

32-13330: MutS

Alternative Name : MutS, Thermus Aquaticus DNA Mismatch Repair Protein, DNA mismatch repair protein MutS.

Description

Source: Escherichia Coli.

Sterile filtered colorless solution.

The MutS DNA Mismatch Protein identifies heteroduplex DNAs comprising mis-paired or unpaired bases. The MutS DNA Mismatch Protein binds in vitro to heteroduplex DNAs comprising mis-paired or unpaired bases over a varied temperature range from 4-70°C and obtains a thermostable ATPase activity. The MutS DNA Mismatch Protein is active at temperature between 0 to 75°C. Since the MutS DNA Mismatch Protein competently binds to 1-4 bases deletion (or insertion) and mismatch base pairs of GT, CT and AG, it is suitable for sensing these mutations. Mutations can be distinguished in polyacrylamide gels or on a solid phase such as Ni agarose or beads or magnetic Ni-NTA particles.

DNA Mismatch Repair Protein MutS Thermus Aquaticus Recombinant produced in E.coli is a single, non-glycosylated polypeptide chain containing 829 amino acids and having a molecular mass of 92.8kDa. The Thermus Aquaticus is fused to a 6 amino acid His-Tag at C-terminus and purified by proprietary chromatographic techniques.

Product Info

Amount :	10 µg / 50 µg
Purification :	Greater than 95.0% as determined by SDS-PAGE.
Content :	The MutS protein is supplied in 20mM Tris-HCl, pH-8, 250mM NaCl, 0.1mM EDTA, 1mM DTT and 50% 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 :	MKIEHMEGML KEGPGPLPP LLQYVELRD QYPDYLLLFQ VGDFYECFGE DAERLARALG LVLTHKTSKD FTTPMAGIPL RAFEAYAERL LKMGFRLAVA DQVEPAEEAE GLVRREVTQL LTPGTLLQES LLPREANYLA AIATGDGWGL AFLDVSTGEF KGTVLKSKSA LYDELFRHRP AEVLLAPELL ENGAFLEDEFK RRFVVMLSEA PFEPEGEGPL ALRRARGALL AYAQRTQGA LSLQPFREFYD PGAFMRLPEA TLRALVFEP LRQDITLFSV LDETRTAPGR RLLQSWLRHP LLDRGPLEAR LDRVEGFVRE GALREGVRRLL LYRLADLERL ATRLELGRAS PKDLGALRRS LQILPELRAL LGEEVGLPDL SPLKEELEAA LVEDPPLKVS EGGLIREGYD PDLDALRAAH REGVAYFLEL EERERERTGI PTLKVGYNV FGYLEVTRP YYERVPKEYR PVQTLKDRQR YTLPEMKEKE REYRLEALI RRREEVFLE VRERAKRQAE ALREAARILA ELDVYAALAE VAVRYGYVRP RFGDRLQIRA GRHPVVERRT EFVPNDLEMA HELVLITGPN MAGKSTFLRQ TALIALLAQV GSFVPAEEAH LPLFDGIYTR IGASDDLGG KSTFMVEMEE VALILKEATE NSLVLLDEVG RGTSSLDGVA IATAVAEALH ERRAYTLFAT HYFELTALGL PRLKNLHVAA REEAGGLVFY HQVLPGPASK SYGVEVAAMA GLPKEVVARA RALLQAMAAR REGALDAVLE RLLALDPDRL TPLEALRLLQ ELKALALGAP LDTMKGKLA ALEHHHHHHH.