Division of Signal Transduction Therapy

Standard Operating Procedure

Preparation of PARK2 [1 - 108]

Enzyme description:- PARK2 [1 – 108]

Clone number:- DU 37370

Source:- Recombinant

Expression system:- *E.coli*,

Tag:- N-terminal GST

Purification method:- GSH Sepharose

Calculated molecular mass:-
Monoisotopic 38, 937.71 daltons
Average Mass 38, 962.79 daltons
[cysteines reduced, methionines have not been oxidised

Theoretical pI:- 5.70

Purity:- >80 %

Enzyme storage buffer:-
50 mM Tris-HCl pH 7.5, 150 mM NaCl, 270 mM sucrose, 0.1 mM EGTA, 0.1 % 2-mercaptoethanol, 0.03 % Brij-35, 1 mM benzamidine, 0.2 mM PMSF

Storage temperature:- -70 °C

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Clone Data Sheet

PARK2 [1 - 108]

Protein	PARK2 [1 - 108]
Clone number	DU 37370
Species	Human
Accession number	NM_004562.2
Tags	N-terminal GST
Bacterially expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFEL GLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLE GAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLN GDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKY LKSSKYIAWPLQGWQATFGGGDHPPKSDLEVLFQGPLGS**MIVFVRFNS** **SHGFPVEVDSDTSIFQLKEVVAKRQGVPADQLRVIFAGKELRNDWTVQ** **NCDLDQQSIVHIVQRPWRKGQEMNATGGDDPRNAAGGCEREPQSLTRV** **DLS**
Native sequence	Amino acids M1 – S108 of human PARK2. [End residue of full length PARK2 is V465] Residue M232 of fusion protein is equivalent to M1 of the native enzyme. The GST tag is located at residues 1 – 220.
Protease cleavage	Prescission site (LEVLFQGP) at residues 221 – 228
Cloning sites	*Bam*H1 and *Not*1 sites of pGex6P-1

Nucleotide sequence of insert

ggatccATGATAGTGTTTGTCAGGTTCAACTCCAGCCATGGTTTCCCA
GTGGAGGTCGATTCTGACACCAGCATCTTCCAGCTCAAGGAGGTGGTT
GCTAAGCGACAGGGGGTTCCGGCTGACCAGTTGCGTGTGATTTTCGCA
GGGAAGGAGCTGAGGAATGACTGGACTGTGCAGAATTGTGACCTGGAT
CAGCAGAGCATTGTTCACATTGTGCAGAGACCGTGGAGAAAAGGTCAA
GAAATGAATGCAACTGGAGGCGACGACCCCAGAAACGCGGCGGGAGGC
TGTGAGCGGGAGCCCCAGAGCTTGACTCGGGTGGACCTCAGCtgagcg
gccgc