

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnacsites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
O14981	BTAF1_HUMAN	Homo sapiens	TATA-binding protein-associated factor 172	21.366884	NaN	S91;S95	28510447	MAVSRLDRLFILLDTGTPVTRKAAA QQLGEVVKLHPHELNNLLSKVLIYL RSANWDTRIAAGQAVEAIVKNVPEW NPVPRTRQEQPTSESSMEDSPTEERL NFDREFDICRLLQHGASLLGSAGAEF EVQDEKSGEVDPKERARQRKLLQK KLGGLNMGEAIGMSTEELFNDELDY TPTSASFVVKQPTLQAAELIDSEFRA GMSNRQKNKAKRMAKLFKQSRSD AVETNEKSNSTGGEPEEKRRKIAN VVINQSANDEKVLIDNIPDSSSLIET NEWPLESFCEELCNDLFNPSWEVR HGAGTGLREILKAHGKSGGKMGDS TLEEMIQHQEWLEDLVIRLLCVFA LDRFGDFVSDEVVAPVRETCAQTLG VVLKHMNETGVHKTVDVLLKLLTQE QWEVRHGGLLGIKYALAVRQDVINT LLPKVLTRIEGLQDLDDVRAVAAA SLVPVVESLVYLQTKVPIINTLWD ALLELDDLASTNSIMTLLSLLTYP QVQCSIQQSLTVLVPRVWPFLLHT ISSVRRAALETFLTLLSTQDQNSSSW LIPILPDMLRHIFQFCVLESSQEILD IHKVWMELLSKASVQYVVAACPW MGAWLCLMMQPSHLPIDLNMLEV KARAKEKTGGKVRQGGQSONKEVLQ EYIAGADTIMEDPATRDFVVMRARM MAAKLLGALCCCICDPGVNVVTQEI KPAESLQQLLHFLNKSALQRISVA LVICEWAALQKECKAVTLAVQPRLL DILSEHLYYDEIAVPFTRMQNECKQL ISSLADVHIEVGNRVNNVLTIDQAS DLVTTVFNEATSSFDLNPQVLQQLD SKRQQVQMTVETNQEWQVLQLRV HTFAACAVVSLQQLPEKLNPIIKPLM ETIKKEENTLVQNYAAQCIKLLQCC TTRTPCPNSKIKNLCSLQVDPYLT CVTCPVPTQSGQENSKGSTSEKDG HHTVTKHRGHTLYRHRQKAAFAITS RGPTPKAVKAQIADLPAGSSGNILVE LDEAQKPYLVQRRGAEFALTTIVKHF GGEMAVKPLHLWDAMVGPLRNTIDI NNFDGKSLLDKGDSPAQELVNSLQV FETAAASMDSELHPLLQVHPLHYM CLOYPSTAVRHHMAARCVGMSKIAT METMNIFLEKVLVPLGAISSVKQE GAIEALACVMEQLDVGIVPYVLLVV PVLGRMSDQTDVSRFMATQCFATLI RLMPLEAGIPDPNMSAELIQLKAK ERHFLEQLLDGKLENYKIPVPINAE LRKYQDGVNWLAFLNKYKLGILC DDMGLGKTLQCSICILAGDHCHRAQE YARSKLAECMPLPSLVCCPPTLTGH WVDEVGKFCREYLNPLHYTGPPTE RIRLQHQVQRHNLIVASYDVVRNDI DFFRNKFNKCYLDEGHVKNKTKL SKAVKQLTANYRIILSGTPIQNNVLE LWSLFDLMPGFLGTERQFAARYGK PILASRDARSSREQEAGVLAMDAL HRQVLPFLRRMKEDVLQDLPPKIIQ DYYCTLSPLQVQLYEDFAKSRACD VDETSSATLSEETKPKLKATGHVF QALQYLRKLCNHPALVLPQHPEFK TTAEKLVQNSSLHDIQHAPKLSALK QLLLDCGLGNGSTSESGTESVVAQH RILIFCQLKMLDIVEHDLKPHLPS VTYLRLDGSIPPGQRHSIVSRFNNDP SIDVLLTTHVGGGLNLTGADTVVF VEHDWNPMDRLQAMDRAHRIGQK RVVNVYRLITRGTLEEKIMGLQKFK MNIANTVISQENSSLSQSMGTDQLLD LFTLDKDGKAEKADTSTSGKASKS ILENLSDLWDQEQYDSEYSLENFM HSLK	None	None	None	None	None	None	None		