



Product description

Product name

AFLIBERCEPT

Catalog number AFF90271

AFLIBERCEPT is a recombinant fusion protein: vascular endothelial growth factor (VEGF)-binding portions from the extracellular domains of human VEGF receptors 1 and 2 fused to the Fc portion of human IgG1.

It is an inhibitor of vascular endothelial growth factor (VEGF) and is used to treat wet macular degeneration and metastatic colorectal cancer.

Protein sequence

AFLIBERCEPT

SDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVVLSPSH GIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG

Product features and protocols

Key features

Purity

Labelling

2

Isotopic incorporation >95%

as determined by SDS-PAGE

Arg-13C₆, 15N₄ | Lys-13C₆, 15N₂

>98%

as determined by LC-MS/MS analysis of digested SIL-mAb

Other features

Expression System	CHO cell line
Protein content	Quantitation is carried out by UV Absorbance at 280 nm
Formulation	10 mM sodium phosphate 40 mM sodium chloride 0.03% polysorbate 20 5% sucrose pH 6.2

Product preparation

- 1. Briefly centrifuge the tube before opening
- 2. Reconstitute by adding the appropriate volume of ultrapure water for a final concentration of 200 μg/ml (e.g. 50 µl for 10 µg or 250 µl for 50 µg)
- 3. Vortex gently to insure complete dissolution
- 4. Wait 15 minutes at Room temperature before proceeding further
- 5. Vortex gently again and centrifuge briefly

Product storage

The product is lyophilized and shipped at room temperature. Store at -80 °C upon receipt.

After reconstitution, the protein can be preserved at 4°C for a few weeks.

Avoid multiple freeze-thaw cycles



How to use our product

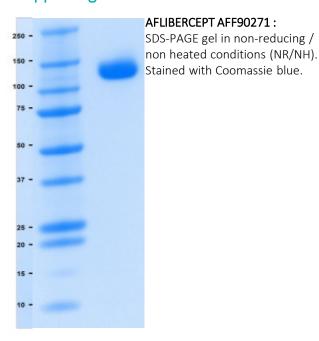


SIL mAbs allow to overcome the process variability since they are added at the very beginning of a sample preparation. This has positive impact on your analyte quantification, especially if the analyte interacts with other species commonly present within the matrix (1).

References



Supporting information



1. G.Picard, D. Lebert, et al. PSAQ standards for accurate MS-based quantification of proteins: from the concept to biomedical applications, J. Mass Spectrom. 2012, 47, 1353-1363



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