

32-6644: ACSF2 Human

Alternative Name : Acyl-CoA Synthetase Family Member 2, PPARG Binding, Long Chain Fatty Acid Acyl Co-A Ligase Like, Acyl-CoA Synthetase Family Member 2, Mitochondrial, EC 6.2.1.26, EC 6.2.1.-, FLJ20920, EC 6.2.1, AVYV493, ACSMW, Acyl-CoA synthetase family member 2, mitochondrial.

Description

Source: E.coli.

Sterile Filtered colorless solution.

Acyl-CoA synthetase family member 2, also known as ACSF2 is a member of the ATP-dependent AMP-binding enzyme family. Acyl-CoA synthetases are a family of enzymes which catalyze the thioesterification of fatty acids with coenzymeA to form activated intermediates, which play a basic part in lipid metabolism as well as homeostasis of lipid-related processes. ACSF2 is required for the complex of lipid synthesis, energy production via beta-oxidation, protein acylation and fatty-acid dependent transcriptional regulation. Moreover, ACSF2 is required for fatty acid import into cells by the process of vectorial acylation.

ACSF2 Human Recombinant produced in E.Coli is a single, non-glycosylated polypeptide chain containing 597 amino acids (42-615 a.a) and having a molecular mass of 66.1kDa. ACSF2 is fused to a 23 amino acid His-tag at N-terminus & purified by proprietary chromatographic techniques.

Product Info

Amount : 5 µg / 20 µg

Purification : Greater than 95% as determined by SDS-PAGE.

Content : ACSF2 protein solution (0.5mg/ml) containing Phosphate Buffered Saline pH 7.4 and 10% glycerol.

Storage condition : Store at 4°C if entire vial will be used within 2-4 weeks. Store, frozen at -20°C for longer periods of time. For long term storage it is recommended to add a carrier protein (0.1% HSA or BSA). Avoid multiple freeze-thaw cycles.

Amino Acid : MGSSHHHHHH SGLVPRGSH MGSLSREVD RMVSTPIGGL SYVQGCTKKH LNSKTVGQCL
ETTAQRVPER EALVVLHEDV RLTFALKEE VDKAASGLLS IGLCKGDRLG MWGPNSYAWV
LMQLATAQAG IILVSVNPAY QAMELEYVLK KVGCKALVFP KQFKTQQYYN VLKQICPEVE NAQPGALKSQ
RLPDLTTVIS VDAPLPGTLL LDEVVAAGST RQHLDQLQYN QQFLSCHDPI NIQFTSGTTG SPKGATLSHY
NIVNNSNILG ERLKLHEKTP EQLRMILPNP LYHCLGVSAG TMMCLMYGAT LILASPIFNG KKALEAISRE
RGFTLYGTPT MFVDILNQP D FSSYDISTMC GGVIAGSPAP PELIRAIINK INMKDLVVAY GTTENSPTVF
AHFPEDTVEQ KAESVGRIMP HTEARIMNME AGTLAKLNTP GELCIRGYCV MLGYWGPQK
TEEAVDQDKW YWTGDVATMN EQGFCKIVGR SKDMIIRGGE NIYPAELEDF FHHPKVQEV
QVVGKDDRM GEEICACIRL KDGEETTVEE IKAFCKGKIS HFKIPKYIVF VTNYPLTISG KIQKFLREQ
MERHLNL.