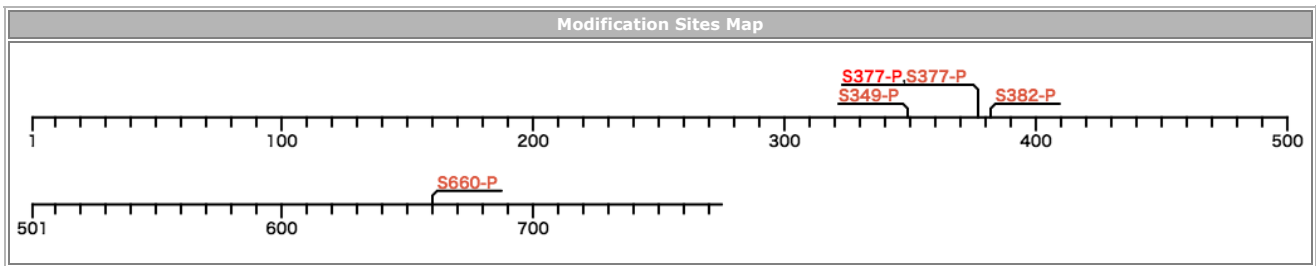


ID	Accession	GeneName	Chr.No.		Description
CMIP_HUMAN	Q8IY22	CMIP	16q23.2	81478775..81745367	C-Maf-inducing protein



Click a modification site to display the information in detail.

Site no	Amino acid	Type	Division	Detail
377	S	P	Lab	130327_HEK_ME_pphos.mgf[F015008]
377	S	P	Lab	130415_HEK_ME_tphos.mgf[F015010]
377	S	P	Paper	J Proteome Res 2008, 7(3), 1346-1351
377	S	P	Paper	J Proteome Res 2013, 12(1), 260-271

Protein Sequence	
MDVTSSSGGG GDPRQIEETK PLLGGDVSAP EGTKMGAVPC RRALLCNGM RYKLLQEGDI QVCVIRHPT FLSKILTSKF LRRWEPHHLT LADNSLASAT PTGYMENSVS YS AIEDVQLL SWENAPKYCL QLTIPGGTVL LQAANSYLRL QWFHSLQWKK KIKYKVVLS NPSRWEVVK EIRTLVDMAL TSPLODD SIN QAPLEIVSKL LSENTNLTQ EHENII VAIA PLENNHPPP DLCEFFCKHC RERPRSMVVI EVFTPVVQRI LKHNMDFGKC PRLRLFTQEQY ILALNELNAG MEVVKKFIQS MHGPTGHCPH PRVLPNLVAV CLAAIYSCYE EFINSRDNSP SLKEIRNGCQ QPCDRKPTLP LRLHPSPDL VSQEATLSEA RLKSVVAVASS EIHVEVERTS TAKPALTASA GNDSEPNLID CLMVSPACST MSIELGPQAD RTLG CYVEIL KLLSDYDDWR PSLASLLQPI PFPKEALAHE KFTKELKYVI QRFAEDPRQE VHSCLLSVRA GKGWGFQLYS PGGVACDDDG ELFASMVHIL MGSCYKTKKF LLSLAEN KLG PCMLLALRGN QTMVEILCLM LEYNIIDNND TQLQIISTLE STDVVGKRYME QLCDRQRELK ELQRKGGPTR LTLPSKSTDA DLARLLSSG S FGNLENLSLA FTNVTSAEAE HLIKPLSLKQ LNLWSTQFGD AGLRLLSEHL TMLQVLNLCE TPVTDAGLLA LSSMKSLCSL NMNSTKLSAD TYEDLKAKLP NLKEVDVRYT EAW	

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