Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of GST-UBE2J2 1-226

Enzyme description:- GST-UBE2J2 1-226

Clone number:- DU20688

Source:- BL21 recombinant

Tag:- N-terminal GST-tag

Purification method:- GSH-Sepharose

Expression level:- 14mg/L

Calculated molecular mass:-

Monoisotopic 52233 Da
Average Mass 52266 Da
[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 6.92

Purity:- 90%

Enzyme storage buffer:-

50mM HEPES pH 7.5, 150mM NaCl, 10% glycerol, 1mM DTT

Storage temperature:- -80°C

Assay:-

Loading with Ubiquitin and UBE1 in the presence of Mg-ATP

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Clone Data Sheet

GST-UBE2J2 1-226

Protein	UBE2J2 1-226
Synonyms	NCUBE2, PRO2121
Clone Number	DU20688
Species	Human
Accession Number	Protein: NP_919296 DNA: NM_194315
Tags	N-terminal GST-tag
Aminoacid sequence of the expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDLEVLFQGPLGS**MSSTSSKRAPTTATQRLKQDYLRIKKDPVPYICAEPLPSNILEWHYVVRGPEMTPYEGGYYHGKLIFPREFPFKPPSIYMITPNGRFKCNTRLCLSITDFHPDTWNPAWSVSTILTGLLSFMVEKGPTLGSIETSDFTKRQLAVQSLAFNLKDKVFCELFPEVVEEIKQKQKAQDELSSRPQTLPLPDVVPDGETHLVQNGIQLLNGHAPGAVPNLAGLQQANRHH**
Native sequence	in bold, missing the C-terminal transmembrane domain.
Protease cleavage	Prescission protease site underlined
Cloning sites	BamH1 / Not1

DNA sequence of insert	GGATCCATGAGCAGCACCAGCAGTAAGAGGGCTCCGACCACGGCAACCCAGAGGCTGAAGCAGGACTACCTTCGCATTAAGAAAGACCCGGTGCCTTACATCTGTGCCGAGCCCCTCCCTTCGAATATTCTCGAGTGGCACTATGTCGTCCGAGGCCCAGAGATGACCCCTTATGAAGGTGGCTATTATCATGGAAAACTAATTTTTCCCAGAGAATTTCCTTTCAAACCTCCCAGTATCTATATGATCACTCCCAACGGGAGGTTTAAGTGCAACACCAGGCTGTGTCTTTCTATCACGGATTTCCACCCGGACACGTGGAACCCGGCCTGGTCTGTCTCCACCATCCTGACTGGGCTCCTGAGCTTCATGGTGGAGAAGGGCCCCACCCTGGGCAGTATAGAGACGTCGGACTTCACGAAAAGACAACTGGCAGTGCAGAGTTTAGCATTTAATTTGAAAGATAAAGTCTTTTGTGAATTATTTCCTGAAGTCGTGGAGGAGATTAAACAAAAACAGAAAGCACAAGACGAACTCAGTAGCAGACCCCAGACTCTCCCCTTGCCAGACGTGGTTCCAGACGGGGAGACGCACCTCGTCCAGAACGGGATTCAGCTGCTCAACGGGCATGCGCCGGGGGCCGTCCCAAACCTCGCAGGGCTCCAGCAGGCCAACCGGCACCAC*TGA*GCGGCCGC