

Anti-Human ZNF597, monoclonal (clone R917.1.1C12)

Recommended name: Zinc finger protein 597

Cat. No. m15-058
Lot. No. 20150817.L.I.K

Quantity: 100 µg
Storage: -20 °C



FOR RESEARCH USE ONLY

NOT FOR USE IN HUMANS

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UniProt / NCBI Summary

UniProt

Primary Accession # [Q96LX8](#)
Secondary Accession # n/a

NCBI

GI # [20987612](#)
GenID [146434](#)
Accession # [BC029899](#)
GenBank Nucleotide # n/a

Molecular Weight 48,076 Da (424 aa)

ZNF597: May be involved in transcriptional regulation. Belongs to the krueppel C2H2-type zinc finger protein family. This gene encodes a protein with multiple zinc finger domains. Loss of the related gene in rodents results in defects in neural development and embryonic lethality in mutant homozygotes. This gene is adjacent to a differentially methylated region (DMR) and is imprinted and maternally expressed.

Subcellular location: nucleus

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Physical Characteristics

Quantity: 100 µg

Concentration: 1.0 mg/ml

Host / Isotype: mouse IgG2b

Clonality: monoclonal; ID R917.1.1C12

Immunogen: recombinant protein corresponding to aa residues 53-182 of human ZNF597

Purification: affinity-chromatography using Protein G

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

Specificity: monospecific for human ZNF597; 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

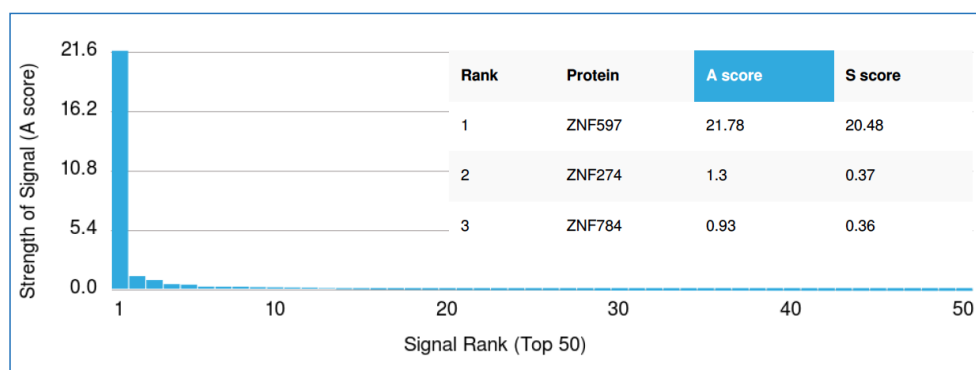
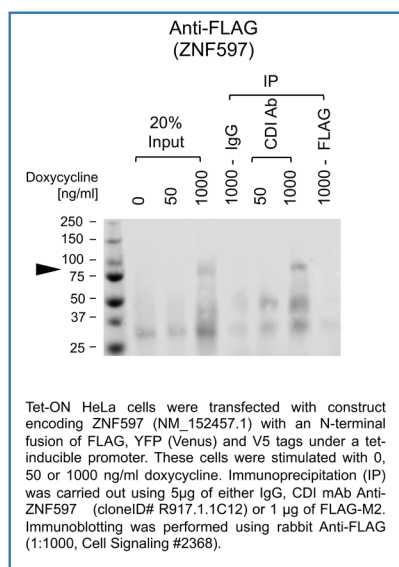
Handling Notes: small volumes of antibody may occasionally become entrapped in the seal of the product vial during shipment and storage; if necessary, briefly centrifuge the vial on a tabletop centrifuge to dislodge any liquid in the container cap.

Tested Research Applications

Immunoprecipitation: recommended; see below.

ChIP-Seq: recommended; see page 2

Quality Assurance



Specificity Analysis with HuProt™ Human Proteome Microarray: Anti Human ZNF597 (clone R917.1.1C12) 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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Continued from page 1.

Selected References:

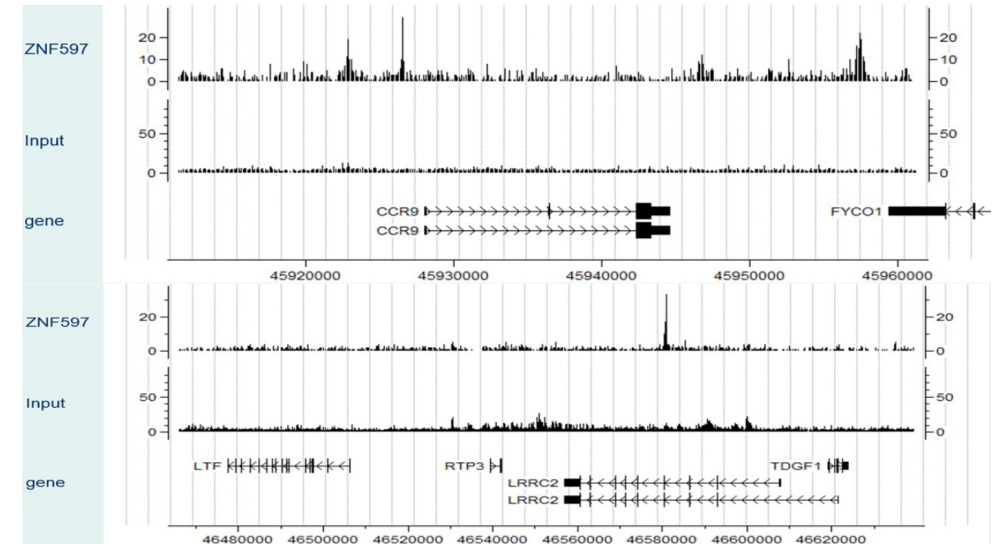
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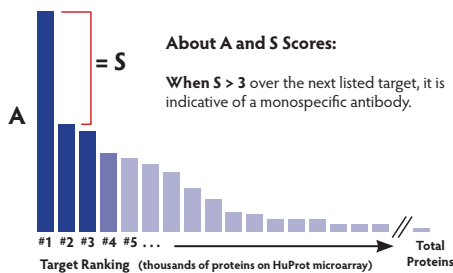
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Tested Research Applications

ChIP-Seq: Recommended



The ChIP was performed with chromatin from 10 million GM12878 cells and 3 µg of Anti-ZNF597 (cloneID # R917.1.1C12) 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 ZNF597 (R917.1.1C12) and control (Input) around the CCR9 and LRRC2 loci are displayed in the CisGenome browser



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](http://cdi-lab.com/HighSpec.html)

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