

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	pl m
Q91V92	ACLY_MOUSE	Mus musculus	ATP-citrate synthase	39.428525	NaN	T131;S263;T447;S451;S455;S459;T629;S653;T672;S829;S1090	33300544;22645316;34887587;37453647;25153642;39627609	MSAKAISEQTGKELLYKYICTTSAIQ NRFKYARVTPDQDWAHLLQDHPWL LSQSLVVKPDQLIKRRGKGLGVGN LSLDGVKSWLKPRLGHEATVKGAKG FLKNFLIEPFVPHSQAEFFVVCYAT REGDYVLFHHHEGGVDVGDVDAKAQ KLLVGVDEKLNTEDIKRHLLVHAPE DKKEVLASFISGLFNFYEDLYFTYLEI NPLVVTKDGVIYILDAAKVDATADYI CKVKWGDIEFPPPPGREAYPEEAYIA DLDAKSGASLKLTLNPKGRIWTMV AGGGASVVSDTICDLGGVNELANY GEYSGAPSEQQTYDYAKTILSLMTRE KHPEGKILIIIGSIANFTNVAATFKGI VRAIRDYQGPKLKEHEVTIFVRRGGPN YQEGLRVMGEVGTGPIPIHVFGTET HMTAIVGMALGHRPIPNOPTAAHT ANFLLNASGSTSTPAPSRTASFSES ADEVAPAKKAKPAMPQGKSATLFSR HTKAIWVGMQTRAVQGMDFDYVC SRDEPSVAAMVYPTGDHKKQKFW GHKEILIPVFKNMADAMKHPVDV LINFASLRSAYDSTMETMNYAQIRTI AIIAEGIPALTRKLIKADQKGVTTIG PATVGGIKPGCFKIGNTGGMLDNILA SKLYRPGSVAYVSRSGGMSNELNNII SRTTDGVYEGVAIGGDRYPGSTFMD HVLRYQDTPGVKMIIVLGEIGGTEEY KICRGIKEGRLTKPVVCWICIGTCATM FSSEVQFGHAGACANQASETAVAKN QALKEAGVFPVRSFDELGEIISVYE DLVAKGAIVPAQEVPPPTVPMDYSW ARELGLIRKPASFMTSICDERGOELI YAGMPITEVFKEEMGIGGVLGLLWF QRRLPKYSQCFIEMCLMVTADHCPA VSGAHTIICARAGKDLVSLTSGLL TIGDRFGGALDAAKMFSAFDSGII PMEFVNKMKKEGKLMIGIHRVKS NNPDMRVQILKDFVKQHFDPATPLLD YALEVEKITTSKPNLILNVDGFIGVA FVDMLRNCGSFTREEADEYVDIGAL NGIFVLGRSMGFIGHYLDQKRLKQG LYRHPWDDISVVLPEHMSM	True	False	4.745	3.634	4.62	2.468	1.733	2.