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Datasheet for 600-106-200

GST Antibody Biotin Conjugated

Overview

Description:	Anti-GST (GOAT) Antibody Biotin Conjugated - 600-106-200
Item No.:	600-106-200
Size:	1 mg
Applications:	ELISA, IF
Reactivity:	GST-Tag
Host Species:	Goat

Product Details

Background:	Biotin conjugated anti-GST antibody is specific for the GST affinity tag. Affinity tags re appended to proteins thereby allowing them to be purified from their crude biological source using an affinity technique. Common affinity tags include glutathione-S-transferase (GST), chitin binding protein (CBP), maltose binding protein (MBP), and the poly-Histidine or HIS-tag.
Synonyms:	goat anti-GST antibody biotin conjugation, biotin conjugated goat anti-GST antibody, Glutathione-S-Transferase, GST antibody, anti-GST antibody, anti-Glutathione-S-Transferase antibody
Host Species:	Goat
Conjugate:	Biotin
Clonality:	Polyclonal
Format:	IgG

Target Details

Reactivity:	GST-Tag
Immunogen Type:	Native Protein
Immunogen:	Glutathione-S-Transferase [Schistosoma japonicum]

Purity/Specificity:	Anti-GST Antibody, Biotin Conjugated, was prepared from monospecific antiserum by immunoaffinity chromatography using GST coupled to agarose beads followed by solid phase adsorption(s) to remove any unwanted reactivities and extensive dialysis against the buffer stated above. Assay by immunoelectrophoresis resulted in a single precipitin arc against anti-biotin, anti-Goat Serum, as well as purified and partially purified Glutathione-S-Transferase [Schistosoma japonicum]. Cross reactivity against Glutathione-S-Transferase from other sources may occur but has not been specifically determined.

Application Details

Tested Applications:	ELISA
Suggested Applications:	IF (Based on references)
Application Note:	Anti-GST Antibody, Biotin Conjugated has been tested by ELISA and is suitable for immunoblotting, immunohistochemistry, immunomicroscopy as well as other antibody based assays using streptavidin or avidin conjugates requiring lot-to-lot consistency. Optimal concentrations in these or other immunoassays should be determined by the researcher.
Assay Dilutions:	All assays should be optimized by the user. Recommended dilutions (if any) may be listed below.
ELISA:	1:10,000 - 1:50,000
IHC:	1:1,000 - 1:5,000
WB:	1:2,000 - 1:10,000

Formulation

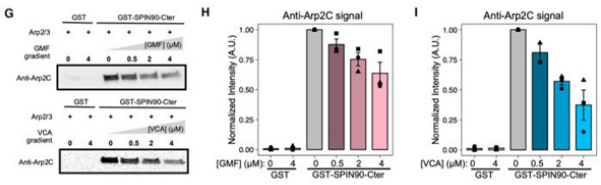
Physical State:	Lyophilized
Concentration:	1.0 mg/mL by UV absorbance at 280 nm
Buffer:	0.02 M Potassium Phosphate, 0.15 M Sodium Chloride, pH 7.2
Preservative:	0.01% (w/v) Sodium Azide
Stabilizer:	10 mg/mL Bovine Serum Albumin (BSA) - Immunoglobulin and Protease free
Reconstitution Volume:	1.0 mL
Reconstitution Buffer:	Restore with deionized water (or equivalent)

Shipping & Handling

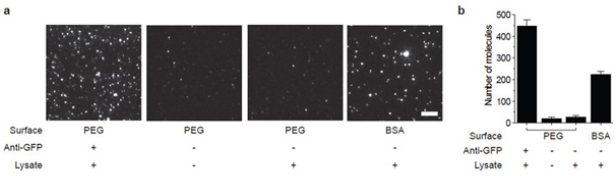
Shipping Condition:	Ambient

Storage Condition:	Store vial at 4° C prior to restoration. For extended storage aliquot contents and freeze at -20° C or below. Avoid cycles of freezing and thawing. Centrifuge product if not completely clear after standing at room temperature. This product is stable for several weeks at 4° C as an undiluted liquid. Dilute only prior to immediate use.
Expiration:	Expiration date is one (1) year from date of receipt.

