

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
A5YKK6	CNOT1_HUMAN	Homo sapiens	CCR4-NOT transcription complex subunit 1	25.911323	T746;S758;T764;S827;T880;S1037;T1038;T1040 (A5YKK6-2);T1041;T1042;S1043;T1044;T1045;T1046;T1047;T1051;T1055;T1058;S1061;T1418;S1775;T1780	S318;S1061	32119511;34725712;36240223;28510447;35132862;35254053;35138101;29237092;33214551;30059200;37340703;29351928;28657654;27655845;23301498;31492838;32574038;30379171	MNLDLSLALSQISYLVNLTCKNYRASQQEIQHIVNRHGPEADRHLLRC LFSHVDFSGDGKSSGKDFHQTQFLI QECALLITKPNFISTLSYADINPLHYQ KSLKPAPHLFAQLSKVLKLSKVQEVIFGLALLNSSSSDLRGFAAQFIKQKLP DLLRSYIDADVSGNQEGGFQDIAIEV LHLLSHLLFGQKGAFGVQEQIDA FLKTLRRDFPQERCPVVLAPLLYPEK RDILMDRILPDSGGVAKTMMESSLA DFMQEVGYGFCASIEECRNIIIVQFGV REVTAQVARVLGMMARTHSGLTD GIPLQISAPGSGIWSDGKDKSDGAQ AHTWNVEVLIDVLKELNPSLNFKEV TYELDHPGFQIRDSKGLHNVVYGIQ RGLGMEVFPVDLIYRPWKHAEGQLS FIQHSLINPEIFCFADYPCHTVATDIL KAPPEDDNREIATWKSOLDLIESLLRL AEVGQYEQVKQLFSFPIKHCPDMLV LALLQINTSWHTLRHELITLMPIFL GNHPNSAILHYAWHGQGSQSPSIRQ LIMHAMAEWYMRGEQYDQAKLSRI LDVAQDLKALSMLLNGTPFAFVIDL AALASRREYLKLDKWLTDKIREHGE PFIQACMTFLKRRCP SILGGLAPEKD QPKSAQLPPETLATMLACLQACAGS VSQELSETILTMVANCSNVMNKAR QPPPGVMPKGRPPSASSLDAISPVQI DPLAGMTSLSIGGSAAPHTQSMQGF PPNLGSFAFSTPQSPAKAFPPLSTPNQ TTAFFSGIGLSSQLPVGGLGTGSLTG IGTGALGLPAVNNDPFVQRKLGTSG LNQPFTFQQSKMKPSDLSQVWPEAN QHFSKEIDDEANSYFQRIYNHPPHP TMSVDEVLEMLQRFKDKSTIKREREV FNCMLRNLFEYRFFPQYPDKELHI TACLFGGIIEKGLVTYMALGLALRYV LEALRKPFSGSKMYFGLAALDRFKN RLKDYPOYCQHSLASISHFMQFPHHL QEYIEYGQSRDPPVKMQGSITTPGS IALAQAQAQAQVPAKAPLAGQVSTM VTTSTTTTVAKTVTVTRPTGVSFKKD VPPSINTTNIDTLLVATDQTERIVEPP ENIQEKIAFIFNNLSQSNMTQKVEE LKETVKEEFMPWVSQYLVMKRVSIE PNFHSLYSNFLDTLKNPEFNKMVL NETYRNIKVLLTSDKAAANFSDRSLL KNLGHWLGMITLAKNKPIHTDLDV KSLLEAYVKGQQLLYVVPFVAKVL ESSIRSVVFRPPNPWTMAIMNVLAELHQEHDLKLNLFKFEIEVLCKNLALDI NELKPGNLLKDKDRLKNLDEQLSAP KKDVKQPEELPPITTTTTSTTPATNTT CTATVPPQPQYSYHDINVYSLAGLAP HITLNPITPLFQAHPQLKQCVRQAIE RAVQELVHPVVDRSIKIAMTTCEQIV RKDFALDSEESRMRIAHHMMRNL TAGMAMITCREPLLSISTNLKNSF

ASALRTASPPQREMMDQAAAQLAQ
DNCELACCFIQKTAVEKAGPEMDKR
LATEFELRKHARQEGRRYCDPVVLT
YQAERMPEQIRLKVGGVDPKQLAVY
EEFARNVPGFLPTNDLSQPTGFLAQ
PMKQAWATDDVAQIYDKCITELEQH
LHAIPPTLAMNPQAQALRSLEVVVL
SRNSRDAIAALGLLQKAVEGLLDATS
GADADLLRYRECHLLVLKALQDGR
AYGSPWCNKQITRCLIECRDEYKYN
VEAVELLIRNHLVNMQQYDLHLAQS
MENGLNYMAVAFAMQLVKILLVDE
RSVAHVTEADLFHTIETLMRINAHS
RGNAPGLPQLMEVVRSNYEAMID
RAHGGPNFMMHSGISQASEYDDPP
GLREKAEYLLREWVNLYHSAAAGR
STKAFSAFVGQMHQQGILKTDLLIT
RFFRLCTEMCVEISYRAQAEQQHNP
AANPTMIRAKCYHNLD AFVRLIALLV
KHSGEATNTVTKINLLNKVLGIVGV
LLQDHDVROSEFQQLPYHRIFIMLL
LELNAPEHVLETINFQTLTAFCNF
HILRPTKAPGFVYAWLELISHRIFIAR
MLAHTPQQGWPMYAQLLIDLFKYL
APFLRNVELTKPMQILYKGTLRVLLV
LLHDFPEFLCDYHYGFCDVIPNCIQ
LRNLILSAFPRNMRLPDPFTP NLKV
DMLSEINIAPRILT NFTGVMPPQFKK
DLDSYLKTRSPVTF LSDLRSNLQVS
NEPGNRYNLQ LINALVLYVGTQAIA
HIHNKGSTPSMSTITHSAHMDIFON
LAVDLDT EGRYFLNAIANQLRYPNS
HTHYFSCTMLYLFAEANTEA IQEQIT
RVLLERLIVNRPHPWGLLITFIELIKN
PAFKFWNHEFVHCAPEIEKLFQSV
QCCMGQKQAQQVMEGTGAS