

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q9WU42	NCOR2_MOUSE	Mus musculus	Nuclear receptor corepressor 2	32.569862	T1175;T1290;S1528;T1532;S1778;S1782;T1783;T1784;T1843;S1844;S1938;S1944;T2089	S54;S67;S149;S152;S215;S493;T549;S550;S747;S750;S938;T945;S955;S1220;T1350;S1449;S1509;S1565;S1746;S1749;S1819;S1963;S2004;S2012;S2015;S2016;S2018;T2020;S2035;S2161;S2181;S2215;S2371	36852467;21606357;35822049;30059200;22517741	MSGSTQPVAQTWRAAEPRYPFHGIS YPVQIARSHTDVGLLEYQHHPDRTY SHLSPGSIQPFQRRRPSLLSEFPQGS ERSQELHLRPESTRFLPELGKPDIEF TESKRPRLELLPDTLLRPSPLLATGQ PSGSEDLTKDRSLAGKLEPVSPSP HADPELELAPSRLSKEELIQNMDRV DREITMVEQQISKLKKKQQQLEEEA AKPPEPEKPVSPPIESKHRSLVQIHY DENRKAEEAAHRILEGLGPOVELPL YNQPSDTRQYHENIKINQAMRKKLI LYFKRRNHARKQWEQRFCQRYDQL MEAWKVERIENPNRRRRAKESKV REYYEKQFPEIRKQRELQERMQSRV GQRGSLMSAARSEHEVSEIIDGL SEQENLEKQMRQLAVIPPLYDADQ QRIKFINMNGLMDDPMKVYKDRQV TNMWSEQERDTRFREKFMQHPKNF GLIASFLERKTVAECVLYYYLTKKNE NYKSLVRRSYRRRGKSQQQQQQQ QQQQQMARSSQEEKEKEKEKEA DKEEEKQDAENEKEELSKEKTDSDTS GEDNDEKEAVASKGRKTANSQGRR KGRITRSMANEANHEETATPQSSSE LASMENESSRWTEEMETAKKGL LEHGRNWSAIARMVGSKTVSQCKN FYFNYKKRQNLDEILQQHKLKMEKE RNARRKKKTPAAASEETAFFPAAE DEEMEASGASANEEELAEAEASQA SGNEVPRVGECSGPAAVNNSDTE VPSRSEATKDTGPKPTGTEALPAAT QPPVPPPEEPVAVAPAEPSVVPDASGP PSPEPSPPAAPPATVDKDEQEAPAA PAPQTEDAKEQKSEAEIDVGKPEEP EASEEPPESVKS DHKEETEEEPEDK AKGTEAIETVSEAPLKVEEAGSKAAV TKGSSSGATQSDSSATCSADEVDE PEGGDKGRLLSPRPSLLTPAGDPRAS TSPQKPLDLKQLQRAAAIPIVTKV HEPPREDTVPPKPVPPVPPPTQHLQP EGDVSQQSGGSPRGKRSRSPVPAEK EAEKPAFFPAFPTEGPKLPTEPPRWS SGLPFPPIPREVIKTS PHAADPSAFSY TPPGHPLPLGLHDSARPVLP RPPISN PPPLISSAKHPGVLERQLGAISQQGM SVQLRVP HSEHAKAPMGPLTMGLPL AVDPKLG TALGSATSGSITKGLPST RAADGPSYRGSITHGTPADVLYKGTI SRIVGEDSPSRLDRARED TLPKGVHI YEGKKGHVLSYEGGMSVSQCSKED GRSSSGPPHETAAPKRTYDMMMEGR VGRTVTSASIEGLMGRAIPEQHS PHLKEQHHRGSITQGI PRSYVEAQEDYL RREAKLLKREGTPPPPPPRDLTETY KPRPLDPLGPKLKP THEGVVATVKE AGRSIHEIPREELRRTPELPLAPRPLK EGSITQGTPLKYDSGAPSTGTTKHDV RSIIGSPGRFPALHPLDIMADARAL ERACYEESLKSRS GTSSGAGGSITRG APVVVPELGKPRQSP LTYEDHGAPFT SHLPRGSPVTTREPTPRLQEGSLLSS KASQDRKLTSTPREIAKSPHSTVPEH HPHPISPYEHLRGTGVDLYRGHIP

LAFDPTSIPRGIPLEAAAAAYLPRHL
APSPTYPHLYPPYLIRGYPDAALEN
RQTIINDYITSQQMHNAASAMAQR
ADMLRGLSPRESSLALNYAAGPRGII
DLSQVPHLPVLPVPTPGTPATAIDRL
AYLPTAPPPFSSRHSSSPLSPGGPTH
LAKPTATSSSERERERERERDKSILT
STTTVEHAPIWRPGTEQSSGAGGSS
RPASHTHQHSPISPRTQDALQORPS
VLHNTSMKGVVTSVEPGTPTVLRWA
RSTSTSSPVRPAATFPPATHCPLGGT
LEGVYPTLMPEVLLPKETSRRVARPER
PRVDAGHAFLLTKPPAREPASSPSKSS
EPRSLAPPSSHTAIARTPAKNLAPH
HASPDPPAPTSASDLHREKTQSKPF
SIQELELRSLGYHSGAGYSPDGVEPI
SPVSSPSLTHDKGLSKPLEELEKSHL
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RPLPESQPSSPLLQTAPGIKQHQRV
VTLAQHISEVITQDYTRHHPQQLSGP
LPAPLYSFPGASCPVLDLRRPPSDLY
LPPPDHGTARGSPHSEGGKRSPEP
SKTSVLGSSEDAIEPVSPEGMTEPG
HARSTAYPLLYRDGEQGEPRMGSKS
PGNTSQPPAFFSKLTESNSAMVSKK
KQEINKKLNTHNRNEPEYNIGQPGT
EIFNMPAITGAGLMTCRSQAVQEHA
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PLGANAFNPLNASASLPAAAMPITTA
DGRSDHALTSPGGGGKAKVSGRPSS
RKAKSPAPGLASGDRPPSVSSVHSE
GDCNRRTPLTNRVWEDRPSSAGSTP
FPYNPLIMRLQAGVMASPPPPGLAA
GSGPLAGPHHAWDEEPKPLLCSQYE
TLSDSE