chromotek® mEos-Trap Agarose

Product Code: meta

Product Information

Description: The ChromoTek mEos-Trap Agarose consists of an anti-mEos Nanobody/VHH, which is coupled to agarose beads. It can be used for the immunoprecipitation of proteins fused to the mEos-tag from cell extracts of various organisms.

Applications: IP, Co-IP

Specificity/Target: Binds specifically to members of the mEos-tag family fused to a protein of interest at N-, C- or internal position. To ensure broad coverage of mEos variants, the Nanobody was optimized for binding to both mEos2 and mEos4b, which are representative of the different lineages of the mEos family. There is no cross-reactivity to other fluorescent proteins such as eGFP.

Binding capacity: 15 µg of recombinant mEOS4b (28 kDa) per 25 µl bead slurry.

Bead Size: 90 µm (cross-linked 4 % agarose beads)

Elution Buffer: 2x SDS-sample buffer (Lämmli), 200 mM glycine pH 2.5

Wash Buffer Compatibility: 2M NaCl, 5 mM DTT, 5 mM β-mercaptoethanol, 5 mM TCEP, 2% NP40, 2% Triton X-100, 0.2% SDS, 1 M Urea

Type: Nanobody

Class: Recombinant

Host: Camelid

Shipment: Shipped at ambient temperature

Storage Buffer: 20 % ethanol

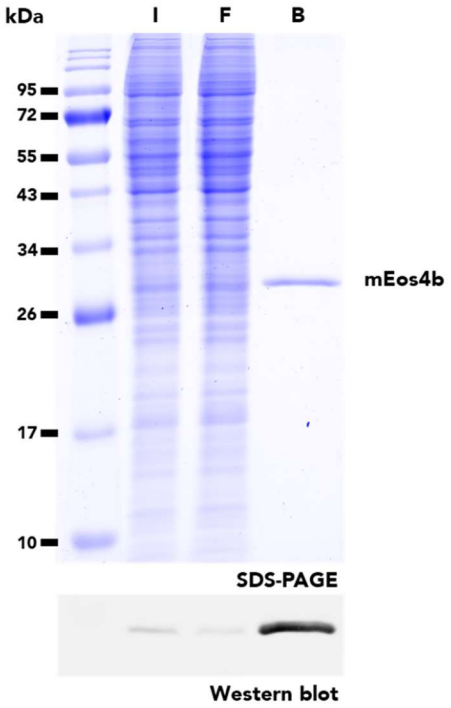
Storage Condition: Upon receipt store at +4°C. Do not freeze!

Stability: Stable for 1 year upon receipt

chromotek® mEos-Trap Agarose

Product Code: meta

Selected Validation Data



Immunoprecipitation of mEos4b protein from transfected HEK293T cells using mEos-Trap Agarose. I: Input, F: Flow-Through, B: Bound.

Suggested Buffer Compositions for IP

Buffer	Composition
Lysis Buffer	10 mM Tris/Cl pH 7.5, 150 mM NaCl, 0.5 mM EDTA, 0.5 % Nonidet™ P40 Substitute (adjust the pH at +4°C)
RIPA Buffer	10 mM Tris/Cl pH 7.5, 150 mM NaCl, 0.5 mM EDTA, 0.1 % SDS, 1 % Triton™ X-100, 1 % deoxycholate (adjust the pH at +4°C)
Dilution Buffer	10 mM Tris/Cl pH 7.5, 150 mM NaCl, 0.5 mM EDTA (adjust the pH at +4°C)
Wash Buffer	10 mM Tris/Cl pH 7.5, 150 mM NaCl, 0.05 % Nonidet™ P40 Substitute, 0.5 mM EDTA (adjust the pH at +4°C)
2x SDS-sample buffer	120 mM Tris/Cl pH 6.8, 20 % glycerol, 4 % SDS, 0.04 % bromophenol blue, 10 % β- mercaptoethanol
Acidic elution buffer	200 mM glycine pH 2.5 (adjust the pH at +4°C)
Neutralization buffer	1 M Tris pH 10.4 (adjust the pH at +4°C)

Note: Use your equivalent cell lysis buffer for other cell types like yeast, plants, insects, bacteria. Consider using a Wash buffer without detergent for Co-IP.

chromotek® mEos-Trap Agarose

Product Code: meta

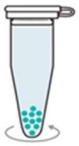
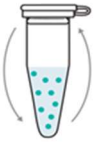
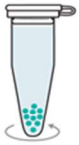
Product Sizes

Product	Product Code	Size
mEos-Trap Agarose	meta-10	10 reactions
	meta-20	20 reactions
	meta-100	100 reactions
	meta-200	200 reactions
	meta-400	400 reactions

chromotek® mEos-Trap Agarose

Product Code: meta

Protocol at a glance

General		• Perform all steps at 4°C • Use your preferred cell lysis buffer and cell lysis conditions
Cell Lysis		• Use 10^6-10^7 cells and 200 µL Lysis buffer. • Perform cell lysis and clear lysate • Mix 200 µl cleared lysate with 300 µL dilution buffer.
Bead Equilibration		• Transfer 25 µL bead slurry into a 1.5 mL tube • Equilibrate beads 3x with 500 µL dilution buffer
Protein binding		• Add 500 µL diluted lysate to beads • Rotate end-over-end for 1 hour at 4°C.
Washing		• Wash beads 3x with 500 µL wash buffer • Transfer beads to a new tube during the last washing step
Elution with SDS-sample buffer		• Resuspend beads in 80 µL 2x SDS-sample buffer • Boil beads for 5 min at 95°C • Analyze the supernatant in SDS-PAGE/ Western Blot

chromotek® mEos-Trap Agarose

Product Code: meta

Immunoprecipitation Protocol

Cell Material

The following protocol describes the preparation of a mammalian cell lysate.

