

## Protein A (PE)

## Cat. No. GTX30957

Applications	ICC/IF, FCM	Package
Species	Staphylococcus aureus	1 ml

## PRODUCT

Protein A (MW 42 kDa) is capable of binding to the Fc portion of immunoglobulins, especially IgGs, from a large number of species. One protein A molecule has been shown to bind at least 2 molecules of IgG simultaneously. The IgG binding domain of Protein A consists of three anti-parallel  $\alpha$ -helices, the third of which is disrupted when the protein is complexed with the Fc region of the immunoglobulins. Protein A will bind the Fc portion of human IgG subclasses, IgM, IgA and IgE; and mouse IgG1 (weakly), IgG2a, and IgG2b. Protein A also binds IgGs from other species, including monkey, rabbit, pig, guinea pig, dog, and cat. Phycoerythrin: Phycoerythrin (R-PE) is a 240 kDa protein from the light-harvesting phycobiliprotein, phycoerythrin is composed of a protein part, organised in a hexameric structure of alpha and beta chains, covalently binding chromophores called phycobilins. In the phycoerythrin family, the phycobilins are: phycoerythrobilin, the typical phycoerythrin acceptor chromophore, and sometimes phycoerythrobilin (marine organisms). Phycoerythrins are the phycobiliprotein which bind the highest number of phycobilins (up to six per alpha-beta subunit dimer). R-PE purified from Poryhyra tenera; A565/A280 >5.0; A 1% 565 nm=82; Amax = 490, 545 and 566 nm; E max = 580 nm. Fluorophore/Protein: A566nm/A280nm=4

## Applications

## Application Note

\*Optimal dilutions/concentrations should be determined by the researcher.

Suggested dilution	Recommended dilution
ICC/IF	Assay dependent
FCM	Assay dependent

Not tested in other applications.

## Properties

Form	Liquid
Buffer	PBS, 10mg/ml BSA
Preservative	0.05% Sodium azide
Storage	Store as concentrated solution. Centrifuge briefly prior to opening vial. Store at 4°C.
Region/Sequence	Native Protein
Expression System	Native Protein
Conjugation	Phycoerythrin (PE) <a href="#">Wavelength</a>



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**Note**

Purchasers shall not, and agree not to enable third parties to, analyze, copy, reverse engineer or otherwise attempt to determine the structure or sequence of the product.



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