Anti-Human ZMYM3, monoclonal (clone JH39.2.2F10)

Recommended name: Zinc finger MYM-type protein 3
Alternative name(s): Zinc finger protein 261

Cat. No.	**m15-026**	**Quantity:**	**100 µg**
Lot. No.	**20150608.L.I**	**Storage:**	**-20˚C**

FOR RESEARCH USE ONLY

NOT FOR USE IN HUMANS

Uniprot / NCBI Summary

UniProt
Primary Accession # Q14202
Secondary Accession # O15089

NCBI
GI # 33870173
GeneID 9203
Accession # BC013009

Molecular Weight 152,379 Da (1370 aa)

Plays a role in the regulation of cell morphology and cytoskeletal organization.

Subunit structure: May be a component of a BHC histone deacetylase complex that contains HDAC1, HDAC2, HMG20B/BRAF35, KDM1A, RCOR1/CoREST, PHF21A/BHC80, ZMYM2, ZNF217, ZMYM3, GSE1 and GTF2I.

Subcellular location: Nucleus.

Continued on page 2.

Physical Characteristics

Quantity: 100 µg

Concentration: 1.0 mg/ml

Host / Isotype: mouse IgG2a

Clonality: monoclonal; ID JH39.2.2F10

Immunogen: recombinant protein corresponding to full-length human ZMYM3

Purification: affinity-chromatography using Protein G

Formulation: 30% glycerol, 1x PBS, 0.02% sodium azide

Specificity: monospecific for human ZMYM3; see microarray analysis below

Reactivity: human

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; if necessary, briefly centrifuge the vial on a tabletop centrifuge to dislodge any liquid in the container cap.

Tested Research Applications

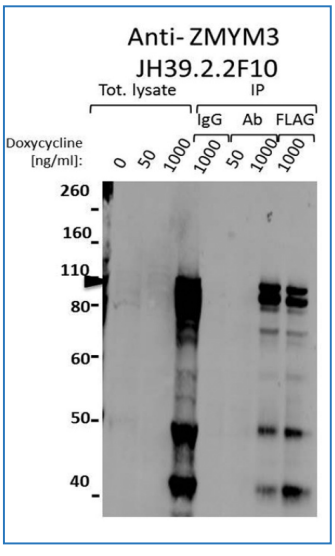
Western Immunoblotting: tested on cells transfected with a construct encoding ZMYM3; utility on native cells under evaluation

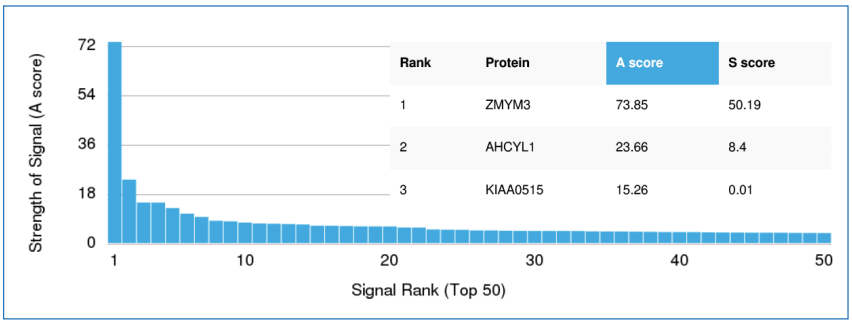
Immunoprecipitation: recommended; see below

ChIP-Seq: recommended; see page 2

Quality Assurance

IP Analysis:
Tet-ON HeLa cells were transfected with construct encoding ZMYM3 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-ZMYM3 (cloneID# JH39.2.2F10) or 1 µg of FLAG-M2. Immunoblotting was performed using rabbit Anti-FLAG (1:1000, Cell Signaling #2368).





Specificity Analysis with HuProt™ Human Proteome Microarray: Anti Human ZMYM3 (clone JH39.2.2F10) was analyzed using the CDI HuProt™ Human Proteome Microarray.

For more information on A/S scores and how they relate to specificity, see page 2.

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Lot-specific Datasheet version tracker: v2.0.0

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Uniprot / NCBI Summary

Continued from page 1.

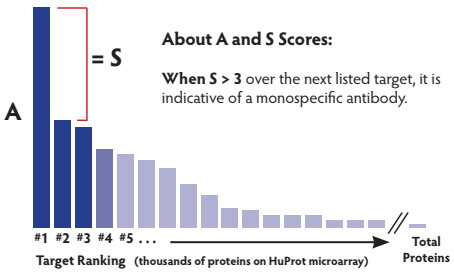
Tissue specificity: Most abundant in brain, moderate in muscle and heart, low in other tissues except placenta. Post-translational modification: Phosphorylation pSer 263, pSer 267, pSer 464, pThr 817. Sequence similarities: Contains 9 MYM-type zinc fingers.

