	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
0	Q9LZX8	BIG2_ARATH	Arabidopsis thaliana	Brefeldin A-inhibited guanine nucleotide-exchange protein 2	27.144759	NaN	S595	28154133	MASSEADSRLSRVVTPALEKIVKNAS WRKHSKLANECKAVIERLNSLQKSP PPSSSAATDSESESSVPGPLNDGGSI EYSLADSELIFSPLINACGTGLAKIIE PAIDCIQKLIAHGYIRGESDPSGGAES LLLFKLIDSVCKCHDLGDESIELPVL KTLLSAINSISLRIHGKCLLLVVRTCY DIYLGSKNVVNQTTAKASLIQILVIVF RRMEADSSTVPIQPIVVAELMEPLEK SDADGTMTQFVQGFITKIMQDIDGV LNPTMSGSGSGSGSGGQDGAYGTTT VETTNPTDLLDSTDKDMLDAKYWEI SMYKSALEGRKGELTDGDAERDDDL EVQIENKLRRDACLVFRALCKLSMK APPKESSADPQSMRGKILALELLKIL LENAGAVFRTSEKFSADIKQFLCLSL LKNSASTLMIIFQLSCSIFISLVARFR AGLKAEIGVFFPMIVLRVVENVAQP NFQQKMIVLRFLDKLCLDSQILVDIF LNYDCDVNSSNIFERMVNGLLKTAQ GVPPGTATTLMPPQEAAMKLEAMK CLVAILKSMGDWLNKQLRLPVSNSL NKSDVIEIDLGPGSPQLANGNADES ADGSDTYSESSGGTSDALAIEQRRAY KLELQEGISLFNRKPTKGIEFLINAG KVGESPEEIAGFLKDASGLNKTLIGD YLGEREDLALKVMHAYVDSFDFRG MEFDEAIRTFLEGFRLPGEAQKIDRI MEKFAERYCKCNPKVFTSADSAYVL AYSVIMLNTDAHNPMVKNKMSADD FIRNNRGIDDGKDLPADYMRSLYERI TKHEIKMKEDDLRLQQKQYANSNR MLGLDGILNIVIRKQWGDSYAETSD DLMKHMQEQFKEKARKSESTYYAA TDVVILRFMIEACWAPMLAAFSVPL DQSDDLIVINICLEGFHHAIHATSLM SMKTHRDAFVTSLAKFTSLHSPADI KQRNIEAIKAILRLADEEGNYLQDAW EHILTCVSRFEQLHLLGEGAPPDATF FASKQNESEKSKQPKQYILPVLKRKG PGKSQYAATGVLRGSYDSMSLGGKG SKNVRQEQMSSIVSNLNLLEQVGE MNQVFSQSQKLNSEAIIDFVKALCK VSMDELRSPSNPRVFSLTKIVEIAHY NMNRIRLVWSSIWQVLSGFFVTIGC SENLSIAIFAMDSLRQLSMKFLEREE LANYNFQNEFMTPFVIVMRRSNDV EIRELIIRCVSQMVLSRVNNVKSGW KSMFMVFTTAAYDDHKNIVFLSFEII EKIIREYFPYITETETTTFTDCVNCLV AFTNNRFSKDISLSSIAFLRYCATKL AEGDLNSPSTNKYKGTSGKIPQSSL HSGKSGKQENGEIVNNNHLYFWFP LLSGLSELSFDPRPEIRKSALQIMFD TLRNHGHLFSLPLWEKVFESVLFPIF DYVRHSIDPSGEDESADQGSSGGEV DELDHDAWLYETCTLALQLVVDLFV KFYTTVNPLLEKVLMLLVSFIKRPHQ SLAGIGIAAFVRLMSDADGLFSEEK WLEVVSALKEAAKTTCPDFSYFLSEE YVARSQRSALNIQNSNAESAAPTAT DGNEESQRTATHLYAAISDAKCRAA VQLLLIQAVMEIYNMYRPQLSAKNT LVLVDALHGVALHAHGINSNTILRSR LQELGPMTQMQDPPLLRLENESYQI CLTFLQNLVADKTKKEEEEEEEEIES LLVNICQEVLNFYIETSSSAKKLQSE SSRASEYRWRIPLGSGKRRELSARAP LIVATLQAMCTLDEASFEKNLKCLFP LLANLISCEHGSNEVQTALADMLGL SVGPVLLQWC	None	None	None	None	None	None	None	None	None