	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membr
0	A2AQH4	BCORL_MOUSE	Mus musculus	BCL-6 corepressor-like protein 1	30.965781	T635	S490;S593;S607;S1024;S1162	36852467;29187734;34678516	MISTAPLYSGVHNWTSSDRIRMCGI NEERRAPLSDEESTTGGCQHFGSQE FCVSSSFSKVELTAVGSGSNARGTN PDGNTTEKLGHRSEDQSDDPQPKM DYVGNPAEAEGLLVPLSSPGDGLKL PTPDSTEASHSRANCSWTPLSTQMS KQVDCSPAGVKALDSRHGVGEKNTF ILATLGTGVPVEGTLPLVTTNFSQLP APICPPAPGSASGTPSVPDPFQVPLS VPAPVPHSGLVPVQVATSASAPSPPL APAAPSVPTLISDSNPLSVSASVLVPV PVSAPHSVPVPLSAPAPTPLTVSVSA PPLALIQAPVPPSAPTLVLASVPTPVL APMPASTPPAAPAPPSVPMPTPTPSS GPPSTPTLIPAFAPTPVPAPTPAPIFTP APTPMPAATPAAIPTSAPIPASFSLSR VCFPAAQAPAMQKVPLSFQPGTVLT PNQPLVYIPPPSCGQPLSVATLPTTL GVSSTLTLPVLPSYLQDRCLPGVLAS PDLRSYPCAFSVARPLASDSKLVSLE VNRLSCTSPSSSTNSQPAPDGVPGP LADTSLTTASAKVLPTSQLLLPAPSG SSVPPHPSKMPGGTDQQTEGTSVTF SPLKSPPQLEREMASPPECSEMPLD LSAKSNRQKLPLPNQRKTPPMPVLT PVHTSSKALLSTVLSRSQRTTQAAGS NVTSCLGSTSSPFVIFPEMVRNGDP STWVKNSTALISTIPGTYVGVANPVP ASLLLNKDPNLGLNRDPRHLPKQEP ISIIDQGEPKSTSATCGKKGSQAGAE GQPSTVKSRYTPARIAPGLPGCQTKE LSLWKPTGLTNMYPRCSINGKPTST QVLPVGWSPYHQASLLSIGISSAGQL TPSQGVPIRPTSIVSEFSGVSPLGSSE TVHGLPEGQPRPGGPFAPEQDAVTK NKNCRIAAKPYEEQVNPVLLTLSPQS GTLALSVQPSSGDMGVNQGSEESES HLCSDSTPKMEGPQAACGLKLAGDT KPKNQVLATYMSHELVLANPQNLC KMPELPLLPHDSHSKELILDVVPSSE RGPSTDLSQLGSQVDLGRVKMEKAD GDVVFNLANCFRADGLPAVPQRGQ AEARANAGQARVKRESIGVFTCKNS WQPDEETESLPPKKVKCNKEKEIEE EPRQQPPPQPHDKPMVRSSLGSKCR KLPGDPQEPTKKSPRGALDSGKEHN GVRGKHKHRKPTKPESQPPGKRTDG HEEGSLEKKAKNSFRDFIPVVLSTRT RSQSGSICSSFAGMADSDMGSQEVF PTEEEEEVAPTPAKRRKVRKTQRDT QYRSHHAQDKTLLSQGRRHLWRAR EMPWRTEAARQMWDTNEEEEDDE EEGLVKRKKRRRQKSRKYQTGEYLI EQEEQRRKGRADSKARKQKTSSQSS EHCLRNRNLLLSSKAQGISDSPNGF LPDNLEEPACLENPEKPSGKRKCKT KHMANASEEARSKGRWSQQKTRSS KSPTPVKPTEPCTPSKYRSAGPEEAS ESPTARQIPPEARRLIVNKNAGETLL QRAARLGYKDVVLYCLQKHSEDVN HRDNAGYTALHEACSRGWTDILNIL LQHGANVNCSSQDGTRPVHDAVVN DNLETIWLLLSYGADPTLATYSGQTA MKLASSDNMKRFLSDHLSDLQGRA EGDPRASWDFYSSSVLEKKDGFACD LLHNPPGSAEQGDDSEQDDFMFEL SDKPLLPCYNLQVSVSRGPCNWFLF SDVLKRLKLSSRIFQARFPHLEITTLP KAEFYRQVASSQLLSPAERPGSLEDR SPPGSSETVELVQYEPELLRLLGSEV EYQSWSS	None	None	None	None	None	None	None	None