For other type of cells, we recommend using 500 µg of cell extract and start the protocol with step Bead equilibration.

Mammalian Cell Lysis

Note: Harvesting of cells and cell lysis should be performed with ice-cold buffers. We strongly recommend adding protease inhibitors to the Lysis buffer to prevent degradation of your target protein and its binding partners.

For one immunoprecipitation reaction, we recommend using ~10^6-10^7 cells.

1. Choice of lysis buffer:
   a. For cytoplasmic proteins, resuspend the cell pellet in 200 µL ice-cold Lysis buffer by pipetting up and down. Supplement Lysis buffer with protease inhibitor cocktail and 1 mM PMSF (not included).
   b. For nuclear/chromatin proteins, resuspend cell pellet in 200 µL ice-cold RIPA buffer supplemented with DNase I (f.c. 75-150 Kunitz U/mL), $MgCl_2$ (f.c. 2.5 mM), protease inhibitor cocktail and PMSF (f.c. 1 mM) (not included).
2. Place the tube on ice for 30 min and extensively pipette the suspension every 10 min.
3. Centrifuge cell lysate at 17,000x g for 10 min at +4°C. Transfer cleared lysate (supernatant) to a pre-cooled tube and add 300 µL Dilution buffer supplemented with 1 mM PMSF and protease inhibitor cocktail (not included). If required, save 50 µL of diluted lysate for further analysis (input fraction).

Bead Equilibration

1. Resuspend the beads by gently pipetting them up and down or by inverting the tube. Do not vortex the beads!
2. Transfer 25 µL of bead slurry into a 1.5 mL reaction tube.
3. Add 500 µL ice-cold Dilution buffer.
4. Sediment the beads by centrifugation at 2,500x g for 5 min at +4°C. Discard the supernatant.

Note: Alternatively, ChromoTek Spin columns (sct-10; -20; -50) can be used to equilibrate the beads.

Protein Binding

1. Add diluted lysate to the equilibrated beads.
2. Rotate end-over-end for 1 hour at +4°C.

Washing

1. Sediment the beads by centrifugation at 2,500x g for 5 min at +4°C.

2. If required, save 50 µL of supernatant for further analysis (flow-through/non-bound fraction).
3. Discard remaining supernatant.
4. Resuspend beads in 500 µL Wash buffer.
5. Sediment the beads by centrifugation at 2,500x g for 5 min at +4°C. Discard remaining supernatant.
6. Repeat this step at least twice.
7. During the last washing step, transfer the beads to a new tube.

Optional: To increase stringency of the Wash buffer, test various salt concentrations e.g. 150-500 mM, and/or add a non-ionic detergent e.g. Triton™ X-100 (see Wash buffer compatibility table for maximal concentrations).

Note: Alternatively, ChromoTek Spin columns (sct-10; -20; -50) can be used to wash the beads.

Elution with 2x SDS-sample buffer (Laemmli)

1. Remove the remaining supernatant.
2. Resuspend beads in 80 µL 2x SDS-sample buffer.
3. Boil beads for 5 min at +95°C to dissociate immunocomplexes from beads.
4. Sediment the beads by centrifugation at 2,500x g for 2 min at +4°C.
5. Analyze the supernatant in SDS-PAGE / Western Blot.

Elution with Acidic Elution Buffer

1. Remove the remaining supernatant.
2. Add 50-100 µL Acidic elution buffer and constantly pipette up and down for 30-60 sec at +4°C or room temperature.
3. Sediment the beads by centrifugation at 2,500x g for 2 min at +4°C.
4. Transfer the supernatant to a new tube.
5. Immediately neutralize the eluate fraction with 5-10 µL Neutralization buffer.
6. Repeat this step at least once to increase elution efficiency.

Note: Elution at room temperature is more efficient than elution at +4°C. Prewarm buffers for elution at room temperature.

Note: Alternatively, ChromoTek Spin columns (sct-10; -20; -50) can be used to separate the beads.

chromotek® mEos-Trap Agarose

Product Code: meta

Related Products

Product	Code
mEos-Trap Magnetic Agarose	metma
mEos-Trap Agarose Kit	metak
mEos-Trap Magnetic Agarose Kit	metmak

Contact

Proteintech North America (HQ)

Proteintech Group, Inc.
5500 Pearl Street, Suite 400
Rosemont, IL 60018 USA

1-888-472-4522
proteintech@ptglab.com

Proteintech Europe

Transmission (6th Fl)
6 Atherton Street
M3 3GS, Manchester, UK

+44 161 839 3007
europe@ptglab.com

ChromoTek & Proteintech Germany

Fraunhoferstr. 1
82152, Planegg-Martinsreid
Germany

+49 89 124 148 850
germany@ptglab.com

Disclaimer

For research use only (RUO), not for diagnostic or therapeutic use.