

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of GST-Parkin 1-76

Enzyme description:- GST-Parkin 1-76 = UBL domain

Clone number:- DU37369

Source:- BL21 recombinant

Tag:- N-terminal GST-tag

Purification method:- GSH-Sepharose

Expression level:- 2mg/L

Calculated molecular mass:-

Monoisotopic 35625 Da

Average Mass 35647 Da

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 6.40

Purity:- 90%

Enzyme storage buffer:-

50mM HEPES pH 8.2, 150mM NaCl, 20% glycerol, 1mM TCEP

Storage temperature:- -80°C

Assay:-

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Clone Data Sheet

GST-Parkin 1-76

Protein GST-Parkin 1-76
Synonyms PARK2, PRKN2
Clone Number DU37369
Species Human
Accession Number Protein: O60260 Gene: NM_004562.2
Tags N-terminal GST-tag

Aminoacid sequence of the expressed protein MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFE
LGLFEPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAIEISM
LEGAVLDIRYGVSR IAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKT
YLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPO
IDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDLEVLFOGPLGSMIVF
VRFNSSHGFPVEVSDTSIFQLKEVVAKRQGV PADQLRVI FAGKELR
NDWTVQNCDL DQQSIVHIVQRPWRK

Native sequence Parkin 1-76 in bold
Protease site Precission Protease site underlined
Cloning sites

DNA sequence of cassette ATGTCCTTACTACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCCACTC
GACTTCTTTTTGGAATATCTTGAAGAAAAATATGAAGAGCATTTGTATGAGCG
CGATGAAGGTGATAAATGGCGAAACAAAAAGTTTGAATTGGGTTTGGAGTTT
CCCAATCTTCCTTATTATATTGATGGTGATGTTAAATTAACACAGTCTATGG
CCATCATACTGTTATATAGCTGACAAGCACAAACATGTTGGGTGTTGTCCAAA
AGAGCGTGCAGAGATTTCAATGCTTGAAGGAGCGGTTTTGGATATTAGATAC
GGTGTTCGAGAATTGCATATAGTAAAGACTTTGAAACTCTCAAAGTTGATT
TTCTTAGCAAGCTACCTGAAATGCTGAAAATGTTTCAAGATCGTTTATGTCA
TAAAACATATTTAAATGGTGATCATGTAACCCATCCTGACTTCATGTTGTAT
GACGCTCTTGATGTTGTTTTATACATGGACCCAATGTGCCTGGATGCGTTCC
CAAAATTAGTTTGTTTTAAAAAACGTATTGAAGCTATCCCACAAATTGATAA
GTACTTGAATCCAGCAAGTATATAGCATGGCCTTTGCAGGGCTGGCAAGCC
ACGTTTGGTGGTGGCGACCATCCTCCAAAATCGGATCTGGAAGTTCTGTTCC
AGGGGCCCTGGGATCCATGATAGTGTGTTGTCAGGTTCAACTCCAGCCATGG
TTTCCCAGTGGAGTTCGATTCTGACACCAGCATCTTCCAGCTCAAGGAGGTG
GTTGCTAAGCGACAGGGGTTCCGGCTGACCAGTTGCGTGTGATTTTCGCAG
GGAAGGAGCTGAGGAATGACTGGACTGTGCAGAATTGTGACCTGGATCAGCA
GAGCATTGTTACATTGTGCAGAGACCGTGGAGAAAATGA