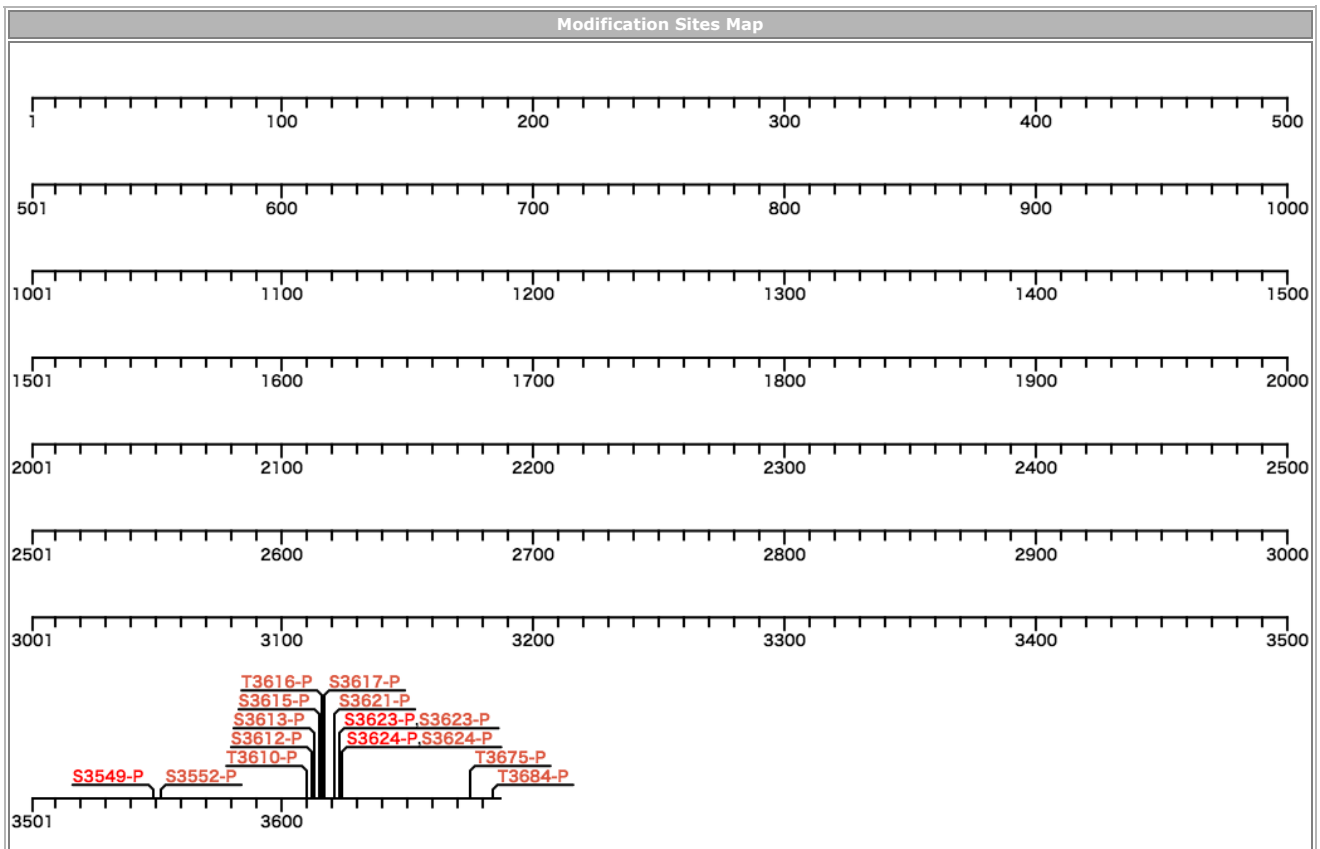


ID	Accession	GeneName	Chr.No.	Description
DMD_HUMAN	P11532	DMD	Xp21.1 31115794..33357558	Dystrophin



Click a modification site to display the information in detail.

