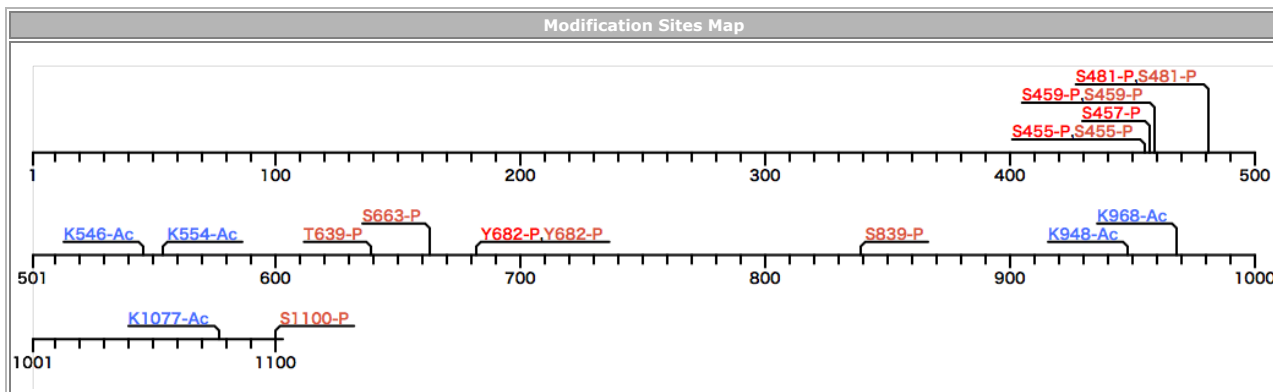


ID	Accession	GeneName	Chr.No.	Description
ACLY_HUMAN	P53396	ACLY	17q21.2 40023161..40086795	ATP-citrate synthase



Click a modification site to display information in detail.

Site no	Amino acid	Type	Division	Detail
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Protein Sequence	
MSAKAISEQT GKELLYKFC TTSAIQNRFK YARVTPDWDW ARLLQDHPWL LSQNLVVKPD QLIKRRGKLG LVGVNLTLDG VKSWLKPRLG QEATVGKATG FLKNFLIEPF VPH SQAEFEY VCIYATREGD YVLFHHEGGV DVGDVDAKAQ KLLVGVDEKL NPEDIKKHLL VHAPEDKKEI LASFISGLFN FYEDLYFTYL EINPLVVTGD GVVYLDLAAK VDATADYI CK VKWGDIEFPP PFGREAYPEE AYIADLDAKS GASLKLTLN PKGRIWTMVA GGGASVVYSD TICDLGGVNE LANYGEYSGA PSEQTYDYA KTIKSLMTR E KHPD GKILII G GSIANFTNV AATFKGIVRA IRDYQGPLKE HEVTIFVRRG GPNYQEGLRV MGEVGGKTTGI PIHVFGTETH MTAIVGMALG HRPINQPPT AAHTANFLN ASGSTSTPAP SRTAS FSES R ADEVAPAKKA KPAMPQDSVP SPRSLQGKST TLFSRHTKAI VWGMQTRAVQ GMLDFDYVCS RDEPSVAAMV YPFTGDHKQK FYWGH KEILI PVFK NMADAM RKHPE VDVLI NFASLSAYD STMETMNYAQ IRTIAIIAEG IPEALTRKLI KKADQKGVTI IGPA TVGGIK PGC FKIGN T G GMLDNILASK LYRPGSVAYV SR SGGMSNEL NNIISRTTDG VYEGVAIGGD RYPGSTFMDH VLR YQDTPGV KMIVVLGEIG GTEEYKICRG IKEGRLTKPI VCWIGTCAT MFSSEVQFGH AGACANQASE TAVAKNQALK EAGVFVPRSF DE LG EIIQSV YEDLVANGVI VPAQEVPPPT VPMDYSWARE LGLIRKPA SF MTSICDERGQ ELIYAGMPIT EVFKEEMGIG GVLG LLWFQK RLPKYSCQFI EMCLMVTADH GPAVS GAHNT IICARAGKDL VSSLTSGLLT IGDRFGGALD AAKMF S K AF DSGIIPMEFV NKMKKEG K LI MGIGHRVKSI NNPDMRVQIL KDYVRQH FPA TPLLDYALEV EKITTSKPP N LILNVDGLIG VAFVDMLRNC GSFTREEADE YIDIGALNGI FVLGRSMGFI GHYLDQ K RLK QGLYRHPWDD ISYVLPEHMS	

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