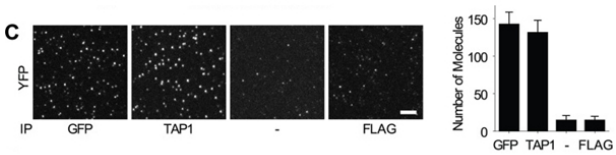
Images



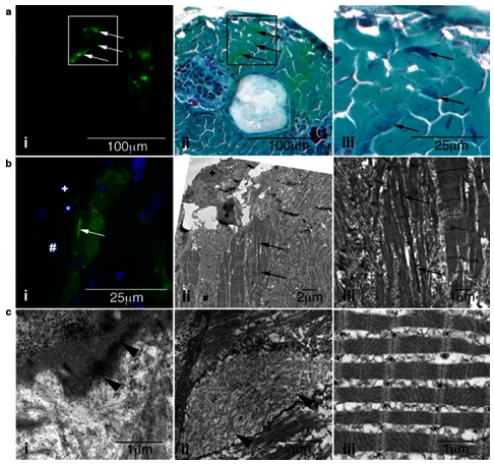
Western Blot
(G–I) GMF and VCA interfere with the SPIN90-Arp2/3 interaction in the absence of filament. (G) Immunoblots from pull-down assays where GST beads, decorated with GST or GST-SPIN90-Cter (the functional domain of SPIN90), were incubated with 0.4 μM Arp2/3 and gradient concentrations of GMF or VCA for 1 h at room temperature. After the unbound protein was washed out, the amount of Arp2/3 attached to the beads was detected by anti-ArpC2 antibody. Ponceau red straining of the membrane verified that the beads were loaded with equal amounts of GST or GST-SPIN90 (Appendix Fig S2). (H, I) Quantification of the amount of ArpC2 remaining on the beads in different conditions.
Data information: In all graphs (H and I): the bars indicate the average values, and the error bars indicate the standard deviations, from three independent repeats of each experiment (data points). Fig 4. PMID: 36939020



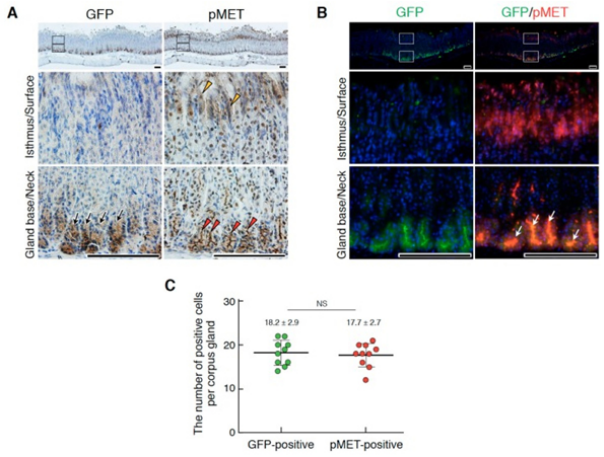
Immunofluorescence Microscopy
PEG passivation hinders non-specific protein adsorption. (a) Typical TIRF image of YFP-tagged protein pulled down using polyclonal anti-GFP antibody from the lysate (a, left). Non-specific binding of the protein to the PEG passivated surface (a, second from right) is comparable to the blank (a, second from left). Significant non-specific adsorption of YFP is observed when the same amount of lysate is added to surface passivated with 1 mg ml−1 BSA (a, right). Scale bar is 5 μm. (b) Bar graph with average number of fluorophores per image. Error bars represent standard deviation of the mean across > 20 images. Fig 2. PMID: 22322217



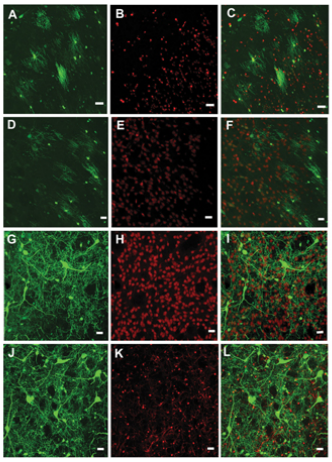
Immunofluorescence Microscopy
TAP/tapasin ratio is 1:2 in human cells. C, representative fluorescent images (left panel) and quantitation (right panel) of tapasin-YFP pulldown in slides coated with goat anti-GFP, the anti-TAP1 antibody 148.3, no antibody, or a control antibody (mouse anti-FLAG). To achieve an optimal density of molecules for imaging, the .220.B4402.tapasin-YFP lysate was diluted 1000-fold (anti-GFP), 20-fold (anti-TAP1), or 10-fold (no antibody and anti-FLAG) in 1% digitonin lysis buffer. The scale bar on the fluorescent images represents 5 µm. The quantitative results are expressed as the means plus the S.D. of at least 20 imaging areas (2500 µm2 each) in one representative experiment. Fig 1. PMID: 22829594



