

**MULTISCREEN™ STABLE CELL LINE
HUMAN RECOMBINANT MGLU8 RECEPTOR**

PRODUCT INFORMATION

Catalog Number: C1195-1a

Lot Number: C1195-1a-120409

Quantity: 1 vial (2×10^6) frozen cells

Freeze Medium: Sigma Freezing Medium (C-6164)

Host cell: CHO-K1

Transfection: Expression vector containing full-length human mGluR8 cDNA (GenBank Accession Number NM_000845) with FLAG tag sequence at N-terminus

Recommended Storage: Liquid nitrogen upon receiving

Propagation Medium: DMEM with GlutaMAX (Gibco 10566), 10% FBS (dialyzed), 2 mM sodium pyruvate, 10 µg/mL puromycin

Stability: Stable after minimum of two months continuous growth

Data sheet

Background: The metabotropic glutamate receptors (mGluRs) have been divided into 3 groups on the basis of sequence homology, putative signal transduction mechanisms, and pharmacologic properties. Group II and group III mGluRs are linked to the inhibition of the cyclic AMP cascade, but differ in agonist selectivity. Group III agonists include L-2-amino-4-phosphonobutyrate (L-AP4) and L-serine-O-phosphate. The human mGluR8 protein shares 67 to 70% sequence similarity with mGluR4 and mGluR7 and 99% amino acid identity with mouse mGluR8.

Application: Functional assays **Figure 1**

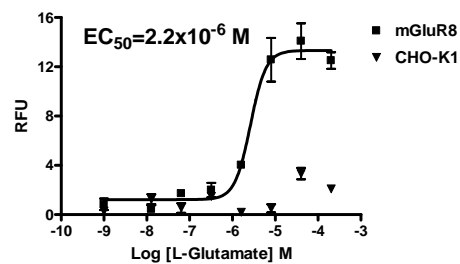


Figure 2

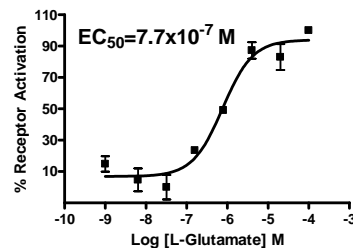


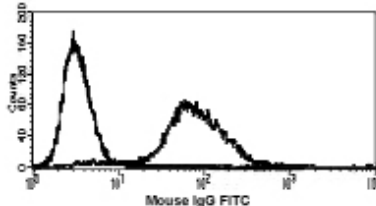
Figure 1. Dose-dependent stimulation of calcium flux upon treatment with ligand, monitored with FlexStation. **Figure 2.** Dose-dependent inhibition of forskolin-stimulated intracellular cAMP level upon treatment with ligand, measured with cAMP HiRange kit (Cisbio 62AM6PEC). **Figure 3.** Receptor expression on cell surface measured by flow cytometry (FACS) using an anti-FLAG antibody. Thin line: parental cells; thick line: receptor-expressing cells.

References

Scherer *et al.* (1996) Localization of two metabotropic glutamate receptor genes, GRM3 and GRM8, to human chromosome 7q. *Genomics* 31:230-233.

Scherer *et al.* (1997) The human metabotropic glutamate receptor 8 (GRM8) gene: a disproportionately large gene located at 7q31.3-q32.1. *Genomics* 44:232-236.

Figure 3



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