Site no	Amino acid	Type	Division	Detail
3623	S	P	Lab	130415_HEK_CE_tphos.mgf[F015009]
3623	S	P	Lab	100510-lungc385.mgf[F017492]
3623	S	P	Paper	Sci Signal 2011, 4(179), rs5

Protein Sequence	
MLWWEVEEDC YEREDVQKKT FTKWVNAQFS KFGKQHIEHL FSDLQDGRRL LDLLEGLTGQ KLPKEKGSTR VHALNNVNKA LRVLQNNVND LVNIGSTDIV DGNHKLTLGL I WNIIHLHWQV KVMKIMAG LQQTNSEKIL LSWVRQSTRN YPQVNVINF TSWSDGLALN ALIHSRHPDL FDWNSVVCQQ SATQRLEHAF NIARYQLGIE KLLDPEDVDT TY PDKKSILM YITSLFQVLP QQVSIEAIEQ VEMLPRPPKV TKEEHFQLHH QMHYSQQITV SLAQGYERTS SPKPRFKSYA YTQAAYVTT S DPTRSPFSSQ HLEAPEDKSF GSSLME SEVN LDYRQTAL EE VLSWLLSAED TLQAQGEISN DVEVVKDQFH THEGYMMDLT AHQGRVGNIL QLQSKLIGTG KLSEDEETEVE QEQMNLNLSR WECLRVASME KQSNLH RVLMLDLQNQKLEL NDWLTKTEER TRKMEEEPLG PDLEDLKRQV QQHVKLQEDL EQEQVRVNSL THMVVVVDES SGDHTATALE ELQKVLGDRW ANICRWTEDR WVLLQ DILLK WQRLTEEQCL FSAWLSEKED AVNKIHTTGF KDQNEMLSSL QKLAVLKADL EKKKQSMGKL YSLKQDLLST LKNKSVTQKT EAWLDFNFARC WDNLVQKLEK STAQIS QAVT TTQPSLTQTT VMETVTTVT REQLVKHQA EELPPPPQK KRQITVDSEI RKRLDVIDITE LHSWITRSEA VLQSPFAIF RKEGNFSDLK EKVNAIEREK AEKFRKLQDA SRSAQALVEQ MVNEGVNAD IKQASEQLNS RWIEFCQLS ERLNWLEYQN NIAFYNLQQL QLEQMTTAE NWLKIQPTTP SEPTAIKSQL KICKDEVNRL SDLPQIERL KIQ SIALKEK GQGPMLFDAD FVAFTNHFKQ VFSVDQAREK ELQITIFDTP PMRYQETMSA IRTWVQSET KLISPLQSVT DYEIMEQRLG ELQALQSSLL EQQSGLYLTS TTVKEM SKKA PSEISRKYQS EFEEIEGRWK KLSSQLVEHC QKLEEQMNNL RKIQNHQITL KKWMAEVDVF LKEEWPALGD SEILKKQLKQ CRLLVSDIQT IQPSLNSVNE GGQKIKNE AE PEFASRLTE LKELNTQWDH MCQQVYARKE ALKGGLEKTV SLQKDLSEMH EWMTQAE EY LERDFEYKTP DELQKAVEEM KRAKEEAQQK EAKVKLLTES VNSVIAQAP P VAQEALKKEL ETLTNYQWL CTRLNGKCKT LEEVWACWHE LLSYLEKANK WLNEVEFKL TTENIPGGAE EISEVLDSE NLMRHSEDP NQIRILAQTL TDGGVMDLI N EELETFSNR WRELHEEAVR RQKLEEQSIQ SAQETESLH LIQESLTFID QLAAYIADK VDAAQMPQEA QKIQSDLTSH EISLEEMKKH NQGKEAAQRV LSQIDVAQKK LQD VSMKFR L FQKPFANFEQR LQESKMILDE VKMHLPALET KSVEQEVVQS QLNHCVNLYK SLSEVKSEVE MVIKTRQIV QKKQNTENPK E LDERVTALK HYNELGAKVT ERKQQ LEKCL KLSRKMREK NVLTEWLAAT DMELTKRSV EGMPSNLDSE VAWGKATQKE IEKQVHLKS ITEVGEALKT VLGGKTELVE DKLSLLNSNW IAVTSRAEEW LNLLEY QKH METFDQNVHD ITKWIQADT LDESEKKKQ QKEDVLKRL KAEINDIRPK VDSTRDQAAN LMANRGDCHR KLVEPQISEL NHRFAAISHR IKTGKASIP L KELEQFN