Division of Signal Tranduction Therapy

Standard Operating Procedure

Preparation of DAZAP T269A T315A [2 - 407]

Enzyme description:- DAZAP T269A T315A [2 - 407]

Clone number:- DU 3267

Source:- Recombinant

Expression system:- *E.coli*

Tag:- N-terminal GST

Purification method:- GSH Sepharose

Calculated molecular mass:-
Monoisotopic 69, 971.63 daltons
Average Mass 70, 016.31 daltons
[cysteines reduced, methionines have not been oxidised

Theoretical pI:- 6.87

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

DAZAP T269A T315A [2 - 407]

Protein	DAZAP T269A T315A [2 - 407]
Clone number	DU 3267
Species	Human
Accession number	NM_018959
Tags	N-terminal GST
Bacterially expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELG LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGA VLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDH VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSS KYIAWPLQGWQATFGGGDHPPKSDLEVLFQGPLGS**NNSGADEIGKLFVG** **GLDWSTTQETLRSYFSQYGEVVDCVIMKDKTTNQSRGFGFVKFKDPNCV** **GTVLASRPHTLDGRNIDPKPCTPRGMQPERTRPKEGWQKGPRSDNSKSN** **KIFVGGIPHNCGETELREYFKKFGVVTEVVMIYDAEKQRPRGFGFITFE** **DEQSVDQAVNMHFHDIMGKKVEVKRAEPRDSKSQAPGQPGASQWGSRVV** **PNAANGWAGQPPPTWQQGYGPQGMWVPAGQAIGGYGPPPAGRGAPPPPP** **PFTSYIVSAPPGGFPPPQGFPQGYGAPPQFSFGYGPPPPPPDQFAPPGV** **PPPPAAPGAAPLAFPPPPSQAAPDMSKPPTAQPDFPYGQYAGYGQDLSG** **FGQGFSDPSQQPPSYGGPSVPGSGGPPAGGSGFGRGQNHNVQGFHPYRR**
Native sequence	Amino acids N2 – R407 (end) of human DAZAP. Residue N232 of the fusion protein is equivalent to N2 of the native enzyme. The GST tag is located at residues 1 – 220. The protein has a T269A and a T315A mutation. Residue T269 is equivalent to residue A499 of the fusion protein. Residue T315 is equivalent to residue A545 of the fusion protein.
Protease cleavage	PreScission (LEVLFQGP) residues 221 - 228
Cloning sites	*Bam*H1 sites of pGEX6P-1

Nucleotide Sequence of insert

ggatccAACAACTCGGGCGCCGACGAGATCGGGAAGCTCTTCGTGGGCG
GTCTTGACTGGAGCACGACCCAAGAGACTCTGCGCAGCTACTTTTCCCA
ATATGGAGAAGTCGTAGATTGTGTTATCATGAAAGATAAAACCACCAAC
CAGTCTCGAGGCTTTGGGTTTGTCAAATTTAAAGACCCAAACTGTGTGG
GGACGGTGCTGGCCAGCAGACCGCACACGCTAGATGGCCGAAACATCGA
CCCCAAGCCATGCACACCCCGGGGGATGCAGCCGGAGAGAACACGGCCG
AAGGAAGGATGGCAGAAAGGACCCAGGAGCGATAACAGTAAATCAAATA
AGATATTTGTCGGTGGAATTCCTCACAATTGTGGTGAGACAGAGCTCAG
GGAATACTTCAAGAAGTTCGGAGTGGTCACGGAGGTAGTCATGATCTAT
GACGCCGAGAAGCAGAGGCCCCGAGGTTTTGGATTTATTACTTTCGAGG
ACGAACAATCAGTGGACCAGGCTGTCAACATGCATTTTCACGACATCAT
GGGCAAAAAAGTGGAAGTTAAACGAGCTGAGCCTCGGGACAGCAAGAGC
CAAGCGCCGGGACAGCCAGGTGCCAGCCAGTGGGGGAGCCGGGTTGTGC
CCAACGCTGCCAATGGCTGGGCAGGCCAGCCCCCGCCCACGTGGCAGCA
AGGATATGGCCCGCAAGGAATGTGGGTGCCGGCAGGACAGGCGATTGGT
GGCTATGGACCGCCCCCTGCAGGAAGAGGAGCCCCCCCGCCACCCCCAC
CGTTCACCTCCTACATCGTGTCCGCCCCTCCTGGAGGCTTTCCCCCTCC
CCAGGGCTTCCCTCAGGGCTACGGTGCCCCGCCACAGTTCAGTTTTGGC
TACGGGCCTCCACCTCCACCGCCAGATCAGTTTGCCCCTCCGGGGGTTC
CTCCTCCACCAGCCGCTCCCGGGGCAGCACCTCTGGCTTTCCCACCGCC
TCCGTCTCAGGCTGCCCCGGACATGAGCAAGCCCCCGACAGCTCAGCCA
GACTTCCCCTATGGTCAGTATGCAGGTTACGGGCAGGACTTGAGTGGCT
TCGGACAGGGCTTCTCAGACCCCAGCCAGCAGCCTCCTTCCTACGGGGG
TCCCTCCGTGCCAGGGTCGGGGGGCCCCCCCGCCGGCGGCAGCGGCTTT
GGACGAGGGCAGAACCACAACGTGCAAGGGTTCCACCCCTACCGACGCt
agggatcc