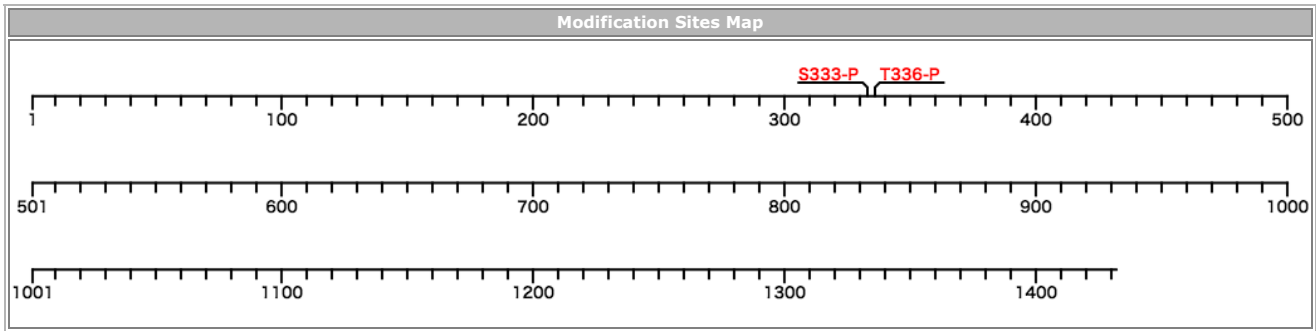


ID	Accession	GeneName	Chr.No.		Description
DAPK1_HUMAN	P53355	DAPK1	9q21.33	90112143..90323548	Death-associated protein kinase 1



Click a modification site to display the information in detail.

Site no	Amino acid	Type	Division	Detail
336	T	P	Lab	140326_OVISE_NES_tita_2_.mgf[F017520]
336	T	P	Lab	140326_OVISE_NES_tita_3_.mgf[F017523]
336	T	P	Lab	110218_pOVSAYO_3.mgf[F017471]
336	T	P	Lab	110218_pRMG2_1.mgf[F017475]
336	T	P	Lab	110218_pRMG2_2.mgf[F017476]
336	T	P	Lab	110218_pRMG2_3.mgf[F017477]
336	T	P	Lab	110218_pRMG2_4.mgf[F017478]
336	T	P	Lab	100627_akimura_pOVISE_1.mgf[F017437]
336	T	P	Lab	140326_OVISE_NES_tita_.mgf[F017518]

Protein Sequence
MTFVFRQENV DYYDTGEE LG SGQFAVVKC REKSTGLQYA AKFIKKRRTK SSRGVSRED IEREVSILKE IQHPNVITLH EVYENKTDVI LILELVAGGE LFDFLAEKES LTEEE ATEFL KQILNGVYYL HSLQIAHFDL KPENIMLLDR NVPKPRIKII DFGLAHKIDF GNEFKNIFGT PEFVAPEIVN YEPLGLEADM WSIGVITYIL LSGASPFLGD TKQETLANVS A VNYEFEDEY FSNTSALAKD FIRLLVKDP KKRMTIQDSL QHPWIKPKDT QQALSRKASA VNMEKFKKFA ARKKWKQSVR LISLCQRLSR SFLSRSNMSV ARSDDTLDEE DSF VMKAIH AINDDNVPLG QHLLGSLSNY DVNQPNKHGT PPLLIAAGCG NIQILQLLIK RGSRIDVQDK GGSNAVYWAA RHGHVDTLKF LSENKCPDLDV KDKSGEMALH VAARY GHADV AQLLCSFGSN PNIQDKEEET PLHCAAWHGY YSVAKALCEA GCNVNIKNRE GETPLLTASA RGYHDIVECL AEHGADLNAC DKDGHIALHL AVRRRCQMEVI KTLLSQ GCFV DYQDRHGNT P LHVACKDGNM PIVVALCEAN CNLDISNKYG RTPHLAANN GILDVVRYLC LMGASVEALT TDGKTAEDLA RSEQHEHVAG LLARLRKTDH RGLFIQQL RP TQNLQPRIKL KLFHSGSGK TTLVESLCKG LLRSFFRRRR PRLSSTNSSR FPPSPLASKP TVSVSINNLY PGCENSVRS RSMMFEPGLT KGMLEVFVAP THHPHCSADD Q STKAIDIQN AYLVNGVDFS VWEFSGNPVY FCCYDYFAAN DPTSIHVVVF SLEEPYEQIQL NQVIFWLSFL KSLVPVEEPI AFGGKLNPL QVVLVATHAD IMNVPRPAGG EFGYD KDTSL LKEIRNRFNG DLHISNKL FV LDAGASGSKD MKVLRNHLQE IRSQIVSVP PMTHLCEKII STLPSPWRKLN GPNQLMSLQQ FVYDVQDQLN PLASEEDLRR IAQQLHST GE INIMQSETVQ DVLLDPRWL CTNVLGKLLS VETPRALHHY RGRYTVEDIQ RLVPSDVEE LLQILDAMDI CARDLSSGTM VDVPAIKTD NLHRSWADEE DEVMVYGGVR IVPVEHLTPF PCGIFHKVQV NLCRWIHQQS TEGDADIRLW VNGCKLANRG AELLVLLVNH GQGIEVQVRG LETEKIKCCL LLDVSCSTIE NVMATTLPLG LTVKHLYLSPQ QLRE HHEPVM IYQPRDFFR QTLKETSLTN TMGGYKESFS SIMCFGCHDV YSQASLGM DI HASDLNLLTR RKLSRLDPP DPLGKDWCLL AMNLGLPDLV AKYNTSNGAP KDFLPS PLHA LLREWTTYPE STVGTLM SKL RELGRRDAAD FLLKASSVFK INLDGNGQEA YASSCSNGTS YNSISSVVSR

Backcolor of amino acid : Yellow -> site of modification, gray -> in front of processing