9853 Pacific Heights Blvd.
Suite D. San Diego,
CA 92121, USA
Tel: 858-263-4982
Email: info@abeomics.com

32-8830: Recombinant E.coli Beta-galactosidase (M443L, C500S)

Gene : lacZ
Gene ID : 945006
Uniprot ID : P00722

Description

Source: E.coli.
MW :112.9kD.
Recombinant E.coli Beta-galactosidase(M443L, C500S) is produced by our E.coli expression system and the target gene encoding Met1-Lys1024(12-41AA deletion) is expressed. beta-galactosidase is an exoglycosidase which hydrolyzes the beta-glycosidic bond formed between a galactose and its organic moiety. It may also cleave fucosides and arabinosides but with much lower efficiency. beta-galactosides include carbohydrates containing galactose where the glycosidic bond lies above the galactose molecule. Substrates of different beta-galactosidases include ganglioside GM1, lactosylceramides, lactose, and various glycoproteins. It is an essential enzyme in the human body. Deficiencies in the protein can result in galactosialidosis or Morquio B syndrome. In E. coli, the gene of beta-galactosidase, the lacZ gene, is present as part of the inducible system lac operon which is activated in the presence of lactose when glucose level is low. beta-galactosidase is important for organisms as it is a key provider in the production of energy and a source of carbons through the break down of lactose to galactose and glucose.

Product Info

Amount : 10 µg / 50 µg
Content : Supplied as a 0.2 µm filtered solution of 20mM Tris,150mM NaCl,pH8.0.
Storage condition : Store at -20°C, stable for 6 months after receipt. Please minimize freeze-thaw cycles.
Amino Acid :
MTMITDSLAVVEARTDRPSQQLRSLNGEWRFAWFPAPEAVPESWLECDLPEADTVVVPSNWQMHGYDAPIYT
NVTYPITVNPPFVPTENPTGCYSLTFNVDESWLQEGQTRIIFDGVNSAFHLWCNGRWVGYGQDSRLPSEFDLS
AFLRAGENRLAVMVLRWSDGSYLEDQDMWRMSGIFRDVSLLHKPTTQISDFHVATRFNDDFSRAVLEAEVQM
CGELRDYLRVTVSLWQGETQVASGTAPFGGEIIDERGGYADRVTLRLNVENPKLWSAEIPNLYRAVVELHTAD
GTLIEAEACDVGFREVRIENGLLLLNGKPLLIRGVNRHEHHPLHGQVMDEQTMVQDILLMKQNNFNAVRCSHY
PNHPLWYTLCDRYGLYVVDEANIETHGMVPMNRLTDDPRWLPAMSERVTRLVQRDRNHPSVIIWSLGNESGH
GANHDALYRWIKSVDPSRPVQYEGGGADTTATDIISPMYARVDEDQPFPAVPKWSIKKWLSLPGETRPLILCEY
AHAMGNSLGGFAKYWQAFRQYPRLQGGFVWDWVDQSLIKYDENGNPWSAYGGDFGDTPNDRQFCMNGLV
FADRTPHPALTEAKHQQQFFQFRLSGQTIEVTSEYLFRHSDNELLHWMVALDGKPLASGEVPLDVAPQGKQLIE
LPELPQPESAGQLWLTVRVVQPNATAWSEAGHISAWQQWRLAENLSVTLPAASHAIPHLTTSEMDFCIELGNK
RWQFNRQSGFLSQMWIGDKKQLLTPLRDQFTRAPLDNDIGVSEATRIDPNAWVERWKAAGHYQAEAALLQCT
ADTLADAVLITTAHAWQHQGKTLFISRKTYRIDGSGQMAITVDVEVASDTPHPARIGLNCQLAQVAERVNWLG
LGPQENYPDRLTAACFDRWDLPLSDMYTPYVFPSENGLRCGTRELNYGPHQWRGDFQFNISRYSQQQLMETS
HRHLLHAEEGTWLNIDGFHMGIGGDDSWSPSVSAEFQLSAGRYHYQLVWCQK