Division of Signal Tranduction Therapy

Standard Operating Procedure

Preparation of TAB3 [2 – 712]

Enzyme description:- TAB3 [2 - 712]

Clone number:- DU3033

Source:- Recombinant

Expression system:- *E.coli*

Tag:- N-terminal GST

Purification method:- GSH Sepharose

Calculated molecular mass:-
Monoisotopic 105, 279.17 daltons
Average Mass 105, 345.83 daltons
[cysteines reduced, methionines have not been oxidised

Theoretical pI:- 8.15

Purity:- >80 %

Enzyme storage buffer:-
50 mM Tris-HCl pH 7.5, 270 mM Sucrose, 150 mM NaCl, 0.1 mM EGTA, 0.1 % 2-mercaptoethanol, 0.02 % Brij-35, 1 mM benzamidine, 0.2 mM PMSF

Storage temperature:- -70 °C

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Clone Data Sheet

TAB3 [2 - 712]

Protein	TAB3 [2 - 712]
Clone number	DU 3033
Species	Human
Accession number	NM_152787.3
Tags	N-terminal GST
Bacterially expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELG LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGA VLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDH VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSS KYIAWPLQGWQATFGGGDHPPKSDLEVLFQGPLGS**AQSSPQLDIQVLHD** **LRQRFPEIPEGVVSQCMLQNNNNLEACCRALSQESSKYLYMEYHSPDDN** **RMNRNRLLHINLGIHSPSSYHPGDGAQLNGGRTLVHSSSDGHIDPQHAA** **GKQLICLVQEPHSAPAVVAATPNYNPFFMNEQNRSAATPPSQPPQQPSS** **MQTGMNPSAMQGPSPPPPPPSYMHIPRYSTNPITVTVSQNLPSGQTVPR** **ALQILPQIPSNLYGSPGSIYIRQTSQSSSGRQTPQSTPWQSSPQGPVPH** **YSQRPLPVYPHQQNYQPSQYSPKQQQIPQSAYHSPPPSQCPSPFSSPQH** **QVQPSQLGHIFMPPSPSTTPPHPYQQGPPSYQKQGSHSVAYLPYTASSL** **SKGSMKKIEITVEPSQRPGTAINRSPSPISNQPSPRNQHSLYTATTPPS** **SSPSRGISSQPKPPFSVNPVYITYTQPTGPSCTPSPSPRVIPNPTTVFK** **ITVGRATTENLLNLVDQEERSAAPEPIQPISVIPGSGGEKGSHKYQRSS** **SSGSDDYAYTQALLLHQRARMERLAKQLKLEKEELERLKSEVNGMEHDL** **MQRRLRRVSCTTAIPTPEEMTRLRSMNRQLQINVDCTLKEVDLLQSRGN** **FDPKAMNNFYDNIEPGPVVPPKPSKKDSSDPCTIERKARRISVTSKVQA** **DIHDTQAAAADEHRTGSTQSPRTQPRDEDYEGAPWNCDSCTFLNHPALN** **RCEQCEMPRYT**
Native sequence	Amino acids A2 – T712 (end) of human TAB3. Residue A232 of the fusion protein is equivalent to A2 of the native enzyme. The GST tag is located at residues 1 – 220.
Protease cleavage	PreScission (LEVLFQGP) residues 221 - 228
Cloning sites	*Bam*H1 and *Eco*R1 sites of pGEX6P-1

Nucleotide Sequence of insert

ggatccGCGCAAAGCAGCCCACAGCTTGATATTCAGGTTCTCCATGATCTTCGACAACGTTTCCCT
GAAATTCCAGAGGGCGTGGTGTCTCAGTGCATGTTACAGAATAACAACAATCTTGAAGCCTGTTGC
CGAGCCCTTTCCCAGGAGAGTAGCAAATACTTATATATGGAATACCATAGTCCAGATGACAATAGG
ATGAATAGAAATCGCCTTTTACATATTAACCTGGGTATCCATTCTCCTAGTAGCTATCACCCAGGA
GATGGAGCCCAACTTAATGGTGGTCGAACACTGGTACATAGCTCAAGTGATGGACATATTGATCCT
CAGCATGCAGCAGGTAAACAGCTGATATGTTTAGTTCAAGAACCACACTCAGCTCCAGCTGTTGTT
GCTGCTACTCCCAACTACAATCCATTTTTTATGAACGAACAGAACAGAAGTGCAGCTACTCCTCCT
TCACAACCACCTCAACAGCCATCTTCCATGCAAACAGGAATGAATCCGTCTGCTATGCAAGGGCCT
TCACCACCACCGCCACCTCCTTCATACATGCACATACCTCGGTATAGTACAAATCCAATTACTGTT
ACAGTATCCCAGAACCTCCCTTCTGGACAGACTGTACCAAGAGCTTTACAAATTCTTCCACAAATT
CCAAGCAATCTCTATGGGTCTCCTGGTTCTATTTATATTAGACAGACATCTCAGAGTTCATCAGGA
AGACAAACTCCTCAGAGTACGCCGTGGCAGTCCTCACCACAGGGCCCAGTGCCTCACTATAGCCAG
CGTCCTTTACCTGTTTATCCACACCAACAGAACTATCAGCCTTCTCAGTATTCTCCCAAACAGCAG
CAGATCCCTCAGTCTGCTTACCATTCACCACCTCCTTCTCAATGTCCTTCACCCTTCAGCTCTCCA
CAGCATCAAGTGCAACCTTCCCAGTTGGGCCACATCTTTATGCCACCTAGTCCTTCAACTACTCCA
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CCATACACAGCATCTAGTTTATCCAAAGGTTCCATGAAGAAGATAGAAATTACAGTTGAACCTTCT
CAAAGACCTGGGACAGCAATTAATAGGAGTCCTTCACCCATCAGTAATCAACCATCTCCACGGAAT
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TACGAAGGGGCTCCATGGAATTGTGATAGCTGCACCTTTCTTAACCACCCAGCACTAAATCGCTGT
GAGCAGTGCGAGATGCCACGGTACACCtgaattc

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