	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
	H3BPE1	H3BPE1_HUMAN	Homo sapiens	NaN	25.886613	NaN	NaN	35008409	MPLLDSSYLPPTIFILTHVLGVAGVLY WKRHARGRADERDRVQKKTFTKWV NKHLMKVRKHINDLYEDLRDGHNL ISLLEVLSGIKLEPAGLKTLRLVSMPS WCHTNNEEQAEEDDDDVPREKGR MRFHRLQNVQIALDFLKQRQVKLV NIRNDDITDGNPKLTLGLIWTIILHF QISDIYISGESGDMSAKEKLLLWTQK VTAGYTGIKCTNFSSCWSDGKMFNA LIHRYRPDLVDMERVQIQSNRENLE QAFEVAERLGVTRLLDAEDVDVPSP DEKSVITYVSSIYDAFPKVPEGGEGIS ATEVDSRWQEYQSRVDSLIPWIKQH TILMSDKTFPQNPVELKALYNQYIHF KETEILAKEREKGRIEELYKLLEVWI EFGRIKLPQGYHPNDVEEEWGKLIIE MLEREKSLRPAVERLELLLQIANKIQ NGALNCEEKLTLAKNTLQADAAHLE SGQPVQCESDVIMYIQECEGLIRQLQ VDLQILRDENYYQLEELAFRVMRLQ DELVTLRLECTNLYRKGHFTSLELVP PSTLTTTHLKAEPLTKATHSSSTSWF RKPMTRAELVAISSSEDEGNLRFVY ELLSWVEEMQMKLERAEWGNDLPS VELQLETQQHIHTSVEELGSSVKEA RLYEGKMSQNFHTSYAETLGKLETQ YCKLKETSSFRMRHLQSLHKFVSRA TAELIWLNEKEEEELAYDWSDNNS NISAKRNYFSELTMELEEKQDVFRS LQDTAELLSLENHPAKQTVEAYSAA VQSQLQWMKQLCLCVEQHVKENTA YFQFFSDARELESFLRNLQDSIKRKY SCDHNTSLSRLEDLLQDSMDEKEQ LIQSKSSVASLVGRSKTIVQLKPRSP DHVLKNTISVKAVCDYRQIEITICKN DECVLEDNSQRTKWKVISPTGNEA MVPSVCFLIPPPNKDAIEMASRVEQ SYQKVMALWHQLHVNTKSLISWNY LRKDLDLVQTWNLEKLRSSAPGECH QIMKNLQAHYEDFLQDSRDSVLFSV ADRLRLEEEVEACKARFQHLMKSM ENEDKEETVAKMYISELKNIRLRLEE YEQRVVKRIQSLASSRTDRDAWQDN ALRIAEQEHTQEDLQQLRSDLDAVS MKCDSFLHQSPSSSSVPTLRSELNL LVEKMDHVYGLSTVYLNKLKTVDVI VRSIQDAELLVKGYEIKLSQEEVVLA DLSALEAHWSTLRHWLSDVKDKNS VFSVLDEEIAKAKVVAEQMSRLTPER NLDLERYQEKGSQLQERWHRVIAQL EIRQSELESIQEVLGDYRACHGTLIK WIEETTAQQEMMKPGQAEDSRVLS EQLSQQTALFAEIERNQTKLDQCQK FSQQYSTIVKDYELQLMTYKAFVESQ QKSPGKRRRMLSSSDAITQEFMDLR TRYTALVTLTTQHVKYISDALRRLEE EEKVVEEEKQEHVEKVKELLGWVST LARNTQGKATSSETKESTDIEKAILE QQVLSEELTTKKEQVSEAIKTSQIFL AKHGHKLSEKEKKQISEQLNALNKA YHDLCDGSANQLQQLQSQLAHQTE QKECRAVAGVIDLGTVEIFPIFKAMQ KGLLDQDTGLVLLESQVIMSGLIAPE TGENLSLEEGIARNLINPQMYQQLR ELQDALALISRLTESRGPLSVVEAIEK RIISETVGLKILEAHLATGGFSLSPSE NCINLEEAFHQGLISAWLHSVLESY LRTSKNLIDPNTAEKIGLLDLMQRCI VHQESGFKLLPVKQLAGGMVSLKSG RKVSIFRAVQEGLIDRQVTVRLLEAQ LFAGGIVDPRTGHRLTVEEAVRHNLI DQDMACAILIRQLQTGGIIDTVTGQR LTIDEAVSNDLVAAKIALVILESLWSF MGLLWPESGEILPITDALEQGIVSTE	None	None	None	None	None	None	None	None	None

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