General References:

van der Maarel SM, Scholten IHGM, Huber I, Phillippe C, Suijkerbuijk RF, Gilgenkrantz S, Kere J, Cremers FPM, Ropers H-H (1995) Cloning and characterization of DXS6673E, a candidate gene for X-linked mental retardation in Xq13.1. *Hum Mol Genet* **5**:887-897. [PubMed]

Hakimi M-A, Dong Y, Lane WS, Speicher DW, Shiekhattar R (2002) A candidate X-linked mental retardation gene is a component of a new family of histone deacetylase-containing complexes. *J Biol Chem* **278**:7234-7239. [PubMed]

Bai SW, Herrera-Abreu MT, Rohn JL, Racine V, Tajadura V, Suryavanshi N, Bechtel S, Wiemann S, Baum B, Ridley AJ (2010) Identification and characterization of a set of conserved and new regulators of cytoskeletal organisation, cell morphology and migration. *BMC Biol* **9**:54-54. [PubMed]



About A and S Scores:

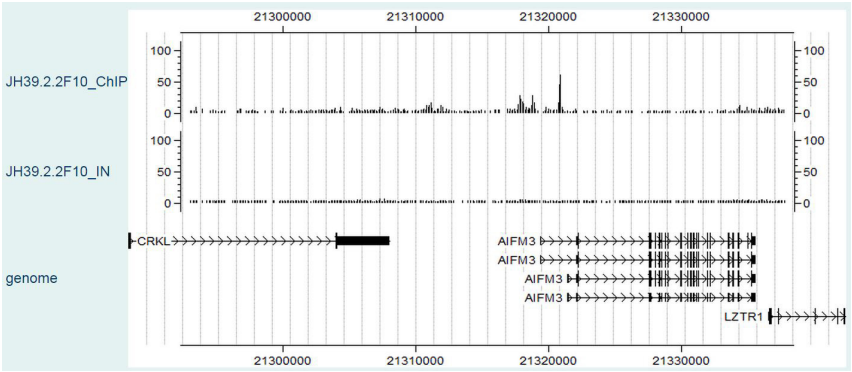
When S > 3 over the next listed target, it is indicative of a monospecific antibody.

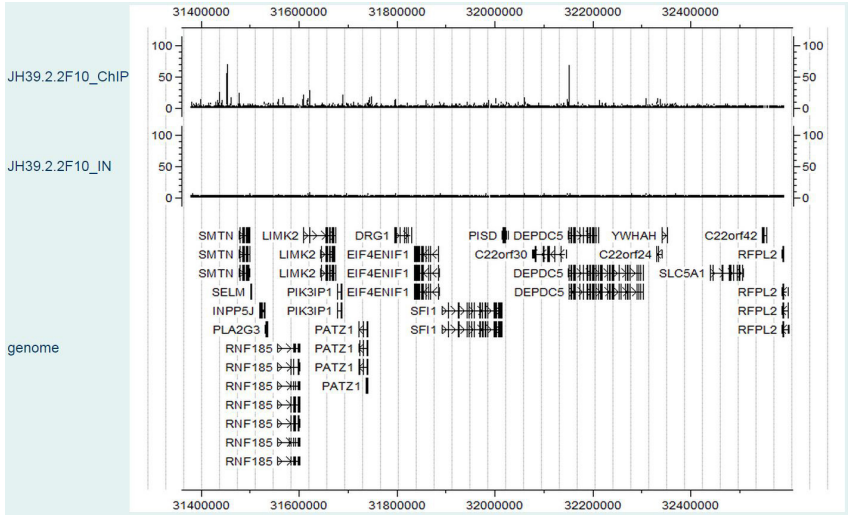
Statistical Analysis: Thousands of GenePix data points (from the microarray) are analyzed in terms of signal strength and ranked accordingly.

SUMMARY: The A-score indicates the number of standard deviations above background seen for the mean signal bound by the target antigen The S-score represents the difference between the A-score of the target antigen and the next best hit on the array. S-scores **greater than 3 standard deviations over the next listed target** are deemed statistically significant and indicate **highly specific antibodies.** More info at cdi-lab.com/HighSpec.html

Tested Research Applications

ChIP-Seq: Recommended





The ChIP was performed with chromatin from 10 million GM12878 cells and 3 µg of Anti-ZMYM3 (cloneID #JH39.2.2F10) 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 ZMYM3 (JH39.2.2F10_ChIP) and control (JH39.2.2F10_IN) around the AIFM3 and a 1,200,000 bp region (chromosome 22: 31,400,000-32,600,000) are displayed in the CisGenome browser.

The development of this antibody was supported by the National Institutes of Health Protein Capture Reagent Program under award U54HG06434 to CDI Laboratories and Johns Hopkins University.

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