

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q6W2J9	BCOR_HUMAN	Homo sapiens	BCL-6 corepressor	26.365742	S365;S453;T555;S560;S586;S637	S336;S340;S365;S367;S423;S1127;S1139;S1290;S1345;S1410	30379171;20068230;30059200;31492838;32574038;29351928;29237092;30620550;23301498	<p> MLSATPLYGNVHSMNSERVRMC GASEDRKILVNDGDASKARLELREE NPLNHNVDASTAHRIDGLAALSM DRTGLIREGLRVPGNIVYSSLCGLGS EKGREAASTLGGGLGFSSERNPEMQ FKPNTPETVEASAVSGKPPNGFSAIY KTPPGIQKSAVATAEALGLDRPASDK QSPLNINGASYLRLPWVNPYMEGAT PAIYPFLDSPNKYSLNMYKALLPQQS YSLAQPLYSPVCTNGERFLYLPPPHY VGPHIPSSLASPMRLSTPSASPAIPPL VHCADKSLPWKMGVSPGNPVDSHA YPHIQNSKQPRVPSAKAVTSGLPGDT ALLLPPSPRPSRVHLPTQPAADTYS EFHKHYARISTSPSVALSKPYMTVSS EFPAARLSNGKYPKAPEGGEGAQPV PGHARKTAVQDRKDGSSPPLLEKQT VTKDVTDKPLDLSSKVVDVDASKAD HMKKMAPTVLVHSRAGSGLVLSGS EIPKETLSPPGNGCAIYRSEIISTAPSS WVVPGSPNEENNGKSMCLKNKAL DWAIQQRSSSCPRMGGTDVITNV SSVSSAGRPASASPANANADGTK TSRSSVETTPSVIQHVGQPPATPAKH SSSSTSSKGAASNPESFKANENGL PPSIFLSPNEAFRSPPIPYPRSYLPY PAPEGIAVSPLSLHGKGPVYHPVLL PNGSLFPGHLAPKGLPYGLPTGRP EFVTYQDALGLGMVHPMLIPHTPIEI TKEEKPERRSRSHERARYEDPTLRN RFSEILETSSTKLHPDVPTDKNLKN PNWNQGKTVVKSDKLVYVDLLREEP DAKTDTNVSKPSFAAESVGSQAEP KPSVEPALQHRDFIALREELGRISD FHETYTFKQPVFTVSKDSVLAGTNK ENLGLPVSTPFLEPPLGSDGPAVTFG KTQEDPKPFCVGSAPPSVDVPTPTTK DGADEAESNDGKVLKPKPSKLAKRI ANSAGYVDRFKCVTTELYADSSQL SREQRALQMEGLQEDSILCLPAAYC ERAMMRFSELEMKEREGGHPATKD SEMCKFSPADWERLKGNDKPKS VTLEEAIAEQNESERCEYSVGNKHR DPFEAPEDKDLPEKYFVERQPVSE PPADQVADMPHSPTLRVDRKRKVS GDSSHTETTAEEVPEDPLLKAKRRR VSKDDWPEREMTNSSSNHLEDPHY SELTNLKVCIELTGLHPKKQRHLLH LRERWEQQVSAADGKPGRQSRKEV TQATQPEAIPQGTNITEEKPRKRAE AKGNRSWSEESLKPSDNEQGLPVFS GSPPMKSLSSSAGGKKQAQPSCAP ASRPPAKQQKIKENQKTDVLCADDEE EDCQAASLLQKYTDNSEKPSGKRLC KTKHLIPQESRRGLPLTGEYVENAD GKVTVRRFRKRPEPSSDYDLSPAKQ EPKPFDRQLQQLPASQSTQLPCSSSP QETTQSRMPPEARRLIVNKNAGET LLQRAARLGYEEVVLYCLENKICDV NHRDNAGYCALHEACARGWLNIVR HLLYGADVNCQAQDGTPLHDAVE NDHLEIVRLLLSYGADPTLATYSGRT </p>

IMKMT HSELM EKFLTDYLNDLQGR NDD DASGTWDFYGS SVCEPDDESG YDVLANPPG PEDQDDDDAYS DVFE FEFSETPLL PCYNIQVSVAQGPRNW LLSDVLKCLKMSSRIFRCNFPNVEI VTIAEA EFYQV SASL FSCSKDLEA FNPESKELLDLVEFTNEIQTLGSSV EWLHPSDLASDNYW
