For Research Use Only

Halo-Trap Magnetic Agarose

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Catalog Number: otma

3 Publications

Basic Information

Catalog Number:
otma

Applications:
IP, CoIP, ChIP, RIP

Conjugate:
Magnetic agarose beads; bead size: ~40 µm (cross-linked 6 % magnetic agarose beads)

Host:
Alpaca

Type:
Nanobody

Class:
Recombinant

Description

The ChromoTek Halo-Trap Magnetic Agarose consists of an anti-Halo-tag Nanobody (VHH), which is covalently bound to magnetic agarose beads. Halo-Trap Magnetic Agarose is used to immunoprecipitate Halo-tag proteins from cell extracts of various organisms like mammals, plants, bacteria, yeast, insects etc. in the presence or absence of a covalently bound ligand. The interaction between Halo-Trap and the Halo-tag protein is reversible.

Binding capacity

12.5 µg of recombinant Halo-tag per 25 µL bead slurry

Specificity/Target

Halo-tag (modified variant of the bacterial haloalkane dehalogenase enzyme from *Rhodococcus rhodochrous*) in the absence or presence of covalently bound chloralkane-based ligands.

Elution buffer

SDS sample buffer
0.2 M glycine pH 2.5

Affinity (K_D)

Dissociation constant K_D of 2 nM

Storage

Storage:
Upon receipt store at +4°C. Do not freeze!

Storage Buffer:
20% ethanol

For technical support and original validation data for this product please contact:

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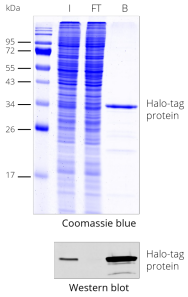
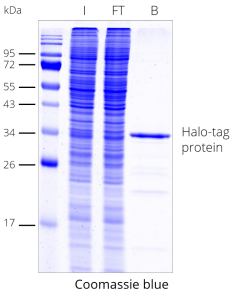
Selected Validation Data



Halo-Trap Magnetic Agarose for immunoprecipitation of Halo-tag proteins. HEK293T cell lysate with Halo-tag protein. Coomassie and Western blot. Halo-tag antibody [28A8], monoclonal mouse IgG1and anti-mouse secondary antibody. I: Input, FT: Flow-Through, B: Bound



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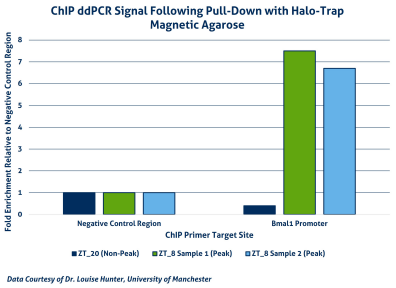

Chromatin Immunoprecipitation (ChIP) utilizing Halo-Trap Magnetic Agarose (otma) was performed on cross-linked chromatin isolated from the liver of a transgenic mouse line expressing a Halo-tagged version of clock factor REVERBα (HaloReverbα). Samples were isolated at timepoints of non-peak (ZT20) or peak (ZT8) binding of the REVERBα protein to the Bmal1 promoter region of the genome. The enriched DNA was then quantified by ddPCR utilizing primers directed at a gene desert (negative control region) or the Bmal1 promoter. Fold enrichment of each sample DNA is relative to that of the negative control region of each sample.