

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q9Y618	NCOR2_HUMAN	Homo sapiens	Nuclear receptor corepressor 2	22.098631	S23;S25;S1126;S1138;T1215;S1323;S1510;T1514;S1516;S1517;S1521;T1525 (Q9Y618-4);T1561;T1562;T1566;S1570 (Q9Y618-4);S1577;T1635;S1636;S1778;T1799 (Q9Y618-4);S1817;T1831;T1909;S1986;T1990;S1997 (Q9Y618-4);S2025;T2131	S54;S67;S149;S152;T156;S215;S493;T553;S554;S750;S753;S939;T946;S956;S1173;S1251;S1323;T1383;S1479;S1539;S1595;S1619;S1775;S1778;S1861;S2005;S2046;S2054;S2057;S2058;S2060;T2062;S2077;S2203;S2223;S2258;S2413	30379171;33214551;20068230;30059200;31492838;28657654;32574038;29351928;29237092;34019948;30620550;28510447	MSGSTQPVAQTWRAPEPRYPHLSLSPVYQIARTHTDVGLLEYQHHSRDYASHLSPGSIQIPQRRRPSLLSEFPQGNERSQELHLRPESHSYLPELGKSEMEFIESKRPRLELLPDPLLRPSPLLATGQPAGSEDLTKDRSLTGKLEPVSPSPHTDPELELVPPRLSKEELIQNMDRVDREITMVEQQISLKLKQQLLEEA AKPPEPEKPVSPPIESKHSRLVQIHYDENRKKAAEAHRILEGLGQVELPLYNQPSDTRQYHENIKINQAMRKKLI LYFKRRNHARKQWEQKFCQRYDQLEMEAWEKKVERIENPNRRRAKESKVRREYYEKQFPEIRKQRELQERMQSRV GQRGSLMSAARSEHEVSEIIDGLSEQENLEKQMRQLAVIPPLYDADQQRIFINMNGLMADPMKVYKDRQVMNMWSEQEKETFREKFMQHPKNFGLIASFLERKTVAEVLYYYLTKKNEYKSLVRRSYRRRGKSSQQQQQQQQQQQQQQQMPRSSQEKEKDEKEKEKAEKEEEKPEVENDKEDLLKEKTDTSGEDNDEKEAVASKGRKTANSQGRRKGRITRSMANEANSEEAITPQQAELASMELNESSRWTEEMETAKKGLLEHGRNWSAIARMVGSKTVSQCKNFYFNKKRQNLDEILQKHKLKMEKERNARRKKKAPAAAEEAAFPVVVEDEEMEASGVSGNEEEMVEEAALHASGNEVPRGECSPATVNNSSDTEISPSPHTEAAKDTGQNGPKPPATLGADGPPPGPPTPPPEDIPAPTEPTPASEATGAPTPPPAPSPSAPPVVPK EEKEEETAAPPVEEGEEQKPPAAEELAVDTGKAEEPVKSECTEEAEEGP AKGKDAEAAEATAEGALKAEEKEGGSGRATTAKSSGAPQSDSSATCSAD EVDEAEGGDKNRLSPRPSLLTPTGDPRANASPKPLDLKQLKQRAAAIPP IQVTKVHEPPREDAAPTTPAPPAPP PQLQPESDAPQQPGSSPRGKSRSP APPADKEAFAAEAQKLPDPPCWTS GLPFPVPPREVIKASPHADPSAFSY APPGHPLPLGLHDTARPVLP RPPTIS NPPPLISSAKHPSVLERQIGAISQGM SVQLHVPYSEHAKAPVGPVTMGLPL PMDPKKLAPFSGVKQEQLSPRGQAG PPESLGVPTAQEASVLRGTALGSVPG GSITKGIPSTRVPSDAITYRGSITHG TPADVLYKGTITRIIGEDSPSRLDRGR EDSLPKGHVITYEGKKGHVLSYEGGM SVTQCSKEDGRSSSGPPHETAAPKR TYDMMEGRVGRAISSASIEGLMGRA IPPERHSPHHLKEQHHRGHSITQGIP RSYVEAQEDYLRREAKLLKREGTPPP PPPSRDLTEAYKTQALGPLKLP AHEGLVATVKEAGRSIHEIPREELRHTPE LPLAPRPLKEGSITQGTPLKYDTGAS TTGSKKHVDVRSLIGSPGRTPFPVHPL DVMADARALERACYEESLKS RPPGTA SSSGSIARGAPVIVPELGKPRQSPL TYEDHGAPFAGHLPRGSPVTTREPT PRLQEGSLSSSKASQDRKLTSTPREI

AKSPHSTVPEHHHPISPYEHLRGRG
VSGVDLYRSHIPLAFDPTSIPRGIPLD
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PASHSHAHQHSPIPRQDALQORP
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DTGHAFLAKPPARSGLEPASSPSKGS
EPRPLVPPVSGHATIARTPAKNLAPH
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ETLSDSE