

Product datasheet for **TP522310**

Ercc6 (NM_001081221) Mouse Recombinant Protein

Product data:

Product Type: Recombinant Proteins

Description: Purified recombinant protein of Mouse excision repair cross-complementing rodent repair deficiency, complementation group 6 (Ercc6), with C-terminal MYC/DDK tag, expressed in HEK293T cells, 20ug

Species: Mouse

Expression Host: HEK293T



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Expression cDNA Clone or AA Sequence: >MR222310 representing NM_001081221
Red=Cloning site Green=Tags(s)

MFHEEVPNSTHPQEQLPSQHANAYKDMPVGQENGGVSEAGECLSSTSCEYGPSTSAEACVLAATRRG
P
TLLHIDRHQIPAVEPSAQALELQGLGVDVYDQAVLEQGVLLQVDSAMHEASCAQLADAEKEYQSVLDD
L
MSCTTSLRQINKIIEQLSPQAASNRDINRKLDSVKRQKYNKEQQLKKITAKQKRLQAILGGAGVQVELDH
ASLEEDDAEPGPSCLSMLMPAQETAWHEELRTGQMTFPGTPAPQKQEKPRKIMLNEASGFKEYLAEQA
QLSFERKKQAATKRTAKKAIVSESSRAAIETKADQRSQVLSQTDKRLKKHSRKLQRRALQFQGVGLPS
GKKPLEPEVRPEAEGDTEGEESGSSPTDGEESSEEGVSLSSDDVSYELKPLRKRQKYQKKVPVQE
IDDDFFPSSEEEDEAMEGRGGGRKVARQDDGDEDYKQRLRRWNRLRLQDKEKRLKLEDDSEESDAEFD
EGFKVPGLFKKLFKYQQTGVRWLWELHCQQAGGILGDEMGLGKTIQIIAFLAGLSYSKIRTRGSNYRFE
GLGPTIIVCPTTMHQQWVKEFTWWPPFRVAVLHETGSYTHKKERLIRDIVYCHGVLITSYSYIRLMQDD
ISRHDWHYVILDEGHKIRNPNAAVTLACKQFRTPHRIILSGSPMQNNLRELWSLDFIFPGKLGTLPVFM
EQFSVPITMGYSNASPVQVKTAYKACVLRDITINPYLLRRMKSDVKMSLSLPDKNEQVLCRLTDEQHK
VYQNFIDSKAVYRILNGENQIFSGVLALRKICNHPDLFSGGPKNASGPPPEDEEEQFGHWRRSGKMIVV
ESLLKIWHRRQQRVLLFSQSRQMLHILEVFLRAHKYSYKMDGTTTTASRQPLITKYNEDTSIFVLLTT
RVGGLGVNLTGANRVIIYDPDWNPDSTQARERAWRIGQKKQVTYRLLTAGTIEEKIYHRQIFKQFLTN
RVLKDPKQRRFFKSNDLYELFTLTSPDASQGTETSAIFAGTGSSIQTPKCQLKKRTSTVLGTDPKCKKPP
VSDTPANAATLIGEPKAAGATGRSVTSGESGPFKGDHDTNGNRASSVAFGEETDAGSTLEHLSVMSGDG
KHSDSPTVDHTSRPPVEASTSEKQGSSYAGARCQAQTEPVPMSEQMEGQFSKYKSKRKHDASEEETTEKR
PQPKQKAKNSKHCRDAKFEGTRVPHLVKKRRYRQQTSEQEGGAKDRSSDDYVLEKLFKKSQGVHVSVRH
D
AIIDGSSPDYVLVEAEANRVAQDALKALRLSRQQCLGAASGVPTWTGHRGISGAPTGVKNRFGQKRDS
SLPVQHPSSLTEKTQNNMKKEGKAHTPEHFGKEDGASVSGAPSSSSLLARMRARNHMLPERLESDSEHLA
EAAVPPCGTEHDDLLVDMRNFIQFAQVDGQASTQEILQEFESKLSVAQSCVFRELLRNLCNFHRTPGG
EGIWKLKPEYC

TRTRPLEQKLISEEDLAANDILDYKDDDDKV

Tag: C-MYC/DDK

Predicted MW: 166.4 kDa

Concentration: >0.05 µg/µL as determined by microplate BCA method

Purity: > 80% as determined by SDS-PAGE and Coomassie blue staining

Buffer: 25 mM Tris-HCl, 100 mM glycine, pH 7.3, 10% glycerol

Note: For testing in cell culture applications, please filter before use. Note that you may experience some loss of protein during the filtration process.

Storage: Store at -80°C after receiving vials.

Stability: Stable for 12 months from the date of receipt of the product under proper storage and handling conditions. Avoid repeated freeze-thaw cycles.

RefSeq:	<u>NP_001074690</u>
Locus ID:	319955
UniProt ID:	<u>F8VPZ5</u>
RefSeq Size:	8422
Cytogenetics:	14 B
RefSeq ORF:	4443
Synonyms:	4732403I04; C130058G22Rik; CSB
Summary:	<p>Essential factor involved in transcription-coupled nucleotide excision repair which allows RNA polymerase II-blocking lesions to be rapidly removed from the transcribed strand of active genes (By similarity). Upon DNA-binding, it locally modifies DNA conformation by wrapping the DNA around itself, thereby modifying the interface between stalled RNA polymerase II and DNA (By similarity). It is required for transcription-coupled repair complex formation. It recruits the CSA complex (DCX(ERCC8) complex), nucleotide excision repair proteins and EP300 to the sites of RNA polymerase II-blocking lesions (By similarity). Plays an important role in regulating the choice of the DNA double-strand breaks (DSBs) repair pathway and G2/M checkpoint activation; DNA-dependent ATPase activity is essential for this function (By similarity). Regulates the DNA repair pathway choice by inhibiting non-homologous end joining (NHEJ), thereby promoting the homologous recombination (HR)-mediated repair of DSBs during the S/G2 phases of the cell cycle (By similarity). Mediates the activation of the ATM- and CHEK2-dependent DNA damage responses thus preventing the premature exit from the G2/M checkpoint (By similarity). Acts as a chromatin remodeler at DSBs; DNA-dependent ATPase-dependent activity is essential for this function (By similarity). Remodels chromatin by evicting histones from chromatin flanking DSBs, limiting RIF1 accumulation at DSBs thereby promoting BRCA1-mediated HR (By similarity). Required for stable recruitment of ELOA and CUL5 to DNA damage sites (By similarity). Involved in UV-induced translocation of ERCC8 to the nuclear matrix (By similarity). Essential for neuronal differentiation and neurogenesis; regulates transcription and chromatin remodeling activities required during neurogenesis (By similarity).[UniProtKB/Swiss-Prot Function]</p>