

| UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence |
|--------------|------------|--------------|----------------------|--------------|---------------|---|--|--|
| Q91V92 | ACLY_MOUSE | Mus musculus | ATP-citrate synthase | 29.37038 | NaN | T131;S263;T447;S451;S455;S459;T629;S653;T672;S829;S1090 | 34887587;22645316;33300544;25153642;37453647 | MSAKAISEQTGKELLYKYICTTSAIQ NRFKYARVTPDPTDWAHLLQDHPWL LSQSLVVKPDQLIKRRGKLGVLGVN LSLDGVKSWLKPRLGHEATVGKAKG FLKNFLIEPFVPHSQAEEFYVCIYAT REGDYVLFHHEGGVDVGDVDAKAQ KLLVGVDEKLNTEDIKRHLLVHAPE DKKEVLASFISGLFNFYEDLYFTYLEI NPLVVTKDGVIYILDAAKVDATADYI CKVKWGDIEFPPPPGREAYPEEAYIA DLDAKSGASLKLTLNPKGRIWTMV AGGGASVVYSDTICDLGGVNELANY GEYSGAPSEQQTYDYAKTILSLMTRE KHPEGKILIGGSIANFTNVAATFKGI VRAIRDYQGPLKEHEVTIFVRRGGPN YQEGLRVMGEVGGTTGIPIHVFGTET HMTAIVGMALGHRPIPNOPTAAHT ANFLLNASGSTSTPAPSRTASFSESR ADEVAPAKKAKPAMPQGSATLFSR HTKAIVWGMQTRAVQGMDFDYVC SRDEPSVAAMVYPFTGDHKQKFYW GHKEILIPVFKNMADAMKKHPEVDV LINFASLSAYDSTMETMNYAQIRTI AIIAEGIPEALTRKLIKKADQKGVTIIG PATVGGIKPGCFKIGNTGGMLDNILA SKLYRPGSVAYVSRSGGMSNELNII SRTTDGVYEGVAIGGDRYPGSTFMD HVLRYQDTPGVKMIVVLGEIGGTEEY KICRGIKEGRLTKPVVCWCIGTCATM FSSEVQFGHAGACANQASETAVAKN QALKEAGVFVPRSFDELGEIISVYE DLVAKGAIVPAQEVPPPTVPMDYSW ARELGLIRKPASFMTSICDERGQELI YAGMPITEVFKEEMGIGGVLGLLWF QRRLPKYSCQFIEMCLMVTADHGPA VSGAHNTIICARAGKDLVSSLTSGLL TIGDRFGGALDAAAKMFSKAFDSGII PMEFVNKMKKEGKLIMGIGHRVKSI NNPDMRVQILKDFVKQHFPATPLLD YALEVEKITTSKKPNLILNVDGFIGVA FVDMLRNCGSFTREEADEYVDIGAL NGIFVLGRSMGFIGHYLDQKRLKQG LYRHPWDDISYVLPEHMSM |