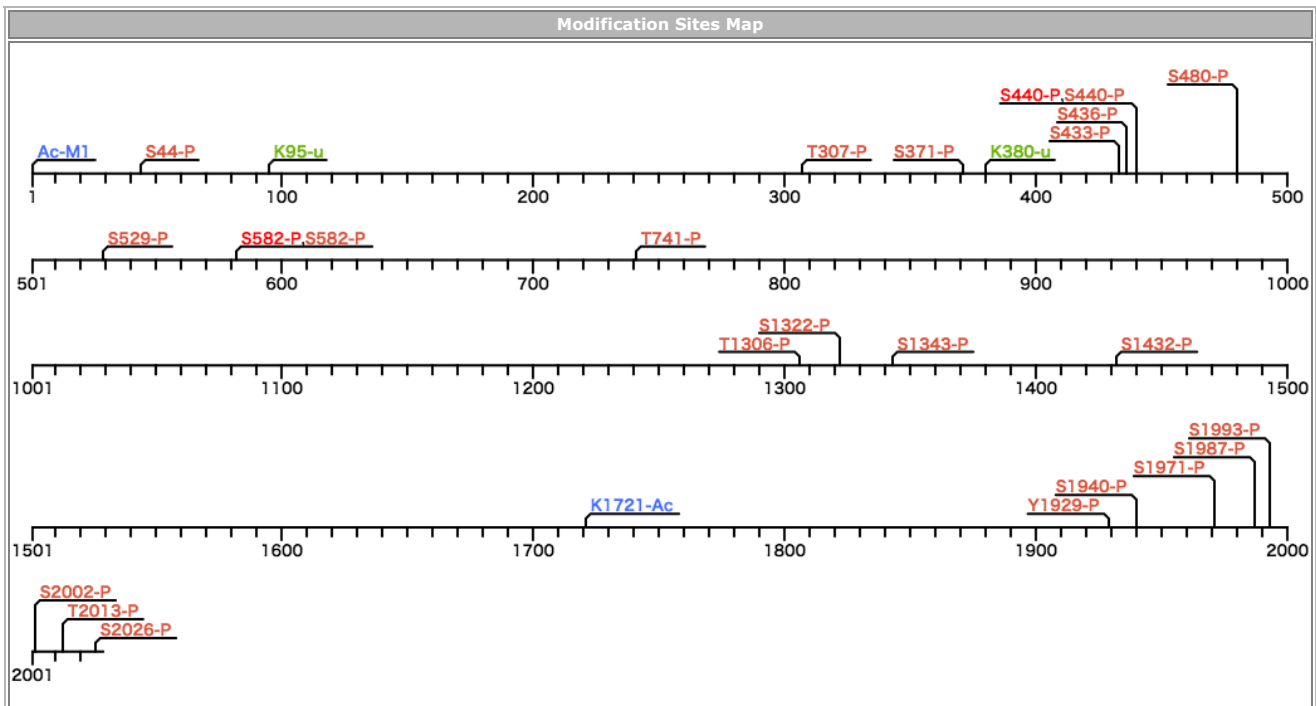


ID	Accession	GeneName	Chr.No.		Description
CTRO_HUMAN	O14578	CIT	12q24.23	120123595..120315095	Citron Rho-interacting kinase



Click a modification site to display the information in detail.

Site no	Amino acid	Type	Division	Detail
582	S	P	Lab	130327_HEK_ME_pphos.mgf[F015008]
582	S	P	Paper	J Proteome Res 2013, 12(1), 260-271
582	S	P	Paper	Mol Cell Proteomics 2012, 11(9), 651-668
582	S	P	Paper	Mol Cell Proteomics 2014, 13(7), 1690-1704

