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Product no AS12 2110

PIP2-1-7 | Plasma membrane aquaporin isoforms 1-7, C-terminal

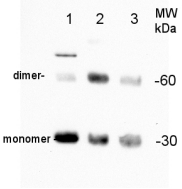
Product information

Immunogen	KLH-conjugated synthetic peptide derived from *Zea mays* PIP2-7 C-terminal, Q9ATM4, conserved also in *Zea mays* PIP2-1, UniProt: Q84RL7, PIP2-2, UniProt: Q9ATM8, PIP2-3 (80 % conservation) UniProt: Q9ATM7, PIP2-4 (80 % conservation) UniProt: Q9ATM6, PIP2-5 (70 % conservation) UniProt: Q9XF58, PIP2-6 (50 % conservation) UniProt: Q9ATM5
Host	Rabbit
Clonality	Polyclonal
Purity	Serum
Format	Lyophilized
Quantity	50 µl
Reconstitution	For reconstitution add 50 µl of sterile water
Storage	Store lyophilized/reconstituted at -20°C; make aliquots to avoid repeated freeze-thaw cycles. Please remember to spin the tubes briefly prior to opening them to avoid any losses that might occur from material adhering to the cap or sides of the tube.

Application information

Recommended dilution	1 : 600 (IP), 1: 3000 (WB)
Expected | apparent MW	30.7 | 30 kDa (*Zea mays*)
Confirmed reactivity	*Lactuca sativa, Pisum sativum, Solanum lycopersicum, Zea mays*
Predicted reactivity	*Arabidopsis thaliana, Artemisia annua, Brassica oleracea, Capsicum annuum, Capsicum chinense, Cicer arietinum, Coffea arabica, Cucumis melo, Cucumis sativus, Fragaria chiloensis, Glycine max, Helianthus annuus, Hordeum vulgare, Malus prunifolia, Medicago trunculata, Mimosa pudica, Nicotiana tabacum, Noccaea caerulescens, Olea europaea, Oryza sativa, Phaseolus vulgaris, Pisum sativum, Prunus mume, Pyrus communis, Spinacia oleracea, Solanum lycopersicum, Solanum tuberosum, Trifolium repens, Triticum urartu, Triticum aestivum, Vitis vinifera* Species of your interest not listed? Contact us
Not reactive in	*Hordeum vulgare*
Additional information	Detection pattern consists of di and monomer of PIP2-7. This antibody has a potential to work in immunolocalization studies, as it is recognizing C-terminal part of the sequence. This product can be sold containing ProClin if requested.
Selected references	Kumar et al. (2024).Dehydration-responsive cytoskeleton proteome of rice reveals reprograming of key molecular pathways to mediate metabolic adaptation and cell survival. Plant Physiol Biochem. 2024 Feb:207:108359. Kumar et al. (2022). Proteomic dissection of rice cytoskeleton reveals the dominance of microtubule and microfilament proteins, and novel components in the cytoskeleton-bound polysome, Plant Physiology and Biochemistry, Volume 170,2022,Pages 75-86,ISSN 0981-9428, https://doi.org/10.1016/j.plaphy.2021.11.037.

Application example



10 µg of total protein from *Zea mays* roots **(1)**, *Phaseolus vulgaris* leaves **(2)** or roots **(3)** extracted with a mixture of 250 mM sorbitol, 50 mM Tris–HCl (pH 8), 2 mM EDTA, and protease inhibitors [1 mM phenylmethylsulfonyl Xuoride, 1 mg ml each of leupeptin, aprotinin, antipain, chymostatin, and pepstatin were separated on 12 **% SDS-PAGE** and blotted 1h to **PVDF**. Blots were blocked with 5% milk in TBS-T for 2h at room temperature (RT) with agitation. Blot was incubated in the primary antibody at a dilution of 1: 3.000 for 1h at RT with agitation. The antibody solution was decanted and the blot was rinsed briefly twice, then washed four times for 5 min in TBS-T at RT with agitation. Blot was incubated in secondary antibody (goat anti-rabbit IgG horse radish peroxidase conjugated, from Agrisera AS09 602) diluted to 1:30 000 in TBS-T for 1h at RT with agitation. The blot was washed as above and developed for 5 min with ECL according to the manufacturers instructions. Exposure time was

60 seconds.

Courtesy of Dr. Ricardo Aroca, CSIC, Spain