

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
P27708	PYR1_HUMAN	Homo sapiens	CAD protein	18.42239	T723;T726;T1080	T456;S1038;S1406;S1859;S1873;T1884;S1900;S1938	16408927;33214551;32119511;34229054;29351928;34019948;23301498	MAALVLEDGSVLRGQPFGAADVSTAG EVVFQTMVGYPEALDTPSYKAQILV LTYPLIGNYGIPPEMDEFGLCKWF ESSGIHVAALVVGECPTPSHWSAT RTLHEWLQQHGIPGLQGVDTRELT KLREQGSLGKLVQNGTEPSSLPFL DPNARPLVPEVSIKTPRVFNTGGAPR ILALDCGLKYNQIRCLCQRGAEVTVV PWDHALDSQEYEGFLSNGPGDPAS YPSVVSTLSRVLSEPNRPVFGICLG HQLLALAIGAKTYKMRYGNRGNQ PCLLVGSGRCFLTSQNHGFAVETDS LPADWAPLFTNANDGSNEGIVHNSL PFFSVQFHPEHQAGPSDMELLDIF LETVKEATAGNPGGQTVRERLTERL CPPGIPTPGSGLPPPRKVLILGSGGLS IGQAGEFDYSGSQAIALKEENIQTL LINPNIATVQTSQGLADKVYFLPITPH YVTQVIRNERPDGVLLTFGGQTALN CGVELTKAGVVLARYGVRVLGTPVETI ELTEDRRAFAARMAEIGEHVAPSEA ANSLEQAQAAERLGYVVLVRAAFA LGGGSGGFASNREELSALVAPAFAH TSQVLVDKSLKGWKEIEYEVVRDAY GNCVTVCNMENLDPLGIHTGESIVV APSQTLNDREYQLLRQTAIKVTQHL GIVGECNVQYALNPESEQYIIIEVNA RLSRSSALASKATGYPLAYVAAKLAL GIPLPELRNSVTGGTAAFEPVSDYCV VKIPRWDLSKFLRVSTKIGSCMKS GEVMGIGRSFEEAFQKALRMVDEN CVGFDHTVKPVSDMELETPDKRIF VVAALWAGYSVDRLYELTRIDRWF LHRMKRIIAHAQLLEQHRGQPLPPD LLQAKCLGFSDKQIALAVLSTELAV RKLRLQELGICPAVKQIDTVAEWP QTNLYLYTYWGTHDLTFRTPHVLV LGGVYRIGSSVEFDWCAVGCQQ RKMGYKTIMVNYNPETVSTDYDMC DRLYFDEISFEVMDIYELENPEGVI LSMGGQLPNNMAMALHRQOCRVL GTSPEAIDSAENRFKFSRLDITIGISQ PQWRELSDESARQFCQTVGYPCVV RPSYVLSGAAMNVAYTDGDLERFLS SAAAVSKEHPVVISKFIQEAKEIDVD AVASDGVAIAISEHVENAGVHSG DATLVTPPDITAKTLERIKAIHVAVG QELQVTGPFNLQIAKDDQLKVIEC NVRVSRSPFVSKTLGVDLVALATRV IMGEEVEPVGLMTGSGVGVKVPQF SFSRLAGADVVLGVEMTSTGEVAGF GESRCEAYLKAMLSTGFKIPKKNILL TIGSYKNKSELLPTVRLLESLSGLYA SLGTADFYTEHGKVTAVDWHFEEA VDGECPPQRSILEQLAEKNFELVINL

SMRGAGGRRLLSSFVTKGYRTRRLAA
DFSVPLIIDIKCTKLFVEALGQIGPAP
PLKVHVDCMTSQKLVRLPGLIDVHV
HLREPGGTHKEDFASGTAALAGGI
TMVCAMPNTRPPIIDAPALALAQKLA
EAGARCDFALFLGASSENAGTLGTV
AGSAAGLKLYLNETFSELRLDSVVQ
WMEHFETWPSHLPVAHAEQQTV
AVLMVAQLTQRSVHICHVARKEEILL
IKAAKARGLPVTCEVAPHHLFLSHD
DLERLGPGKGEVRPELGSRQDVEAL
WENMAVIDCFASDHAPHTLEEKCG
SRPPPGFPGLETMLPLLLTAVSEGR
SLDDLLQRLHHPRRIFHLPPQEDT
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VLVPPGYGQDVRKWPQGAVPQLPPS
APATSEMTTTTPERPRRGIPGLPDGRF
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VAPELMGTPDGTCPYPPPVPRQAS
PQNLGTPGLLHPQTSPLLHSLVGQH
ILSVQQFTKDQMSHLFNVAHTLRM
MVQKERSLDILKGVMMASMFYEVST
RTSSSFAMARLGGAVLSFSEATSS
VQKGESLADSVQTMSCYADVVLRH
PQPGAVELAAKHCRRPVINAGDGVG
EHPTQALLDIFTIREELGTVNGMTIT
MVGDLKHGRTVHSLACLLTQYRVSL
RYVAPPSLRMPPTVRAFVASRGTKQ
EEFESIEEALPDTDVLYMTRIQKERF
GSTQEYEACFGQFILTPHIMTRAKKK
MVMHMPMPRVNEISVEVSDPRAA
YFRQAENGMYIRMALLATVLGRF