Protein Sequence	
<p>MLKFKYGARN PLDAGAAEPI ASRASRLNLF FQGKPPFMTQ QQMSPLSREG IALDFVLFE ECSQPALMKI KHVSNFVRKY SDTIAELQEL QPSAKDFEVR SLVGCGHFAE VQV VREKATG DIYAMKVMKK KALLAQEQVS FFEERNILS RSTSPWIPQL QYAFQDKNHL YLMEYQPGG DLLSLLNRYE DQLDENLIQF YLAELILAVH SVHLMGYVHR DIKPENI LVD RTGHILKLVDF GSAKMNSNK MVNAKLPIGT PDYMAPEVLT VMNGDGKGT YGLDCDWWSVG VIAYEMIYGR SPFAEGTSAR TFNNIMNFQR FLKFPDDPKV SSDFLDLI QS LLCGQKERLK FEGLCCHPFF SKIDWNNIRN SPPPFVPTLK SDDDTSNFDE PEKNSWVSS PCQLSPSGFS GEELPFVGF S YSKALGILGR SESVVSGLDS PAKTSSMEKK LLIKSKELQD SQDKCHKMEQ EMTRLHRRV S EVEAVLSQKE VELKASETQR SLEEQDLATY ITECSSLKR S LEQARMEV S Q EDDKALQLLH DIREQSRKLQ EIKEQEYQAQ VE EMRLMMNQ LEEDLV SARR RSDLYESEL R ESRLAAEEFK RKATECQHL LKAKDQGKPE VGEYAKLEKI NAEQQLKIQE LQEKLEKAVK ASTEATELLQ NIRQAKERAE RELEK LQNRE DSSEGIRKLL VEAEELKEKH REAQVSAQHL EVHLKQKEQH YEEKIKVLDN QIKKDLADKE TLENMMQRHE EEAHEKGKIL SEQKAMINAM DSKIRSLEQR IVELSEA NKL AANSSLFTR NMKAQEEMIS ELRQKQFYLE TQAGKLEAQN RKLEEQL EKI SHQDHS DKNR LLELETRLRE VSLEHEEQKL ELKRQLTELQ LSLQERESQL TALQAARAAL ESQLRQAKTE LEETAEAE E EIQALTAHRD EIQRKFDALR NSCTVITDLE EQLNQLTEDN AELNNQNFYL SKQLDEASGA NDEIVQLRSE VDHLRREITE REMQLTSQKQ TME ALKTTCT MLEEQVMDLE ALNDELLEKE RQWEAWRSVL GDEKSQFE CR VRELQRLD T EKQSRARADQ RITESRQVVE LAVKEHKA EI LALQALKEQ KLKAE S LSDK LNDL EKKHAM LEMNARS LQK KLETERELKQ RLLEEQA KLQ QMDLQKNHI FRLTQGLQEA LDRADLLKTE RSDLEYQLEN IQVLYSHEKV KMEGTISQQT KLIDFLQAKM DQPAKK KKGL FSRRKEDPAL PTQVPLQYNE LKLALEKEKA RCALEEALQ KTRIELRSAR EEAHRKATD HPHPS T PATA RQQIAMS AIV R S PEHQPSAM SLLAPPSRRR KE S STPEEFS RRLKERMHHN IPHRFNVGLN MRATKCAVCL DTVHFGRQAS KCLECV MCH PKCSTCLPAT CGLPAEYATH FTEAFCRDKM N S PGLQTKEP SSSLHLEGWM KVPRNNKRGQ QGWD RKYIVL EGSKVLIYDN EAREAGRPV EEFELCLPDG DVSIHGAVGA SELANTAKAD VPYILKMESH PHTTCWPGRT LYLLAPSPD KQRWVTALES VVAGGRVSRE KA EADAKLLG NSLLKLEGGD RLD MNCTLPF SDQVVLVGTE EGLYALNVLK NSLTHVPGIG AVFQIYIKD LEKLLMIAGE ERALCLVDVK KVKQSLAQSH LPAQPDISP IFEAVK GCHL FGAGKIENGL CICAAMPSKV VILRYNENLS KYCIRKEIET SEPCSCIHT NYSILIGTNK FYEIDMKQYT LEEFLDKNDH SLAPAVFAAS SNSFPVSIQ VNSAGQREY L LCFHEFGVF VDSYGRRSRT DDLKWSRLPL AFAYREP YLF VTHFNSLEVI EIQRSSAGT PARAYLDIPN PRYLGPAISS GAIYLASSYQ DKLRVICCKG NLVKESGTEH HRGPST SRSS PNKRGPPT YN EHITKRVAS S PAPPEGPSHP REPSTPHRYR EGRTELRRDK S PGRPLEREK SPGRMLSTRR ERS PGR LFED S SRGRLPAGA VRT PLSQV NK VWDQS S V</p>	

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