

| UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence |
|--------------|------------|--------------|-------------|--------------|---------------|--|-------------------|---|
| B2RQC6 | PYR1_MOUSE | Mus musculus | CAD protein | 16.639257 | NaN | T456;S1038;S1406;S1859;T1884;S1900;S1938 | 22645316;24788674 | MAALVLEDGSVLQGRPFGA AVSTAG EVVFQTMVGYPEALDTPSYKAQILV LTYPLIGNYGIPSDEEDEFGLSKWFE SSEIHVAGLVVGECCPTPSHWSANC TLHEWLQQRGIPGLQGVDTRELTKK LREQSLLGKLVQKGTEPSALPFVD PNARPLAPEVSIKTPRVFNAGGAPRI CALDCGLKYNQIRCLCQLGA EVT VV PWDHELDSQKYDGLFLSNGPGDPA SYPGVVSTLSRVLSEPNRPFVFGICL GHQLLALAIGAKTYKMRYGNRGHN QPCLLVGTGRCFLTSQNHGFAVDAD SLPAGWAPLFTNANDCSNEGIVHDS LPFFSVQFHPEHRAGPSDMELLFDV FLETVREAAAGNIGGQTVRERLAQR LCPPELPIPGSGLPPPRKVLILGSGGL SIGQAGEFDYSGSQA IKALKEENIQT LLINPNIA TVQTSQGLADKVYFLPITL HYVTQVIRNERPDGVLLTFGGQTAL NCGVELTKAGVLARYGVRVLGTPVE TIELTEDRRAFAARMAEIGE HVAPSE AANSLEQAQAAAERLGY PVLVRAAF ALGGLGSGFASTKEELSALVAPAF HTSQVLIDKSLKGWKEIEYEVVRDAY GNCVTVCNMENLDPLGIHTGESIVV APSQTLNDREYQLLRRTAIKVTQHL GIVGECNVQYALNPES EQYIIIEVNA RLSRSSALASKATGYPLAYVA AKLAL GIPLPELRNSVTGGTAAFEP SLDYCV VKIPRWDLSKFLRVSTKIGSCMKSV GEVMGIGRSFEEAFQKALRMVDEN CVGFDHTVKPVSDMELETPTDKRIF VAAAALWAGYSVERLYELTRIDCWF LHRMKRIVTHAQLLEQHRGQALPQ DLLHQAKCLGFS DKQIALAVLSTELA VRKLRQELGICPAVKQIDTVA AEWPA QTNYLYLTYWGNTHDLDFRAPHVLV LGSVYRIGSSVEFDWCAVGC IQQL RKMGYKTIMVNYNPETVSTDYDMC DRLYFDEISFEVVM DIYELENPEGVI LSMGGQLPNNMAMALHRQQCRVL GTSPEAIDSAENRFKFSRLLDTIGISQ PQWRELSDLESARQFCHTVGYPCVV RPSYVLSGAAMNVAYTDGDLERFLS SAAAVSKEHPVVISKFIQEAKEIDVD AVACDGIVSAIAISEHVENAGVHSGD ATLVTPPQDITPKTLERIKAI VHAVGQ ELQVTGPFNLQLIAKDDQLK VIECNV RVSRSFPFVSKTLGVDLVALATRIIM |

GEKVEPVGLMTGSGVVGKVPQFSF
SRLAGADVVLGVEMTSTGEVAGFGE
SRCEAYLKAMLSTGFKIPEKNILLTIG
SYKNKSELLPTVRLLESGLYSLYASL
GTADFYTEHGKVTAVDWHFEEAV
DGECPPQRSILDQLAENHFELVINLS
MRGAGGRRLSSFVTKGYRTRRLAAD
FSVPLIIDIKCTKLFVEALGQIGPAPP
LKVHVDCMTSQKLVRLPGLIDVHVH
LREPGGTHKEDFASGTAAALAGGVT
MVCAMPNTRPPIIDAPALALAQKLAE
AGARCDFTLFLGASSENAGTLGAVA
GSAAGLKLYLNETFSELRLDSVAQW
MEHFETWPAHLPIVAHAERQSVAAV
LMVAQLTQRPVHICHVARKEEILLIK
TAKAQLPVTCEVAPHHFLFNREDL
ERLGP GKGEVRPELGSREDMEALW
ENMAVIDCFASDHAPHTLEEKCGPK
PPPGFPGLETMLPLLLTAVSEGRSL
DDLLQRLHHNPRRIFHLPLQEDTYV
EVDLEHEWTVPSHMPFSKARWTPF
EGQKVKGTVRRVVLRGEVAYIDGQV
LVPPGYGQDVRKWPQGVVPPPPST
PATTEITTTPERPRRVIPGLPDGRFHL
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SVKQFTKDQMSHLFNVVAHTLRMMV
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SSSFAAMARLGGAVLSFSEATSSV
QKGESLADSVQTMSCYADVIVLRHP
QPGAVELAAKHCRRPVINAGDGVGE
HPTQALLDIFTIREELGTVNGMTITM
VGDLKHGRTVHSLACLTLQYRVSLR
YVAPPSLRMPPSVRDFVASRGTQKE
EFESIEEALPDTDVLYMTRIQKERFG
SVQEYEACFGQFILTPHIMTRAKK
MVMHPMPRVNEISVEVSDPRAA
YFRQAENGMYIRMALLATVLRGFR