

California Bioscience

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Product Datasheet

Product Name	Advanced Glycosylation End Product-Specific Receptor Human Recombinant, HEK
Cata No	CB501458
Source	HEK 293
Synonyms	Advanced glycosylation end product-specific receptor, Receptor for advanced glycosylation end products, AGER, SRAGE, RAGE, MGC22357.

Description

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 HEK cells is a single, glycosylated, polypeptide chain containing 331 amino acids and having a molecular mass of 35.2 kDa.

sRAGE Human is fused to Flag tag at C-Terminus. sRAGE Human is purified by proprietary chromatographic techniques.

Physical Appearance

Sterile Filtered White lyophilized (freeze-dried) powder.

Purity

Greater than 95% as determined by SDS-PAGE.

Formulation

The sterile filtered concentrated (0.5mg/ml) protein solution was lyophilized with 50mM Tris-HCl pH-7.5 & 50mM NaCl.

Reconstitution

Add deionized water to a working concentration of 0.5mg/ml and let the lyophilized pellet dissolve completely.

Stability

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.

Sequence

AQNITARIGE PLVLKCKGAP KKPPQRLEWK LNTGRTEAWK VLSPQGGGPW DSVARVLPNG SLFLPAVGIQ DEGIFRCQAM NRNGKETKSN YRVRVYQIPG KPEIVDSASE LTAGVPNKVG TCVSEGSYPA GTLSWHLDGK PLVPNEKGVS VKEQTRRHPE TGLFTLQSEL MVTPARGGDP RPTFSCSFSP GLPRHRALRT APIQPRVWEP VPLEEVQLVV EPEGGAVAPG GTVTLTCEVP AQPSPQIHWM KDGVPLPLPP SPVLILPEIG PQDQGTYSCV ATHSSHGPQE SRAVSISIIE PGEEGPTAGS VGGSGLGTLA **AAADYKDDDDK**