	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	pla me
0	Q96BY7	ATG2B_HUMAN	Homo sapiens	Autophagy-related protein 2 homolog B	21.027803	T2025	S255;S379;S497;S840;S886;S899;S1008;T1012;S1016;S1018;T1022;S1526	30379171;28657654;23301498	MPWPFSESIKKRACRYLLQRYLGHF LQEKLSLEQLSLDLYQGTGSLAQVPL DKWCLNEILESADAPLEVTEGFIQSI SLSVPWGSLLQDNCALEVRGLEMVF RPRPRPATGSEPMYWSSFMTSSMQ LAKECLSQKLTDEQGEGSQPFEGLE KFAETIETVLRRVKVTFIDTVLRIEHV PENSKTGTALEIRIERTVYCDETADE SSGINVHQPTAFAHKLLQLSGVSLF WDEFSASAKSSPVCSTAPVETEPKLS PSWNPKIIYEPHPQLTRNLPEIAPSD PVQIGRLIGRLELSLTLKQNEVLPGA KLDVDGQIDSIHLLLSPRQVHLLLD MLAAIAGPENSSKIGLANKDRKNRP MQQEDEYRIQMELNRYYLRKDSLSV GVSSEQSFYETETARTPSSREEEVFF SMADMDMSHSLSSLPPLGDPPNMD LELSLTSTYTNTPAGSPLSATVLQPT WGEFLDHHKEQPVRGSTFPSNLVH PTPLQKTSLPSRSVSVDESRPELIFRL AVGTFSISVLHIDPLSPPETSQNLNP LTPMAVAFFTCIEKIDPARFSTEDFK SFRAVFAEACSHDHLRFIGTGIKVSY EQRQRSASRYFSTDMSIGQMEFLEC LFPTDFHSVPPHYTELLTFHSKEETG SHSPVCLQLHYKHSENRGPQGNQA RLSSVPHKAELQIKLNPVCCELDISIV DRLNSLLQPQKLATVEMMASHMYT SYNKHISLHKAFTEVFLDDSHSPAN CRISVQVATPALNLSVRFPIPDLRSD QERGPWFKKSLQKEILYLAFTDLEFK TEFIGGSTPEQIKLELTFRELIGSFQE EKGDPSIKFFHVSSGVDGDTTSSDD FDWPRIVLKINPPAMHSILERIAAEE EEENDGHYQEEEEGGAHSLKDVCD LRRPAPSPFSSRRVMFENEQMVMP GDPVEMTEFQDKAISNSHYVLELTL PNIYVTLPNKSFYEKLYNRIFNDLLL WEPTAPSPVETFENISYGIGLSVASQ LINTFNKDSFSAFKSAVHYDEESGS EEETLQYFSTVDPNYRSRRKKKLDS QNKNSQSFLSVLLNINHGLIAVFTD VKQDNGDLLENKHGEFWLEFNSGS LFCVTKYEGFDDKHYICLHSSSFSLY HKGIVNGVILPTETRLPSSTRPHWLE PTIYSSEEDGLSKTSSDGVGGDSLN MLSVAVKILSDKSESNTKEFLIAVGL KGATLQHRMLPSGLSWHEQILYFLN IADEPVLGYNPPTSFTTFHVHLWSC ALDYRPLYLPIRSLLTVETFSVSSSVA LDKSSSTLRIILDEAALHLSDKCNTV TINLSRDYVRVMDMGLLELTITAVKS DSDGEQTEPRFELHCSSDVVHIRTC SDSCAALMNLIQYIASYGDLQTPNKA DMKPGAFQRRSKVDSSGRSSSRGPV LPEADQQMLRDLMSDAMEEIDMQQ GTSSVKPQANGVLDEKSQIQEPCCS DLFLFPDESGNVSQESGPTYASFSH HFISDAMTGVPTENDDFCILFAPKAA MQEKEEEPVIKIMVDDAIVIRDNYFS LPVNKTDTSKAPLHFPIPVIRYVVKE VSLVWHLYGGKDFGIVPPTSPAKSYI SPHSSPSHTPTRHGRNTVCGGKGR NHDFLMEIQLSKVKFQHEVYPPCKP DCDSSLSEHPVSRQVFIVQDLEIRDR LATSQMNKFLYLYCSKEMPRKAHS NMLTVKALHVCPESGRSPQECCLRV SLMPLRLNIDQDALFFLKDFFTSLSA EVELQMTPDPEVKKSPGADVTCSLP RHLSTSKEPNLVISFSGPKQPSQND SANSVEVVNGMEEKNFSAEEASFR DQPVFFREFRFTSEVPIRLDYHGKH VSMDQGTLAGILIGLAQLNCSELKLK RLSYRHGLLGVDKLFSYAITEWLNDI KKNQLPGILGGVGPMHSLVQLVQGL KDLVWLPIEQYRKDGRIVRGFQRGA ASFGTSTAMAALELTNRMVQTIQAA AETAYDMVSPGTLSIEPKKTKRFPH HRLAHQPVDLREGVAKAYSVVKEGI TDTAQTIYETAAREHESRGVTGAVGE	False	False	2.675	3.89	1.799	3.739	1.512	1.4

									VLRQIPPAVVKPLIVATEATSNVLGG MRNQIRPDVRQDESQKWRHGDD								