S D I QKLEPLEAE IQQGVNKEE DFNKDMNEDN EGTVKELLQR GDNLQQRITD ERKREEIKI QQLLQTKHNA LKDLRSQRRK KALEISHQWY QYKRQADDLL KCLDDIEKKL AS LPEPRDR KIKEIDRELQ KKEELNAVR RQAEGLESDG AAMAVEPTQI QLSKRWEIRE SKFAQFRRLN FAQIHTVREE TMMVMTEMDP LEISVPSTY LTEIHVSQA LLEVEQ LLNA PDLCAKDFED LFKQEESLKN IKDSLQSSG RIDIHSKKT AALQSATPVE RVKLEQALSQ LDFQWEKVNK MYKDRQGRFD RSVEKWRFRH YDIKIFNQWL TEAEQFLR KT QIPENWEHAK YKWLKELQD GIGQRQTVVR TLNATGEEII QSSKTDASI LQEKLGSLNL RWQEVCKQLS DRKKRLEEQK NILSEFQRDL NEFVLWLEEA DNIAISIPLEP GKEQQLKEK EQVKLLVEEL PLRQGIKQL NETGGPVLVS APISPEEQDK LENKLLQTNL QWIKVSRALP EKQGEIEAQI KDLGQLEKLL EDLEEQLNHL LLWLSPIRNQ LEIYN QPNQE GPFDVKETEI AVQAKQPDVE EILSKGQHLV KEKPATQPVK RKLEDLSEW KAVNRLLEL RAKQPD LAPG LTTIGASPTQ TVTLVTQPVV TKETAISKLE MPSSMLLEV P ALADFNRAWT ELTDWLSLLD QVIKSQRVMV GDLEDINEMI IKQKATMQDL EQRRPQLEEL ITAAQNKLNK TSNQEARTII TDRIERIQNQ WDEVEQHLQN RRQQLNEMLK DSTQWLEAKE EAEQVLGQAR AKLESWKEGP YTVDAIQKKI TETKQLAKDL RQWQTNVDVA NDALAKLLRD YSADDTKRVH MITENINASW RSIHKRVSR EAAL EETHRL L QQFPDLDEK FLAWLFEAET TANVLQDATR KERLLED SKG VKELMKQWQD LQGEIAHTD VYHNLNDSQ KILRSLEGSD DAVLLQRRLD NMNFKWSEL R KSLNIRSHL EA SSDQWKRL HLSLQELLVW LQLKDDLSR QAPIGGDFPA VQKQNDVHRA FKRELKTKEP VIMSTLETVR IFLTEQPLEG LEKLYQEPRE LPPEERAQNV TRLLRQKQAE VNT EW EKLNL HSADWQRKID ETLERLQELQ EATDEL DKL RQAEVIGKSW QPVGDL LIDS LQDHLEKVA LRG EIAPLKE NVSHVNDLAR QLTLGIQLS PYNLSTLEDL NTRWKLLO VA VEDRVRLHE AHRDFGPASQ HFLSTSVQGP WERAISPNNV PYYINHETQT TCWDHPKMT E LYQSLADLNN VRFSA YRTAM LRLRLQKALC LDLLLSAAC DALDQHNLK Q NDQPM DILQI INCLTTIYDR LEQEHNNLVN VPLCVDMLCN WLLNVYDTGR TGRIRVLSFK TGIISLCAH LEDKYRYLFK QVASSTGFCD QRRLGLLHD SIQIPRQLGE VA SFGGSNIE PSVRS CFQFA NNPETEAL FLDWMRLPEQ SMVWLPVLRH VAAETAHQ AKCNICKECP IIFRYSRLK HFNYDICQSC FFSGRVAKGH KMHYPMVEYC TPTT SGEDVR DFAKVLKKNF RTKRYFAKHP RMGYLPVQTV LEGDNMTPV TLINFWPVD S APASSQLSH DDTHSRIEHY ASRLAEMENS NGSYLNDSIS PNESIDDEHL LIQHVC QSLN QDSPLSQPRS PAQILISLES EERGERLIL ADLEENRNL QA EYDRKQKQ HEHKGLSLP SPPEMPTSP QSPRDAELIA EAKLLRQHKG RLEARMQILE DHNKQLESQ L HRLRQLLEQP QAEAKVNGT <b>VSSPSTSLQR</b> <b>SDSS</b> QPM L LRVVGSQTSDSM GEEDLLSPPQ DTSTGLEEVM EQLNNSFPSS RGRNTPGKPM REDT M	

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