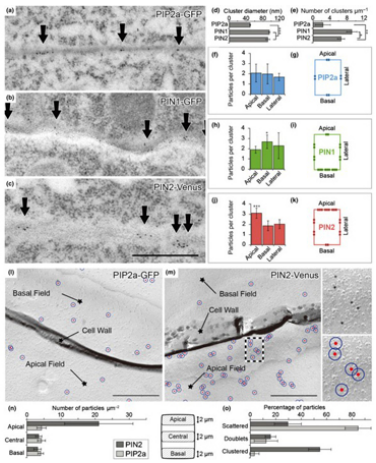
Immunofluorescence Microscopy
Characterization of skeletal muscle pathology in Tg (ACTA1 D286G-eGFP) high zebrafish. a Skeletal muscle expressing i mosaic ACTA1D286G-eGFP, and ii overlaid with a light microscopy image of the same section showing Gomori trichrome staining, and iii enlarged. Dark regions (indicative of nemaline bodies) of disrupted muscle correspond to eGFP expression (arrows). b Correlative light and electron microscopy of Tg(ACTA1 D286G-eGFP) high fish muscle at 2 dpf. b i Fluorescent image and corresponding ii electron microscopy image of skeletal muscle section containing a dense, elongated nemaline body (arrow) and enlarged in (iii). Sections are matched using nuclei positions (asterisk, plus and hash). c i Accumulations of actin filaments (arrowheads) and ii diffuse regions of filamentous actin (arrowheads), as well as ii disrupted sarcomeric regions are evident in Tg(ACTA1 D286G-eGFP) high skeletal muscle, at 2 dpf unlike the iii uniform sarcomeres observed in Tg(ACTA1-eGFP) zebrafish. Fig 2. PMID: 25931053



Immunofluorescence Microscopy
Localizations of Lgr5+ stem cells and pMET in the corpus epithelium of the adult stomach. (A) Immunohistochemical staining for GFP and pMET. (B) Double immunofluorescence staining for GFP and pMET. In (A), black arrows, Lgr5-driven GFP; red arrowheads, pMET in the glandular base region; yellow arrowheads, pMET in the isthmus and/or surface regions. In (B), white arrows indicate the co-localization of pMET and GFP in Lgr5+ stem cells. The images in the lower panel are magnified images of the boxed areas in the upper panel. Tissues were obtained from Lgr5-DTR-EGFP mice. Scale bars represent 200 μm. (C) The numbers of GFP- and pMET-positive cells per corpus gland. These values were obtained by counting in 10 glands (n = 10). Data were tested for significance using an unpaired two-tailed t-test. NS, not significant. Fig 6.
PMID: 31212972

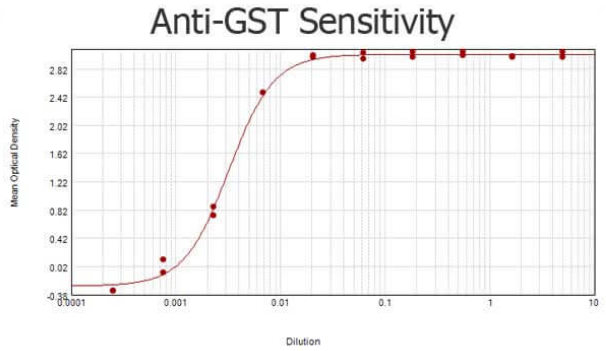


Immunofluorescence Microscopy
Confocal images of AAV9-hSyn and AAV9AU-hSyn mediated transduction in the rat striatum. (A–C) AAV9-JetI-GFP gene expression primarily co-localizes with the oligodendrocyte marker, Olig2, while (D–F) the general lack of GFP co-localization is with the neuronal marker, NeuN. In contrast (G–I), AAV9AU-JetI-GFP gene expression exhibits substantial co-localization with NeuN, but little co-localization with Olig2. Scale bars equal 20 μm. AAV, adeno-associated virus; GFP, green fluorescent protein. Fig 1.
PMID: 32940068



