

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
O75376	NCOR1_HUMAN	Homo sapiens	Nuclear receptor corepressor 1	30.564292	S3;S4;S24;T28;T32;S46;S51;S54;S123;S1039;S1040;T1042;S1050;T1064;S1073;T1075;S1082;S1114;T1449;S1450;S1453;S1454;S1457;T1479;S1480;S1487;T1491;S1493;S1545;S1806;S1812;S1857;S1861;S1913;T1925;T1926;S2069;S2070;T2078;S2079;T2080;S2086;S2219;T2233;T2242;T2299	S172;S224;S999;S1111;S1195;S1196;S1249;S1263;S1281;S1322;T1367;S1450;S1472;S1592;S1977;S1981;S2102;S2120;S2136;S2151;S2184;T2399;S2436;S2438	31637018;30379171;33214551;20068230;27655845;31492838;32119511;30059200;28657654;32574038;29351928;29237092;34019948;26374642;30620550;23301498	MSSSGYPPNQGAFSTEQSRYPHSHV QYTFPNTRHQQEFAVDPYRSSHLEV SQASQLLQQQQQLRRRPSLLSEF HPGSDRPQERRTSYEPFHGPGSPVD HDSLESKRPRLEQVSDSHFQRVSA VLPLVHPLPEGLRASADAKKDPAFG GKHEAPSSPISGQPCGDDQNASPSK LSKEELIQSMDRVDREIAKVEQQILK LKKKQQQLEEEAAKPEPEKPVSPPP VEQKHRSIVQIYDENRKKAEAAHKE FEGLGPKVELPLYNQPSDTKVYHENE KTNQVMRKKLILFFKRRNHARKQRE QKICQRYDQLMEAWEEKVDRIENN PRRKAKESKTREYYEKQFPEIRKQRE QQERFQRVGQRGAGLSATIARSEHE ISEIIDGLSEQENNEKQMRQLSVIPP MMFDAEQRRVKFINMNGLMEDPDM KVYKDRQFMNVVTDHEKEIFKDKFI QHPKNFGLIASYLERKSVPCVLYYY LTKKNENYKALVRRNYGKRRGRNQ QIARPSQEEKVEEKEDKAEKTEKK EEKKDEEEKDEKEDSKENTKEKDK IDGTAEEETEEREQATPRGRKTANSQ GRRKGRITRSMTNEAAAAASAAAAA TEEPPPPPLPPPEPISTPEVTSRWTE EEMEVAKKGLVEHGRNWAAIAKMV GTKSEAQCKNFYFNYKRRHNLNLDNL LQQHKQKTSRKPREDVVSQCESVA STVSAQEDEDIEASNEEENPEDSEV EAVKPSSEDSPENATSRGNTEPAVEL EPTTETAPSTSPSLAVPSTKPAEDES VETQVNDSSISAETAEQMDVDQQEH SAEEGSVCDPPPATKADSVDVVEVRV PENHASKVEGDNTKERDLDRASEK VEPRDEDLVVAQQINAQRPEPQSDN DSSATCSADEDVDGEPERQRMFPM DSKPSLLNPTGSILVSSPLKPNPLDL PQLQHRAAVIPPMVSCVTPCNIPIGTP VSGYALYQRHIKAMHESALLEEQRQ RQEQIDLECRSSTSPCGTSKSPNRE WEVLQPAPHQVITNLPEGVRLPTR PTRPPPLIPSSKTTVASEKPSFIMGG SISQGTPTGYLTSHNQASYTOETPKP SVGSISLGLPRQGESAKSATLPYIKQ EEFSPRSQNSQPEGLLVRAQHEGVV RGTAGAIQEGSITRGTPTSKISVESIP SLRGSITQGTALPQTGIPTEALVKGS ISRMPIEDSSPEKGREAAASKGHVY EGKSGHILSYDNIKNAREGTRSPRTA HEISLKRSYESVEGNIKQGMRES PVSAPLEGLICRALPRGSPHSDLKER TVLSGSIMOGTPRATTESFEDGLKYP KQIKRESPIRAFEGAITKGPYDGIT TIKEMGRSIEIIPRQDILTQESRKT EYVQSTRPIEGSISQGTPIKFDNNSG QSAIKHNKSLITGPKLSRGMPPLE IVPENIKVVERGKYEDVKAGETVRSR HTSVVSSGPSVLRSTLHEAPKAQLSP GIYDDTSARRTPVSYQNTMSRGS MNRSDVTISSNKNSTNHERKSTLTP TQRESIPAKSPVPGVDPVVSHPDFP HHRGSTAGEVYRSHLPHLDPAMPF HRALDPAAYLFRQLSPTPGYPS

QYQLYAMENTRQITLNDYITSQQMQ
VNLRPDVARGLSPREQLGLPYPAT
RGIIDLTNMPPTILVPHPGGTSTPPM
DRITYIPGTQITFPPRPYNSASMSPG
HPTHLAAAASAERERERERERERER
ERIAAASSDLYL RPGSEQPGRPGSHG
YVRSPSPSVRTQETMLQQRPSVFQG
TNGTSVITPLDPTAQLRIMPLPAGGP
SISQGLPASRYNTAADALAAALVDA
SAPQMDVSKTKESKHEAARLEENLR
SRSAAVSEQQQLEQKTLEVEKRSVQ
CLYTSSAFPSGKPKQHSSVVYSEAGK
DKGPPPKSRYEEELRTRGKTTITAA
FIDVIITRQIASDKDARERGSQSSDSS
SSLSSHRYETPSDAIEVISPASSPAPP
QEKLQTYQPEVVKANQAENDPTRQY
EGPLHHYRPQQESPSPQQQLPPSSQ
AEGMGQVPRTHRLITLADHICQIITQ
DFARNQVSSQTPQQPPTSTFQNSPS
ALVSTPVRTKTSNRYSPEQAQSVH
HQRPGSRVSPENLVDKSRGSRPGKS
PERSHVSSEPYEPISPPQVPVVHEKQ
DSLILLSQRGAEPAEQRNDARSPGSI
SYLPSFFTKLENTSPMVKSKKQEIFR
KLNSSGGGSDMAAAQPGTEIFNLP
AVTTSGSVSSRGHSFADPASNLGLE
DIIRKALMGSFDDKVEDHGVVMSQP
MGVVPGTANTSVVTSGETRREEGDP
SPHGGVCKPKLISKNSRKS KSPIP
GQGYLGTERPSSVSVHSEGDYHRQ
TPGWAWEDRPSSTGSTQFPYNPLT
MRMLSSTPPTPIACAPSAVNQAAPH
QQNRIWEREPAPLLSAQYETLSDSD
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