



Polyclonal Anti- Glucocorticoid Receptor, GR (Sepharose Bead Conjugate)

Catalogue No. PA1107-S

Lot No. 08F01

Ig type: rabbit IgG

Size: 100µg/vial

Specificity

Human, mouse, rat. No cross reactivity with other proteins.

Recommended application

(Immunoprecipitation(IP))

Immunogen

A synthetic peptide corresponding to a sequence at the C-terminal of human GR, identical to the related rat and mouse sequence.

Purification

Immunogen affinity purified.

Formulation

50% slurry in PBS pH 7.2 with 0.01mg NaN₃ preservative.

Storage

Store at 4°C for frequent use.

Description:

This Antagene antibody is immobilized via covalent binding of primary amino groups to N-hydroxysuccinimide (NHS)-activated sepharose beads. It is useful for immunoprecipitation assays

BACKGROUND

Glucocorticoid receptor (GR) maps to the distal long arm of chromosome 5. The human glucocorticoid receptor (hGR) gene contains a total of 10 exons and has a minimum size of 80 kilobases. The identification of complementary DNAs encoding the human glucocorticoid receptor (hGR) predicts two protein forms (alpha and beta; 777 and 742 amino acids long, respectively) which differ at their carboxy termini and both forms of the receptor are related, with respect to their domain structure, to the v-erb-A oncogene product of avian erythroblastosis virus (AEV), which suggests that steroid receptor genes and the c-erb-A proto-oncogene are derived from a common primordial regulatory gene. Transcriptional regulation by the glucocorticoid receptor (GR) is mediated by hormone binding, receptor dimerization, and coactivator recruitment.

REFERENCE

1. Encio, I. J.; Detera-Wadleigh, S. D. : The genomic structure of the human glucocorticoid receptor. *J. Biol. Chem.* 266: 7182-7188, 1991.
2. Weinberger, C.; Hollenberg, S. M.; Rosenfeld, M. G.; Evans, R. M. : Domain structure of human glucocorticoid receptor and its relationship to the v-erb-A oncogene product. *Nature* 318: 670-672, 1985.
3. Bledsoe, R. K.; Montana, V. G.; Stanley, T. B.; Delves, C. J.; Apolito, C. J.; McKee, D. D.; Consler, T. G.; Parks, D. J.; Stewart, E. L.; Willson, T. M.; Lambert, M. H.; Moore, J. T.; Pearce, K. H.; Xu, H. E. : Crystal structure of the glucocorticoid receptor ligand binding domain reveals a novel mode of receptor dimerization and coactivator recognition. *Cell* 110: 93-105, 2002.

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