

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	go ap
Q01705	NOTC1_MOUSE	Mus musculus	Neurogenic locus notch homolog protein 1	69.199757	S94;T405;T617;S784;T900;S1856 (Q01705-2)	T1851	24730386;28395734;33789105;22645316;22310717;38474544;24573683;28089369;30016717;26192747;38359610;37838775;35290457	MPRLLTPLLCLLTPALAAARGLRCSQ PSGTCNLNGRCEVANGTEACVCSGA FVGQRQDSNPCLSTPCKNAGTCH VVDHGGTVDYACSCPLGFSGLCLT PLDNACLANPCRNGGTCDLLLTLTEY KCRCPGWSGKSCQQADPCASNPC ANGGQCLPFESSYICRCPGFHGPT CRQDVNECSQNPGLCRHGGTCHNE IGSYRCACRATHGPHCELPHYVPCSP SPCQNGGTCRPTGDTTHECACLPGF AGQNCENVDVDCPGNNCKNGGAC VDGVNTYNCRCPPPEWTGQYCTEDV DECQLMPNACQNGGTCNTHGGY NCVCVNGWTGEDCSENIDDCASAA CFOGATCHDRVASFYCECPHGRTGL LCHLNDACISNPCNEGSNCDTNPV NGKAICTCPSGYTPACSQDVDECA LGNANPCEHAGKCLNLTGSEFCQCLQ GYTGPRCEIDVNECISNPCQNDATC LDOIGEFQCICMPGYEGVYCEINTDE CASSPCLHNGHCKMDFKINEFQCQCP KGFNGHLCQYDVDECASTPCKNGA KCLDGPNTYTCVCTEGYTGTHCEVD IDECDDPCHYGSKDGVATFTCLC QPGYTGHHCEININECHSQPCRHG GTCQDRDNSYLCLLCKGTTGPNCEI NLDDCASNPCDSGTCLDKIDGYECA CEPGYTGSMCNVNIDECAGSPCHN GGTCEDGIAGFTCRCEGYHDPTCL SEVNECNSNPCIHGACRDGLNGYK CDCAPGWSGTNCDINNECESNPC VNGGTCCKDMTSGYVCTCREGFSGP NCQTNINECASNPCLNQGTCIDDVA GYKCNCLPYTGATCEVVLAPCATSP CKNSGVCKESEDYSEFSCVCPTGWQ GQTCVEDINECVKSPCRHGASQNT NGSYRCLCQAGYTGRNCESDIDDCR PNPCHNGGSCDTGINTAFCDCLPGF QGAFCCEEDINECASNPCQGANCT DCVDSYTCCTPVGFNGIHCENNTPD CTESSCFNGGTCVDGINSFTCLCPP GFTGSYCYDVNECDSRPCLHGGTC QDSYGTYKCTCPQGYTGLNQNLRV WCDSAPCKNGGRCWQNTNTQYHCE CRSGWTGVNCDVLSVSEVAQKR GIDVTLQCQHGGLCVDEGDKHYCHC QAGYTGSYCEDEVECESPNPCQNGA TCTDYLGGFCKCVAGYHGSNCSEE INECLSQPCQNGGTCIDLNSYKCS CPRGTQGVHCEINVDVCHPPLDPAS RSPKCFNNGTCVDQVGGYTCCTPPG FVGRCEDVNECLSNPCDPRGTQ NCVQRVNDFHCECRAHGTGRRCES VINGCRGKPKNGGVCVAVASNTARG FICRCPAGFEGATCENDARTCGSLR CLNGGTCISGPRSPCTCLGSLFTGPE CQFPASSPCVGSNPNYNGTCEPTS ENPFYRCLCPAKFNGLLCHILDYSFT GGAGRDIPPPQIEEACELEPCQVDAG NKVCNLQCNHACGWDGDCSLN FNDPWKNCTQSLQWKFSDGHCD SQCNASAGLFDGDFDQCLTEGOCNP LYDQYCKDHFSDGHCDQGCNSAEC EWDGLDCAHVPERLAAGTLVVLV LPPDQLRNNFSHFLRELSHVLHTNV VFKRDAQGQMIFFPYGHEEELRKH PIKRSTVGWATSLLPGTSGGRQRR ELDPMDIRGSIVYLEIDNRQCVQSSS OCFQSATDVAFLGALASLGSNLNIPY KIEAVKSEPVPEPLPSQLHLMYVAAA AFVLLFFVCGVLLSRKRRRQHGQL WFPEGFVKSEASKKRREPLGEDSV GLKPLKNASDGALMDDNQNEWGD EDLETKKFRFEPPVLPDLSQTDH RQWTQQHLDAADLRMSAMAPTPO GEVDADCMDVNVVRGPDGFTPLMIA SCSGGGLETGNSEEEEDAPAVISDFI YQAGSLHNQTDRTGETALHLAARYS RSDAAKRLLLEASADANIQDNMGRTF LHAAVSADAQGVFQILLRNRATDLD	True	True	4.55	5.0	2.812	5.0	4.4

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FK