

Product Name Thermus thermophilus MutS DNA mismatch repair protein

Catalog #: EG-198

Description The Tth MutS DNA mismatch protein recognizes heteroduplex DNAs containing mispaired or unpaired bases. This 91.8-kDa protein binds in vitro to heteroduplex DNAs containing mispaired or unpaired bases over a wide temperature range from 4 to 70 °C and has a thermostable ATPase activity. This thermostable Tth MutS is active at temperature between 0 to 75°C. Since Tth MutS efficiently binds to 1-4 bases deletion (or insertion) and mismatch base pairs of GT, CT and AG, it is useful for detecting these mutations. Mutations can be detected in polyacrylamide gels or on a solid phase such as Ni agarose or magnetic Ni-NTA particles.

Applications

- Remove mismatch DNA (error correction) from gene synthesis reaction
- Mutation detection and removal
- Rapid isothermal SNP detection

Source E. coli

Fusion Tag 6XHis tag at **N-terminus**

Purification Method FPLC

Purity ~ 95% as determined by SDS-PAGE

Accession # WP_011173381

Gene Name Thermus thermophilus MutS DNA mismatch repair protein

MW 91.8 kDa

Protein Sequence

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1 MGSSHHHHH MGNMLKGEGP GPLPPLLQY VELRDYDPDY LLLFQVGDFY ECFGEDAERL
61 ARALGLVLTH KTSKDFTTPM AGIPIRAFDA YAERLLKMGF RLAVADQVEP AEEAEGLVRR
121 EVTQLLTPGT LTQEALLPRE ANYLAAIATG DGWGLAFLDV STGEFKGTLL KSKSALYDEL
181 FRHRPAEVLV APRLRENEAF VAEFRKRFPV MLSEAPFEPQ GEGPLALRRA QGALLAYARA
241 TQGGALSVRP FRLYDPGAFV RLPEASLKAL EVFEPLRGQD TLFGVLDETR TAPGRRLQA
301 WLRHPLLERG PLEARLDRVE RFVREGALRE GVRRLFLRLA DLERLATRLE LSRASPRDLA
361 ALRRSLEILP ELKGLLGEEV GLPDLSGLE ELRAALVEDP PLKVSEGGI REGYDPDLDA
421 LRRHAEGVA YFLDLEAREK ERTGIPTLKV GYNAVFGYYL EVTRPYYEKV PQEYRPVQTL
481 KDRQRYTLPE MKERERELYR LEALIKRREE EVFLALRERA RKEAEALREA ARILAELDVY
541 AALAEVAVRH GYTRPRFGER LRIRAGRHPV VERRTAFVPN DLEMAHELVL VTGPNMAGKS
601 TFLRQTALIA LLAQIGSFVP AEEAELPLFD GIYTRIGASD DLGGKSTFM VEMEEVALVL
661 KEATERSLV LDEVGRGTSS LDGVAIATAL AEALHERRCY TLFATHYFEL TALALPRLKN
721 LHVAKEEEG GLVFYHQVLP GPASKSYGVE VAEMAGLPKE VVERARALLS AMAARREGAL
781 EEVLERLLAL DPDRLTPLEA LRFLHELKAL ALGLPLGSMK G
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Storage Buffer 20 mM Tris-HCl, pH 8.0, 250 mM NaCl

Storage -20 to -80 °C.

Shipping 4°C or dry ice

References

1. Protein-mediated error correction for de novo DNA synthesis. [Nucleic Acids Res.](#) 2004 Nov 23;32(20):e162.
2. Correcting errors in synthetic DNA through consensus shuffling. [Nucleic Acids Res.](#) 2005 Mar 30;33(6):e55.
3. MutS as a tool for mutation detection. [Acta Biochim Pol.](#) 2005;52(3):575-83. Epub 2005 Aug 4.
4. One tube mutation detection using sensitive fluorescent dyeing of MutS protected DNA. [Nucleic Acids Res.](#) 2000 Apr 15;28(8):E36.
5. Rapid SNP diagnostics using asymmetric isothermal amplification and a new mismatch-suppression technology. *Nature Methods* - 4, 257 - 262 (2007)
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