

DESCRIPTION

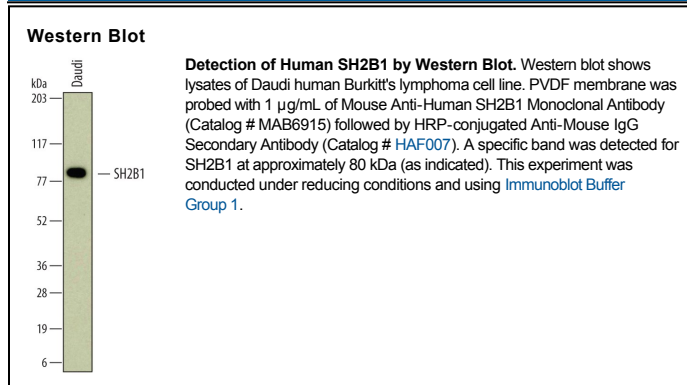
Species Reactivity	Human
Specificity	Detects human SH2B1 in direct ELISAs and Western blots.
Source	Monoclonal Mouse IgG _{2A} Clone # 700320
Purification	Protein A or G purified from hybridoma culture supernatant
Immunogen	<i>E. coli</i> -derived recombinant human SH2B1 Pro317-Leu467 Accession # Q9NRF2
Formulation	Lyophilized from a 0.2 µm filtered solution in PBS with Trehalose. See Certificate of Analysis for details. *Small pack size (-SP) is supplied as a 0.2 µm filtered solution in PBS.

APPLICATIONS

Please Note: Optimal dilutions should be determined by each laboratory for each application. *General Protocols* are available in the *Technical Information* section on our website.

	Recommended Concentration	Sample
Western Blot	1 µg/mL	See Below

DATA



PREPARATION AND STORAGE

Reconstitution	Sterile PBS to a final concentration of 0.5 mg/mL.
Shipping	The product is shipped at ambient temperature. Upon receipt, store it immediately at the temperature recommended below. *Small pack size (-SP) is shipped with polar packs. Upon receipt, store it immediately at -20 to -70 °C
Stability & Storage	Use a manual defrost freezer and avoid repeated freeze-thaw cycles. <ul style="list-style-type: none"> ● 12 months from date of receipt, -20 to -70 °C as supplied. ● 1 month, 2 to 8 °C under sterile conditions after reconstitution. ● 6 months, -20 to -70 °C under sterile conditions after reconstitution.

BACKGROUND

SH2B1 (SH2 adaptor protein B1), also called PSM (Pro-rich, PH and SH2 domain-containing signaling mediator) is an adaptor protein that mediates signaling between receptor tyrosine kinases and JAK signaling pathways. The 756 amino acid (aa) human SH2B1 contains an N-terminal Phe-zipper dimerization domain (aa 26-82), a nuclear localization sequence (aa 224-233), a PH domain (aa 267-376), and a pY-binding SH2 domain (aa 526-614). Within the region used as an immunogen, human SH2B1 shares 92% aa sequence identity with human and mouse SH2B1. Potential isoforms of 683 and 671 diverge after aa 632; a potential 426 aa form also shows an alternate start site at aa 246.