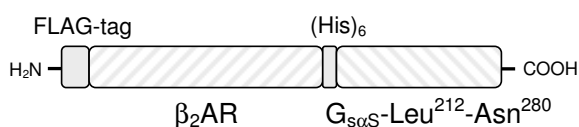


β_2 -AR- $G_{s\alpha S}$ -Leu²¹²-Asn²⁸⁰

β_2 -Adrenergic Receptor $G_{s\alpha S}$ fusion protein
human, recombinant, Sf9 insect cells

| Cat. No. | Amount |
|----------|--------|
| PR-546 | 1 ml |



For *in vitro* use only
Quality guaranteed for 12 months
Store at -80°C

Avoid freeze / thaw cycles

Form

Membrane suspension. Supplied in 75 mM Tris-HCl
pH 7.4, 12.5 mM MgCl₂ and 1 mM EDTA.

Molecular Weight

98 kDa

Activity

1.4 - 5.7 pmol/mg

Description

β_2 -Adrenergic receptor- $G_{s\alpha S}$ -Leu²¹²-Asn²⁸⁰ is a fusion protein in which the $G_{s\alpha S}$ -Leu²¹²-Asn²⁸⁰ N-terminus is linked to the β_2 -adrenoceptor (β_2 AR) C-terminus via a hexahistidine (His₆)-tag.

The β_2 AR is activated by the catecholamine epinephrine and couples to the G-protein G_s to mediate adenylate cyclase (AC) activation. β_2 ARs are found in numerous tissues and cell types including vascular and bronchial smooth muscle cells, leukocytes and liver.

β_2 ARs mediate smooth muscle relaxation, inhibition of leukocyte function and activation of glycogenolysis.

$G_{s\alpha S}$ is the short splice variant of the α -subunit of the heterotrimeric G-protein G_s . G_s activates the effector AC. $G_{s\alpha S}$ differs from the long splice variant ($G_{s\alpha L}$) by the absence of a 15-amino acid insert between the raslike domain and the α -helical domain $G_{s\alpha S}$ (cat.# PR-505) possesses a higher GDP-affinity than $G_{s\alpha L}$ (cat.# PR-501).

GTP-binding proteins possess a highly conserved aspartate residue in the NKXD motif that is critical for high-affinity interaction with GTP. In small GTP-binding proteins, the D/N-mutation switches base-specificity from guanine to xanthine. In contrast to all other known G_α D/N mutants, the exchange of Asp²⁸⁰ to Asn²⁸⁰ in $G_{s\alpha S}$ does not lead to an inactivation in nucleotide binding.

Mutation of Gln²¹² to Leu²¹² (Q/L mutation) in the catalytic site abolishes the intrinsic GTPase activity and increases GDP-affinity, resulting in a constitutively activated $G_{s\alpha S}$. The Q/L-D/N double mutant is a $G_{s\alpha}$ with constitutive activity and specificity for XTP

(cat.# NU-602), XppNHp (cat.# NU-403) and XTP- γ S (cat.# NU-404) relative to the respective guanine nucleotides.

The β_2 AR- $G_{s\alpha S}$ -Leu²¹²-Asn²⁸⁰ fusion protein ensures a defined 1:1 stoichiometry of the receptor and the $G_{s\alpha S}$ -Leu²¹²-Asn²⁸⁰ subunit as well as high coupling efficiency. In contrast to the β_2 AR- $G_{s\alpha S}$ -Asn²⁸⁰ fusion protein (cat.# PR-545), the β_2 AR- $G_{s\alpha S}$ -Leu²¹²-Asn²⁸⁰ fusion protein does not exhibit high-affinity XTPase activity.

The fusion protein contains a N-terminal FLAG-tag® for immunochemical detection.

Selected References:

- Graziano *et al.* (1989) Synthesis in *Escherichia coli* of GTPase-deficient mutants of $G_{s\alpha}$. *J. Biol. Chem.* **264**:15475.
Seifert *et al.* (1998) Different effects of $G_s\alpha$ splice variants on β_2 -adrenoreceptor-mediated signaling. *J. Biol. Chem.* **273**:5109.



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Gille *et al.* (2003) GDP affinity and order state of the catalytic site are critical for function of xanthine nucleotide-selective $G_{\alpha s}$ proteins. *J. Biol. Chem.* **278**:7822.