Immunofluorescence Microscopy
Visualization and quantification of Arabidopsis PIN clusters by immunogold electron microscopy (IEM) and sodium dodecyl sulfate-digested freeze-fracture replica labeling (SDS-FRL). (a–c) IEM analysis with GFP antibody on high-pressure frozen 3-d-old root tips in PIP2a-GFP (a), PIN1-GFP (b) and PIN2-Venus (c). Arrows indicate the gold particles. Bar, 500 nm. (d) Quantitative analysis of the cluster diameter in PIP2a-GFP (50.1 ± 1.1 nm), PIN1-GFP (95.9 ± 1.7 nm) and PIN2-Venus (92.4 ± 4.7 nm) based on the gold particles from IEM. Ten representative images from each line were quantified. (e) Quantification of the number of clusters with radii >55 nm in PIP2a-GFP (2.31 ± 1.7), PIN1-GFP (9.1 ± 1.2)

and PIN2-Venus (6.5 ± 0.8). Ten representative images from each line were quantified. (f–k) Quantitative analysis of IEM particles in PIP2a-GFP, n = 18 (f, g), PIN1-GFP, n = 15 (h, i), and PIN2-Venus, n = 9 (j, k) at apical, basal and lateral polar domains. Average particle number per cluster (f, h, j). PIN1 and PIN2 both show significant differences in average particle number per cluster between apical and basal domains (h, j), and schematic cluster distribution (g, i, k) in single root cells are presented. (l) Specific PIP2a-GFP immunolabeling for epidermal cells at the plasma membrane leaflet facing the protoplasm (membrane P-face) in SDS-FRL. The PIP2a-GFP labeling in epidermal cells is similar in apical and in basal fields. Bars, 500 nm. (m) Characterization of PIN2-Venus distribution in SDS-FRL. Immunogold particles labeling GFP (10-nm gold). Many more particles can be detected in apical fields compared to basal fields. Particles are nonhomogeneously distributed in the plasma membrane, forming loose aggregations and tight clusters. For quantitative analysis, gold particles were marked in red. A 27.5-nm-radius circle around the particle center was drawn in blue (enlargement of the boxed area on the right). Clusters were defined as particles residing within overlapping blue circles (center-to-center distance ≤ 55 nm). Bar, 500 nm. (n) Quantification of immunogold particle densities in PIN2-Venus and PIP2a-GFP epidermal cells in SDS-FRL. In PIN2-Venus cells the number of particles per area was significantly higher in domains close to the apical surface (distance ≤ 2 μm from the apical edge) compared to central (2 μm around the midline) and basal domains (distance ≤ 2 μm from the basal edge) (apical: 21.1 ± 10.2, central: 3.3 ± 0.8, basal: 3.1 ± 1.0). In PIP2a-GFP cells numbers were similar in all domains (aplical 3.2 ± 1.8, central 2.5 ± 1.1, basal 2.7 ± 1.5). (o) Characterization of immunogold particle distribution in PIN2-Venus and PIP2a-GFP epidermal cells. Scattered, single particles; doublets, two particles with a center-to-center distance ≤55 nm; clusters, at least three particles with a nearest-neighbor distance ≤55 nm. PIN2: scattered: 29.4 ± 10.6, doublets: 15.9 ± 6.1, clustered: 54.7 ± 12.8; PIP2a: scattered: 84.5 ± 10.2, doublets: 12.3 ± 9.2, clustered: 3.2 ± 3.7. Values are means ± SD. Mann–Whitney U-test: *, $P < 0.1$; **, $P < 0.01$; ***, $P < 0.001$. Fig 2. PMID: 32810889



ELISA
ELISA results of purified Goat anti-GST Antibody Biotin Conjugated tested against purified GST. Each well was coated in duplicate with 1.0 µg of GST (p/n 000-001-200). The starting dilution of antibody was 5µg/ml and the X-axis represents the Log10 of a 3-fold dilution. This titration is a 4-parameter curve fit where the IC50 is defined as the titer of the antibody. Assay performed using 3% fish gelatin as blocking buffer, Streptavidin Peroxidase Conjugated and TMB substrate p/n TMBE-1000

References

- Cao L et al. Regulation of branched versus linear Arp2/3-generated actin filaments. *EMBO J.* (2023)

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