPTION

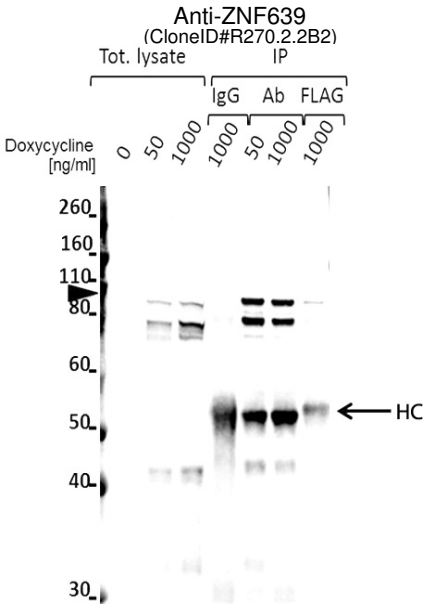
Quality Assurance (continued)

IMMUNOPRECIPITATION - Predicted MW 92.16kDa



Tet-ON HeLa cells were transfected with construct encoding ZNF639 (NM_016331.1) with an N-terminal fusion of FLAG, YFP (Venus) and V5 tags under a tet-inducible promoter. These cells were stimulated with 0, 50 or 1000 ng/ml doxycycline. Immunoprecipitation (IP) was carried out using 5µg of either IgG, CDI mAb Anti-ZNF639 (cloneID# R270.2.2B2) or 1 µg of FLAG-M2 (Sigma). Immunoblotting was performed using rabbit Anti-FLAG (1:1000, Cell Signaling #2368). We observe that such fusion proteins are generally expressed as a doublet, with the upper band corresponding to the expected size of the ZNF639 with an N-terminal fusion of FLAG, YFP (Venus) and V5 tags.

WESTERN BLOT - Predicted MW 92.16kDa



Tet-ON HeLa cells were transfected with construct encoding ZNF639 (NM_016331.1) with an N-terminal fusion of FLAG, YFP (Venus) and V5 tags. under a tet-inducible promoter. These cells were stimulated with 0, 50 or 1000 ng/ml doxycycline. Immunoprecipitation (IP) was carried out using 5µg of either IgG, CDI mAb Anti-ZNF639 (cloneID# R270.2.2B2) or 1 µg of FLAG-M2 (Sigma). Immunoblotting was performed using 0.2µg/ml CDI mouse mAb Anti-ZNF639 (cloneID# R270.2.2B2). HC=Heavy chain.

Cautionary notes for IP and WB experiments:

1. No or low signal seen in Flag IP lane
2. No or low signal seen in Flag IP lane

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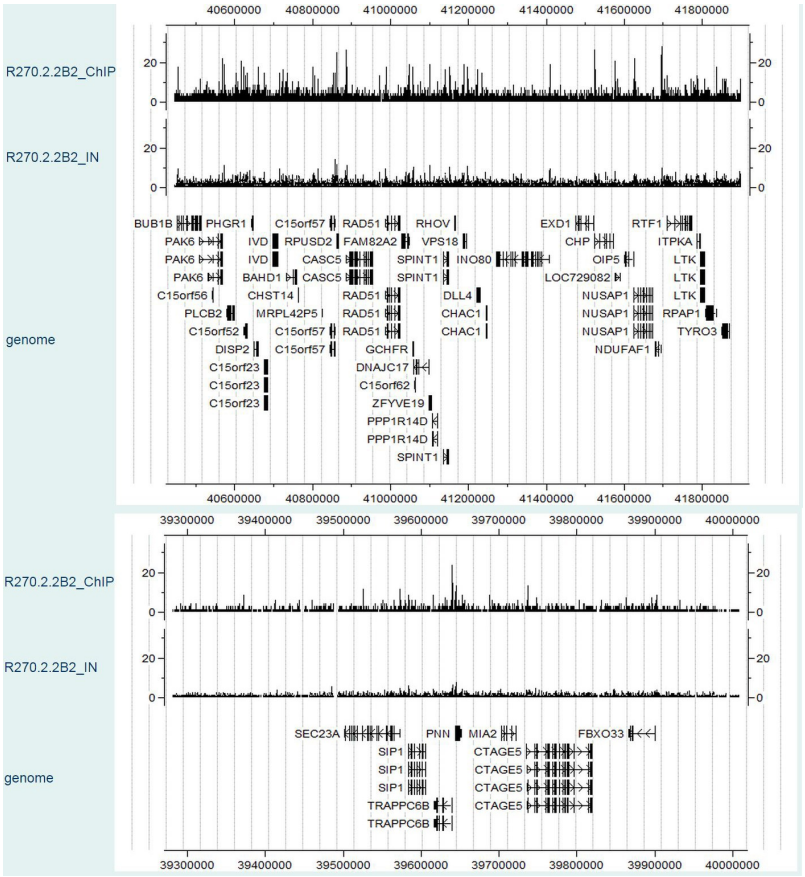
PRODUCT DESCRIPTION

Quality Assurance (continued)

CHIP SEQ



The ChIP was performed with chromatin from 10 million K562 cells and 3 µg of Anti-ZNF639 (cloneID #R270.2.2B2) antibody. The ChIP DNA was sequenced on an Illumina HiSeq platform and read counts were calculated at consecutive 100 bp bins across the human genome hg19. Normalized read-count levels for ChIP-seq of ZNF639 (R270.2.2B2_ChIP) and control (R270.2.2B2_IN) around the PNNanda 1,500,000 bp region (chromosome 15: 40,400,000-41,900,000) are displayed in the CisGenome browser.

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