

UniprotKB ID	Entry name	organism	full name	oglcnaicscore	oglcnaicsites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
C8YR32	LOXH1_MOUSE	Mus musculus	Lipoxygenase homology domain-containing protein 1	25.019509	S246	NaN	34418053	MMAQKKRRKKIDDFLGLYEEELN YDSEEDGELEHEHYKAKVYEVVTA TGDVRGAGTDANVFITLFGENGLSP KLHLTSKSESFAFEKANVDVFRVRTN NVGLYKIRIEHDNTGLNASWYLDRV IVTDMKRPHLRYYFNCNNWLSKVE GDRQWCRDLLASFDPMDMPRGNK YEIKVYTGDIVAGTADVFIFIGEY GDTGERRLENEKDNFEKGAEDKFTL DAPDLGQLMKINVGHNKGGSGAGW FLSKIIIEDIGNKRRKYDFPLNRWLAL DEDDGKIQRDILVGGAEETTAITYIVTV FTGDIRGAGTKSKIYLVMYGARGNK NSGKIFLEGGVFDRGRTDIFHIDLAV LLSPLSRVSIHGHNIGVNRGWYCEK VVILCPFTGIQQTFFPCSNWLDEKKAD GLIERQLYEMVSLRKKRLKKYPWSL WVWTTDLKAGTNSPIFIQIYGKKGGR TDEILLNPNNKWFKPGIHEKFRMELP DLGRFYKIRAWHDRQNPQSGWHLE KMTLMNTINKDKYFNFCNRWLDA NEDDNEIVREMTAEGPTVRRIMGM ARYRVTVCTGELEGAGTDANVYLCL FGDVGDTGERLLYNCRNNTDLFEK GNADEFTIESVTMRKVRVRVRHDG KSGSGWYLDRLVREEGQPESDN VEFPCLRWLDKDDGQLVRELLPS DSNATLKNFRYHISVKTGDVSGAST DSRVYIKLYGEKSDTIKQVLLVSDNN LKDYFERGRVDEFTLETLNIGTINRL VIGHDSTGMHAGWFLGVSQIRVPRQ GKQYTFPANRWLDKNQADGRLEVE LYPSEVVEIQKLVHYEIEIWTGDVGG AGTTSRVFVQIYGEEGKTEVLFSSR SKVFDRGSKDIFQTDFTIYIDLAL TKIRIRHDNTGNRPGWFLDRVDITD VNNETTYFPCORWLAVEEDDGQLS RELLPVDESIVLPSEDEEGGGQGDN NPLDNLALEQDKSTTFVTKTGDK KNAGTDANVFITLFGTQDNNGMTLL KSSKTNSDKFERDSIEIFTVETLDLG DLWKVRIGHDNTGKAPGWVFDWVE VDAPSLGKCMTFPCGRWLAKNEDD GSIVRDLFHAELQTRLYTPFVPEITL YTSDFVFAAGTDANIFIVYGCDAVCT RQKFLCTNKREQKLFERKSASRFIV ELEDVGEIIEKIRIGHDNTGINPGWH CSHVDIRRLLEPKDGTETLTFPCDR WLATSEDDKKTIRELVPYDIFTEKYM KDGSLRQVYKEVEEPLDIVLYSVQIF TGNVPGAGTDAKVYITTYDGLDGTGE RYLGKSENRTNKFEGTADTFIIEAA DLGVYKIKLRHDNTKWCADWYVEK VEIWNDTNEDEFLFCGRWLSLKE DGRLERLFYEKEYTGDRSSNCSSPA DFWEIALSSKMADVDIDVTGPMVD YVQDGPVIPPYVSVTTGKHKEAATDS RAFVLLIGEDDECTNRIWLDYPOGK RGFSCGSVEEFYVGGGLDVGIKKIEL GHDGASPESCWLVEELCLAVPTQGT KYTLRCNCWLAKDRGDVTSRVFDL LDAMVVNIGKKVLYEMTVWTGDVV GGGTDNIFMTLYGINGSTEEVQLD KKKARFERQNDTFIMEILDIAFPTK MRIRIDMGSRPEWFLEIRILLKNMN TGDLTMFYGDWLSQKKGKTLVC EICAVIDGEEMMEWTSYTVSVKTSDI LGAGTDANVFIIIFGENGDSCTLALK QSANWNKFERNNTDTFNFSDMLS GHLCKLRVWHDNKGIFPGWHLSYV DVKDNSRDETRFRQCDCWLSKSEG DRQTLRDFACANNEIRDELEETTYEI VIETGNGGETRENVWLILEGRKNRS KEFLVNSSRQRAFRTGTTDFEFD SIFLGDIASLCVGHAREDRFIPKREL VWHVKTTTTMEYGNVYFFNCDCLI	None	None	None	None	None	None	None		

