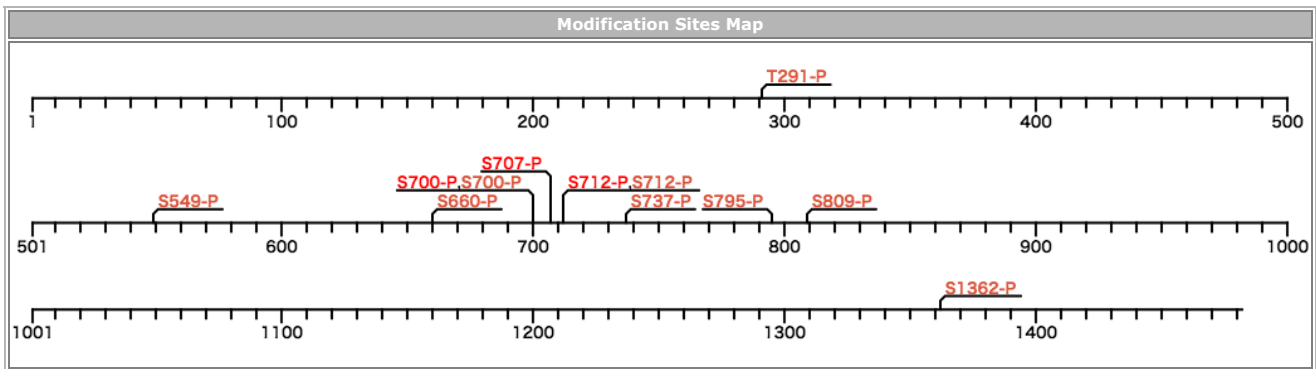


ID	Accession	GeneName	Chr.No.		Description
CFTR_HUMAN	P13569	CFTR	7q31.2	117105838..117356025	Cystic fibrosis transmembrane conductance regulator



Click a modification site to display the information in detail.

Site no	Amino acid	Type	Division	Detail
700	S	P	Lab	110218_pRMG2_1.mgf[F017475]
700	S	P	Lab	110218_pRMG2_2.mgf[F017476]
700	S	P	Lab	110218_pRMG2_3.mgf[F017477]
700	S	P	Lab	110218_pRMG2_4.mgf[F017478]
700	S	P	Paper	Mol Cell Proteomics 2014, 13(7), 1690-1704

Protein Sequence	
MQRSPLEKAS VVSKLFFSWT RPILRKGYRQ RLELSDIYQI PSVDSADNLS EKLEREWDRE LASKKNPKLI NALRRCCFFWR FMFYGIFLYL GEVTKAVQPL LLGRIIASYD PDNK EERSIA IYLGIGLCLL FIVRTLLHP AIFGLHHIGM QMRIAMFSLI YKTKLSSR VLDKISIGQL VSLLSNLNK FDEGLALAHF VWIAPLQVAL LMGLIWELLQ ASAFGLGLF I VLALFQAGL GRMMMKYRDQ RAGKISERLV ITSEMIENIQ SVKAYCWEEA MEKMIENLRQ T <sup>Y</sup> ELKLRKAA YVRYFNSSAF FFSGFFVFL SVLPYALIKG IILRKIFTTI SFCIVLR MAV TRQFPWAVQT WYDSLGAINK IQDFLQKQEQY KLEYNLTTT EVMENVTAF WEEGFGELFE KAKQNNNRK TSNGDDSLFF SNFSLGTPV LKDINFKIER QLLAVAGS T GAGKTSLLMV IMGELEPSEG KIKHSGRISF CSQFSWIMPG TIKENIIFGV SYDEYRYSV IKACQLEEDI SKFAEKDNIV LGEGGITL <sup>S</sup> G GQRARISLAR AVYKDADLYL LDS PFGYLDV LTEKEIFESC VCKLMANKTR ILVTSKMEHL KKADKILILH EGSSYFYGTG SELQNLQPDF SSKLMGDSF DQFSAERRN <sup>S</sup> ILTETLHRFS LEGDAPVSWT ETKKQSF KQT GEFGEKRKN <sup>S</sup> ILNPIN <sup>S</sup> IRK F <sup>S</sup> IVQKTPQL MNGIEEDSDE PLERRL <sup>S</sup> LVP DSEQGEA <sup>I</sup> LP RISVISTGPT LQARRRQSVL NLMTHSVNQG QNIHRKTAS TRKV <sup>S</sup> LAPQA NLTELDIY <sup>S</sup> R RLSQETGLEI SEEINEEDLK ECFDDMESI PAVTTWNTYL RYITVHKSLI FVLIWCLVIF LAEVAASLVV LWLLGNTPLQ DKGNSHRSR NSYAVIITST SSYYVF YIYV GVADTLAMG FFRGLPLVHT LITVSKILHH KMLHSVLQAP MSTLNTLKAG GILNRFSDI AILDDLLPLT IFDFIQLLI VIGAI <sup>A</sup> VVAV LQPIYFVATV PVIVAFIMLR AYFL QTSQQL KQLESEGRSP IFTHLVTLK GLWTLRAFGR QPYFETLFHK ALNLHTANWF LYLSTLRWFQ MRIEMIFVIF FIAVTFISIL TTGEGEGRVG IILTLAMNIM STLQWAVNS S IDVDSL <sup>M</sup> RSV SRVFKFIDMP TEGKPTKSTK PYKNGQLSKV MIIENSHVKK DDIWPSGGQM TVKDLTAKYT EGGNAIL <sup>E</sup> NI SFSISPGQRV GLLGRTGSGK STLLSAFLRL LN TEGEIQID GVSWDSITLQ QWRKAFGVIP QKVFIFSGTF RKNLDPYEQW SDQE <sup>I</sup> WKVAD EVGLRSVIEQ FPGKLD <sup>F</sup> VLV DGGCVLSHG <sup>H</sup> KQLMCLARSV L <sup>S</sup> KAKILLD EPSA HLD <sup>P</sup> V <sup>T</sup> YQIIRRTLKQ AFADCTVILC EHRIEAMLEC QQFLVIEENK VRQYDSIQKL LNERSLFRQA ISPSDRVKLF PHRNSKCKS KPQIAALKEE TEEEVQDTRL	

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