32-13455: sRAGE Human

Alternative Name : Advanced glycosylation end product-specific receptor, Receptor for advanced glycosylation end products, AGER, SRAGE, RAGE, MGC22357.

Description

Source: Escherichia Coli.
Sterile Filtered White lyophilized (freeze-dried) powder.
sRAGE is a member of the immunoglobulin superfamily of cell surface molecules. sRAGE is a receptor for various molecules, including the amyloidogenic form of serum amyloid A, amyloid-beta protein, members of the S100/calgranulin superfamily and advanced glycation end products. sRAGE lies within the major histocompatibility complex (MHC) class III region on chromosome 6. Alternative splicing results in two transcript variants encoding different isoforms. sRAGE mediates interactions of nonenzymatic glycosylated proteins which accumulate in vascular tissue during aging & at an increasing rate in diabetes. sRAGE is a receptor for amyloid beta peptide.
sRAGE Human Recombinant produced in E.Coli is a single, non-glycosylated, polypeptide chain containing 339 amino acids and having a molecular mass of 36.5 kDa. The Human sRAGE is fused to a 14 a.a. His tag at N-Terminus.The Human sRAGE is purified by proprietary chromatographic techniques.

Product Info

Amount :	2 µg / 10 µg
Purification :	Greater than 95% as determined by SDS-PAGE.
Content :	The sterile filtered (0.4 µm) concentrated (0.5mg/ml) protein solution was lyophilized with 30mM acetate buffer pH-4. Add 0.1M Acetate buffer pH4 to a working concentration of 0.5mg/ml and let the lyophilized pellet dissolve completely.
Storage condition :	Store lyophilized protein at -20°C. Aliquot the product after reconstitution to avoid repeated freezing/thawing cycles. Reconstituted protein can be stored at 4°C for a limited period of time.
Amino Acid :	MRGSHHHHHH GMASAQNITA RIGEPLVLKC KGAPKKPPQR LEWKLNTGRT EAWKVLSPQG GGPWDSVARV LPNGSLFLPAV GIQDEGIFRCQ AMNRNGKETKS NYRVRVYQIP GKPEIVDSASE LTAGVPNKVG TCVSEGSYPA GTLSWHLDGKPL VPNEKGVSVK EQTRRHPETG LFTLQSELMV TPARGGDPRP TFSCSFSPGL PRHRALRTAP IQPRVWEPVPL EEVQLVVEPE GGAVAPGGTV TLTCEVPAQP SPQIHWMKDGVP LPLPPSPVLI LPEIGPQDQG TYSCVATHSS HGPQESRAVS ISIIEPGEEG PTAGEGFDKV REAEDSPQHM